RESEARCH ARTICLE Legume Research- An International Journal, Volume 49 Issue 7: 1080-1090 (July 2026)

SSR based Molecular Diversity and Marker-trait Association in Mungbean (*Vigna radiata* L.) under Deficit Moisture Stress

Ravada D. Bandhavi[1], D. Lenka[2], Swapan K. Tripathy[3], Jayashree Kar[2], R. Khan[2]

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Background: In recent years, breeding of climate resilient varieties particularly for deficit moisture stress is the major focus for sustainable crop production. Molecular markers being independent of environmental influence, SSR based genotyping and marker-trait association can address such a complex trait with utmost precision for molecular breeding in mungbean.

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Key words: Deficit moisture stress, Genetic diversity, Marker-trait associations, Mungbean, SSR primers.

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Ravada D. Bandhavi[1], D. Lenka[2], Swapan K. Tripathy[3], Jayashree Kar[2], R. Khan[2]

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Background: In recent years, breeding of climate resilient varieties particularly for deficit moisture stress is the major focus for sustainable crop production. Molecular markers being independent of environmental influence, SSR based genotyping and marker-trait association can address such a complex trait with utmost precision for molecular breeding in mungbean.

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Key words: Deficit moisture stress, Genetic diversity, Marker-trait associations, Mungbean, SSR primers.

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Ravada D. Bandhavi[1], D. Lenka[2], Swapan K. Tripathy[3], Jayashree Kar[2], R. Khan[2]

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Background: In recent years, breeding of climate resilient varieties particularly for deficit moisture stress is the major focus for sustainable crop production. Molecular markers being independent of environmental influence, SSR based genotyping and marker-trait association can address such a complex trait with utmost precision for molecular breeding in mungbean.

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Key words: Deficit moisture stress, Genetic diversity, Marker-trait associations, Mungbean, SSR primers.

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Ravada D. Bandhavi[1], D. Lenka[2], Swapan K. Tripathy[3], Jayashree Kar[2], R. Khan[2]

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Background: In recent years, breeding of climate resilient varieties particularly for deficit moisture stress is the major focus for sustainable crop production. Molecular markers being independent of environmental influence, SSR based genotyping and marker-trait association can address such a complex trait with utmost precision for molecular breeding in mungbean.

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Key words: Deficit moisture stress, Genetic diversity, Marker-trait associations, Mungbean, SSR primers.

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Each individual RNA-free gDNA sample was primed and amplified using ten gene specific SSR primers (Table 1) in a reaction volume 20 µl. Amplifications were set up in a Gene Amp PCR (Applied Biosystems), programmed for 5 min at 94°C, 40 cycles of 1 min at 92°C, 1 min at varying annealing temperature specific to primer (53-58°C, Table 1) and 2 min at 72°C and final extension for 10 min at 72°C. The amplified DNA was electrophoresed in an agarose gel at a constant voltage of 50V and scanned by gel doc system (Fire Reader-Uvtec, Cambridge, UK) for detection of gene specific SSR alleles. The amplifications were checked at least twice for their reproducibility and the size of the amplicons was determined by comparing with the lambda DNA ladder (100 bp) with known size (bp) fragments.

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GP 134= RCM 14	1	80.0	14.2	9.2	0.438	0.12	0.22	0.09	1	31.77	41.27	31.88	3.21	2.14	6.91	6.47	8.83	3.55	2.43
GP 179= TARM 1	0	78.5	15.7	9.7	0.46	0.19	0.25	0.10	0	31.91	39.26	32.58	3.46	3.24	6.87	6.05	10.05	2.66	2.66
GP 129=RCM 5	0	73.3	9.5	9.5	0.24	0.11	0.20	0.08	0	31.77	38.27	31.90	3.28	2.21	6.74	5.32	9.02	3.45	2.85
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GP 227=SML 668	1	76.5	4.02	9.7	0.22	0.09	0.21	0.05	0	33.75	41.00	33.71	3.33	3.27	11.53	5.25	11.03	2.40	3.05
GP 62=OUM 99-4	2	66.7	14	9.7	0.438	0.12	0.23	0.10	1	30.69	40.69	41.25	6.78	2.35	14.36	6.05	10.58	2.33	3.60
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GP 227=SML 668	1	76.5	4.02	9.7	0.22	0.09	0.21	0.05	0	33.75	41.00	33.71	3.33	3.27	11.53	5.25	11.03	2.40	3.05
GP 62=OUM 99-4	2	66.7	14	9.7	0.438	0.12	0.23	0.10	1	30.69	40.69	41.25	6.78	2.35	14.36	6.05	10.58	2.33	3.60
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GP 134= RCM 14	1	80.0	14.2	9.2	0.438	0.12	0.22	0.09	1	31.77	41.27	31.88	3.21	2.14	6.91	6.47	8.83	3.55	2.43
GP 179= TARM 1	0	78.5	15.7	9.7	0.46	0.19	0.25	0.10	0	31.91	39.26	32.58	3.46	3.24	6.87	6.05	10.05	2.66	2.66
GP 129=RCM 5	0	73.3	9.5	9.5	0.24	0.11	0.20	0.08	0	31.77	38.27	31.90	3.28	2.21	6.74	5.32	9.02	3.45	2.85
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GP 134= RCM 14	1	80.0	14.2	9.2	0.438	0.12	0.22	0.09	1	31.77	41.27	31.88	3.21	2.14	6.91	6.47	8.83	3.55	2.43
GP 179= TARM 1	0	78.5	15.7	9.7	0.46	0.19	0.25	0.10	0	31.91	39.26	32.58	3.46	3.24	6.87	6.05	10.05	2.66	2.66
GP 129=RCM 5	0	73.3	9.5	9.5	0.24	0.11	0.20	0.08	0	31.77	38.27	31.90	3.28	2.21	6.74	5.32	9.02	3.45	2.85
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GP 134= RCM 14	1	80.0	14.2	9.2	0.438	0.12	0.22	0.09	1	31.77	41.27	31.88	3.21	2.14	6.91	6.47	8.83	3.55	2.43
GP 179= TARM 1	0	78.5	15.7	9.7	0.46	0.19	0.25	0.10	0	31.91	39.26	32.58	3.46	3.24	6.87	6.05	10.05	2.66	2.66
GP 129=RCM 5	0	73.3	9.5	9.5	0.24	0.11	0.20	0.08	0	31.77	38.27	31.90	3.28	2.21	6.74	5.32	9.02	3.45	2.85
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GP 16= Dhauli	7	26.7	3.5	2.6	0.22	0.08	0.14	0.05	9	28.75	36.15	28.65	3.20	2.80	7.20	5.90	8.80	2.11	1.63
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GP 134= RCM 14	1	80.0	14.2	9.2	0.438	0.12	0.22	0.09	1	31.77	41.27	31.88	3.21	2.14	6.91	6.47	8.83	3.55	2.43
GP 179= TARM 1	0	78.5	15.7	9.7	0.46	0.19	0.25	0.10	0	31.91	39.26	32.58	3.46	3.24	6.87	6.05	10.05	2.66	2.66
GP 129=RCM 5	0	73.3	9.5	9.5	0.24	0.11	0.20	0.08	0	31.77	38.27	31.90	3.28	2.21	6.74	5.32	9.02	3.45	2.85
GP 173=T 34-1-5	1	80.0	4.05	9.3	0.32	0.09	0.26	0.09	1	31.51	39.76	32.97	5.28	2.23	10.50	5.22	10.19	2.97	2.96
GP 227=SML 668	1	76.5	4.02	9.7	0.22	0.09	0.21	0.05	0	33.75	41.00	33.71	3.33	3.27	11.53	5.25	11.03	2.40	3.05
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GP 134= RCM 14	1	80.0	14.2	9.2	0.438	0.12	0.22	0.09	1	31.77	41.27	31.88	3.21	2.14	6.91	6.47	8.83	3.55	2.43
GP 179= TARM 1	0	78.5	15.7	9.7	0.46	0.19	0.25	0.10	0	31.91	39.26	32.58	3.46	3.24	6.87	6.05	10.05	2.66	2.66
GP 129=RCM 5	0	73.3	9.5	9.5	0.24	0.11	0.20	0.08	0	31.77	38.27	31.90	3.28	2.21	6.74	5.32	9.02	3.45	2.85
GP 173=T 34-1-5	1	80.0	4.05	9.3	0.32	0.09	0.26	0.09	1	31.51	39.76	32.97	5.28	2.23	10.50	5.22	10.19	2.97	2.96
GP 227=SML 668	1	76.5	4.02	9.7	0.22	0.09	0.21	0.05	0	33.75	41.00	33.71	3.33	3.27	11.53	5.25	11.03	2.40	3.05
GP 62=OUM 99-4	2	66.7	14	9.7	0.438	0.12	0.23	0.10	1	30.69	40.69	41.25	6.78	2.35	14.36	6.05	10.58	2.33	3.60
GP 16= Dhauli	7	26.7	3.5	2.6	0.22	0.08	0.14	0.05	9	28.75	36.15	28.65	3.20	2.80	7.20	5.90	8.80	2.11	1.63
Phulbani Local	2	65.5	5.2	3.82	0.33	0.08	0.18	0.06	4	27.70	38.20	26.58	2.76	2.83	7.48	5.18	8.68	1.96	1.92
Vigna glaberescence	1	80.0	10.5	8.2	0.3	0.09	0.20	0.10	2	59.05	75.25	81.58	14.88	4.38	33.08	5.63	9.93	1.90	6.03

DT Score : Drought tolerance score.

DF: Days to 50% flowering, DM: Days to maturity, PHT: Plant height (cm), NC: No. of clusters per plant, NP/C: No. of pods per cluster, NP/Pl.: No. of pods per plant, PL: Pod length (cm), NS/P: No. of seeds per pod, SW: 100-seed weight(g), Y/Pl.: Seed yield per plant (g).

Table 1: Amplified products and polymorhic information of a set of SSR primer pairs used in the study.

Primer	Source	Primer Sequence (3′-5′)	GC content (%)	Tm (°C)	Tan (°C)	No. of monom--orphic alleles	No. of polym--orphic alleles	Total No. of alleles	% of polymo--rphism	MAF	PIC	Rp	Range of ampli-con size (bp)
ICCM-0249	Chickpea	5″-TTTCTTCGCATGGGCTTAAC-3″	45.00	55.25	54°C	0	8	8	100.0	0.90	0.806	5.4	120-1200
	(Nayak *et al.,* 2010)	5″-GGAGATTTGTTGGGTAGGCTC-3″	52.38	59.82									
TAA170	Chickpea	5″-TATAGAGTGAGAAGAAGCAAAGAGGAG-3″	40.74	61.93	53°C	1	3	4	75.0	1.00	0.505	4.8	180-800
	(Winter *et al.*,1999)	TATTTGCATCAATGTTCTGTAGTGTTT-3″	40.74	61.93									
TM-VF	*Vicia faba*	5″- CTTGCAGTCAAGCTCCCTTC-3″	55.00	59.35	54°C	2	5	7	71.4	1.00	0.48	8.8	300-1180
	(Amar *et al.*, 2016)	5′-CCTTGTCCCAAGACAGACCA-3″	55.00	59.35									
RD20A	Soya bean	5″- GTGGCACATGACTGAAGGAA	50.00	57.3	56°C	1	0	1	0.00	1.00	0	1	300
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	et al., 2012)												
RD22	Soya bean	5″- AATGCCGAAAGCCATTACAG	45.00	55.25	53°C	2	0	2	0.00	0.20	0.487	0.6	460-1110
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GmDREB2	(Soya bean)	5″- GGGGAATTCATGGAAGAACCGGGTTTA-3″	48.15	64.97	58°C	0	2	2	100	0.10	0.99	0.4	820-1140
	(Savitri *et.al.*, 2019)	5″- GGGCTCGAGATCTTCAGGTTTGGGATA- 3″	51.85	66.48									
codA gene	Mungbean	5′- CCACCATGATATTCGGCAAC-3′	50.00	57.3	53°C	0	9	9	100	0.70	0.088	7.2	380-2800
	(Baloda *et al*., 2017)	5′- GTGGAGGCTATTC GGCTA -3′	55.56	55.97									
HSP20	Mungbean	5′- AGGTGGAAGTGGAAGATGGG-3′	55.00	59.35	57°C	0	1	1	100	1.00	0	2	130
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VrUBC1	Mungbean	5′- GGCCTCTAAGCGGATTCTGAAG-3′	50.00	62.72	57°C	0	1	1	100	1.00	0	2	78
	(Chung *et al*., 2013)	5′- CTAGCCCATTGCATACTTCTGAGTCC-3′	50.00	64.8									

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	(Nayak *et al.,* 2010)	5″-GGAGATTTGTTGGGTAGGCTC-3″	52.38	59.82									
TAA170	Chickpea	5″-TATAGAGTGAGAAGAAGCAAAGAGGAG-3″	40.74	61.93	53°C	1	3	4	75.0	1.00	0.505	4.8	180-800
	(Winter *et al.*,1999)	TATTTGCATCAATGTTCTGTAGTGTTT-3″	40.74	61.93									
TM-VF	*Vicia faba*	5″- CTTGCAGTCAAGCTCCCTTC-3″	55.00	59.35	54°C	2	5	7	71.4	1.00	0.48	8.8	300-1180
	(Amar *et al.*, 2016)	5′-CCTTGTCCCAAGACAGACCA-3″	55.00	59.35									
RD20A	Soya bean	5″- GTGGCACATGACTGAAGGAA	50.00	57.3	56°C	1	0	1	0.00	1.00	0	1	300
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RD22	Soya bean	5″- AATGCCGAAAGCCATTACAG	45.00	55.25	53°C	2	0	2	0.00	0.20	0.487	0.6	460-1110
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GmDREB2	(Soya bean)	5″- GGGGAATTCATGGAAGAACCGGGTTTA-3″	48.15	64.97	58°C	0	2	2	100	0.10	0.99	0.4	820-1140
	(Savitri *et.al.*, 2019)	5″- GGGCTCGAGATCTTCAGGTTTGGGATA- 3″	51.85	66.48									
codA gene	Mungbean	5′- CCACCATGATATTCGGCAAC-3′	50.00	57.3	53°C	0	9	9	100	0.70	0.088	7.2	380-2800
	(Baloda *et al*., 2017)	5′- GTGGAGGCTATTC GGCTA -3′	55.56	55.97									
HSP20	Mungbean	5′- AGGTGGAAGTGGAAGATGGG-3′	55.00	59.35	57°C	0	1	1	100	1.00	0	2	130
	(Tian *et al.,* 2016)	5′- GGAAGCCAGAACCTCCTCAT-3′	55.00	59.35									
Ap2	Mungbean	5′- TTGATGGAAGCTGGGGTGAT-3′	50.00	57.3	56°C	0	1	1	100	1.00	0	2	140
	(Tian *et al*., 2016)	5′- CTCAGAAAACGCCTGCCATT-3′	50.00	57.3									
VrUBC1	Mungbean	5′- GGCCTCTAAGCGGATTCTGAAG-3′	50.00	62.72	57°C	0	1	1	100	1.00	0	2	78
	(Chung *et al*., 2013)	5′- CTAGCCCATTGCATACTTCTGAGTCC-3′	50.00	64.8									

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ICCM-0249	Chickpea	5″-TTTCTTCGCATGGGCTTAAC-3″	45.00	55.25	54°C	0	8	8	100.0	0.90	0.806	5.4	120-1200
	(Nayak *et al.,* 2010)	5″-GGAGATTTGTTGGGTAGGCTC-3″	52.38	59.82									
TAA170	Chickpea	5″-TATAGAGTGAGAAGAAGCAAAGAGGAG-3″	40.74	61.93	53°C	1	3	4	75.0	1.00	0.505	4.8	180-800
	(Winter *et al.*,1999)	TATTTGCATCAATGTTCTGTAGTGTTT-3″	40.74	61.93									
TM-VF	*Vicia faba*	5″- CTTGCAGTCAAGCTCCCTTC-3″	55.00	59.35	54°C	2	5	7	71.4	1.00	0.48	8.8	300-1180
	(Amar *et al.*, 2016)	5′-CCTTGTCCCAAGACAGACCA-3″	55.00	59.35									
RD20A	Soya bean	5″- GTGGCACATGACTGAAGGAA	50.00	57.3	56°C	1	0	1	0.00	1.00	0	1	300
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RD22	Soya bean	5″- AATGCCGAAAGCCATTACAG	45.00	55.25	53°C	2	0	2	0.00	0.20	0.487	0.6	460-1110
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GmDREB2	(Soya bean)	5″- GGGGAATTCATGGAAGAACCGGGTTTA-3″	48.15	64.97	58°C	0	2	2	100	0.10	0.99	0.4	820-1140
	(Savitri *et.al.*, 2019)	5″- GGGCTCGAGATCTTCAGGTTTGGGATA- 3″	51.85	66.48									
codA gene	Mungbean	5′- CCACCATGATATTCGGCAAC-3′	50.00	57.3	53°C	0	9	9	100	0.70	0.088	7.2	380-2800
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HSP20	Mungbean	5′- AGGTGGAAGTGGAAGATGGG-3′	55.00	59.35	57°C	0	1	1	100	1.00	0	2	130
	(Tian *et al.,* 2016)	5′- GGAAGCCAGAACCTCCTCAT-3′	55.00	59.35									
Ap2	Mungbean	5′- TTGATGGAAGCTGGGGTGAT-3′	50.00	57.3	56°C	0	1	1	100	1.00	0	2	140
	(Tian *et al*., 2016)	5′- CTCAGAAAACGCCTGCCATT-3′	50.00	57.3									
VrUBC1	Mungbean	5′- GGCCTCTAAGCGGATTCTGAAG-3′	50.00	62.72	57°C	0	1	1	100	1.00	0	2	78
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VrUBC1	Mungbean	5′- GGCCTCTAAGCGGATTCTGAAG-3′	50.00	62.72	57°C	0	1	1	100	1.00	0	2	78
	(Chung *et al*., 2013)	5′- CTAGCCCATTGCATACTTCTGAGTCC-3′	50.00	64.8									

Note : Tm: Primer melting temperature, Tan: Primer annealing temperature, MAF: Major allele frequency, PIC: Polymorphic information content, Rp: Resolving power.

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Primer	Source	Primer Sequence (3′-5′)	GC content (%)	Tm (°C)	Tan (°C)	No. of monom--orphic alleles	No. of polym--orphic alleles	Total No. of alleles	% of polymo--rphism	MAF	PIC	Rp	Range of ampli-con size (bp)
ICCM-0249	Chickpea	5″-TTTCTTCGCATGGGCTTAAC-3″	45.00	55.25	54°C	0	8	8	100.0	0.90	0.806	5.4	120-1200
	(Nayak *et al.,* 2010)	5″-GGAGATTTGTTGGGTAGGCTC-3″	52.38	59.82									
TAA170	Chickpea	5″-TATAGAGTGAGAAGAAGCAAAGAGGAG-3″	40.74	61.93	53°C	1	3	4	75.0	1.00	0.505	4.8	180-800
	(Winter *et al.*,1999)	TATTTGCATCAATGTTCTGTAGTGTTT-3″	40.74	61.93									
TM-VF	*Vicia faba*	5″- CTTGCAGTCAAGCTCCCTTC-3″	55.00	59.35	54°C	2	5	7	71.4	1.00	0.48	8.8	300-1180
	(Amar *et al.*, 2016)	5′-CCTTGTCCCAAGACAGACCA-3″	55.00	59.35									
RD20A	Soya bean	5″- GTGGCACATGACTGAAGGAA	50.00	57.3	56°C	1	0	1	0.00	1.00	0	1	300
	(Neves-Borges	5″- ATCTTTCCAGCAGCACCTCT-3”	50.00	57.3									
	et al., 2012)												
RD22	Soya bean	5″- AATGCCGAAAGCCATTACAG	45.00	55.25	53°C	2	0	2	0.00	0.20	0.487	0.6	460-1110
	(Neves-Borges	5″- GCTTTGTTTTCCCTGCGTTA-3″	45.00	55.25									
	et al., 2012)												
GmDREB2	(Soya bean)	5″- GGGGAATTCATGGAAGAACCGGGTTTA-3″	48.15	64.97	58°C	0	2	2	100	0.10	0.99	0.4	820-1140
	(Savitri *et.al.*, 2019)	5″- GGGCTCGAGATCTTCAGGTTTGGGATA- 3″	51.85	66.48									
codA gene	Mungbean	5′- CCACCATGATATTCGGCAAC-3′	50.00	57.3	53°C	0	9	9	100	0.70	0.088	7.2	380-2800
	(Baloda *et al*., 2017)	5′- GTGGAGGCTATTC GGCTA -3′	55.56	55.97									
HSP20	Mungbean	5′- AGGTGGAAGTGGAAGATGGG-3′	55.00	59.35	57°C	0	1	1	100	1.00	0	2	130
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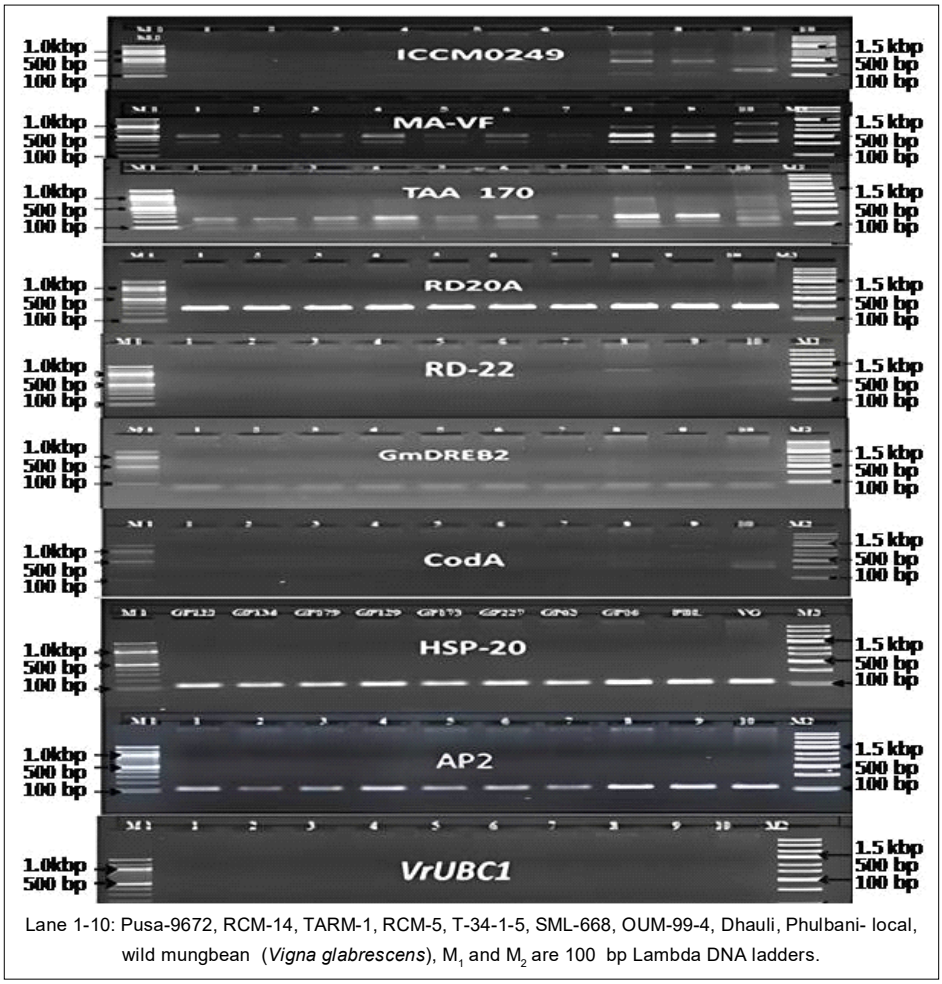
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SSR based genotyping

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Lane 1-10: Pusa-9672, RCM-14, TARM-1, RCM-5, T-34-1-5, SML-668, OUM-99-4, Dhauli, Phulbani- local, wild mungbean (*Vigna glabrescens*), M_1 and M_2 are 100 bp Lambda DNA ladders.

