RESEARCH ARTICLE Agricultural Reviews, Volume 46 Issue 5: 815-822 (October 2025)

Population Structure of *Oryza alta* Swallen as a Potential Wild Rice Variety for Cultivated Rice Improvement

Fimanekeni Ndaitavela Shivute[1,2], Xiang-Dong Liu[2], Mohammed Abdullah Abdulraheem Ghaleb[3] **10.18805/ag.RF-274**

ABSTRACT

Background: *O. alta* is an important wild rice harboring many elite genes. However, the wild rice belongs to the allotetraploid (CCDD) and has a complex genetic background. It is difficult to utilize its genetic resource in rice breeding. Therefore, it is necessary to systematically observe the segregation (population structure) of the offspring of its inbred population, to provide a better basis for further gene editing and selection.

Methods: Total of 371 plants from self-bred offspring of *O. alta* which were planted in the experimental field of South China Agricultural University were employed in which the main agronomic traits, of *O. alta* were investigated. Population structure of self-crossed ten generations of *O. alta* was conducted by investigating about ten agronomic traits of this wild rice.

Result: My investigation found significant differences in most of the main agronomic traits that include reduction in plant height, confirming the consistence of *O. alta* new line compared to the conventional breed. Furthermore, the experiment observed strong panicles, thicker and wider leaves in new lines as compared to typical wild and cultivated rice, approving that populating the structure of *O. alta* will surely allow the study of genomic DNA variations and pave way to DNA analysis of wild rice line using re-sequencing.

Key words: Breeding, *Oryza alta* swallen, Population, Structure.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important food crops in the world. About half of the world's population uses rice as a staple food especially developing countries (Zhang *et al.,* 2020). Rice accounts for about 40% of the total grain output in China (Zhang *et al.,* 2018; Chaudhar *et al.,* 2018). It's important for human health as it contains bioactive compounds, including minerals and vitamins (Fukagawa and Ziska, 2019) and provide about 20% of the world's dietary energy needs (Cordero-Lara, 2020), while providing 76% of the calorific intake of the population of Southeast Asia (Bita and Gerats, 2013). Rice farmers feed and have fed more people than any other important cereal crop like wheat, barley and maize (Mohapatra and Sahu, 2021). Therefore, domestication of rice became one of the most crucial developments analogous to human civilization culture and food habit. With the continuous growth of the world's population and the continuous development of the economy (Zheng *et al.,* 2019), the requirements for the quality of human life have risen sharply (Malik, 2018) the relative arable land area has decreased (Fei *et al.,* 2021; Xie *et al.,* 2018; Li *et al.,* 2017) and the ecological environment has deteriorated (Jiang *et al.,* 2021; Zhou *et al.,* 2021) making the food scarcity prominent and attracted courtesy from all walks of life (Guo *et al.,* 2022). Furthermore, the acceleration of urbanization has caused imbalance between people and land in urban area (Zhai *et al.,* 2021; Peng *et al.,* 2023) hence demand for land increased with pressure on land resources, which led to declining crop production. Competition for land and how to use limited land resources to meet people's needs for food has become a challenge for agricultural scientific research. The increasing world population needs higher rice productivity (Yu *et al.,* 2018).

Crop improvements helps us to meet the challenge of feeding a population by breeding better varieties as faster as we can. Identification of traits contributing towards genetic diversity in each population can help in formulating effective selection criteria (Thakur and Sarma, 2023). Technologies such as genotyping, marker-assisted selection, high-throughput phenotyping, genome editing, genomic selection and de novo domestication could be galvanized by using speed breeding to enable plant breeders to keep pace with a changing environment and ever-increasing human population (Hickey *et al.,* 2019).

[1]Zero Emission Research Initiative (ZERI), Multi-disciplinary Research Services, University of Namibia, Namibia.
[2]College of Agriculture, South China Agricultural University, China.
[3]Department of Crop Science and Genetic Improvement, Faculty of Agriculture, Food and Environment, Sana's University, Sanaa, Yemen.

