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Selection Criteria for Identification of Turkey Berry (*Solanum torvum*) Genotypes for Variability, Heritability and Genetic Advance

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ABSTRACT

Background: Breeders can determine the likelihood of passing on advantageous traits to the following generation by using heritability, which calculates the portion of phenotypic variation that can be attributed to genetic factors.

Methods: The present study was conducted at College Orchard on clay loam soil in the years 2022-2023 at the Department of Vegetable Science, Horticultural College and Research Institute, TNAU, Coimbatore. The experimental orchard site at HC and RI is located in the tropical plain topography at 11 degrees north latitude, 77 degrees east longitude and 411 metres above mean sea level (MSL). There are 20 genotypes of turkey berry for variability, heritability and genetic advance study. These genotypes are collected from different areas of Tamil Nadu and other Indian states. One season measurements have been taken of the following traits: plant height, internodal length, number of branches per plant, stem girth, number of stem prickles, number of leaves, leaf area cm^2, number of leaf prickles per plant, days of first flowering, number of flowers/clusters, number of flowers per plant, number of fruits/clusters, the number of fruit clusters per plant, fruit diameter, the individual fruit weight and the fresh fruit yield (gm/plant). As part of the current study, five randomly chosen plants from each genotype in each replication were tagged to record the observations.

Result: The results from this study revealed that higher values of PCV, GCV, heritability and GAM are indicative of a greater influence of environmental factors, according to variability studies. These data demonstrated that there was a high level of variability for these traits in the germplasm and that selection for these traits might be successful. These data were combined with high estimates of genetic advance for traits like the number of leaf prickles per plant, number of flowers per cluster, fruit diameter, number of fruits per cluster, leaf area, stem girth, number of stem prickles per plant and internodal length. The promising accessions discovered in this study could be applied to projects aimed at improving crops, such as pre-breeding for turkey berries.

Key words: Genetic advance, Heritability, Turkey berry, Variability.

INTRODUCTION

Turkey berry (*Solanum torvum* Sw.), also known as prickly nightshade or wild eggplant, is a small, perennial fruit-bearing plant belonging to the Solanaceae family. Native to South Asia, this species is widely distributed in tropical and subtropical regions across the globe, including Africa, the Caribbean and Southeast Asia. Turkey berry is known for its various culinary and medicinal uses and its potential as a valuable crop has been recognized in recent years. Understanding the genetic characteristics of any crop is crucial for its improvement and successful cultivation. Variability, heritability and genetic advance are key parameters that play a pivotal role in plant breeding programs. These factors provide valuable insights into the extent of genetic variation present within a population, the level of inheritance of important traits and the potential progress that can be achieved through selective breeding.

Variability refers to the differences observed among individuals within a population for specific traits. In turkey berry, variability analysis can help identify plants with desirable characteristics, such as high fruit yield, disease resistance and nutritional content. Heritability estimates the proportion of phenotypic variation attributed to genetic

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factors, which aids breeders in determining the likelihood of passing on favourable traits to the next generation. The degree of genetic diversity in the population, which is greatly derived from germplasm, determines how easily any crop can be genetically improved (Gavade and Ghadage, 2015). The concept of heritability primarily pertains to the extent to which a genotype can be effectively selected based on its phenotypic expression. However, it does not provide insights into the expected genetic advancement that can be achieved within a single cycle of selection. When heritability and genetic progress are studied together, heritable variation can be used more accurately and effectively (Johnson *et al*., 1955). The term "genetic advance" refers to an increase in the mean genotypic values of chosen families over the base population. This aids the breeder in choosing the progeny from the previous generation. To achieve sustainable crop improvement and maximize the potential of turkey berry as a valuable agricultural commodity, it is essential to understand the genetic basis of its traits and the magnitude of variability and heritability. This knowledge will enable breeders to make informed decisions and develop superior cultivars with improved yield, nutritional content and resistance to biotic and abiotic stresses. In this study, we explore the variability, heritability and genetic advance of essential traits in turkey berry using a diverse collection of germplasm. By analysing this data, we aim to contribute valuable information for the enhancement of turkey berry breeding programs, ultimately facilitating the development of improved cultivars that meet the demands of modern agriculture and benefit farmers and consumers alike.