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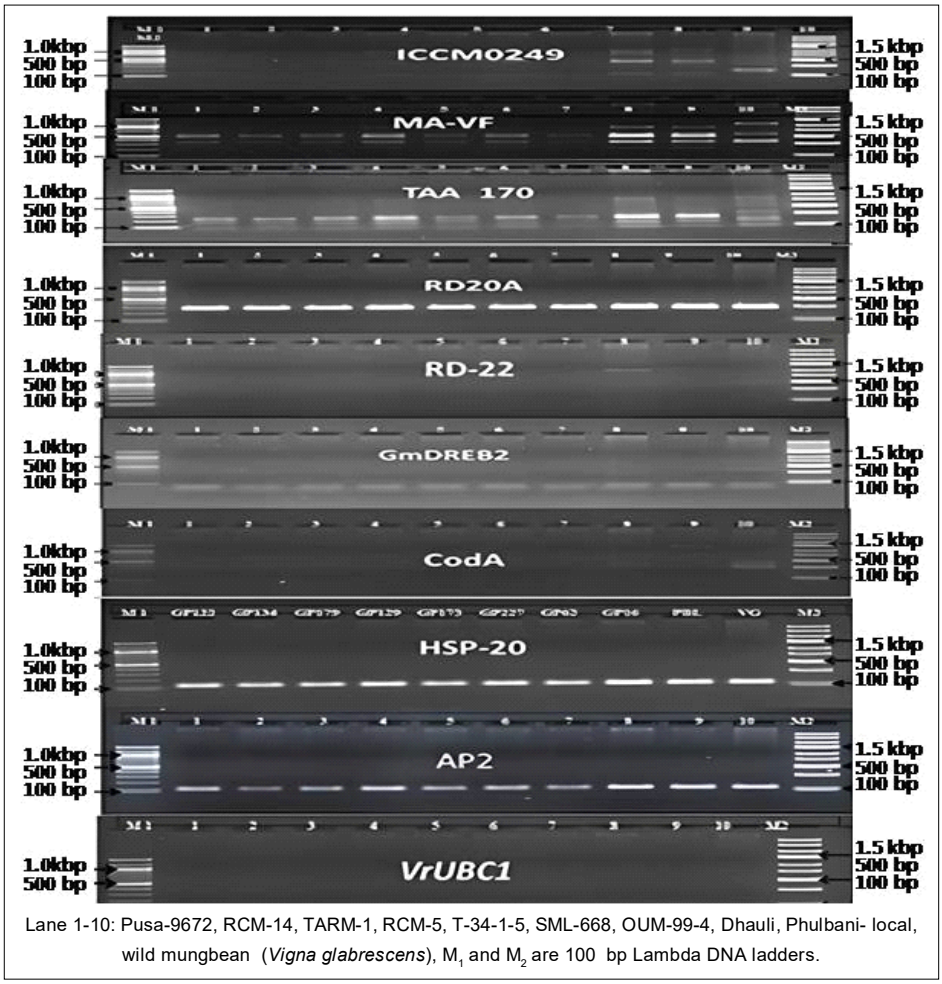
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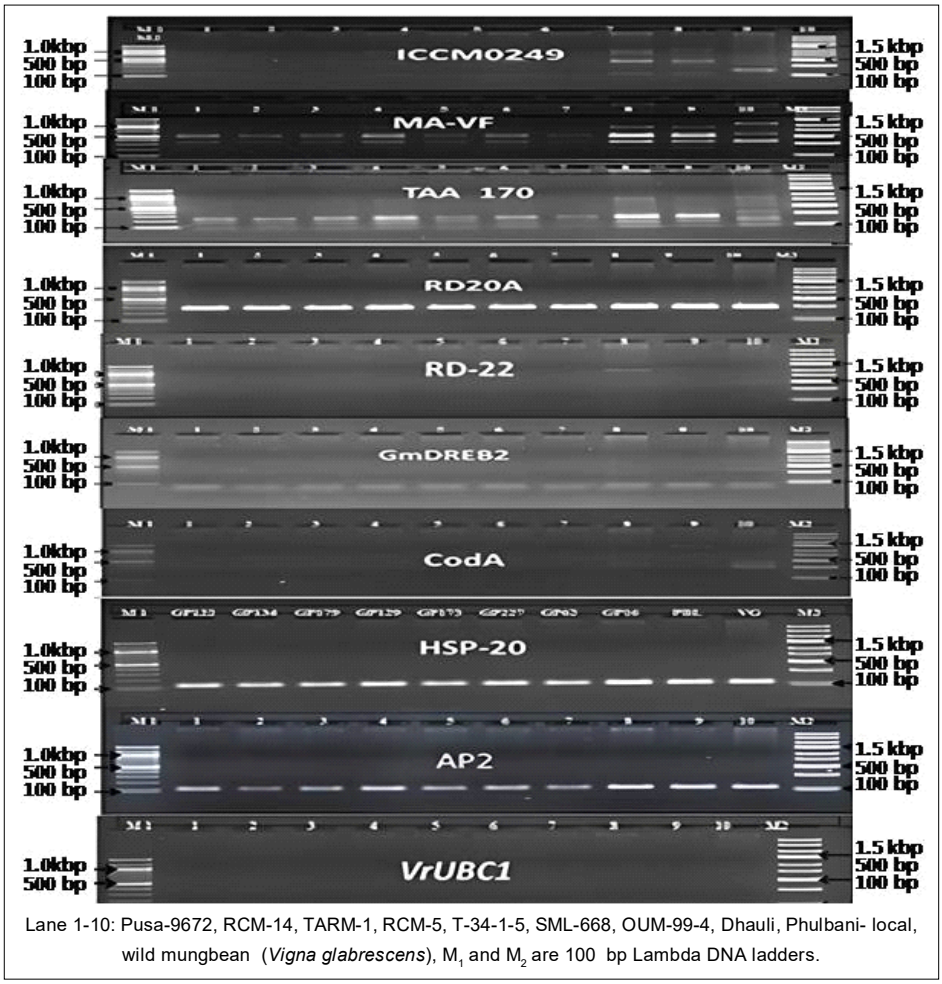
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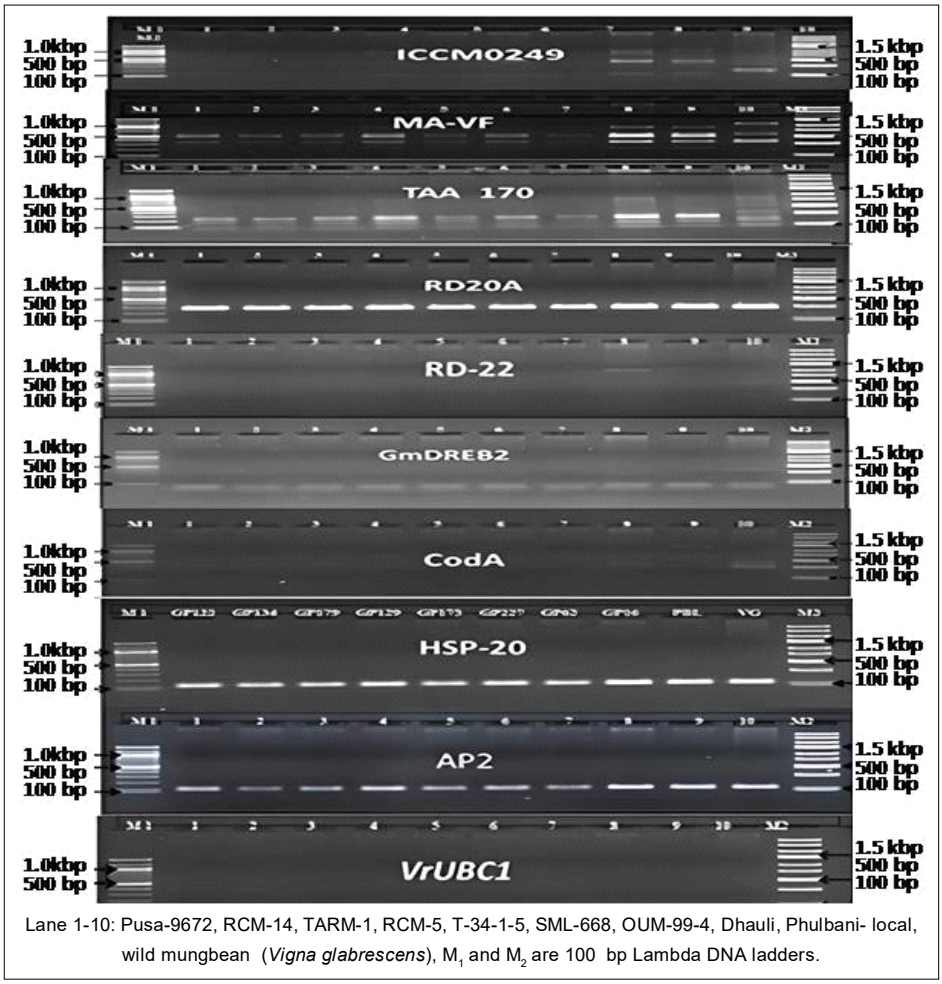
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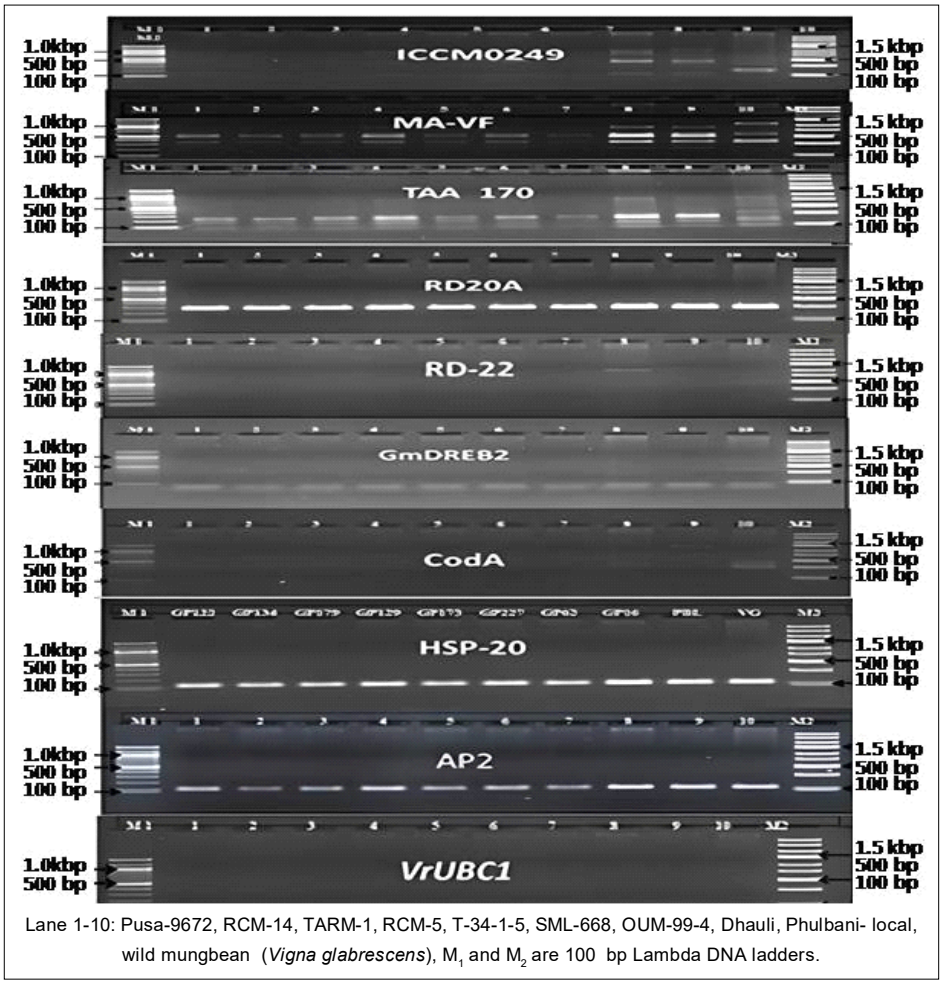
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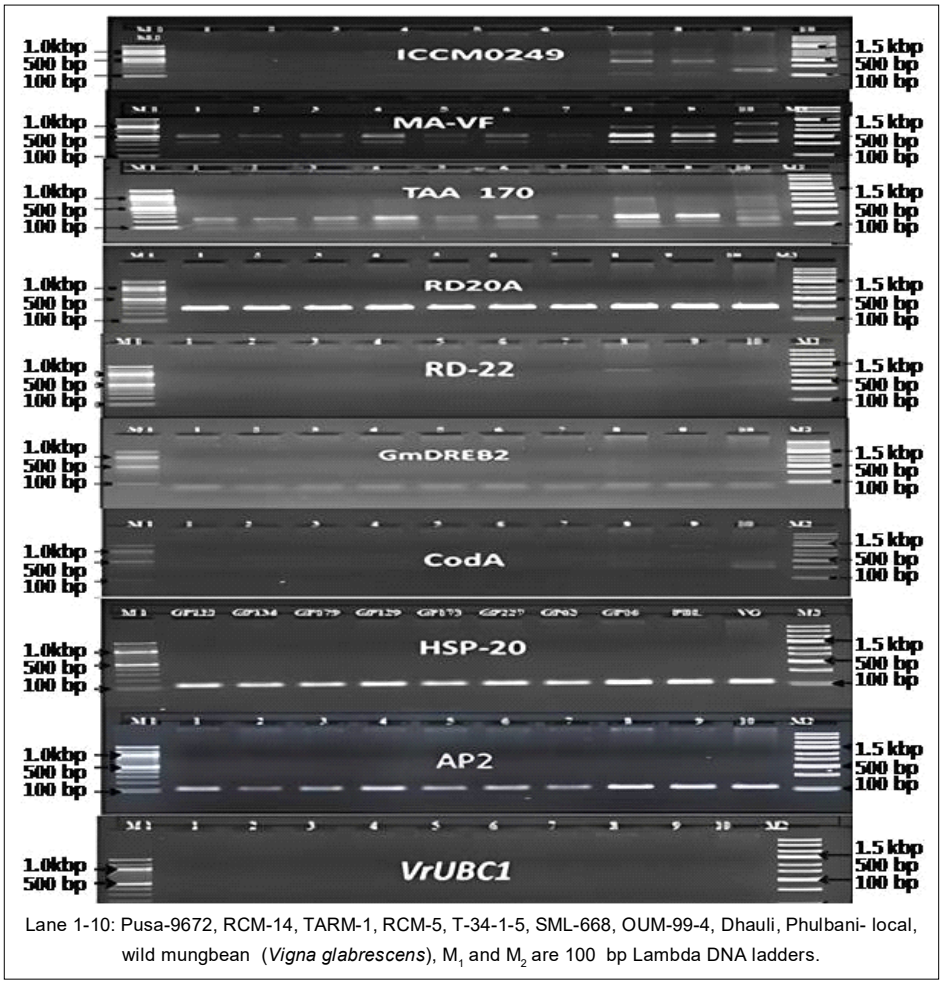
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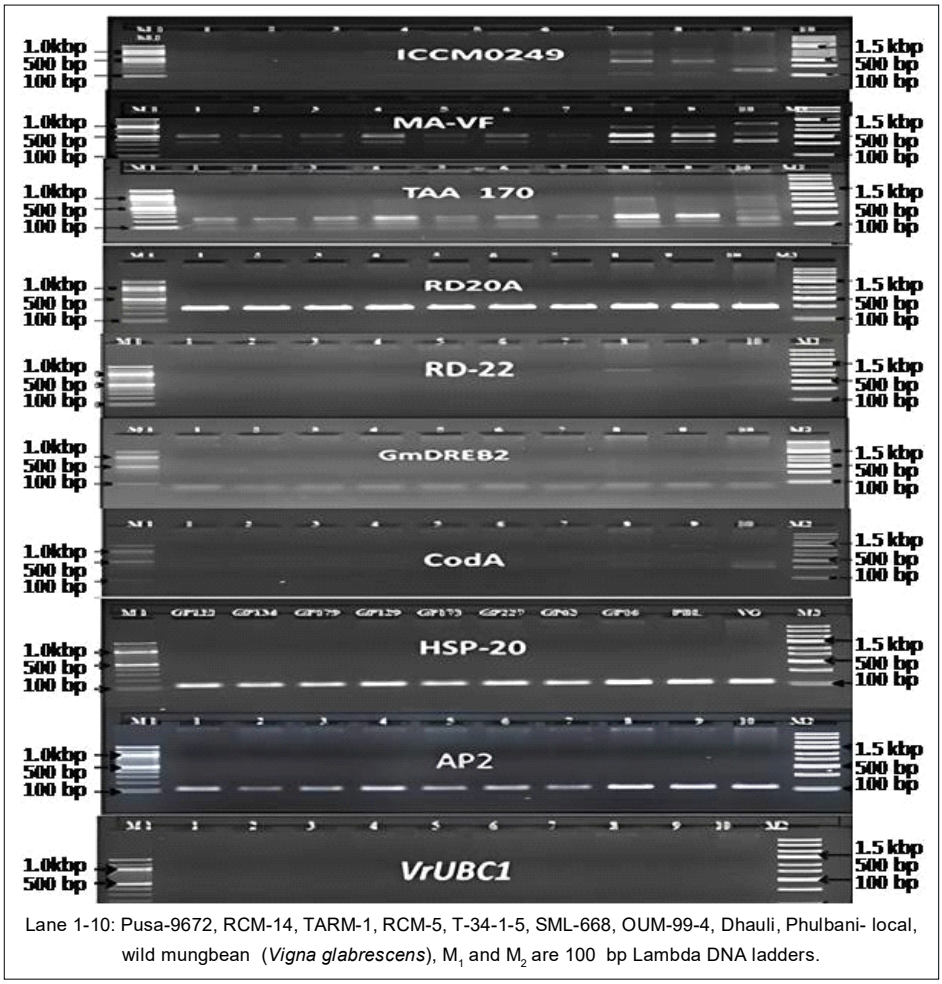
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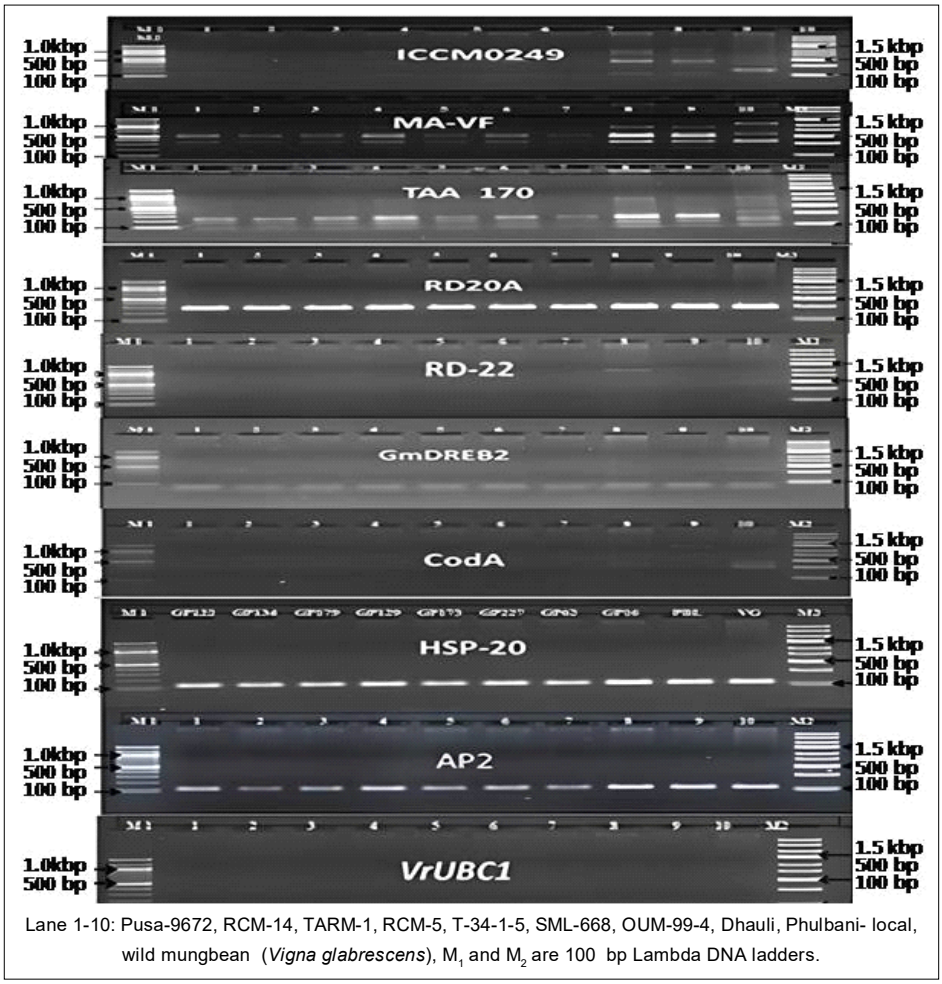
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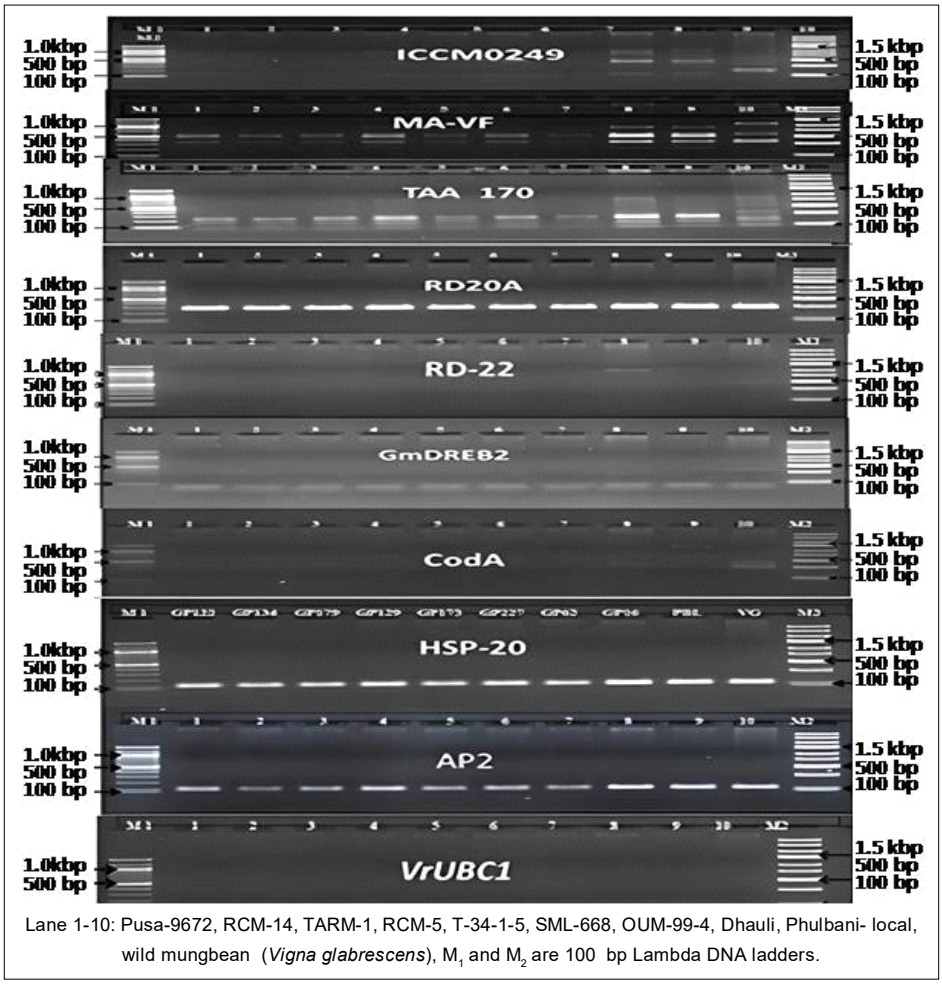
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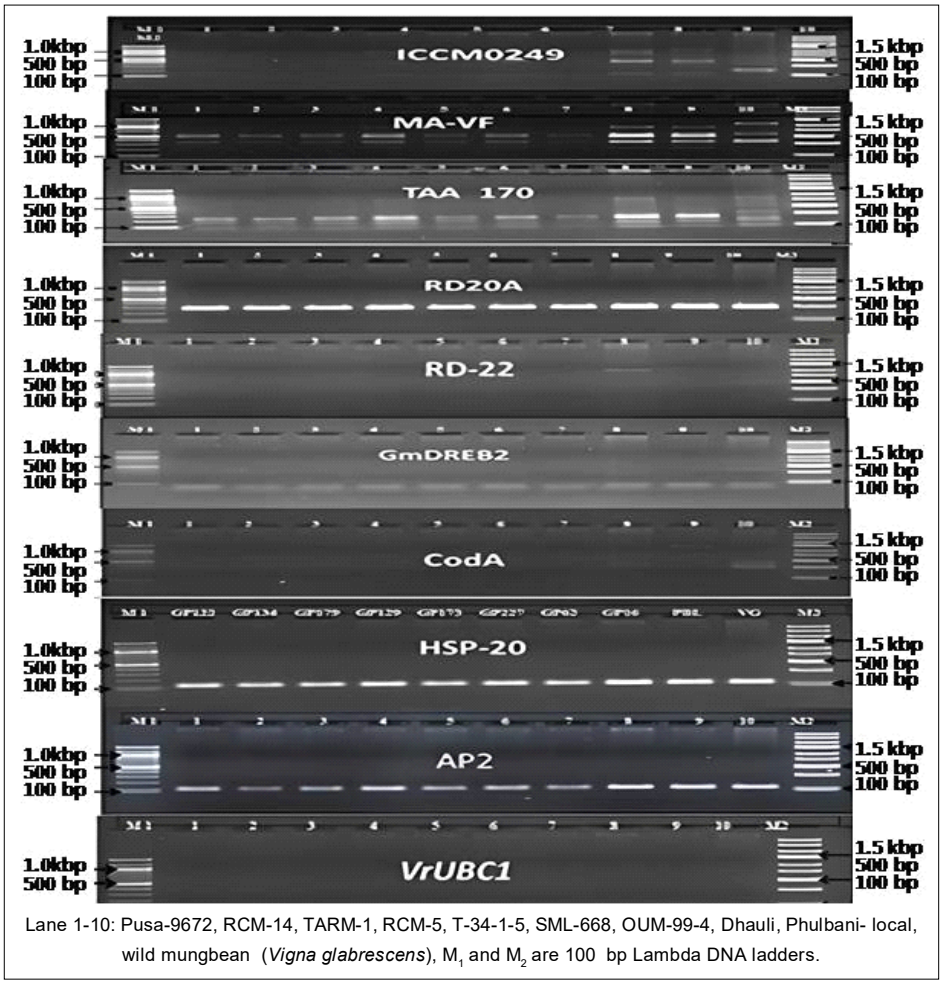
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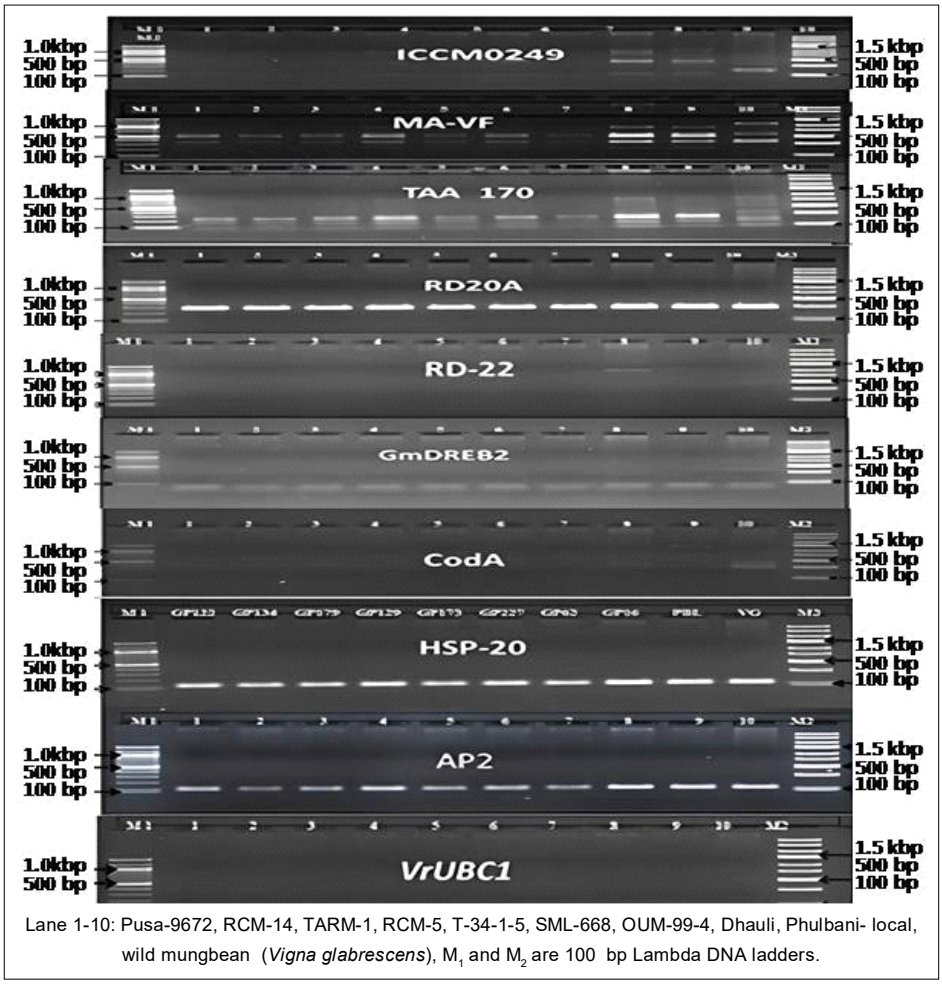
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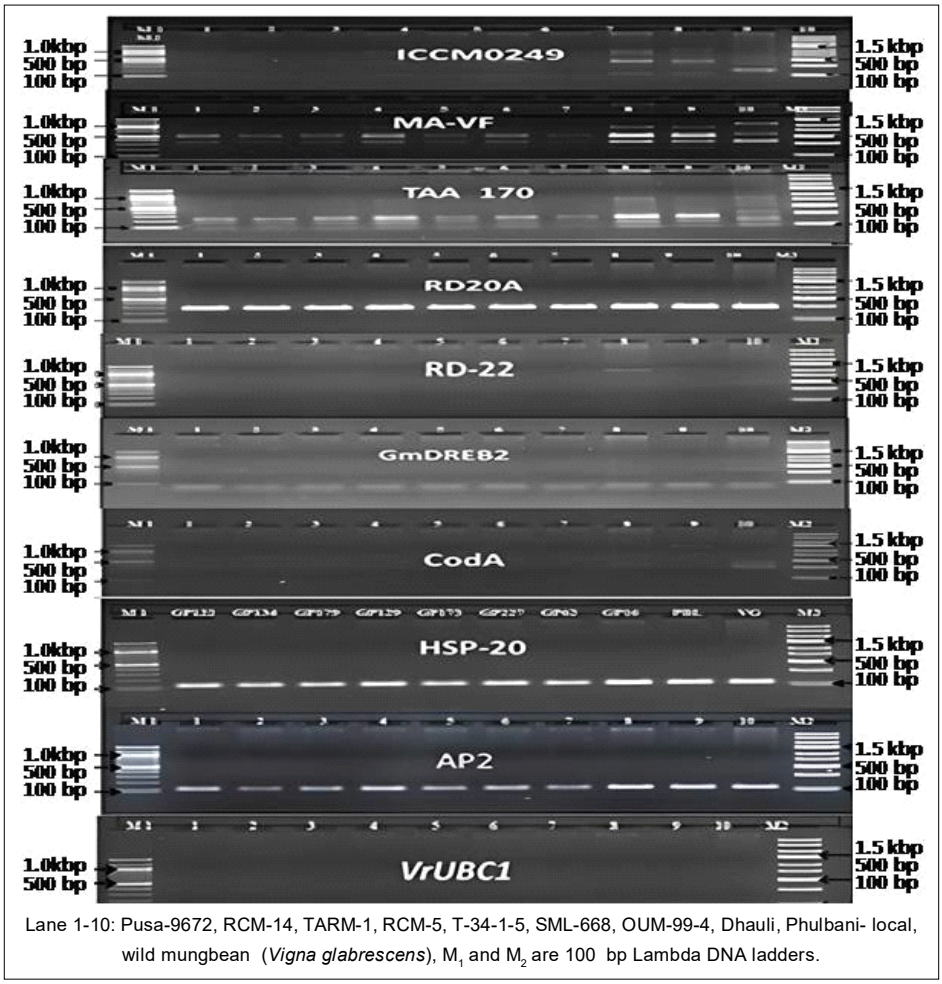
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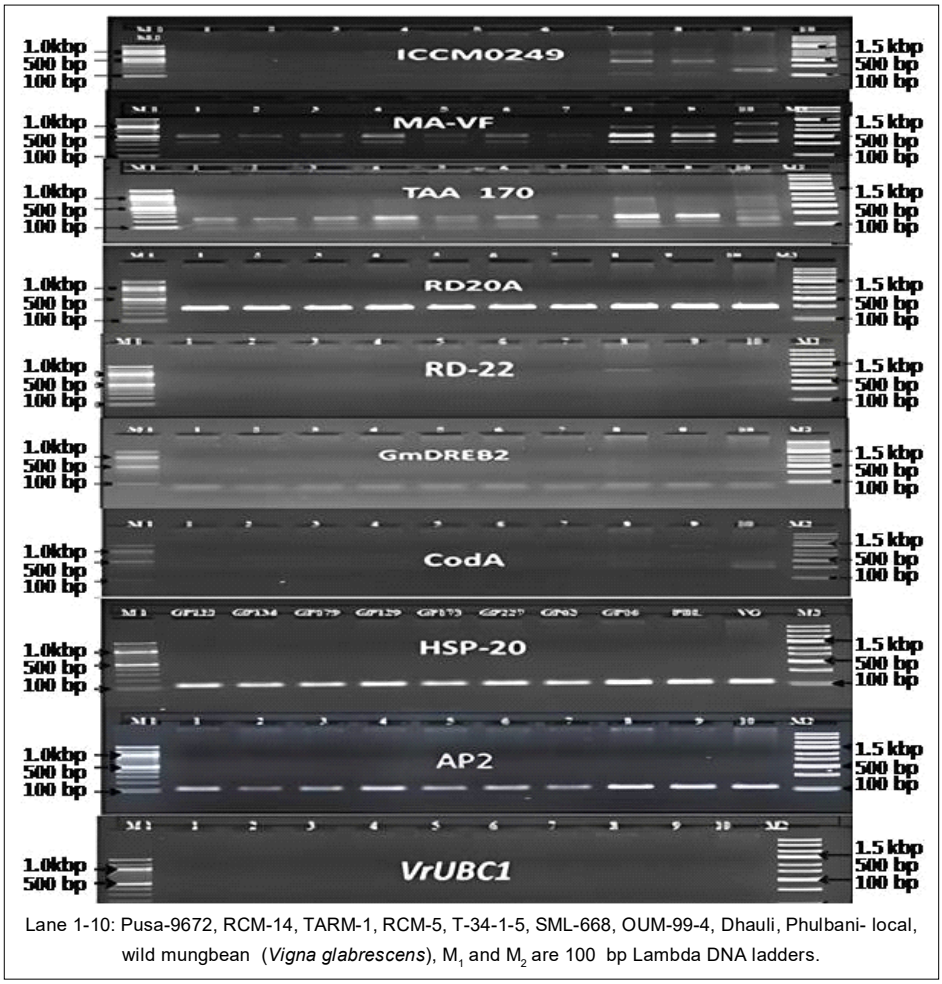
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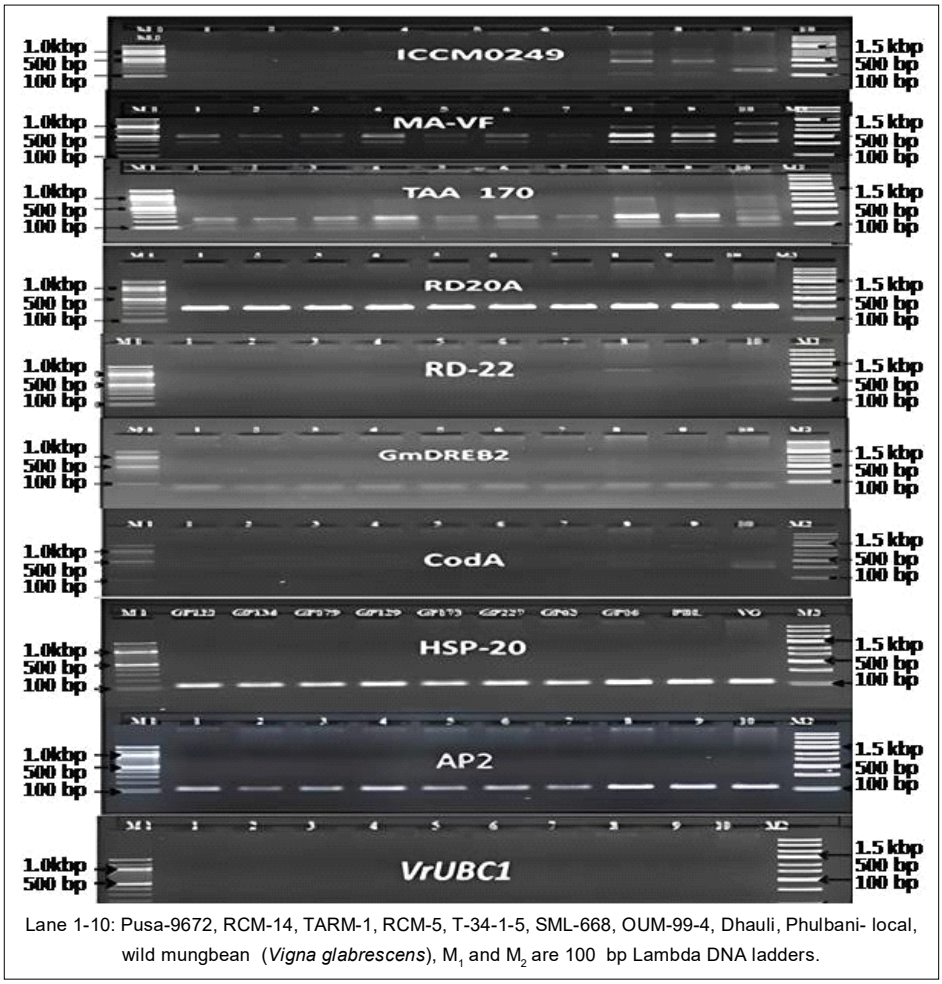
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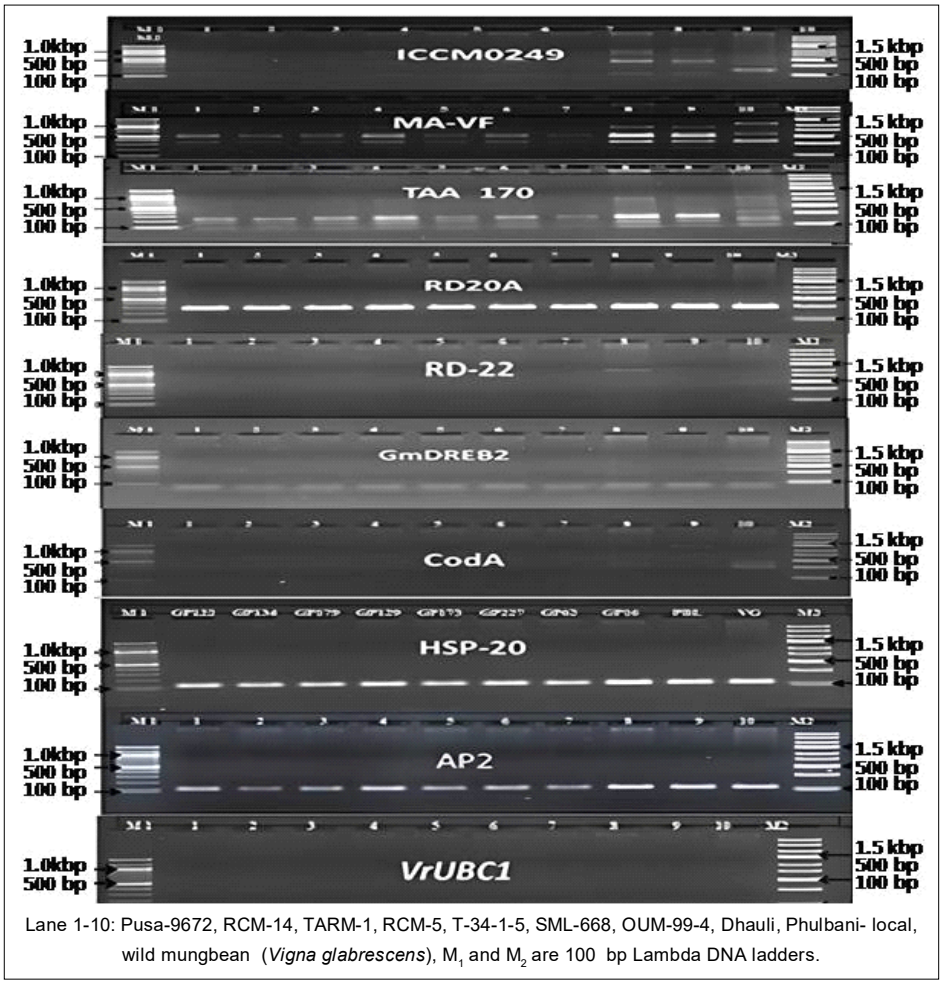