Corresponding Author: Fimanekeni Ndaitavela Shivute, Zero Emission Research Initiative (ZERI), Multi-disciplinary Research Services, University of Namibia, Namibia.
Email: fshivute@unam.na

How to cite this article: Shivute, F.N., Xiang-Dong Liu. and Ghaleb, M.A.A. (2025). Population Structure of *Oryza alta* Swallen as a Potential Wild Rice Variety for Cultivated Rice Improvement. *Agricultural Reviews*. **46(5):** 815-822. doi: 10.18805/ag.RF-274.

Submitted: 09-06-2023 **Accepted:** 12-04-2024 **Online:** 10-01-2025

The development of molecular markers combined with high throughput technologies have paved the way for achieving the desirable traits as well as induced biotic and abiotic stress tolerance in plant, which enhanced the crop breeding (Nair and Pandey, 2024). To address widespread malnutrition influencing global health, novel high-yielding rice cultivars with better nutritional quality need to be bred (Rana *et al.,* 2020). Rice is a salt-susceptible crop and, so improving the salt tolerance of rice would increase the potential of saline-alkali land and ensure food security (Qin *et al.,* 2020). Therefore, research on how to improve rice yield, quality, tolerance and resistance has become an important task for rice breeders (Peng *et al.,* 2009; Shabir *et al.,* 2017; Kumar *et al.,* 2020; Khan *et al.,* 2021) aiming to increase food production, alleviate poverty and for economic emancipation.

Cultivated rice (*Oryza sativa* L.) has very low genetic diversity (Qi *et al.,* 2006, Zhou *et al.,* 2022, Hour *et al.,* 2020). So far, a few wild rice landraces have been identified as a source gene transfer and utilized in rice improvement (Zhang *et al.,* 2019). The resistance of wild rice species and its gene assortment are due to the complex geographic environment and various ecological factors of wild rice; in which varieties of excellent characteristics have been formed (Nautiyal *et al.,* 2021; Shamim *et al.,* 2022). The history of using the beneficial genes of wild rice for breeding is long overdue. In 1930s, Ding Ying used Guangdong common wild rice as parents to bred “Zhongshan No. 1”, a production species with strong cold tolerance and stress resistance (Ding *et al.,* 2021; Liu *et al.,* 1998). In the 1970s, China used various ecological types of common wild rice to hybridize with cultivated rice (Guo *et al.,* 2016). At present, more than 95% of the sterile lines used in the hybrid combination in rice production are of wild type or wild type cytoplasm (Liao 2021; Xu *et al.,* 2022) with more than 20 excellent traits been identified in wild rice, mainly for disease and insect resistance, stress resistance, excellent rice quality and cytoplasmic male sterility (Sangeetha *et al.,* 2020; Huang and Liu, 2022; Long *et al.,* 2023). At the same time, wild rice is used in breeding system for strong growth advantages such as strong tillering ability (Singh *et al.,* 2022), fast growth (Varshney *et al.,* 2021), root system development (Bheemanahalli *et al.,* 2019, Panda *et al.,* 2021), strong regeneration ability (Yu *et al.,* 2021; Zhang *et al.,* 2023), functional leaf senescence resistance (Shi *et al.,* 2023), large anthers (Cao *et al.,* 2022), exposed stigma (Zheng *et al.,* 2020), long flowering time (Zsögön *et al.,* 2022) and wide compatibility (Zheng *et al.,* 2020; Peng *et al.,* 2021).