MATERIALS AND METHODS

The field study was conducted in the College Orchard on clay loam soil in the years 2022-2023 at the Department of Vegetable Science, Horticultural College and Research Institute, TNAU, Coimbatore. The experimental orchard site at HC and RI is located in the tropical plain topography at 11 degrees north latitude, 77 degrees east longitude and 411 metres above mean sea level (MSL) (Fig 1). A yearly rainfall total of 830 mm was noted. The experiment's randomised block design called for three replications. Plants and rows of the turkey berry genotype were spaced apart by 2 metres and 2 metres, respectively, in a 30-centimeter square of soil. Each genotype produced 10 plants that were multiplied by three in the vicinity of 60 cents. In this study, samples from various locations in Tamil Nadu and other Indian states were used to conduct analyses on twenty genotypes. A list of the genotypes and their sources can be found in Table 1. All suggested packages of practises were used to grow a good crop. Information about the first flowering days was compiled based on genotype. The following characteristics have been measured from season to season: plant height (PH),

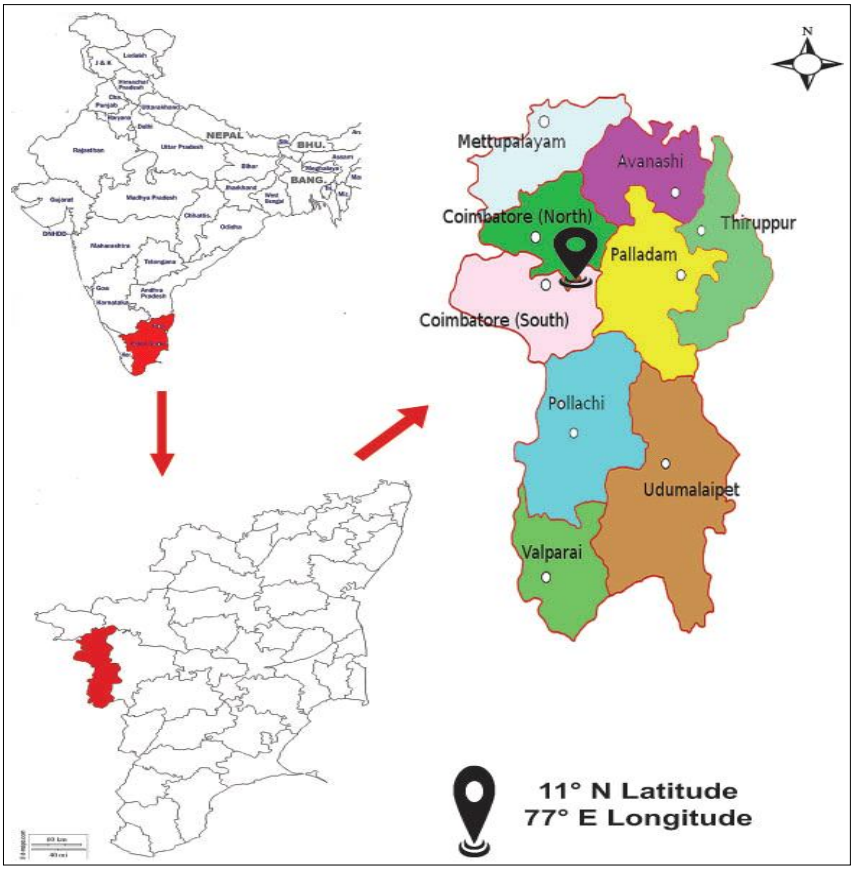

Fig 1: Map of the research area in schematic form.

internodal length (INL), number of branches per plant (NBP), stem girth (SG), number of stem prickles (NSP), number of leaves (NL), leaf area cm^2 (LA), number of leaf prickles per plant (NLP), days of first flowering (DFF), number of flowers/cluster (NFLC), number of flower clusters per plant (NFLCP), number of fruits/cluster (NFRC), the number of fruit clusters per plant (NFRCP), fruit diameter (FD), the individual fruit weight (IFW) and the fresh fruit yield (gm/plant) (FFYP). Five randomly particular plants from each genotype in each replication were tagged as part of the current study in order to record the observations.