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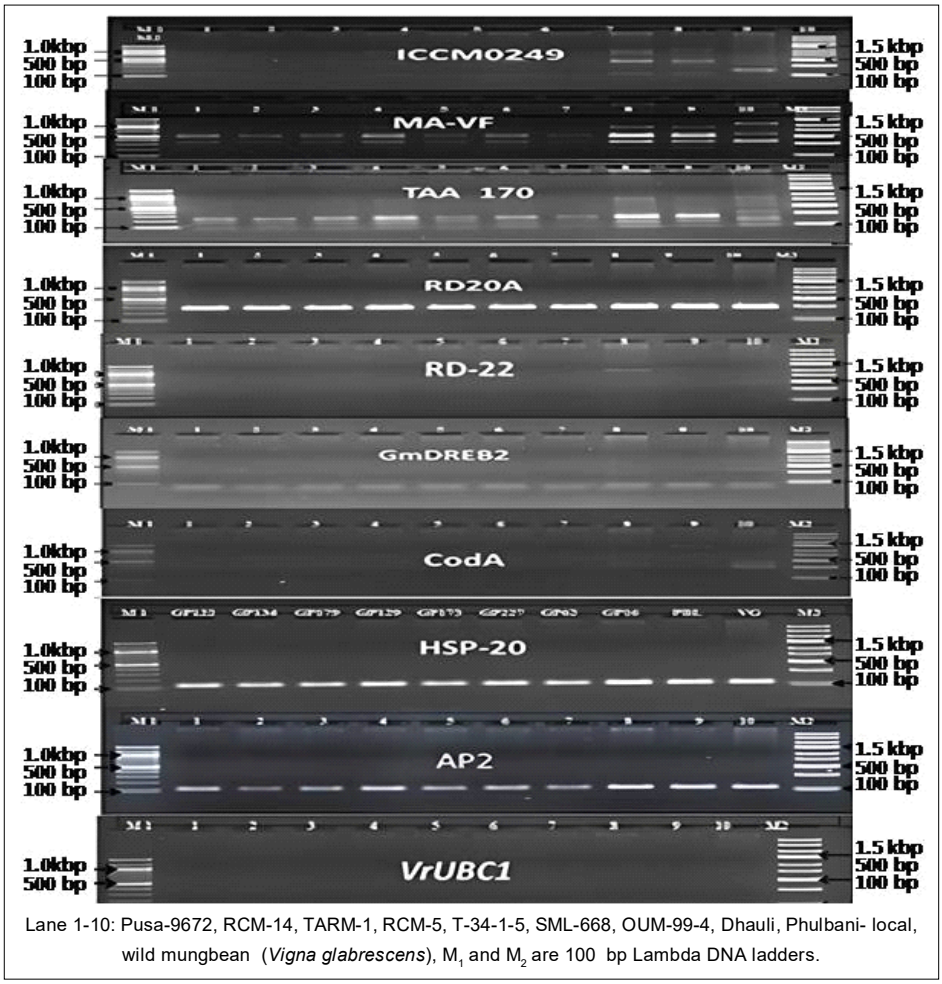
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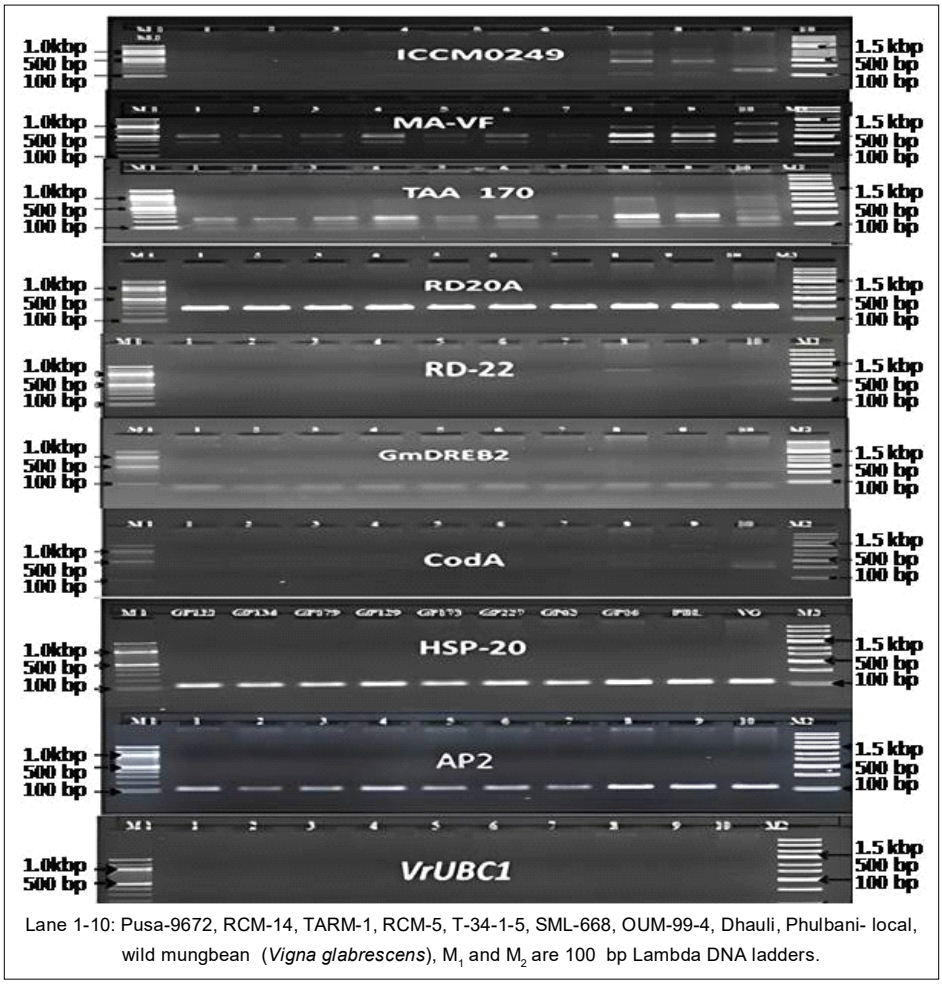
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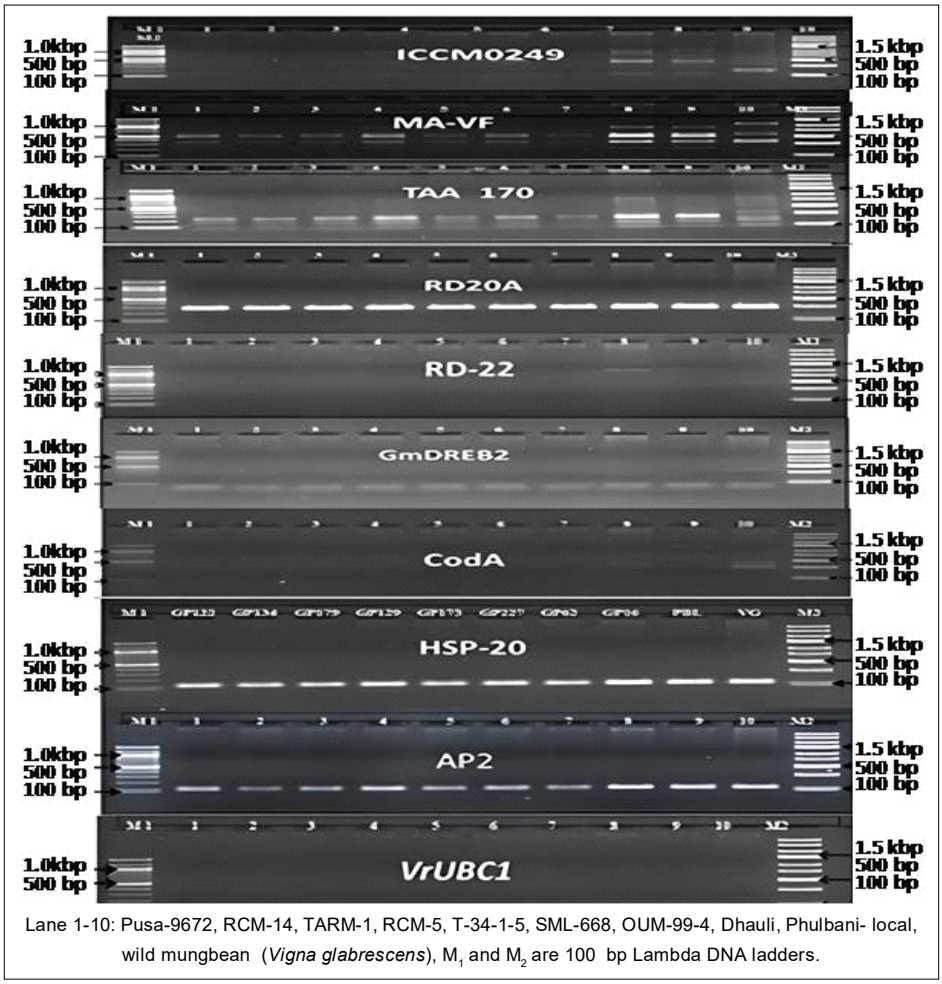
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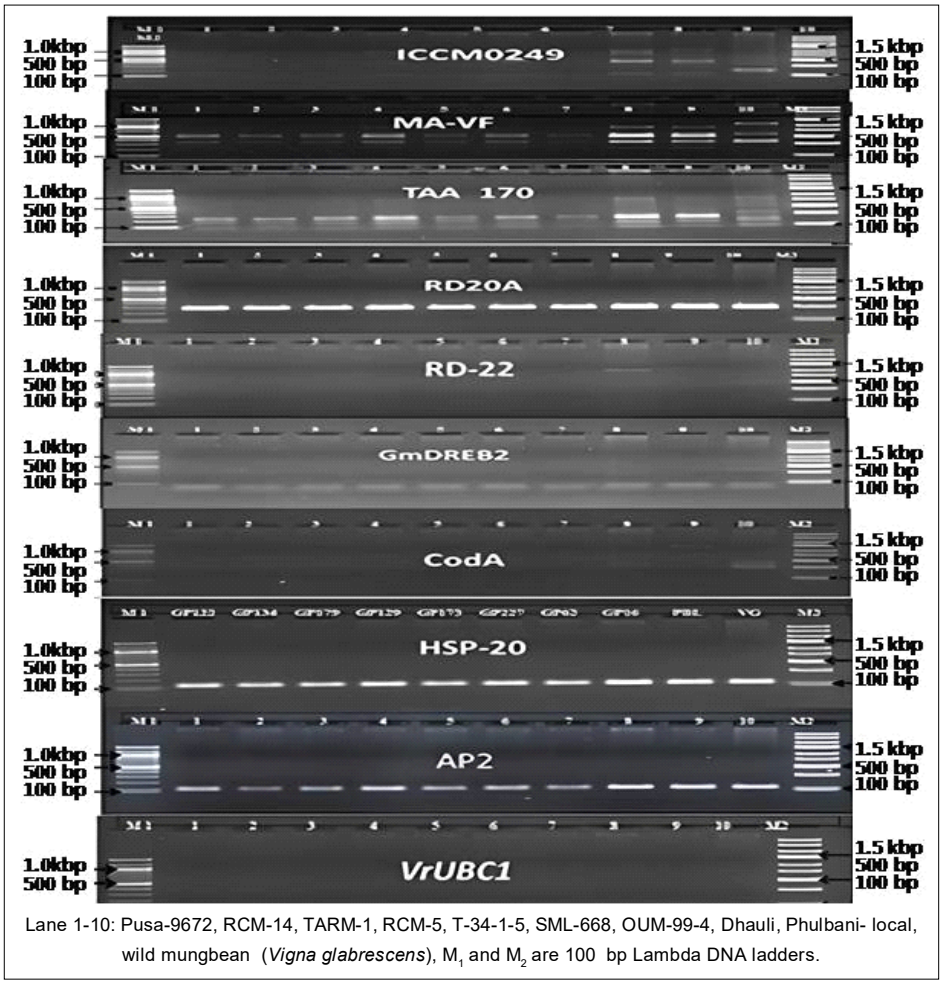
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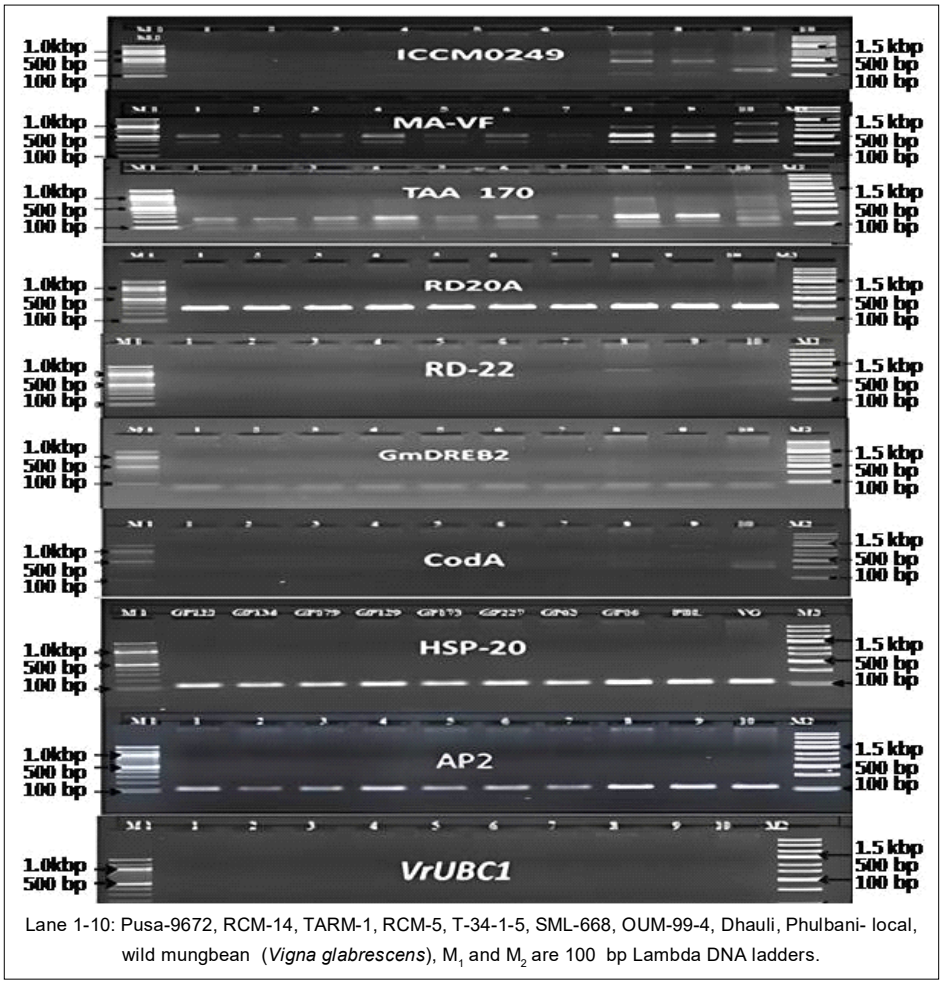
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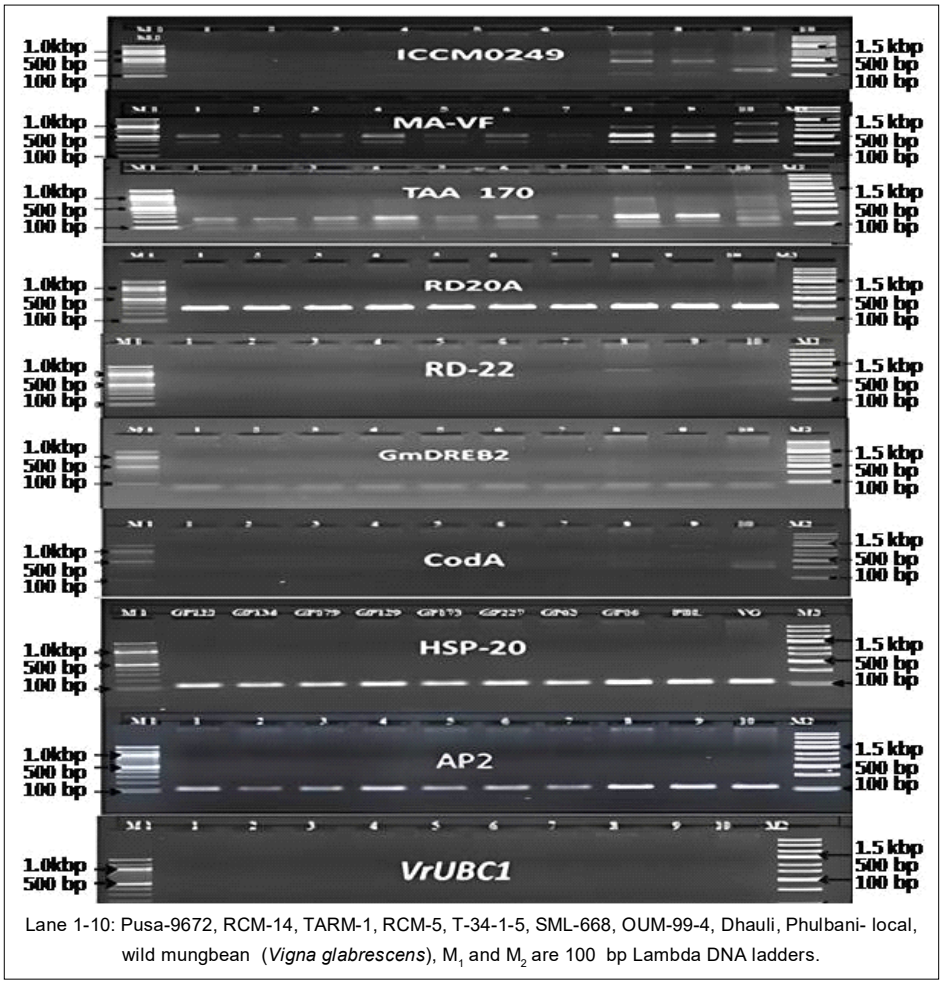
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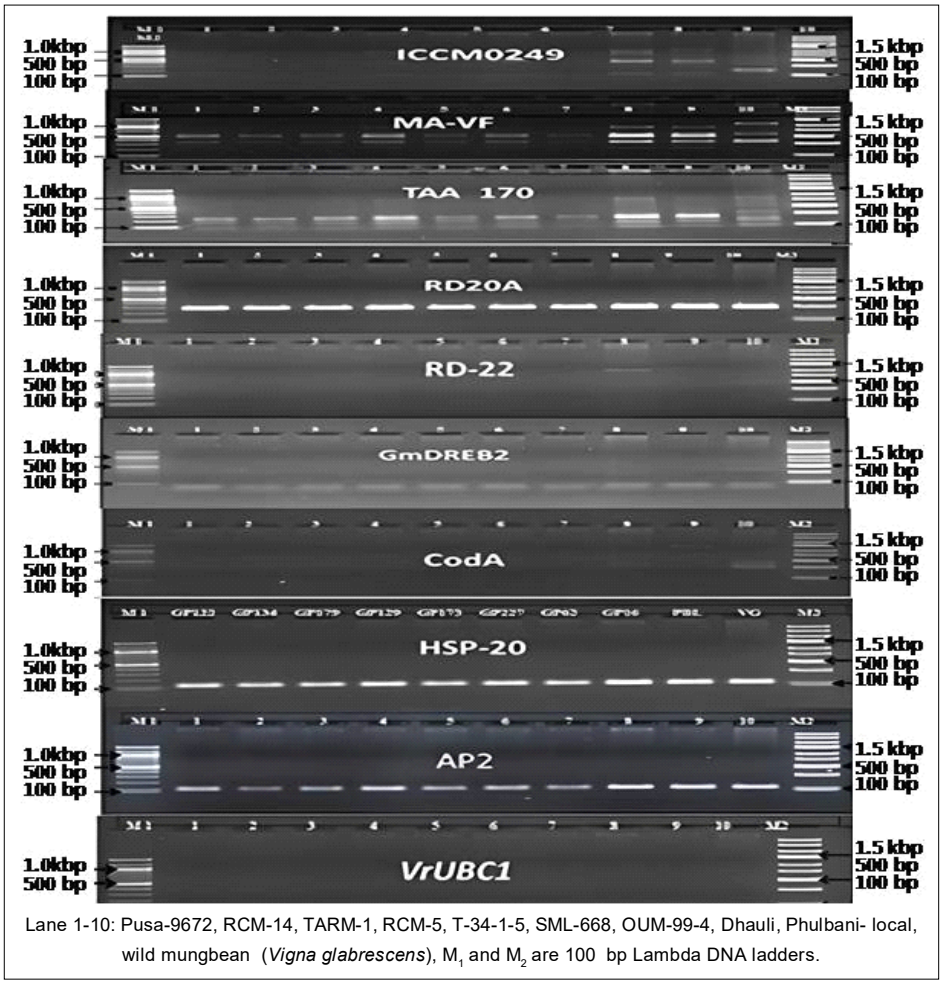
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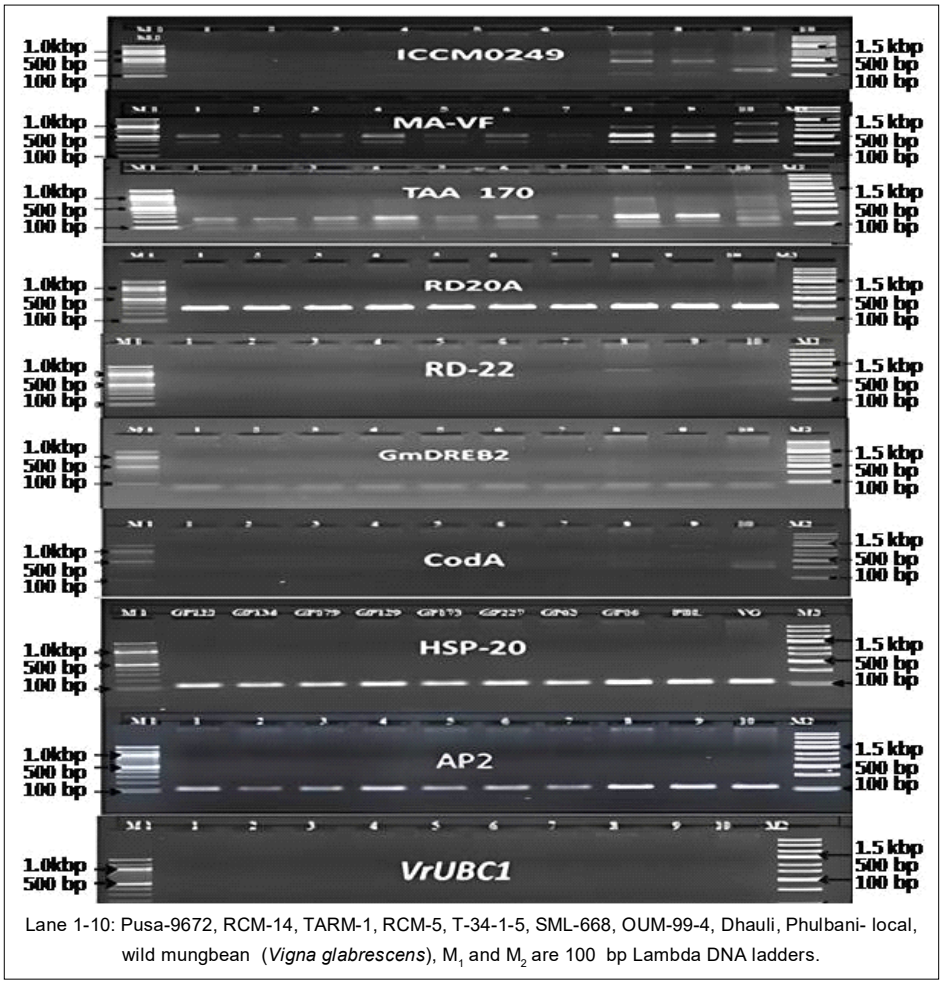
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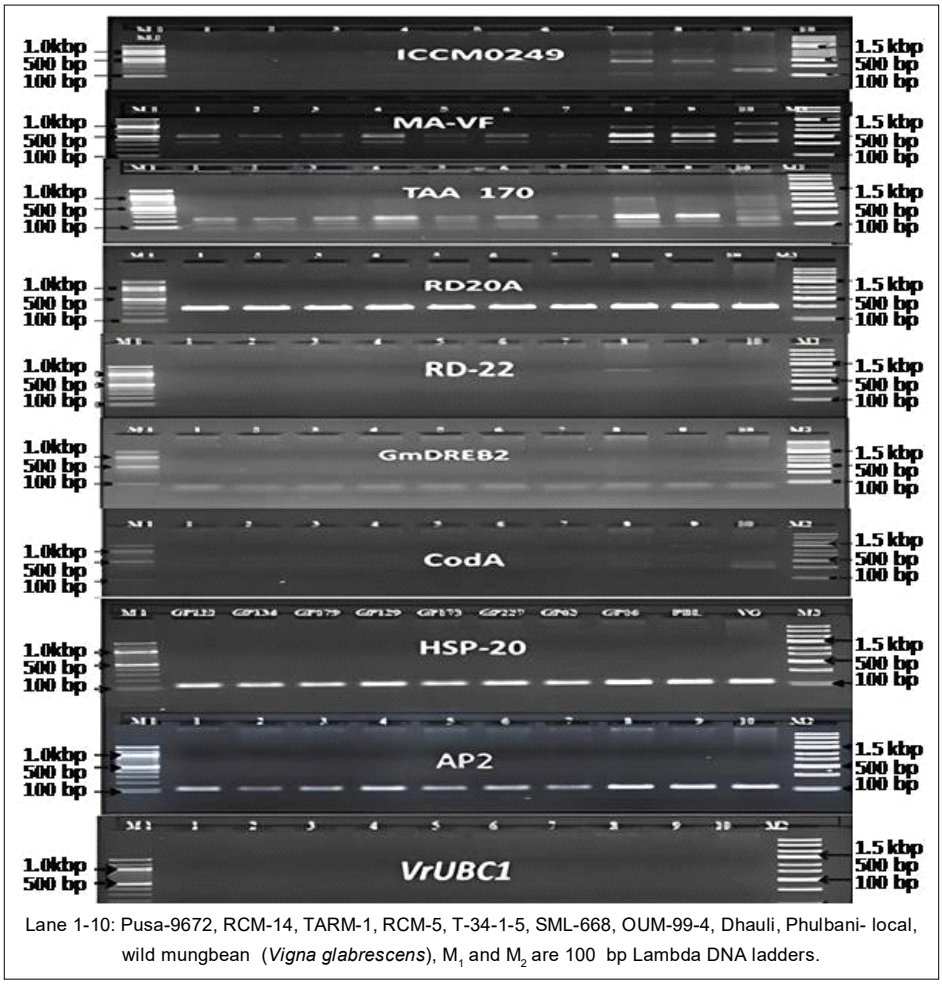
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Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
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Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Markar	Forward primer seq	Reverse primer seq	crop	Reference
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Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