The realm of genetic diversity within rice is immense and undermining it provides the opportunity to utilize them in rice improvement programs (Jegadeeswaran *et al.,* 2024). Understanding genetic diversity of the wild species would help implementing the conservation practices measures (Gouda *et al.,* 2020; Wambugu and Henry, 2022). Zhang *et al.* (2021) further concluded that studying the population structure of wild rice will shed light to its effective conservation and utilization. Wild rice is an important part of rice germplasm resources (Liu *et al.,* 2021). Therefore, its domestication will give rise to desirable agronomic traits (He *et al.,* 2021). It has excellent characters that are not available in cultivated rice (Civan *et al.,* 2018; Gupta *et al.,* 2021). Due to its wide distribution and the complexity of the ecological environment, wild species formed strong genetic diversity during the long evolutionary process (Lakew *et al.,* 2021; Li *et al.,* 2023) hence at present, disease resistance, insect resistance, cold tolerance, heat tolerance and others have been discovered from wild rice. The natural community of wild rice has been lost in large quantities due to human inhibition (Lv *et al.,* 2018; Wang *et al.,* 2021; Yao *et al.,* 2022) and thus loss of wild rice germplasm resources worldwide is thoughtful. Protection of wild rice is of predominantly important and studies on wild rice are necessary to intensify yield, conserve and protect wild rice species. Therefore, the structure of *O.alta* must be populated to understand the main agronomic traits of this wild rice and enable the utilization and conservation of wild relatives elite genes.

The purpose of this study is to systematically observe the segregation (population structure) of *O. alta* offspring and its inbred lines to provide improved base for advanced gene editing and selection using of *O. alta* wild rice. The study is highly significant as it is only if the rice structure is populated and studied that genomic DNA variations of the wild rice line will be analyzed using re-sequencing.

MATERIALS AND METHODS

Materials

Total of 371 plants from self-bred offspring of *O. alta* which were planted in the experimental field of South China Agricultural University were used in the experiment.

Character investigation and statistical methods

The methods and standards of character investigation refer to the DUS testing guidelines for new plant varieties in the People’s Republic of China was used as a testing. The investigated traits included: (1) Plant height; (2) Panicle length; (3) Panicle number; (4) Grain length and width, the ratio of grain length to width is obtained; (5) Filled and empty panicle; (6) Seed setting rate; (7) Total grains; (8) Flag leaf length and width and so on. The obtained data were statistically analyzed by SPSS version 17.0 software and Microsoft Excel 2003.

RESULTS AND DISCUSSION

Analysis of main agronomic traits in self-crossing generation of *O. alta*

Significant differences between *O. alta* and *O. sativa* in plant height, leaf, panicle and other traits (Fig 1 to 5) were observed. As shown in Table 1, the main agronomic characters are different among plants from the self-crossing

generation of *O. alta*. Plant height of *O. alta* ranged from 1.97 m to 3.03 m with an average height of 2.39 m. Among the tested plants, 46% of the plants were taller than 2.0 m in (Fig 1). The panicle number was distributed in the range of 4 to 21 and more than 74% of total plants obtained 6 to 15 panicles. The panicle length ranged between 34.5 cm to 113 cm with more than 89% ranging at 50-110 cm. The length of flag leaf of *O. alta* ranged from 31 cm to 58.7 cm and more than 82% were between 35-555 cm. The width of flag leaf ranged from 3.6 cm to 6.25 cm with more than 86% ranging between 3.6 cm to 5.5 cm. The flag leaf length/width (ratio) of *O. alta* ranged from 5.38 to 12.35 cm and more than 72% plants were between 7.5 to 10.5 cm.



Fig 1: Plants of *O. alta* before flowering.



Fig 2: Plants of *O. alta* during flowering.



Fig 3: Plants of *O. alta* during flowering (Collecting seeds).

As presented in Table 1, the number of filled grains of *O. alta* ranged from 4 to 2017.5, while empty grains ranged from 235 to 1700. The total grains of *O. alta* ranged from 299.5 to 2497.5, with majority at the range of 500 to 1800 grains. The seed setting rate ranged from 6 to 76%, with average 18.5% (Fig 5). More than 87% had their seed setting less than 20%. The grain length of *O. alta* ranged from 6.22 mm to 8.69 mm and more than 86% were at the range of 7.0 mm to 8.0 mm. The grain length/width (ratio) of *O. alta* were distributed in the range of 2.55 to 3.91 mm and more than 91% ranged 2.75 to 3.5 mm. The pollen fertility of the wild rice ranged from 0.25% to 84%, with average 27.51%.