Table 1: List of Turkey berry (*Solanum torvum*) genotypes used in the present study.

Genotypes	Source
St001	Himachal Pradesh
St002	Tirupur, Tamil Nadu
St003	Madurai, Tamil Nadu
St004	Trivandrum, Kerala
St005	TNAU, Coimbatore, Tamil Nadu
St006	OUAT, Bhubaneswar, Odisha
St007	Theni, Tamil Nadu
St008	Haveri, Karnataka
St009	Thiruvarur, Tamil Nadu
St010	Dindigul, Tamil Nadu
St011	Ram Nagar, Tamil Nadu
St012	Kolkata, West Bengal
St013	Guntur, Andhra Pradesh
St014	Ranchi, Jharkhand
St015	Nabarangpur, Odisha
St016	Patna, Bihar
St017	Kannur, Kerala
St018	Tirunelveli, Tamil Nadu
St019	IIHR, Bangalore, Karnataka
St020	Kanyakumari, Tamil Nadu

In order to determine the significance of genotypic effects, the data were analysed using (Cochran and Cox 1957) methods using the mean values of arbitrary plants from all genotypes in individual replication. Using (Burton, 1952) formulas, the coefficients of variation for genotypes and phenotypes were calculated. The genetic advance was estimated using the (Johnson *et al.,* 1955) method and wide-ranging sense heritability was calculated in accordance with Lush (1940). Genetic advance (GA), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorised in accordance with (Sivasubramanyam and Menon, 1973) and (Johnson *et al.,* 1995) from classified heritability.

RESULTS AND DISCUSSION

The mean sum of squares for sixteen different characters in the genotypes of turkey berry are displayed in Table 2. For all sixteen characters, the analysis of variance revealed incredibly significant variations among genotypes. In Table 3, the findings for the sixteen characters' mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in the broadest sense (h^2) and probable genetic advance as a percentage of mean (GAM) are presented.

The term "variability" describes the existence of differences among members of a population. Variability is crucial for broad adaptability and resistance to biotic and abiotic factors; as a result, a plant breeder's understanding of the level of genetic variability present in a population is crucial for launching an intelligent breeding programme. The magnitude of variation resulting from different phenotypic and genotypic values is measured by the phenotypic and genotypic variances. Since the mean values and units of measurement of the characters may vary, it is impossible to compare the magnitude of variability for different characters using the absolute values of phenotypic and genotypic

Table 2: Mean squares of the sixteen characters studied in Turkey berry.

Characters	Genotype (df =19)	Replication (df =2)	Error (df =38)	S.E.	C.V. (%)	C.D. 5%
Plant height (cm)	2117.302**	0.099	316.83	10.27	11.881	29.41
Inter nodal length (cm)	29.064**	0.692	1.921	0.80	10.025	02.29
Number of branches/plants	6.938**	0.49	1.116	0.61	11.899	1.74
Stem girth (cm)	10.216**	0.072	0.473	0.39	8.627	1.13
Number of stem prickles	1275.524**	0.472	64.363	4.63	10.378	13.25
Number of leaves	123.584**	0.103	117.108	6.24	10.128	17.88
Leaf area (cm^2)	18280.036**	0.083	442.851	12.15	8.72	34.77
Number of leaf prickles/plant	6055.396**	0.54	47.794	3.99	10.663	11.42
Days of 1st flowering	682.729**	0.009	124.823	6.45	9.162	18.46
Number of flowers/clusters	273.474**	0.027	4.571	1.23	9.33	3.53
Number of flower cluster/plant	65.053**	0.094	7.833	1.61	10.096	4.62
Number of fruits/clusters	145.604**	0.031	2.79	0.96	10.469	2.76
Number of fruit cluster/plant	49.392**	0.826	13.417	2.11	12.709	6.05
Fruit diameter (cm)	0.224**	0.094	0.004	0.03	6.598	0.09
Individual fruit weight (g)	0.013**	0.046	0.004	0.03	5.115	0.10
Fresh fruit yield (g/plant)	138444.837**	0.124	7676.253	50.55	14.65	144.76

variances. As a result, the phenotypic and genotypic levels of the coefficients of variation were applied.