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Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Suppl. Table 2: List of SSR primers screened.

Markar	Forward primer seq	Reverse primer seq	crop	Reference
Satt383	CGATTACACCACG ATAATTTCCTCTG	CTTTCCATAATTTGGCAACCTCTTAG	soybean	Mishra *et al*., 2022
Satt557	GCGGGATCACCA TGTAAATAGTG	GCGCTCAGCCTTAAATT TGAA	soybean	Mishra *et al*., 2022
ICCM0249	TTTCCTGCAGGGCTAAC	GGAGATTTGTGGGTAGCCTC	chikpea	Nayak *et al*., 2010
CEDG144	CAGTTACGAGTCTTGAACTTCAGC	CAGCTCTGTACAAAGCTGTAACTG	Mungbean	Suman *et al*., 2019
STMS11	GTAACTTGTAATAATTCCTCCTCT	ATACATAACCCCCAAC	chikpea	Winter *et al*., 1999
Satt009	CAACTTGAAATTACTAGAGAAAT	CTTACTAGCGTATTAACCCTTG	Soybean	Cregan *et al*., 1999
Satt197	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA	Soybean	Cregan *et al*., 1999
SoySSR9.1	GGAAGATTGAT TCAAAAGTCA	CGAGAAAGTGATTGTGAGAA	Soybean	Nugroho *et al*., 2020
Satt540	CTGGCGAATCAAGCTTTGTAAC	CCGTGATTGCGAAGAGGATATT	Soybean	Mishra, 2022
Ts72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG	Chikpea	Winter *et al*., 2000
TA47	TTTTTATAGGTGTCTTTTTGTTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT	Chikpea	Winter *et al*., 2000
RD20A	GTGGCACATGACTGAAGGAA	ATCTTTCCAGCAGCACCTCT	Soya bean	Neves-Borges et.al.,2012
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA	Chikpea	Winter et al.,2000
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA	Chikpea	Winter et al.,2000
VrDREB2A	CTGCTCTTGCTTATGATGAA	ATGTAGTGGTAGTAGTAGTAGTG	Mungbean	Alsamadany, 2022
VrbZIP17	GGCATCATCATCTCCATG	GAGTTTGAGGTCGTTCCA	Mungbean	Alsamadany, 2022
VrHsfA6a	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	Mungbean	Alsamadany, 2022
Ap2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
CEDG066	AGTAAAACAAGAACCCTCCCAAG	GTATTAAAATTTGGGGTGGTGG	Mungbean	Suman *et al*., 2019
CEDG071	GGTCCATTGAGACGGATCGAG	TCCCACCTCAGCGGAATCC	Mungbean	Suman *et al*., 2019
RD29B	AGCTGGAAGAGCCATCATG	CTCTGTCAGGGGACTGAGCAA	Soybean	Neves Borges *et al*., 2012
ERD1	CGTCCAGAATTTGCTCAACAG	TGGGGTTATAGCCTTGTTGG	Soybean	Neves Borges *et al*., 2012
FBOX	CTAATGGCACAATTGCAGCTCTC	AGATAGGGAAGATGGTGCAGGT	Soybean	Neves Borges *et al*., 2012
LEA	CAGTGGCAGTGGGTGGTG	CAGGGTTATGGGACGCAAGG	Mungbean	Tian *et al*., 2016
CP47	TGGGTGTCTGATCCTTATGGAC	CCTGCCGCAATATGATGAGAAG	Mungbean	Tian *et al*., 2016
codA gene	CCACCATGATATTCGGCAAC	GTGGAGGCTATTC GGCTA	Mungbean	Baloda *et al*., 2017
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SUT	TGTCTCCGTCACAGCACCAC	GGAGGAGCCAACCAAGTTACAG	Mungbean	Tian *et al*., 2016
ADH	CGAACCTGAAGCGTGTCC	CGAGTTGCGGAAGATGCC	Mungbean	Tian *et al*., 2016
FAH	TGACAGCAGCGACGAGGTAGG	AGGACCAGGAGCAGCCATCAC	Mungbean	Tian *et al*., 2016
AP2	TTGATGGAAGCTGGGGTGAT	CTCAGAAAACGCCTGCCATT	Mungbean	Tian *et al*., 2016
SMP	GTCACCGCCTTATCAGCTTG	CCACACATAACACACGCACT	Mungbean	Tian *et al*., 2016
VgActin	TTCCTTTTCTTCGTTTTTCATGCT	AAACCGAGGCACCTAATTCTTG	Mungbean	Tian *et al*., 2016
ICCM0249	TTTCTTCGCATGGGCTTAAC	GGAGATTTGTTGGGTAGGCTC	Chickpea	Nayak *et al*., 2010
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT-3"	Chickpea	Winter *et al*., 1999
TM-VF	CTTGCAGTCAAGCTCCCTTC	CCTTGTCCCAAGACAGACCA	Vicia faba	Ammar *et al*., 2017
SODC	ACAAGACCAGAAACACGAACAG	CCACCTCCTCCTCAATCCATAG	Mungbean	Tian *et al*., 2016

Supplementary Table 2: Continue....