Fig 4: Plants of *O. alta* (providing support).



Fig 5: Seeds of *O. alta*.

Analysis of main agronomic traits of self-crossed 10th generation in *O. alta*

The main agronomic traits were investigated in the plants to the 10th self-bred generation of *O. alta*. The results showed that the panicle characters of *O. alta* separated after continuous self-bred for several generations, however, their characters remained consistent.

As presented in Table 1, panicle length variation ranged were 34.5~57.1 cm. The varying ranges of awn length were 14.7~51.0 mm. The variation ranges of effective panicle number were 2~9. The variation of flag leaf length was 30.0~79.8 cm. The variation of flag leaf width was 3.6~6.1 cm. The variations in filled grain number were ranged from 20 to 1947. The variation of pollen fertility was 0.3%~84.4%, the average pollen fertility is 27.5%. The variation of the seed setting rate range was 21.2%~72.3%, the average

Table 1: The main agronomic traits of *O. alta*.

Traits	Mean ± S.E.	Minimum value	Maximum value
Plant height (m)	2.39±0.01	1.97	3.03
No. of panicle	8.64±0.25	4.00	21.00
Panicle length (cm)	67.90±0.82	34.50	113.00
Flag leaf length (cm)	41.98±0.27	31.00	58.75
Flag leaf width (cm)	4.61±0.02	3.60	6.25
Flag leaf length/width (ratio)	9.21±0.09	5.38	12.35
Penultimate leaf length (cm)	39.87±0.21	32.30	52.50
Penultimate leaf width (cm)	4.53±0.03	3.25	5.85
Penultimate leaf length/width (ratio)	8.91±0.08	7.08	13.12
Antepenultimate leaf length (cm)	46.57±0.31	34.50	58.00
Antepenultimate leaf width	4.99±0.03	3.85	6.25
Antepenultimate leaf length/width (ratio)	9.42±0.07	7.22	12.15
Filled grains	201.55±13.18	14.00	2017.50
Empty grains	768.75±17.47	235.00	1700.00
Total grains	970.30±24.03	299.50	2497.50
Seed set rate	18.50±0.40	6.00	76.00
Grain width (mm)	2.51±0.01	2.08	2.85
Grain length (mm)	7.75±0.03	6.22	8.69
Grain length/width (ratio)	3.12±0.02	2.55	3.91
Pollen fertility (%)	27.51±21.69	0.25	84.35
Grains weight per panicle (g)	2.97±0.97	1.58	4.51

seed setting rate is 52.9%. The variation of grain weight per panicle range was 1.6~4.5 g, with average 3.0 g.

Correlation analysis of main agronomic characteristics of *O. alta* population

As shown on Table 2, plant height positively correlated with grain quantity, total grains and seed setting rate with correlation coefficients variation of 0.43, 0.40 and 0.47, respectively. At the same time, plant height negatively correlated with grain length and width with coefficient variation of 0.19 and -0.20 respectively.

Consistency analysis of *O. alta* G7

After self-crossing *O. alta* to the 10th generation, a line with outstanding characters was selected from its offspring and named G7.

Consistency analysis of heading date of *O. alta* G7

To further investigate G7 traits thoroughly, four lines were selected from the self-crossing off springs of *O. alta* G7 (G7-1, G7-2, G7-3, G7-4). According to the observations made within four new lines, significant differences were observed in the heading date. G7-1 took 19 days from the beginning of flowering to the end. G7-3 took 11 days, G7-4 took 5 days and G7-2 took 15 days from the beginning of flowering to the end.