Indicating the presence of high variability in the genotypes for selection, a relatively high estimate of genotypic coefficient of variation and phenotypic coefficient of variation (GCV of more than 20%) occurred for inter nodal length (21.75%), stem girth (22.60%), number of stem prickles (25.99%), leaf area (cm^2) (31.95%), number of leaf prickles/plant (69.02%), number of flowers/cluster (41.31%), number of fruits/cluster (43.24%), fruit diameter (28.31%) and fresh fruit yield (g/plant) (34.91%). The choice of these characters for improvement could be interpreted as being successful. The results are in consonance with (Lokesh *et al*., 2013; Kumar *et al*., 2011; Gavade and Ghadage, 2015; Ramesh Kumar and Arumugam, 2013; Arunkumar *et al*., 2013 and Kumar *et al*., 2012).

For the number of leaves (10.22%), days until first flowering (14.45%), number of flower clusters per plant (18.71%) and number of flower clusters per plant (17.49%), moderate phenotypic coefficients of variation (10-19%) were noted. Plant height (16.35%), the number of branches per plant (15.68%), number of leaves (1.37%), days of first flowering (11.18%) the number of flower clusters per plant (15.75%) and the number of fruit clusters per plant (12.01%) all showed a moderate coefficient of genotypic variation. These characters have the potential to be selected to develop in the desired way. The results of (Ramesh Kumar and Arumugam, 2013; Lokesh *et al.,* 2013 and Gavade and Ghadage, 2015) are in agreement with this. Kumar *et al.* (2012) also reported similar findings. Low estimates of phenotypic coefficient of variation were detected in individual fruit weight (6.43%) and individual fruit weight (3.90%) detected low in genotypic coefficient of variation. Similar results were reported by (Gavade and Ghadage, 2015 and Kumar *et al*., 2012).

In general, the PCV values were higher than the GCV values, indicating that the apparent variation is caused by environmental influences in addition to genotypes. The traits under study were less influenced by the environment, however, as evidenced by the small differences between PCV and GCV values; therefore, selection for the improvement of such characters will be beneficial.

Although the studied characters were least affected by environmental factors, their heritability in a broad sense was high (>60%), indicating that the selection of such characters for improvement may be successful. The outcomes support the conclusions made by (Lokesh *et al*., 2013). However, as explained by (Johnson *et al*., 1955), heritability combined with genetic advancement as a percentage of mean was more useful than heritability alone in predicting the resultant effect for choosing the best individual.

High variation for selecting the best genotypes for these features was suggested by strong GCV and PCV levels. The expression of the remaining characters was influenced by genetic effects and due to small differences between PCV and GCV, which suggested that they were relatively resistant

Table 3: Estimates of genetic progress, heritability and variability expressed as a percentage of the mean for sixteen characters.