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

Supplementary Table 2: Continue....

RD22	AATGCCGAAAGCCATTACAG	GCTTTGTTTTCCCTGCGTTA	Soya bean	Neves-Borges *et al*., 2012
GmDREB2	GGGGAATTCATGGAAGAACCGGGTTTA	GGGCTCGAGATCTTCAGGTTTGGGATA	Soya bean	Savitri *et al*., 2019
ACT11	CGGTGTTTCATCTTGGGATC	GTCTTTCGCTCAATAACCCTA	Soybean	Neves-Borges *et al*., 2012
HSP20	AGGTGGAAGTGGAAGATGGG	GGAAGCCAGAACCTCCTCAT	Mungbean	Tian *et al*., 2016
SoySSR5.1	ATGAAGCCCAGAGAGTACAAC	CCCAAGTCTGAACATTACTCA	Soybean	Nugroho *et al*., 2020
VrUBC1	ATGGCCTCTAAGCGGATTCTGAAG-3'	CTAGCCCATTGCATACTTCTGAGTCC	Mungbean	Chung *et al*., 2013
DMB-SSR182	TAGAGCCTTCTGGTTTTTCACA	AGGAGGAGGATTTTGATGATGA	Mungbean	Suman *et al*., 2019
CEDG068	TCTCCATAGGAACCCCTGAAAG	TGGGATCAGTGAATTCGCCAG	Mungbean	Suman *et al*., 2019
CEDGAG001	CTCATCAGGGACATCCTCCC	GATCGTGATCGATCCAACGGTC	Mungbean	Suman *et al*., 2019
CEDG008	AGGCGAGGTTTCGTTTCAAG	GCCCATATTTTTACGCCCAC	Mungbean	Suman *et al*., 2019
CEDG056	TTCCATCTATAGGGGAAGGGAG	GCTATGATGGAAGAGGGCATGG	Mungbean	Suman *et al*., 2019
CEDG091	CTGGTGGAACAAAGCAAAAGAGT	TGCGTCTTGGTGCAAAGAAGAAA	Mungbean	Suman *et al*., 2019
CEDG264	GATTCCCTTCCTAGCTATGG	CTGCTGGACATGAAGATTCAG	Mungbean	Suman *et al*., 2019

Supple. Table 3: Genotyping data

	Amplicons	ICCM 0249_1	ICCM 0249_2	ICCM 0249_3	ICCM 0249_4	ICCM 0249_5	ICCM 0249_6	ICCM 0249_7	ICCM 0249_8	TAA 170_1	TAA 170_2	TAA 170_3	TAA 170_4	MA-VF_1	MA-VF_2	MA-VF_3	MA-VF_4	MA-VF_5	MA-VF_6	MA-VF_7	RD-20A_1	RD 22_1	RD-22_2	GmDREB2_1	GmDREB2_2	Cod A_1	Cod A_2	Cod A_3	Cod A_4	Cod A_5	Cod A_6	Cod A_7	Cod A_8	Cod A_9	HSP 20_1	Ap 2_1	Vr UBC1_1
Genotype	Size (bp)	1200	1150	980	740	600	490	400	120	800	320	250	180	1180	1000	950	610	520	350	240	300	1110	460	1140	820	2800	2700	1610	1350	810	750	630	490	380	130	140	78
GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

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GP122= PUSA 9672		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GP134= RCM14		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP179= TARM 1		0	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1
GP129=RCM5		1	0	1	0	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	1	1	0	1	0	1	0	0	1	1	1	1
GP173=T 34-1-5		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP227=SML668		0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1
GP62=OUM 99-4		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
GP16= Dhauli		1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	1
Phulbani Local		1	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	0	1	1	1	1	1	1
Vigna glaberescence		0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1

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Presence or absence of specific band is the inherent feature of each genotype. Primer GmDREB 2 and ICCM-0249 produced 820 bp and 740 bp amplified products which were specific to Dhauli and Phulbani local respectively (Supple. Table 3). *Vigna glabrescens* produced unique molecular finger print by a number of primers *e.g.*, ICCM-0249, TAA-170, MA-VF, RD 22, GmDREB-2 and Cod-A which amplified 600 bp, 320 bp, 1180 bp, 460 bp, 1180 bp, 460 bp, 1140 bp and 810 bp amplicons respectively. In contrast, all test genotypes except *Vigna glabrescens* amplified 250 bp and 520 bp allele by primer TAA-170 and MA-VF respectively. These results suggest that SSR markers can be used as an accurate and efficient tool for identification of mungbean genotypes (Liu *et al.*, 2013).

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Molecular diversity

Available literature revealed use of SSR markers for study of genetic diversity in germplasm (Liu *et al.,* 2013; Ganguly and Bhat, 2012). *Vigna glabrescens* maintained high genetic dissimilarity with TARM-1(0.32), OUM-99-4(0.34), Phulbani local (0.35) and RCM-14(0.36) (Table 2) indicating better scope of using them in hybridization to achieve transgressive segregants. Similar molecular diversity has

Table 2: Similarity coefficient values between paired test genotypes for DNA profiles using SSR markers.

Genotype	Pusa-9672	RCM-14	TARM-1	RCM-5	T 34-1-5	SML -668	OUM-99-4	Dhauli	Phulbani Local	*V. glabrescens*
	1	2	3	4	5	6	7	8	9	10
PUSA -9672	1.0									
RCM -14	0.76	1.0								
TARM-1	0.70	0.92	1.0							
RCM-5	0.62	0.59	0.54	1.0						
T-34-1-5	0.65	0.84	0.77	0.50	1.0					
SML-668	0.94	0.72	0.66	0.60	0.61	1.0				
OUM-99-4	0.59	0.77	0.83	0.45	0.91	0.58	1.0			
Dhauli	0.63	0.48	0.44	0.75	0.41	0.66	0.37	1.0		
Phulbani local	0.55	0.46	0.42	0.68	0.38	0.59	0.34	0.79	1.0	
V. glaberesence	0.52	0.36	0.32	0.43	0.39	0.50	0.35	0.41	0.35	1.0

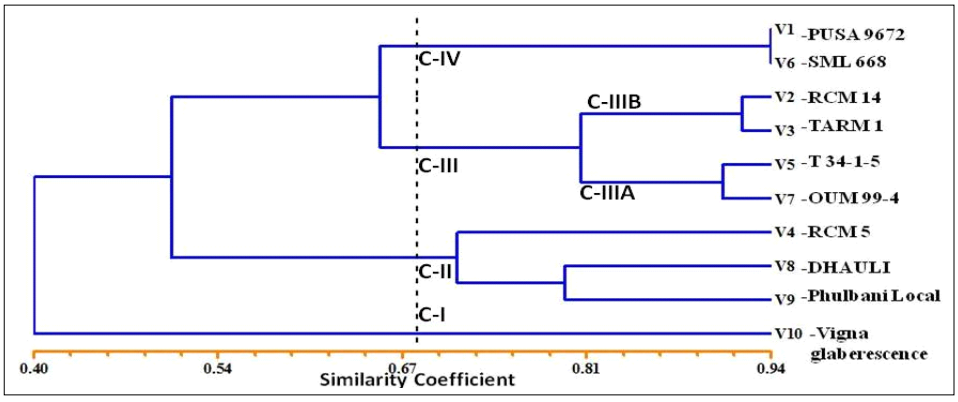


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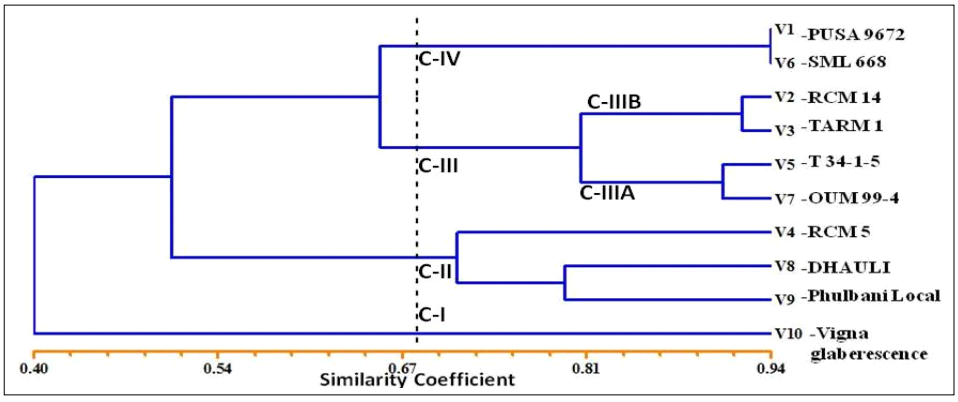


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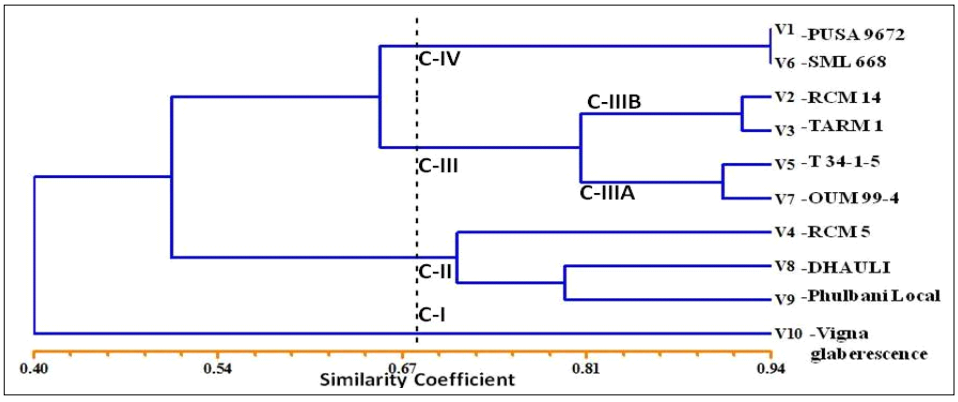


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RCM -14	0.76	1.0								
TARM-1	0.70	0.92	1.0							
RCM-5	0.62	0.59	0.54	1.0						
T-34-1-5	0.65	0.84	0.77	0.50	1.0					
SML-668	0.94	0.72	0.66	0.60	0.61	1.0				
OUM-99-4	0.59	0.77	0.83	0.45	0.91	0.58	1.0			
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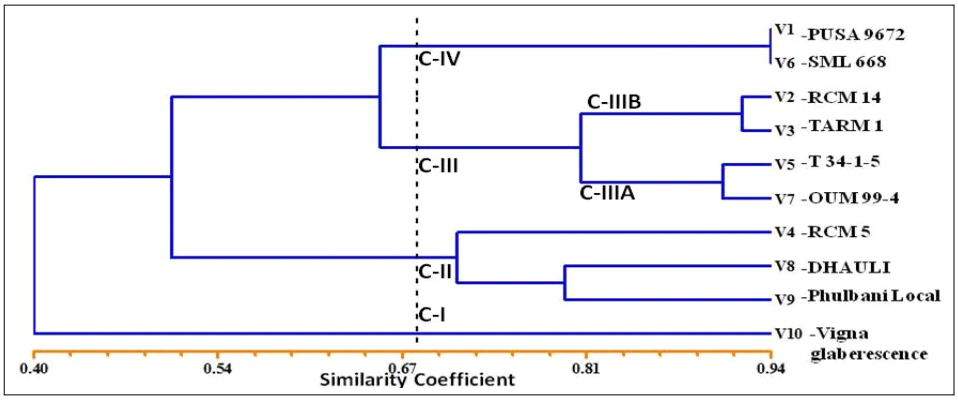


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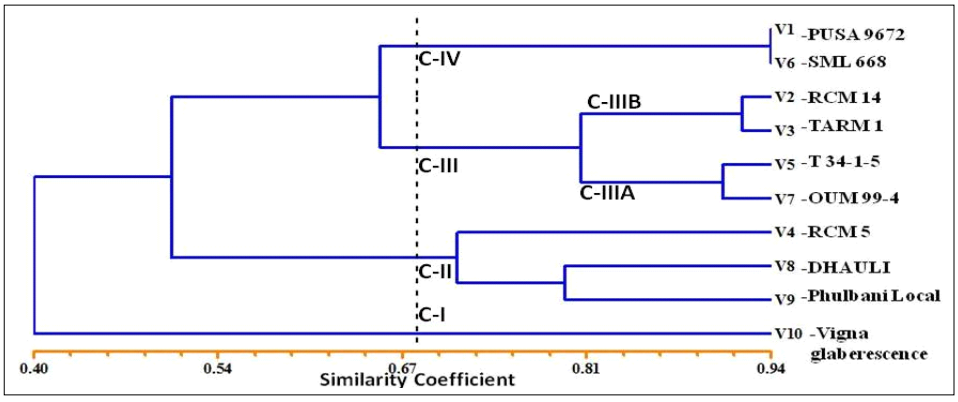


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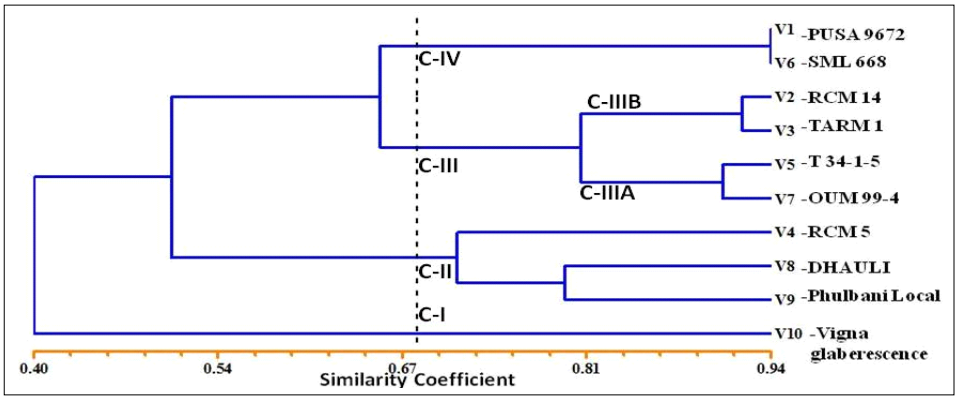


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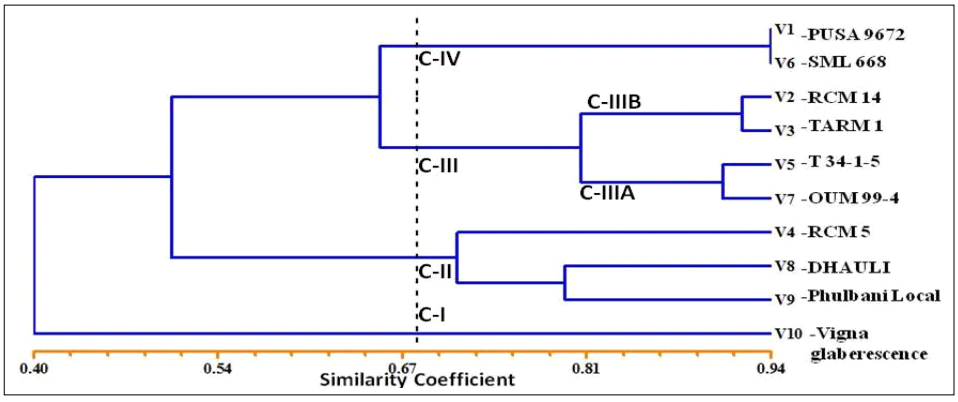


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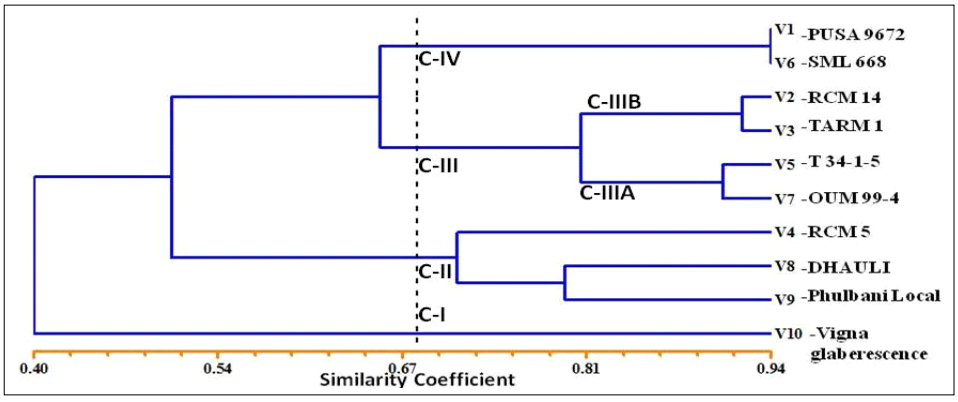


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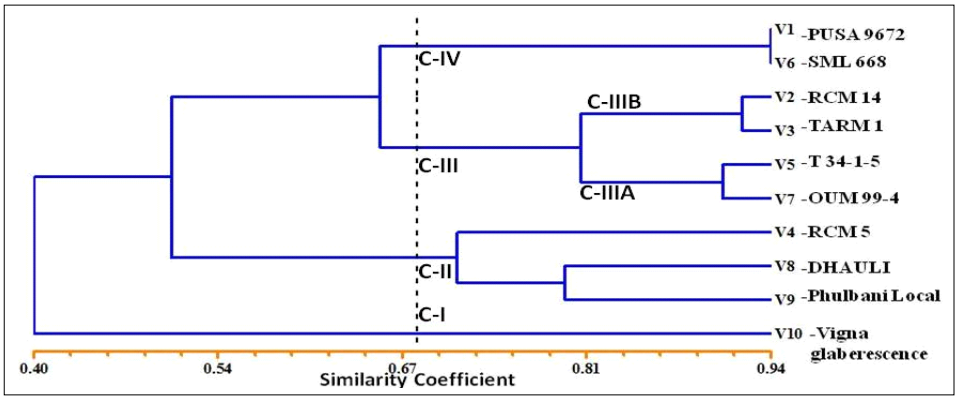


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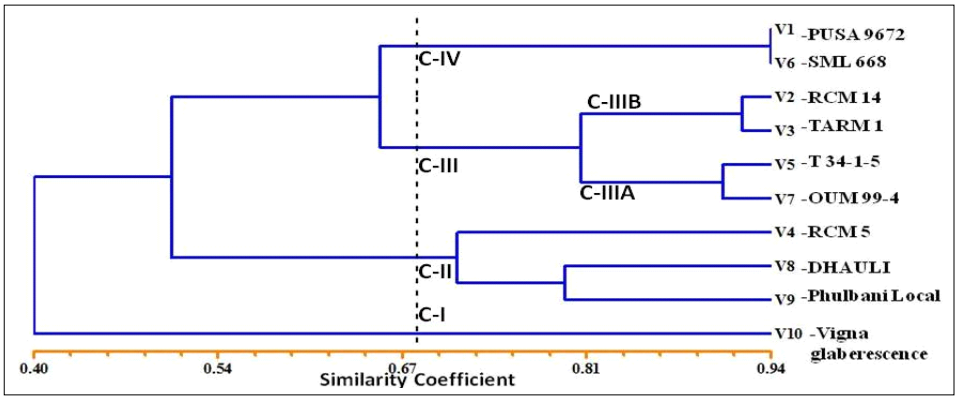


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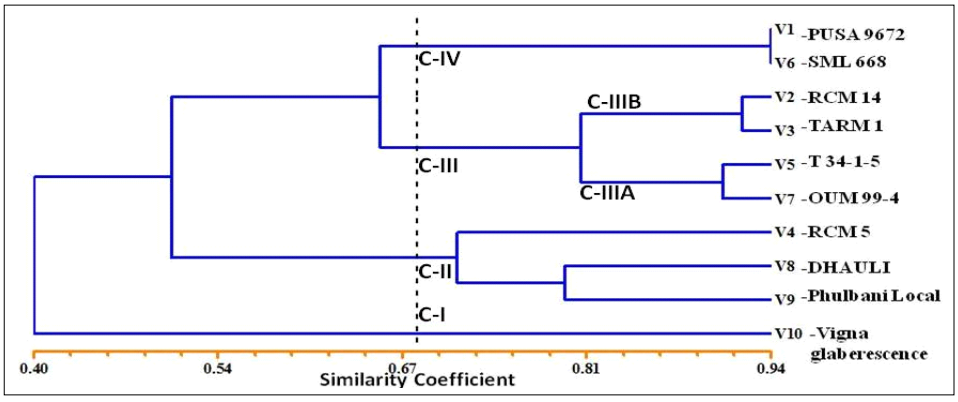