Consistency analysis of panicle traits of *O. alta* G7

The effective panicle number variation coefficient of G7-1 is 0.26, G7-3 is 0.26 and the variation coefficient of G7-4 is 0.30 as shown in Table 3. The variation ranges of effective ear number of G7-1, G7-3, G7-4 and G7-2 are: 2-6, 2-6, 2-

Table 2: Correlation analysis of main agronomic characters of *O. alta* population.

Traits	Filled grain	Empty grains	Total grains	Seed setting	Grain length	Grain width
Plant height	0.42**	0.05	0.40**	0.47**	-0.19*	-0.20*
Panicle number	0.02	0.29**	0.30**	-0.06	-0.00	0.05
Panicle length	0.21**	0.06	0.23**	0.20**	-0.12	-0.07
Flag leaf	0.03	-0.11	-0.09	0.07	0.13	0.02
Flag leaf width	0.10	0.11	0.14	0.08	0.26**	0.20*
Flag leaf length/width	-0.05	-0.20*	-0.19*	-0.01	-0.13	-0.18*

Table 3: Variation parameters of effective panicle number of *O. alta* G7.

Strain	Mean	Standard deviation	Minimum	Maximum	Range	Coefficient of variation
G7-1	4.13	1.06	2.00	6.00	4.00	0.26
G7-3	3.56	0.92	2.00	6.00	4.00	0.26
G7-4	4.20	1.27	2.00	8.00	6.00	0.30
G7-2	4.62	1.65	2.00	9.00	7.00	0.36

Table 4: Variation parameters of real grain number of *O. alta* G7.

Strain	Mean	Standard deviation	Minimum	Maximum	Range	Coefficient of variation
G7-1	242.05	310.65	100.00	2047.00	1947.00	1.28
G7-3	178.00	45.56	86.00	281.00	195.00	0.26
G7-4	289.80	107.55	20.00	611.00	591.00	0.37
G7-2	198.62	86.72	30.00	375.00	345.00	0.44

Table 5: Variation parameters of empty grain number of *O. alta* G7.

Strain	Mean	Standard deviation	Minimum	Maximum	Range	Coefficient of variation
G7-1	42.79	21.03	9.00	103.00	94.00	0.49
G7-3	36.44	30.61	9.00	164.00	155.00	0.84
G7-4	67.60	89.91	9.00	390.00	381.00	1.33
G7-2	101.90	68.87	18.00	332.00	314.00	0.68

Table 6: Variation parameters of seed setting rate of *O. alta* G7.

Strain	Mean %	Standard deviation	Minimum%	Maximum%	Range%	Coefficient of variation
G7-1	81.80	8.43	60.81	98.02	37.21	0.10
G7-3	83.42	10.12	53.01	95.54	42.54	0.12
G7-4	83.49	18.65	4.88	96.78	91.91	0.22
G7-2	65.31	22.01	12.77	93.00	80.23	0.34

8 and 2-9 respectively. The results indicated that the number of effective panicles in the offspring of *O. alta* G7 did not differentiate and the number of effective panicles in the plant line was small.

Consistency analysis of filled grain number, empty grain number and seed setting rate of *O. alta* G7

Coefficient of variation of G7-1 filled grain number is 1.28, G7-3 is 0.26, G7-4 is 0.37 and G7-2 is 0.44. G7-1, G7-3, G7-4 and G7-2 ranged from -105 real grains are 100~1947, 86~281, 20~611 and 30~375 (Table 4). The results indicated that the number of seeds in the progeny lines of *O. alta* G7 varied with low consistency and significant difference was observed between the lines.

Table 5 shows that the coefficient of variation of G7-1 empty grain number is 0.49, G7-3 is 0.84, G7-4 is 1.33 and G7-2 is 0.68. G7-1, G7-3, G7-4 and G7-2 filled grains ranged 9~103, 9~164, 9~381 and 18~332, respectively. The number of empty seeds in the G7 progeny line of *O. alta* varied with pitiable consistency and differentiation occurred in the line.