Characters	Maximum value	Minimum value	Mean	Genotypic. variance	Phenotypic. variance	Env. variance	PCV (%)	GCV (%)	h^2	Genetic adv (%) (i=5%)	GA as per cent of mean
Plant height (cm)	149.83	98.47	149.81	600.158	916.989	316.831	20.21	16.35	65.4	27.251	18.19037
Inter nodal length (cm)	19.35	7.84	13.82	9.047	10.968	1.921	23.95	21.75	82.5	40.705	294.5369
Number of branches/plants	11.92	6.11	8.87	1.94	3.056	1.116	19.69	15.68	63.5	25.75	290.3044
Stem girth (cm)	10.60	4.35	7.97	3.247	3.72	0.473	24.19	22.60	87.3	43.5	545.7967
Number of stem prickles	97.03	60.87	77.30	403.723	468.083	64.36	27.98	25.99	86.3	49.726	64.32859
Number of leaves	118.17	97.01	106.85	2.162	119.266	117.104	10.22	1.37	18.3	0.382	0.357511
Leaf area (cm^2)	344.78	87.84	241.32	5945.744	6388.584	442.84	33.12	31.95	93.1	63.498	26.31278
Number of leaf prickles/plant	112.19	0	64.83	2002.532	2050.326	47.794	69.83	69.02	97.7	140.514	216.7422
Days of 1st flowering	150.46	96.21	121.94	185.975	310.788	124.813	14.45	11.18	59.8	17.821	14.61456
Number of flowers/clusters	37.69	7.47	22.91	89.634	94.205	4.571	42.35	41.31	95.1	83.021	362.3789
Number of flower cluster/plant	33.63	18.35	27.72	19.075	26.909	7.834	18.71	15.75	70.9	27.323	98.56782
Number of fruits/clusters	24.46	5.05	15.95	47.605	50.395	2.79	44.49	43.24	94.5	86.581	542.8276
Number of fruit cluster/plant	34.96	20.94	28.83	11.993	25.41	13.417	17.49	12.01	47.2	17.006	58.98717
Fruit diameter (cm)	1.46	0.47	0.95	0.074	0.078	0.004	29.07	28.31	94.8	56.811	5980.105
Individual fruit weight (g)	1.33	1.14	1.23	0.002	0.006	0.004	6.43	3.90	36.8	4.884	397.0732
Fresh fruit yield (g/plant)	1115.14	226.30	598.66	43589.672	51265.791	7676.119	37.85	34.9	85	66.312	11.07674

to environmental variation, selection could be successfully conducted based on phenotypic performance.

Heritability in conjunction with genetic progress aids in illustrating the genetic advancement brought on by phenotypic selection. The estimated level of heritability in a broad sense varied for all attributes, ranging from 18.3% for the number of leaves to 97.70% for the number of leaf prickles/plant. Due to the high broad sense heritability values, which show that the phenotypes accurately reflected their genotypes, decisions based on quantitative performance could be trusted.

A high degree of heritability coupled with high genetic advance occurred (Table 3) was noted in the current study for traits such number of leaf prickles/plant (97.70%), number of flowers/cluster (95.1%), fruit diameter (94.8%), number of fruits/cluster (94.5%), leaf area (93.1%), stem girth (87.3%), number of stem prickles/plant (86.3%) and inter nodal length (82.5%). These traits are controlled by additive genes and selection will be advantageous for enhancing them. These results agree with the findings of (Lokesh *et al.,* 2013; Kumar *et al*., 2012; Shekar *et al*., 2012; Arunkumar *et al*., 2013; Ramesh Kumar and Arumugam 2013 and Gavade and Ghadage, 2015). Characteristics with high heritability and GAM show that additive gene action predominates and they can be enhanced through breeding using the selection method. Low genetic advance and heritability indicate a trait's strong reliance on environmental influences and selection efforts based on such traits may fail. According to Burton (1952), GCV, high heritability and genetic advance would give the clearest picture possible regarding the degree of advancement anticipated from selection. The genetic architecture of fruit yield is built upon the balance, or overall net effect, that is produced by the interaction of yield components.

CONCLUSION

Higher values of PCV, GCV, heritability and GAM indicate a lesser influence of environmental factors, according to variability studies, which have demonstrated this. Together with high estimates of genetic advance for traits like the number of leaf prickles per plant, number of flowers per cluster, fruit diameter, number of fruits per cluster, leaf area, stem girth, number of stem prickles per plant and internodal length, these data showed that there was a high level of variability for these traits in the germplasm and that selection for these traits might be successful. The promising accessions discovered in this study could be applied to projects aimed at improving crops, such as pre-breeding for turkey berries.

Conflict of interest

All authors declared that there is no conflict of interest.

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