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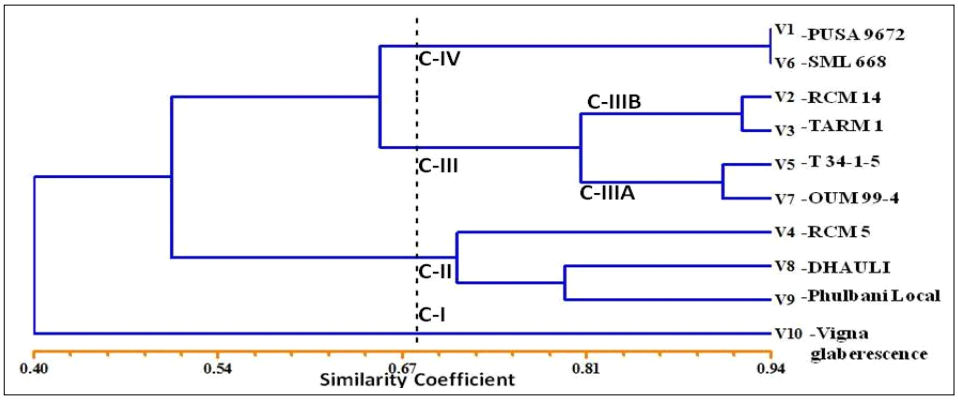


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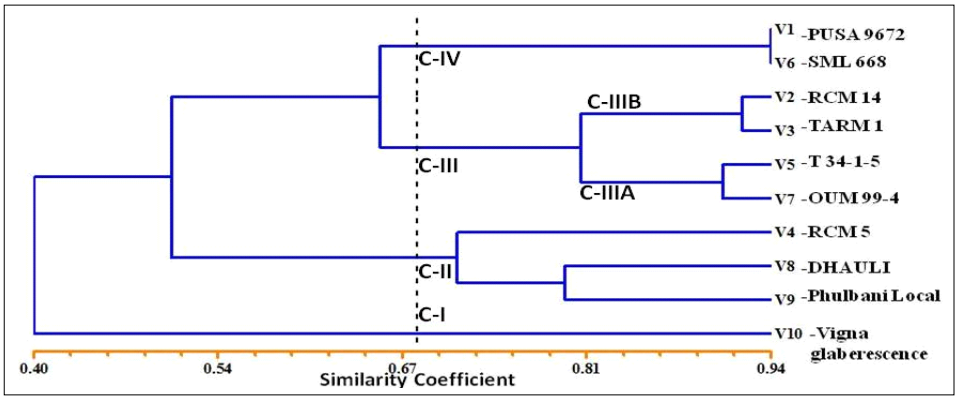


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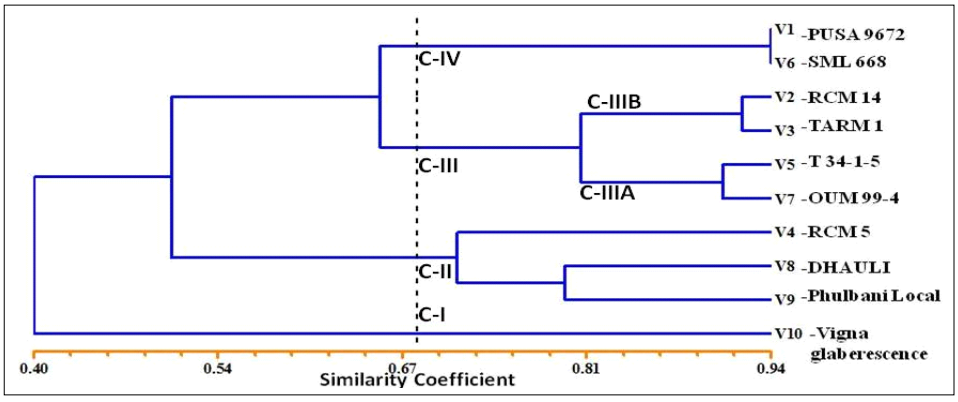


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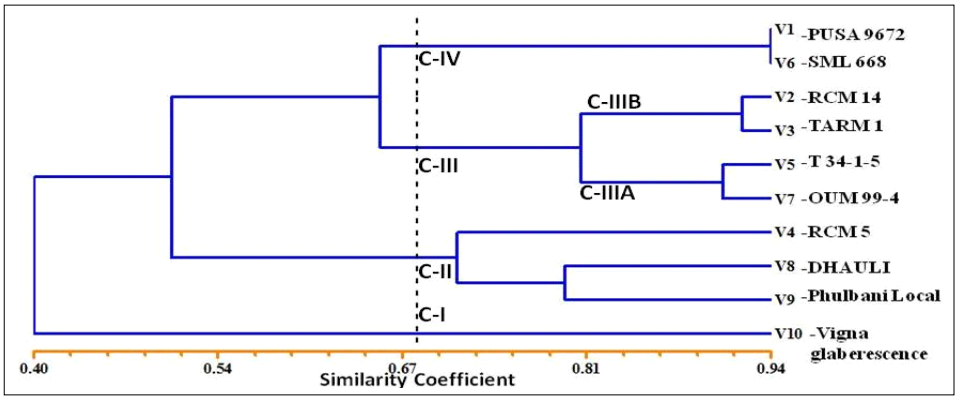


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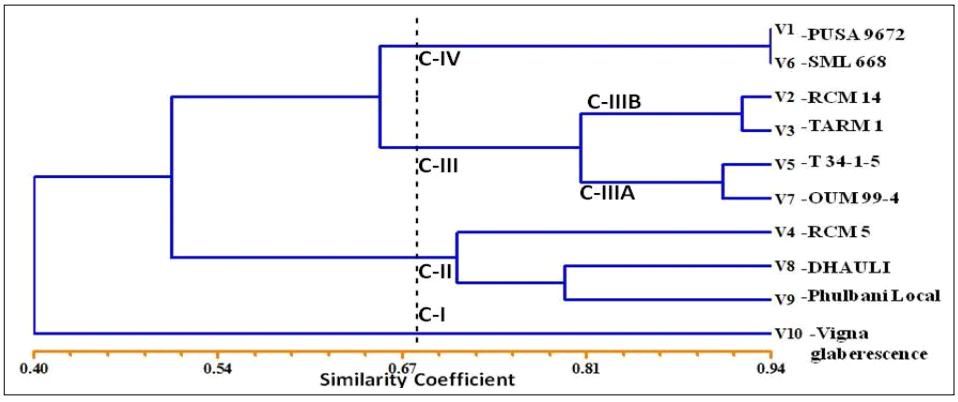


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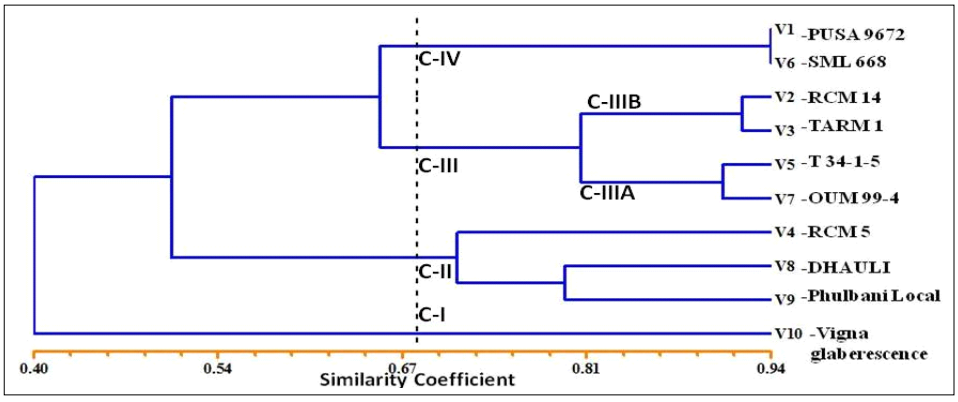


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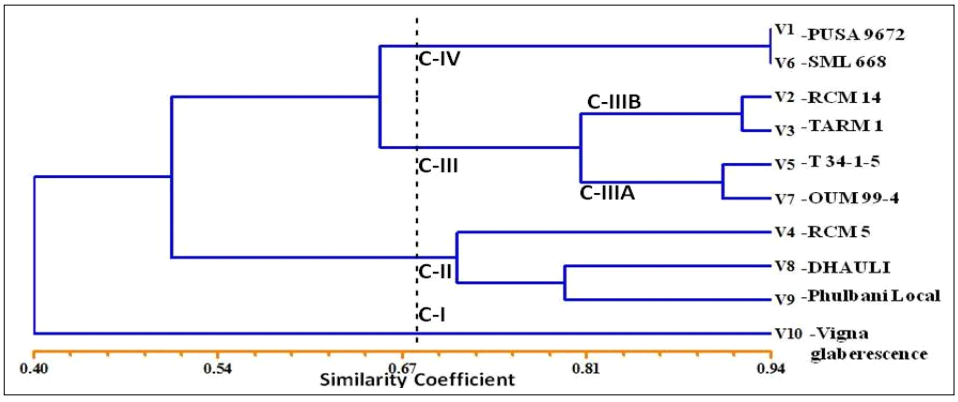


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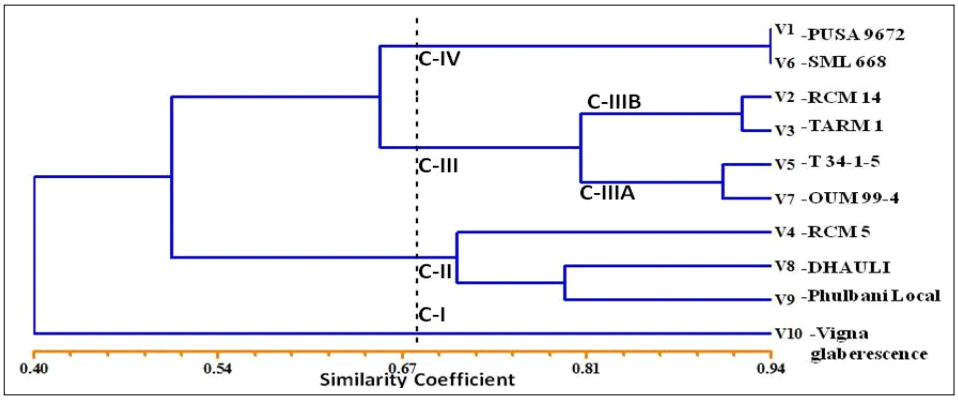


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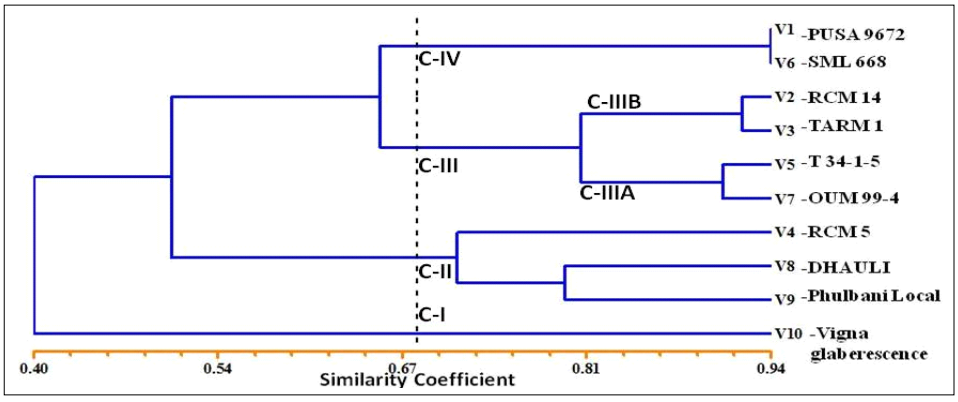


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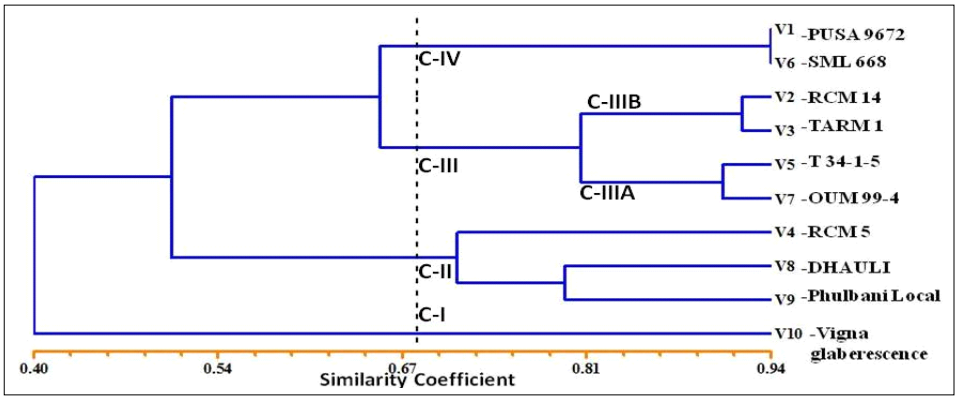


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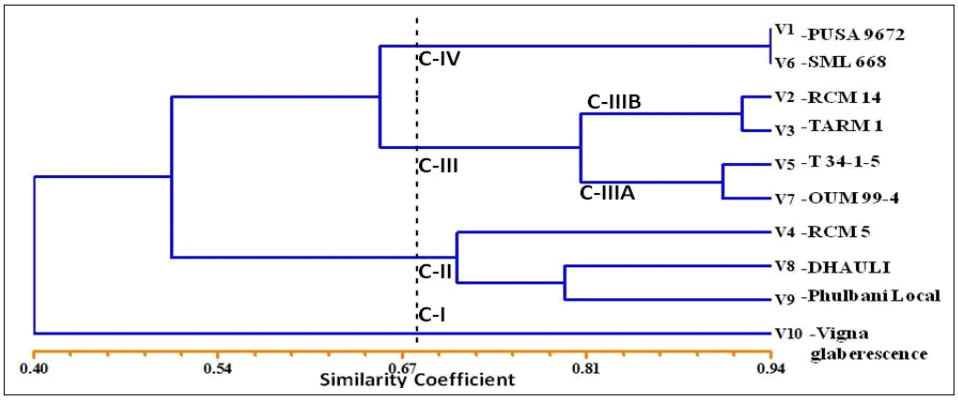


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Available literature revealed use of SSR markers for study of genetic diversity in germplasm (Liu *et al.,* 2013; Ganguly and Bhat, 2012). *Vigna glabrescens* maintained high genetic dissimilarity with TARM-1(0.32), OUM-99-4(0.34), Phulbani local (0.35) and RCM-14(0.36) (Table 2) indicating better scope of using them in hybridization to achieve transgressive segregants. Similar molecular diversity has

Table 2: Similarity coefficient values between paired test genotypes for DNA profiles using SSR markers.

Genotype	Pusa-9672	RCM-14	TARM-1	RCM-5	T 34-1-5	SML -668	OUM-99-4	Dhauli	Phulbani Local	*V. glabrescens*
	1	2	3	4	5	6	7	8	9	10
PUSA -9672	1.0									
RCM -14	0.76	1.0								
TARM-1	0.70	0.92	1.0							
RCM-5	0.62	0.59	0.54	1.0						
T-34-1-5	0.65	0.84	0.77	0.50	1.0					
SML-668	0.94	0.72	0.66	0.60	0.61	1.0				
OUM-99-4	0.59	0.77	0.83	0.45	0.91	0.58	1.0			
Dhauli	0.63	0.48	0.44	0.75	0.41	0.66	0.37	1.0		
Phulbani local	0.55	0.46	0.42	0.68	0.38	0.59	0.34	0.79	1.0	
V. glaberesence	0.52	0.36	0.32	0.43	0.39	0.50	0.35	0.41	0.35	1.0

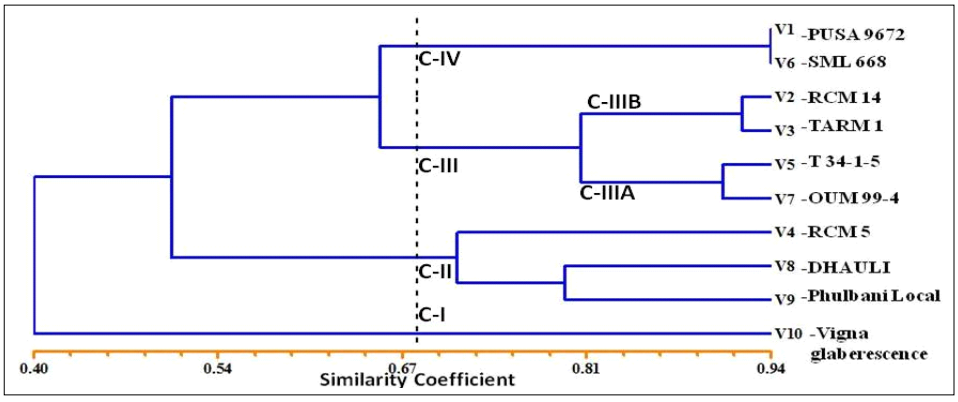


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considered to be sufficient to distinguish between cultivars of broccoli (Hu and Quaros, 1991).

CodA revealed maximum number of polymorphic bands (9) with the widest size variation of amplicons (380-2800 bp) followed by the Primer ICCM-0249 (Fig 1, Table 1), while HSP-20, AP-2 and Vr UBC1 produced only one fragment each. Higher polymorphism of the above marker may be attributed to appreciable variation in number of tandem repeats within the core sequence in the genome across the panel of genotypes under study. Overall, 19 polymorphic bands were recorded out of total 36 bands resulting 52.8% polymorphism indicating subtle response of some primers towards genetic variation. While, Mathivathana *et al.* (2018) reported polymorphism only in primers: VrSSR_6_746 and VrSSR_1_31 out of ten primers used across six mungbean genotypes.

Presence or absence of specific band is the inherent feature of each genotype. Primer GmDREB 2 and ICCM-0249 produced 820 bp and 740 bp amplified products which were specific to Dhauli and Phulbani local respectively (Supple. Table 3). *Vigna glabrescens* produced unique molecular finger print by a number of primers *e.g.*, ICCM-0249, TAA-170, MA-VF, RD 22, GmDREB-2 and Cod-A which amplified 600 bp, 320 bp, 1180 bp, 460 bp, 1180 bp, 460 bp, 1140 bp and 810 bp amplicons respectively. In contrast, all test genotypes except *Vigna glabrescens* amplified 250 bp and 520 bp allele by primer TAA-170 and MA-VF respectively. These results suggest that SSR markers can be used as an accurate and efficient tool for identification of mungbean genotypes (Liu *et al.*, 2013).

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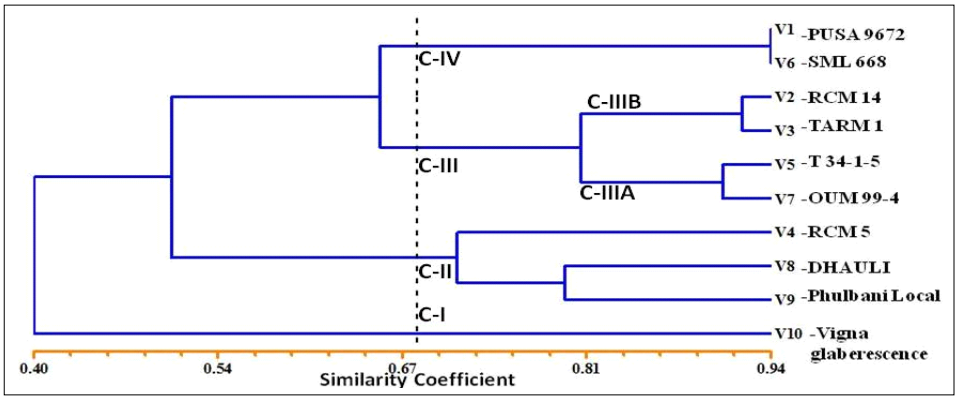


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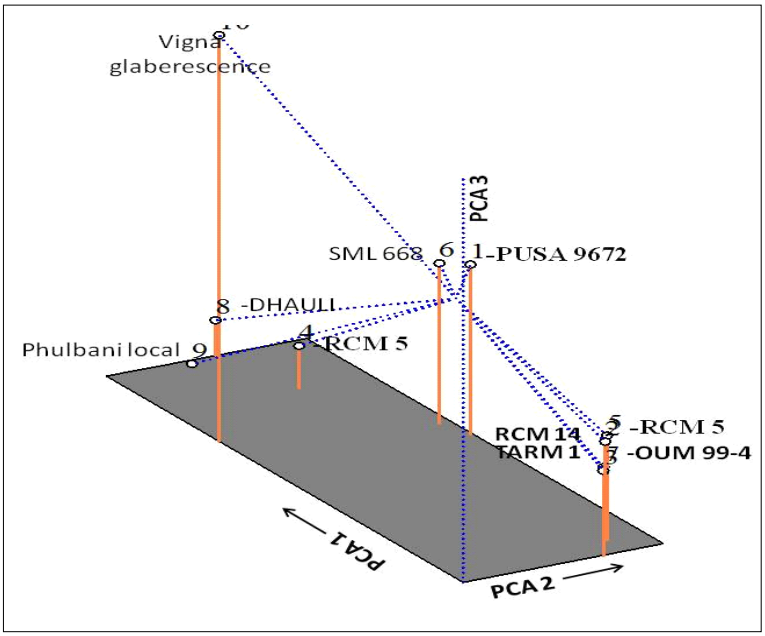


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Germination %	RD 22	RD 22_1	-28.2**	0.017	0.530
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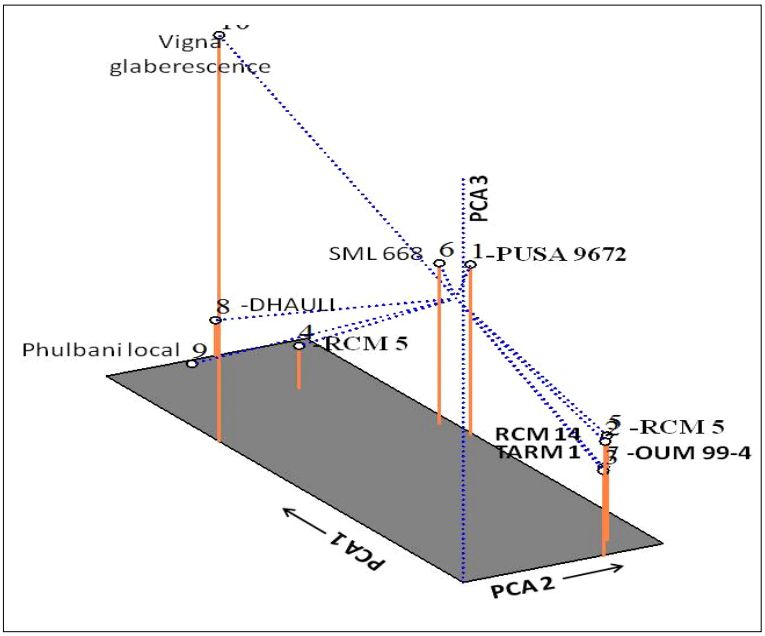