The coefficient of variation of G7-1 seed setting rate is 0.10, G7-3 is 0.12, G7-4 is 0.22 and G7-2 is 0.34. G7-1, G7-3, G7-4 and G7-2 seed setting rate raged from 60.81~98.02%, 53.01~95.54%, 4.88~96.78% and 12.77~93%, respectively (Table 6). Furthermore, seed setting rate in the offspring lines of *O. alta* G7 varied with poor consistency and differentiation occurred between lines with seed setting rates of G7-1 and G7-3 above 50%.

The result indicated reduction in plant height, confirming the consistence of *O. alta* new line compared to conventional breed. Taller plants hardly stand strong on their own especially at maturity when the seeds are set, therefore decrease in plant height of *O. alta* in this experiment is considered a milestone achievement and it will be needless to provide support to plants at maturity. Furthermore, the experiment observed strong panicles, thicker and wider leaves in new lines as compared to typical wild and cultivated rice. Thicker and wider leaves are good for plant photosynthesis. However, the seed set rate observed was very low and discouraging as well high shattering rate experienced. Therefore, further research on this wild rice will be fruitful.

CONCLUSION

The present study was conducted on 371 plants from self-bred offspring of *O. alta*. Population structure of self-crossed ten generations of *O. alta* was conducted and observations were recorded on the main agronomic traits. The results showed significant differences in most of the main agronomic traits such as reduction in plant height, strong panicles, thicker and wider leaves in new lines with low seed setting as well as high seed-shattering ability in the offspring.

ACKNOWLEDGEMENT

I am indeed grateful to my supervisors: Prof. Xiang-dong Liu for his support, encouragement and his highly valuable inputs into this paper. I must express my special thanks to Prof. Qasim, Dr. Wu and my special fellow students Zhang Liushen Zhong Yi plus all other laboratory staffs for providing all necessary support and help throughout this paper's experiments. Thank you!

Conflict of interest

All authors declare that they have no conflict of interest.

REFERENCES

Bheemanahalli, R., Hechanova, S., Kshirod, J.K. and Jagadish, S.V. (2019). Root anatomical traits of wild rice reveal links between flooded rice and dryland sorghum. *Plant Physiology Reports*. **24:** 155-167.

Bita, C.E. and Gerats, T. (2013). Plant tolerance to high temperature in a changing environment: Scientific fundamentals and production of heat stress-tolerant crops. *Frontiers in Plant Science*. **4:** 273.

Cao, Z., Tang, H., Cai, Y., Zeng, B., Zhao, J., Tang, X., Lu, M., Wang, H., Zhu, X., Wu, X. and Yuan L. (2022). Natural variation of HTH5 from wild rice, Oryza rufipogon Griff., is involved in conferring high temperature tolerance at the heading stage. *Plant Biotechnology Journal*. **20(8):** 1591.

Chaudhari, P.R., Tamrakar, N., Singh, L., Tandon, A. and Sharma, D. (2018). Rice nutritional and medicinal properties: A review article. *Journal of Pharmacognosy and Phytochemistry*. **7(2):** 150-156.

Civáň, P. and Brown, T.A. (2018). Role of genetic introgression during the evolution of cultivated rice (*Oryza sativa* L.). *BMC Evolutionary Biology*. **18:** 1-11.

Cordero-Lara, K.I. (2020). Temperate japonica rice (*Oryza sativa* L.) breeding: History, present and future challenges. *Chilean Journal of Agricultural Research*. **80(2):** 303-314.

Ding, C., Chen, C., Su, N., Lyu, W., Yang, J., Hu, Z. and Zhang, M. (2021). Identification and characterization of a natural SNP variant in ALTERNATIVE OXIDASE gene associated with cold stress tolerance in watermelon. *Plant Science*. **304:** 110735.

Fei, R., Lin, Z. and Chunga, J. (2021). How land transfer affects agricultural land use efficiency: Evidence from China's agricultural sector. *Land Use Policy*. **103:** 105300.