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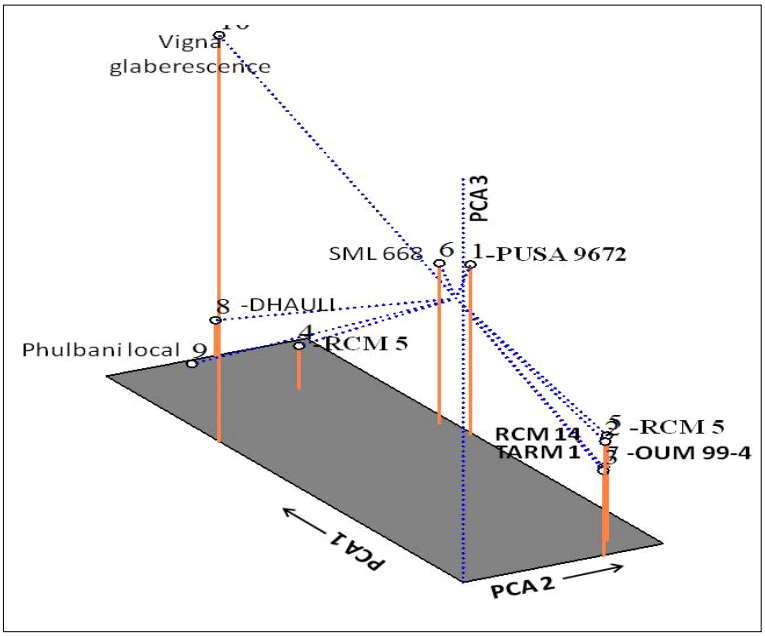


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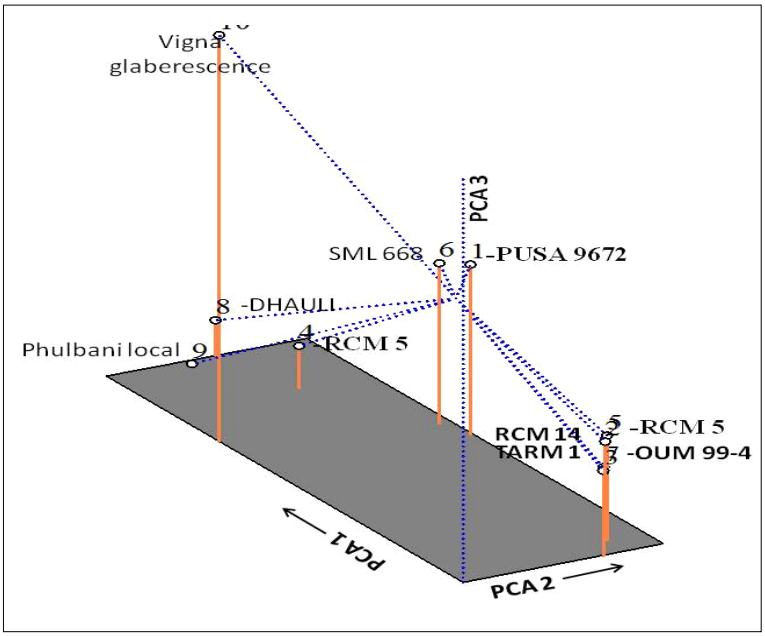


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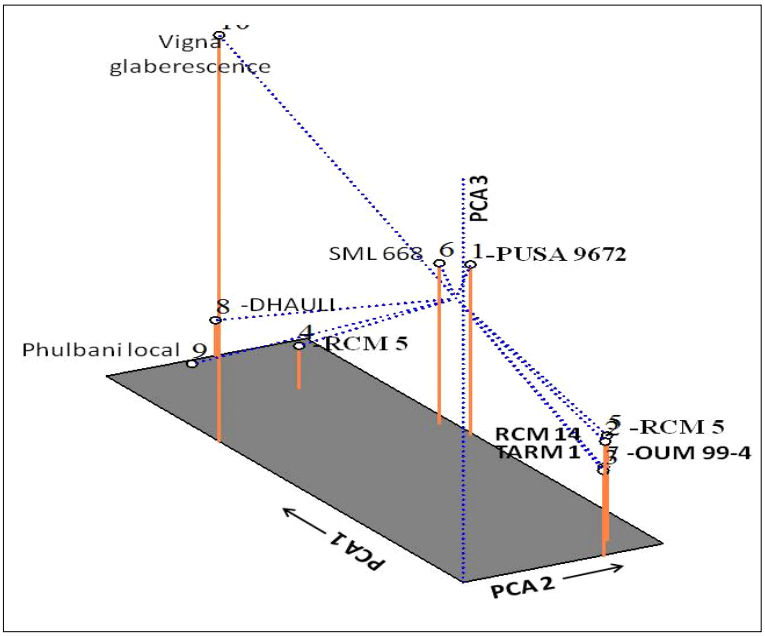


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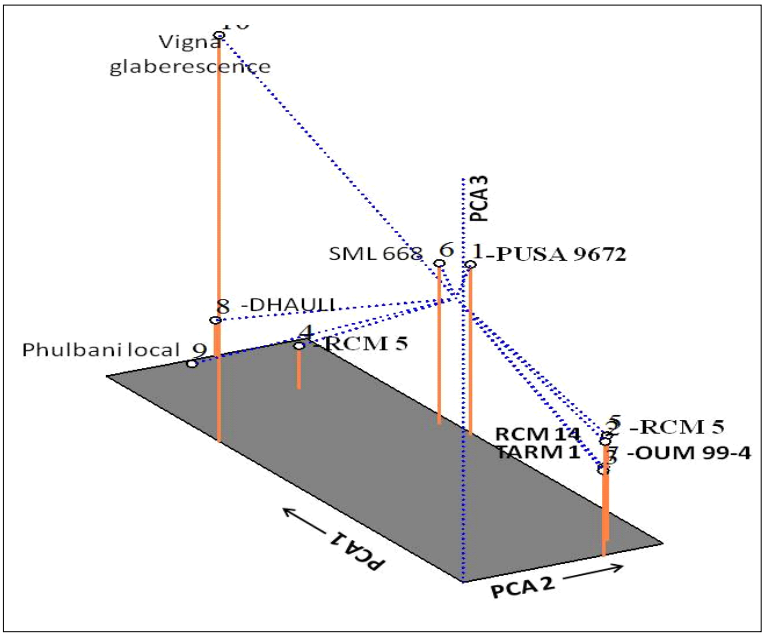


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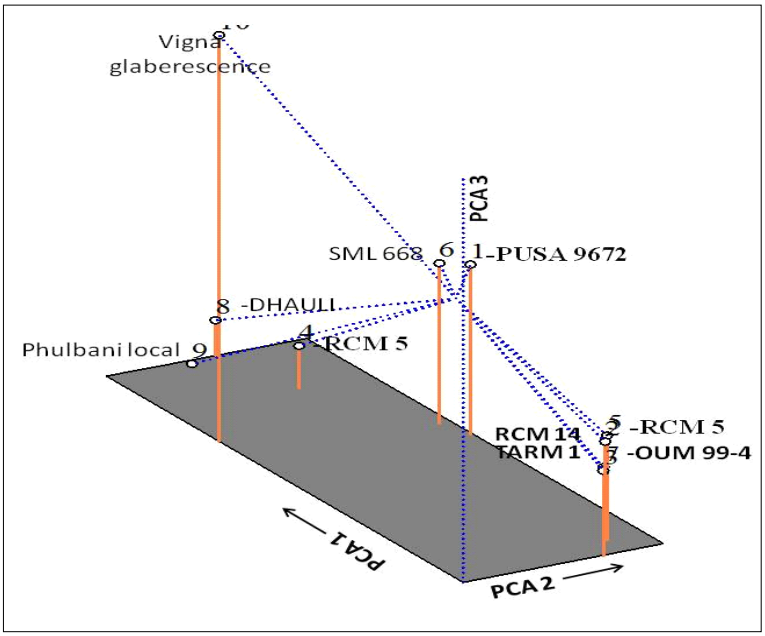


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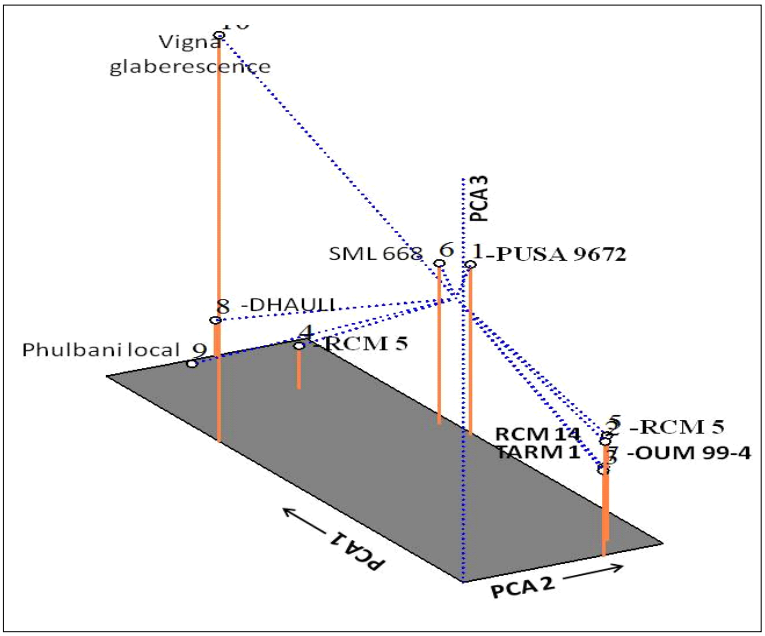


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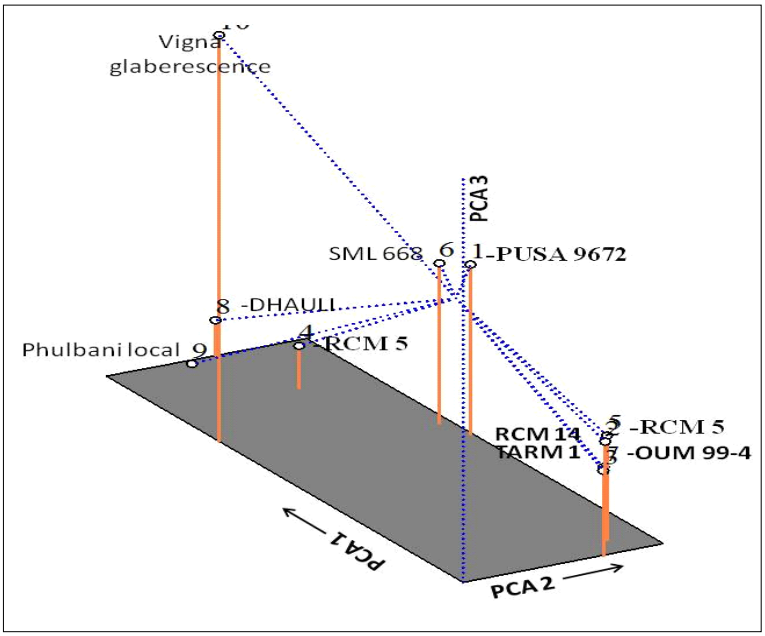


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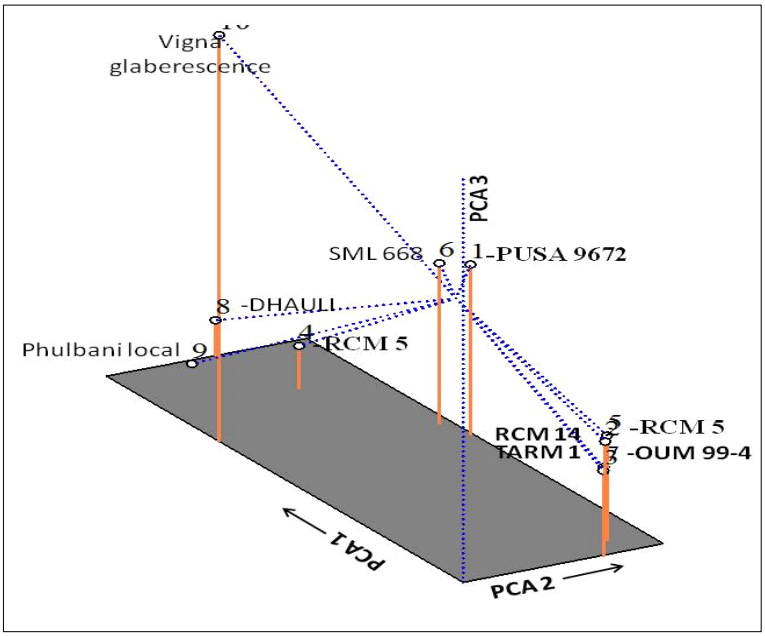


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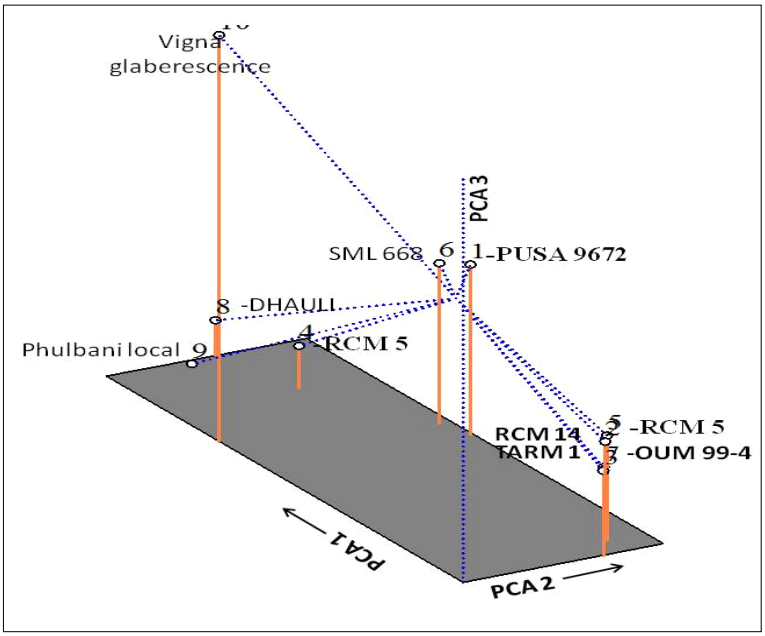


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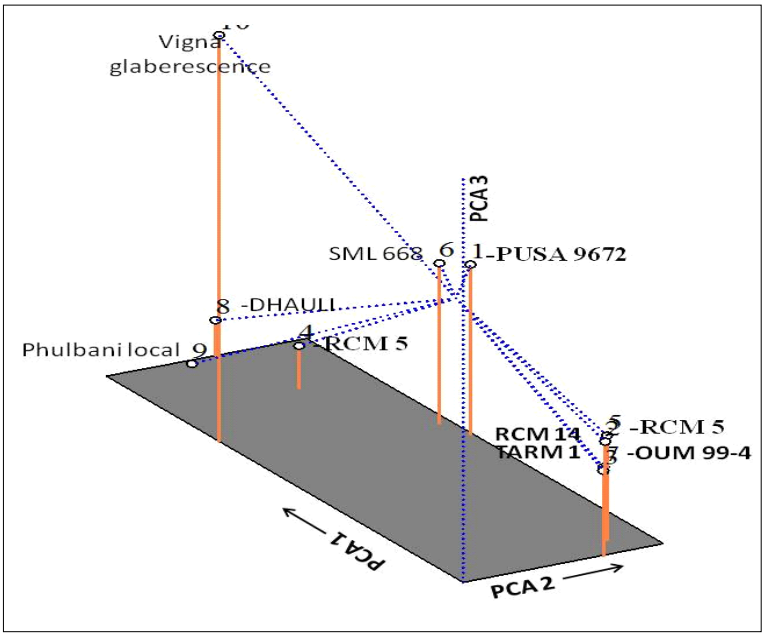


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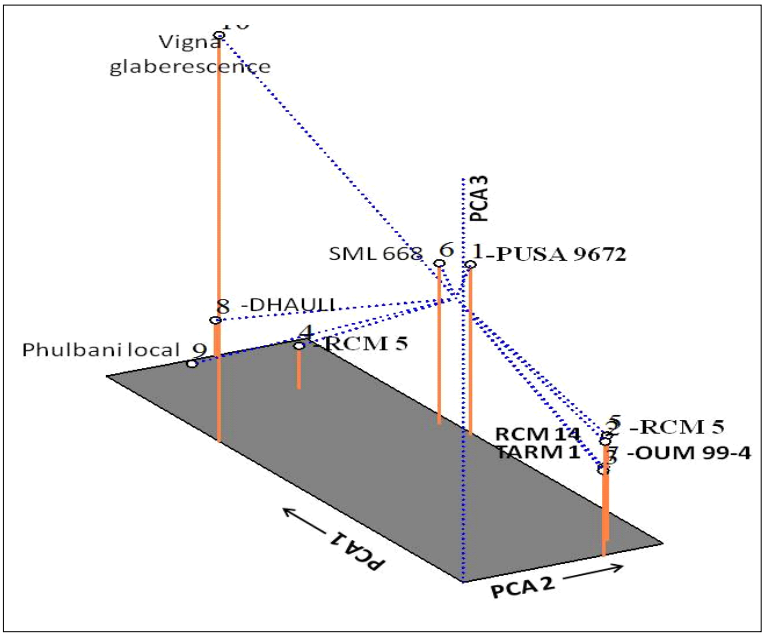


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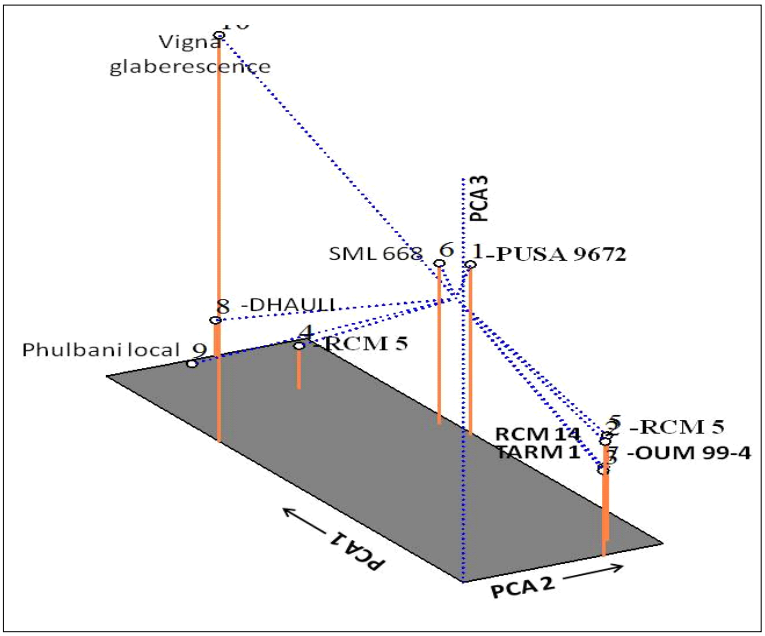


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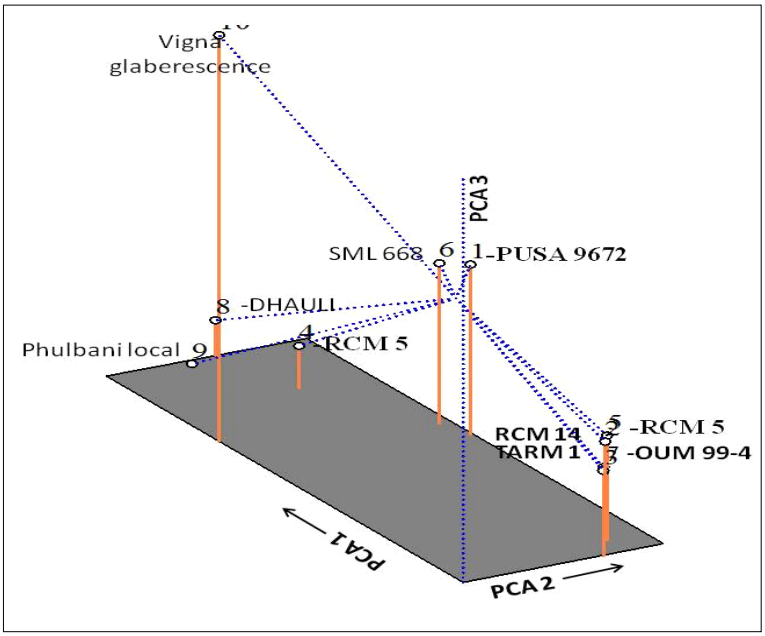


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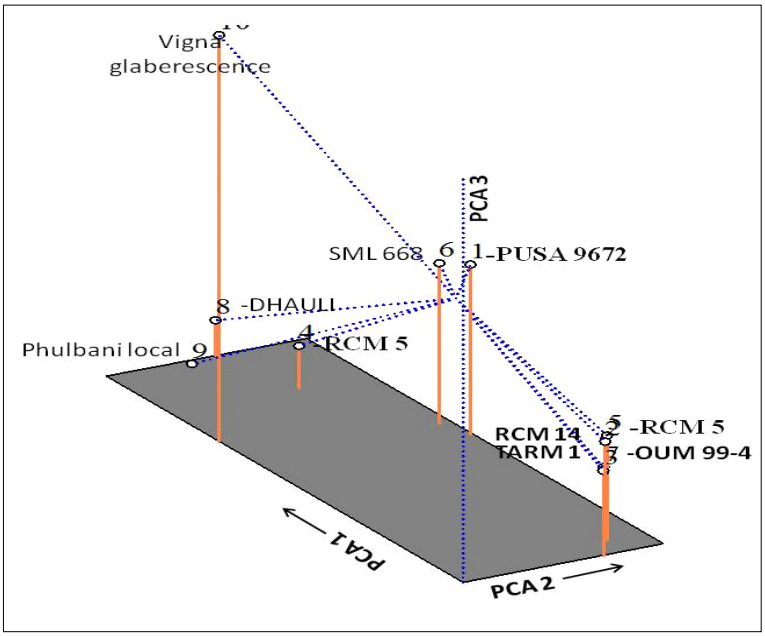


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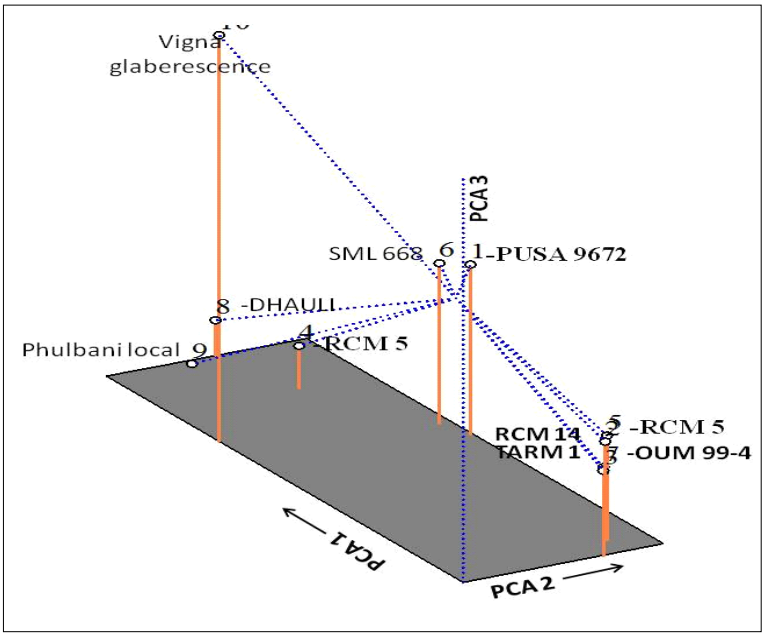


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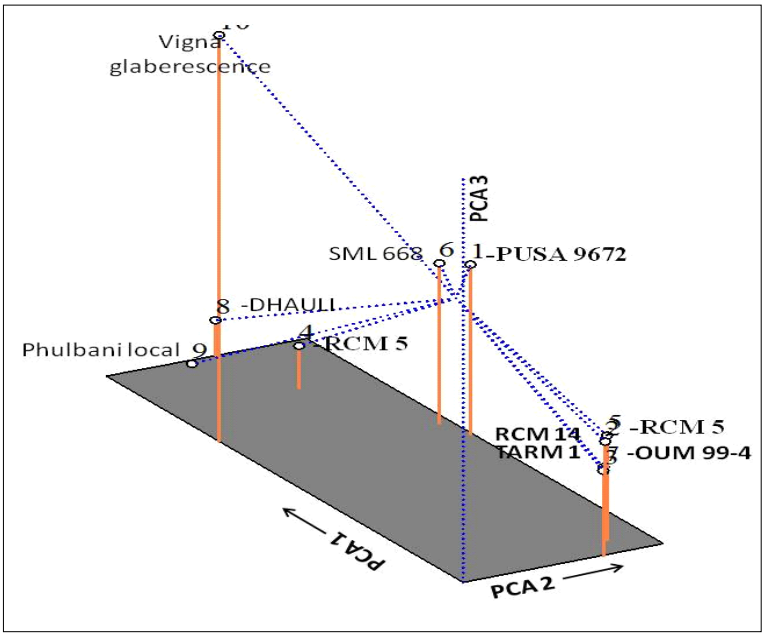


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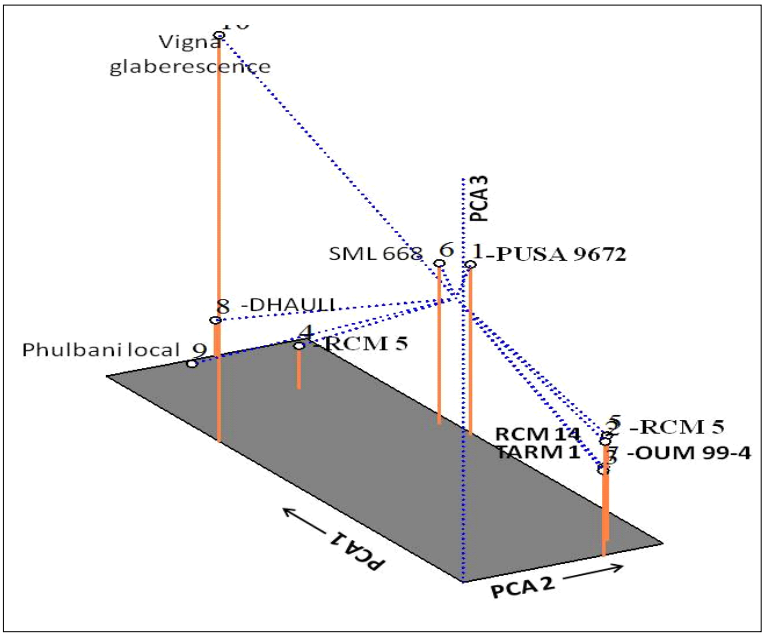


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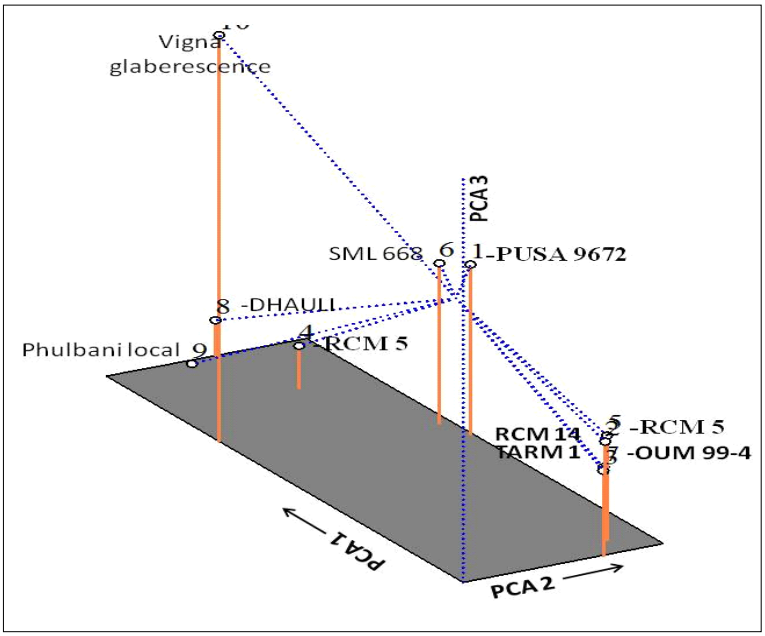


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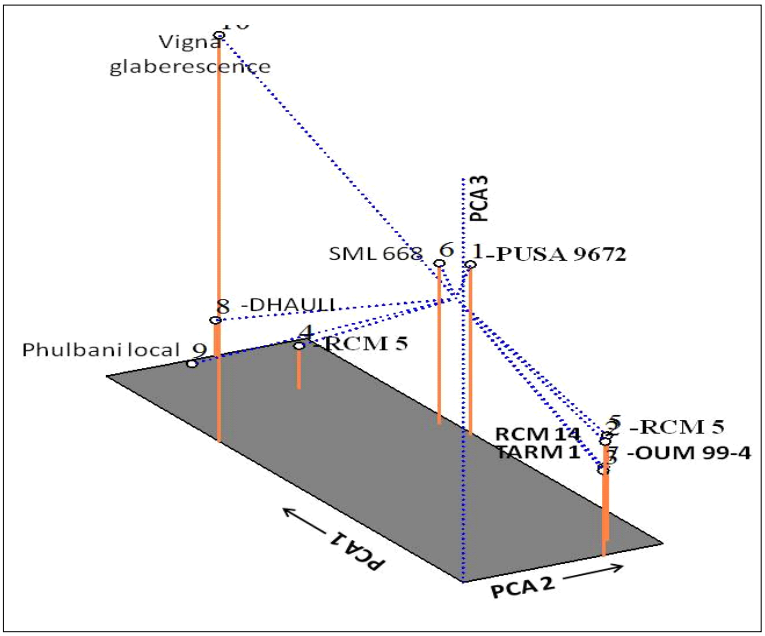


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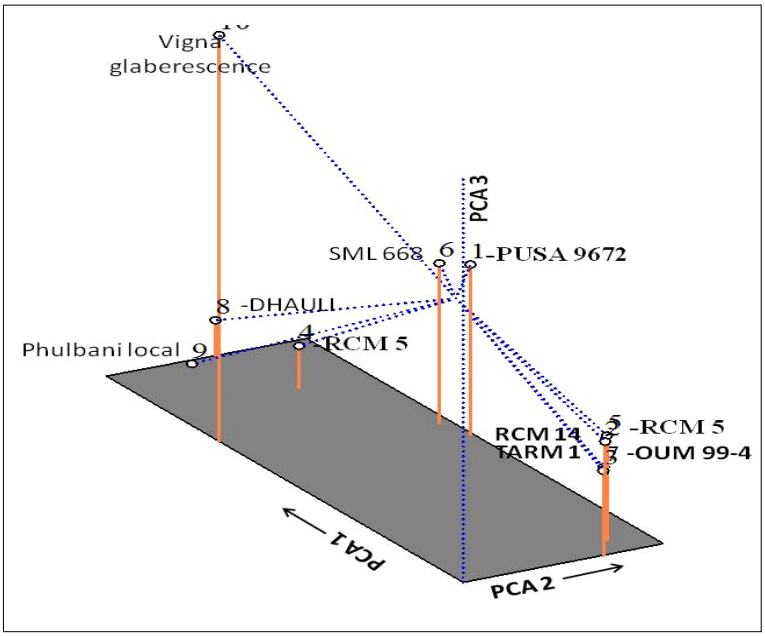


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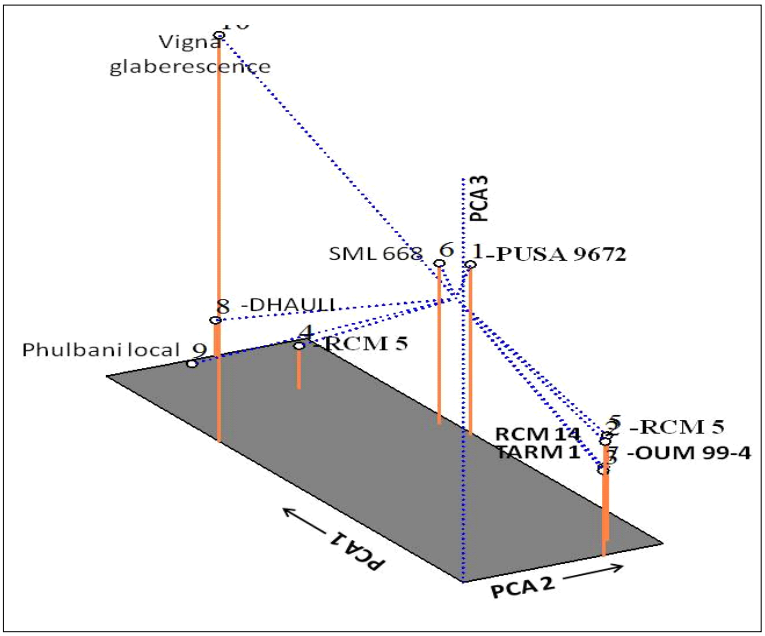


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The grouping of genotypes using UPGMA analysis (Fig 2) was found to be more or less consistent with that of three dimensional scaling based on PCA values (Fig 3). The erstwhile mentioned divergent genotypes (*Vigna glabrescens* with TARM-1, OUM-99-4 and RCM-14) which were initially separated from rest of the test genotypes in the UPGMA clustering were also shown to be sorted out to diverse extreme positions in case of three- dimensional scaling with vectors (Fig 3). This supports the findings of Tripathy *et al.* (2015) in mungbean and Baisakh *et al.* (2021) in urdbean. However, the deficit moisture stress tolerant genotypes *e.g*., SML-668 and PUSA-9672 with inherent high yield potential (> 3.0 g/plant) (Ravada, 2023) formed a distinct cluster (Fig 3). Therefore, the above divergent and high yielding test genotypes may serve as valuable materials for further genetic improvement in mungbean using recombination breeding.

Marker-trait association (MTA) under deficit moisture stress

Deficient moisture stress tolerance is a highly complex trait having involvement of a number of genetic factors. Breeding for the trait in mungbean can be accomplished by using MTA (Elakhdar *et al*., 2016), which enables indirect selection on markers avoiding the phenotypic assessment of traits. But, untill now, little information is available on MTA for abiotic stresses except cold tolerance for 230 germplasm lines in mungbean (Dash, 2021) and frost tolerance for

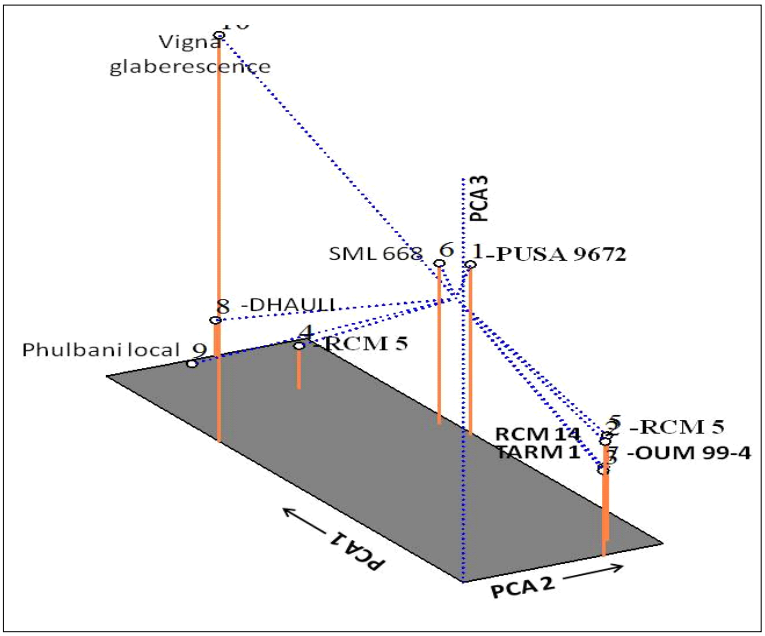


Fig 3: 3D -PCA plot of ten mung bean test genotypes using SSR data.

Table 3: Marker trait association using deficit moisture stress related SSR markers.

Phenotypic trait	Primer	Molecular marker	b-value	P-value	R^2
Deficit moisture stress tolerance score	ICCMO249	ICCMO249_6	2.619**	0.06	0.374
	CodA	CodA_3	6.1**	<0.001	0.873
Germination %	RD 22	RD 22_1	-28.2**	0.017	0.530
	CodA	CodA_3	-46.69**	<0.001	0.812
Root length	GmDREB2_2	GmDREB2_2	-6.169**	0.016	0.537
	CodA	CodA_1	-4.065**	0.015	0.544
	TAA170	TAA170_1	-3.537**	0.028	0.471
No. of clusters/pl	ICCM0249	ICCM0249_5	11.002**	<0.001	0.890
	CodA	CodA_4	-5.717**	0.013	0.561
No. of seeds/pod	CodA	CodA_1	-1.294**	0.014	0.554
Seed yield/pl	TAA170	TAA170_2	3.321**	0.001	0.757
	RD 22	RD 22_2	3.321**	0.001	0.757
	CodA	CodA_4	-1.65**	0.038	0.437

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Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

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Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

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Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

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Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

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Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

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Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

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Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

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Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

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Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

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Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

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Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

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Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., van Toai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E. (1999). An integrated genetic linkage map of the soybean genome. *Crop Sci*. **39:** 1464-1490. doi: 10.2135/cropsci1999.3951464x.

Chen, H., Qiao, L., Wang, L., Wang, S., Blair, M.W. and Cheng, X. (2015). Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR marker. *Gene*. **566(2):** 175-183.

Dahiya P.K., Linnemann A.R., Van Boekel, M.A.J.S. and Khetarpaul, N. (2015). Mung bean: Technological and nutritional potential. *Critical Reviews in Food Science and Nutrition*. **55(5):** 670-688. doi.org/10.1080/10408398.2012.671202.

Dar, M.I., Naikoo, M.I., Rehman, F., Naushin, F. and Khan, F.A. (2016). Proline Accumulation in Plants: Roles in Stress Tolerance and Plant Development. In: Osmolytes and Plants Acclimation to Changing Environment: Emerging Omics Technologies. [N. Iqbal *et al.* (eds.)]. pp.155-166. doi: 10.1007/978-81-322-2616-1_9.

Dash, L., Rath, L.K. and Tripathy, S.K. (2022). Molecular signatures of elite brinjal varieties towards grouping and marker-trait association for shoot and fruit borer resistance. *J. Environ Biol*. **44:** 91-98.

Dash, S. (2021). Characterization and genetic analysis of mungbean [*Vigna radiata* (L.) Wilczek] under cold stress. Ph.D. Thesis submitted to Odisha Univ.of Agril. and Tech. (OUAT), Bhubaneswar, Odisha. p-120.

Doyle, J.J. and Doyle, J.L. (1990), Isolation of DNA from plant tissue. *Focus*. **12:** 13.

Dutta, P. and Bera, A.K. (2008). Screening of mungbean genotypes for drought tolerance. *Legume Research*. **31(2):** 145-148.

Elakhdar, A., Abd EL-Sattar, M., Amer, K., Rady, A. and Kumamaru, T. (2016). Population structure and marker-trait association of salt tolerance in barley (*Hordeum vulgare* L.). C.R. *Biologies*. **339:** 454-461.

Galvan, M.Z., Bornet, B., Balatti, P.A.andBranchard, M. (2003). Inter simple sequence repeat (ISSR) marker as a tool for the assessment of both genetic diversity and gene pool origin in common bean (*Phaseolus vulgaris* L.). *Euphytica*. **132:** 297-301.

Ganguly, P.R. and Bhat, K.V. (2012). Study of the pattern of variation for microsatellite markers in black gram, *Vigna mungo* (L.) Hepper germplasm. *Int. J. Biomed. Life Sci*. **3:** 168.

Hu, J. and Quaros, C.F. (1991). Identification of broccoli and cauliflower cultivars with RAPD markers. *Plant Cell Reports*.**10:** 505-511.

Idris, F.M., Urga, K., Admassu, H., Fentie, E.G., Kwon, S.M. and Shin, J.H. (2025). Profiling the nutritional, phytochemical and functional properties of mung bean varieties. *Foods*. **14(4):** 571. https://doi.org/10.3390/foods14040571.

Ihsan, M.Z., Shahzad, N., Kanwal, S., Naeem, M., Khaliq, A., El-Nakhlawy, F.S. and Matloob, A. (2013). Potassium as foliar supplementation mitigates moisture induced stresses in mung bean (*Vigna radiata* L.) as revealed by growth, photosynthesis, gas exchange capacity and Zn analysis of shoot. *Int. J. Agron. and Plant Prod*. **4:** 3828-3835.

Jaccard, P. (1908) Nouvelles recherches Sur la distribution florale. *Bulletin Society Vaud Science National*. **44 (1908):** 223.

Jincya, M., Prasad Rajendra Babu, V., Jeyakumara, P., Senthila, A. and Manivannan, N. (2019). Evaluation of green gram genotypes for drought tolerance by PEG (polyethylene glycol) induced drought stress at seedling stage. *Legume Research*. **44(6):** 684-691. doi: 10.18805/LR-4149.

Lei, L., Wang, L., Wang, S. and Wu, J. (2020). Marker-trait association analysis of seed traits in accessions of common bean (*Phaseolus vulgaris* L.) in China. *Front. Genet*. **11:** 698. doi.org/10.3389/fgene.2020.00698.

Liu, R., Fang, L., Yang, T., Zhang, X., Hu, J., Zhang, H., Han, W., Hua, Z., Hao, J. and Zong, X. (2017). Marker-trait association analysis of frost tolerance of 672 worldwide pea (*Pisum sativum* L.) collections. *Science Reports*. **7:** 5919.

Liu, Y., Cheng, X.Z., Wang, L.X., Wang, S.H., Bai, P. and Wu, C.S. (2013). Genetic diversity research of mungbean germplasm resources by SSR markers in China. *Sci. Agric. Sin.* **46:** 4197-4209.

Lucas, M.R., Huynh, B.L., Vinholes, P.S., Cisse, N., Drabo, I., Ehlers, J.D., Roberts, P.A. and Close, T.J. (2013). Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front. *Plant Sci.* **4:** 95. doi:10.3389/fpls.2013.00095.

Mishra, N., Tripathi, M.K., Tripathi, N., Tiwari, S., Gupta, N. and Sharma, A. (2022). Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. *Innovations in Science and Technology*. **3(4):** 49-61.

Mathivathana, M.K., Jagadeeshselvam, N., Madhumitha, B., Karthikeyan, A., Pandiyan, M., Karthikeyan, G., Vanniarajan, C., Raveendran, M., Senthil, N. and Sudha, M. (2018). Screening and identification of SSR markers for genetic diversity for mungbean [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.* **7(4):** 789-793.

Michel, B.E. and Kaufmann, M.R. (1973). The osmotic potential of polyethylene glycol 6000. *Plant Physiology*. **51:** 914-916.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., Jüngling, R. *et al.* (2010). Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. *Theor. Appl. Genet*. **120(7):** 1415-41. doi: 10.1007/s00122-010-1265-1.

Neves-Borges, A.C., Guimarães-Dias, F., Cruz, F., Mesquita, R.O., Nepomuceno, A.L., Romano, E., Loureiro, M.E., Grossi-de-Sá, M.F. and Alves-Ferreira, M. (2012). Expression pattern of drought stress marker genes in soybean roots under two water deficit systems. *Genetics and Molecular Biology*. **35(1-suppl):** 212-221.

Nugroho, K., Kosmiatin, M., Husni, A., Tasma, I.M. and Lestari, P. (2020). Identification of soybean [*Glycine max* (L.) Merr.] mutants and improved varieties having diverse drought tolerance character using SSR marker. *IOP Conf. Ser. Earth Environ. Sci.* **482:** 012014.

Savitri, E.S. and Fauziah, S.M. (2019). Characterization of drought tolerance of GmDREB2 soybean mutants [*Glycine max* (L.)] by ethyl methane sulfonate induction. AIP Conf. Proc. 020017-1-020017-7.

Offia, O.B.I. and Madubuike, U.B. (2014). The dehulling efficiency and physicochemical properties of pre-conditioned mung bean [*Vigna radiata* (L.) Wilczek] seeds and flour. *Afr. J. Food Sci. and Tech*. **6:** 1-11. doi.org/10.14303/ajfst.2014.104.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

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Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

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Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

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Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.

Panigrahi, J., Mishra, R.R., Sahu, A.R., Rath, S.C., Seth, S. and Mishra, S.P. (2013). Marker-assisted breeding for simple inherited traits conferring stress resistance in crop plants. *The Ecoscan*. **3:** 23-26.

Pratap, A., Gupta, S., Basu, P.S., Tomar, R., Dubey, S., Rathore, M., Prajapati, U.S., Singh, P. and Kumari, G. (2019). Towards development of climate smart mungbean: Challenges and opportunities, In: Climate smart mungbean. ICAR-Indian Institute of Pulses Research, Kalyanpur, Kanpur, India. p.235-264.

Prevost, A.and Wilkinson, M.J. (1999). A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theor. Appl. Genet*. **98:** 107.

Rakshit, S., Winter, P., Benko-Iseppon, A.M., Muchlbauer, F.J. and Kahl, G. (2003). DAF marker tightly linked to a major locus for Aschochyta blight resistance in chickpea (*Cicer arietinum* L.). *Euphytica*. **132:** 23-30.

Ravada, D.B. (2023). Characterization and identification of elite Mungbean [*Vigna radiata* (L.) Wilczek] genotypes under deficient moisture stress. Ph.D. Thesis submitted to the Odisha Univ. of Agriculture and Technology, Bhubaneswar, India.

Rohlf, F.J. (2002). NTSYS-pc. Numerical taxonomy and multi-variance analysis system, version 2.02. Setauket, New York. p.1-202.

Rojas, O. (2020). Agricultural extreme drought assessment at global level using the FAO-Agricultural Stress Index System (ASIS). *Weather and Climate Extremes*. **27:** 100184.

Suman, S., Rani, B., Sharma, V.K., Kumar, H., Shahi, V.K. (2019). SSR marker based profiling and diversity analysis of mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Legume Research*. **42(5):** 585-594. doi: 10.18805/LR-3918.

Saini, M., Singh, S., Hussain, Z. and Yadav, A. (2010). RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek]: I. Assessment of genetic diversity. *Indian J. Biotechnol.* **9:** 137-146.

Tian, X., Li, S., Liu, Y. and Liu, X. (2016). Transcriptomic Profiling Reveals Metabolic and Regulatory Pathways in the Desiccation Tolerance of Mungbean [*Vigna radiata* (L.) R. Wilczek]. *Front. Plant Sci*. **7:** 1-12. doi.org/10.3389/fpls.2016.01921.

Tripathy, S.K., Sardar, S.S., Pal, S., Mohapatra, B.P., Das, A.B. and Rout, G.R. (2015). RAPD markers for genetic characterization in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **38(3):** 279-288. doi: 10.5958/0976-0571.2015.00023.5.

Winter, P., Benko-Iseppon, A.M., Hüttel, B., Ratnaparkhe, M., Tullu, A., Sonnante, G., Pfaf, T. *et al.* (2000). A linkage map of chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum* × *C. reticulatum* cross: localization of resistance genes for *Fusarium* wilt races 4 and 5. *Theor. Appl. Genet*. **101:** 1155-1163. doi: 10.1007/s001220051592.

Winter, P., Pfaff, T., Udupa, S.M., Sharma, P.C., Sahi, S., Arreguin-Espinoza, R., Weigand, F., Muehlbauer, F.J. and Kahl, G. (1999). Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*C. arietinum* L.) genome. *Mol. Gen. Genet*. **262:** 90-101. doi.org/10.1007/s004380051063.

Younis, A., Ramzan, F., Ramzan, Y., Zulfiqar, F., Ahsan, M. and Lim, K.B. (2020). Molecular markers improve abiotic stress tolerance in crops: A review. *Plants*. **9:** 1374. doi: 10. 339 0/plants9101374.