Fukagawa, N.K. and Ziska, L.H. (2019). Rice: Importance for global nutrition. *Journal of Nutritional Science and Vitaminology*. **65(Supplement):** S2-S3.

Gouda, A.C., Ndjiondjop, M.N., Djedatin, G.L., Warburton, M.L., Goungoulou, A., Kpeki, S.B., N'Diaye A. and Semagn, K. (2020). Compari-sons of sampling methods for assessing intra-and inter-accession genetic diversity in three rice species using geno-typing by sequencing. *Scientific Reports*. **10(1):** 1-14.

Guo, J., Xu, X., Li, W., Zhu, W., Zhu, H., Liu, Z., Zhang, G. (2016). Overcoming inter-subspecific hybrid sterility in rice by developing indica-compatible japonica lines. Scientific Reports. 6: 1-9.

Guo, J., Yu, Z., Ma, Z., Xu, D. and Cao, S. (2022). What factors have driven urbanization in China? *Environment, Development and Sustainability*. **24(5):** 6508-6526.

Gupta, M.K., Gouda, G., Sabarinathan, S., Donde, R., Dash, G.K., Ponnana, M., Pati, P., Rathore, S.K., Vadde, R. and Behera, L. (2021). Brief Insight into the Evolutionary History and Domesti-cation of Wild Rice Relatives. *Bioinformatics in Rice Research: Theories and Techniques*. pp. 71-88.

He, W., Chen, C., Xiang, K., Wang, J., Zheng, P., Tembrock, L.R., Wu, Z. (2021). The history and diversity of rice domestication as resolved from 1464 complete plastid genomes. *Frontiers in Plant Science*. **12:** 781793.

Hickey, L.T., N. Hafeez, A., Robinson, H., Jackson, S.A., Leal-Bertioli, S.C., Tester, M., Gao, C., Godwin, I.D., Hayes, B.J. and Wulff, B.B. (2019). Breeding crops to feed 10 billion. *Nature Biotechnology*. **37(7):** 744-754.

Hour, A.L., Hsieh, W.H., Chang, S.H., Wu, Y.P., Chin, H.S. and Lin, Y.R. (2020). Genetic diversity of landraces and improved varieties of rice (*Oryza sativa* L.) in Taiwan. *Rice*. **13:** 1-12.

Huang, Z. and Liu, W. (2022). Hybrid Rice Production. In Modern Techniques of Rice Crop Production Singapore: Springer Singapore. pp. 629-645.

Jegadeeswaran, M., Nithya, V.N., Salini, A.P., Vanitha, J., Mahendran, R. and Maheswaran, M. (2024). Assessing genetic diversity and population structure of rice genotypes using ISSR markers. *Agricultural Science Digest*. **44(3):** 453-459. doi: 10.18805/ag.D-5855.

Jiang, L., Liu, Y., Wu, S. and Yang, C. (2021). Analyzing ecological environment change and associated driving factors in China based on NDVI time series data. *Ecological indicators*. **129:** 107933.

Khan, M.I.R., Palakolanu, S.R., Chopra, P., Rajurkar, A.B., Gupta, R., Iqbal, N. and Maheshwari, C. (2021). Improving drought tolerance in rice: Ensuring food security through multi dimensional approaches. *Physiologia Plantarum*. **172(2):** 645-668.

Kumar, A., Sandhu, N., Venkateshwarlu, C., Priyadarshi, R., Yadav, S., Majumder, R.R. and Singh, V.K. (2020). Development of introgression lines in high yielding, semi-dwarf genetic backgrounds to enable improvement of modern rice varieties for tolerance to multiple abiotic stresses free from undesirable linkage drag. *Scientific Reports*. **10(1):** 1-13.

Lakew, T., Tanaka, K. and Ishikawa, R. (2021). Genetic diversity of African wild rice (*Oryza longistaminata* Chev. et Roehr) at the edge of its distribution. *Genetic Resources and Crop Evolution*. **68:** 1769-1784.

Li, X., Liu, T., Li, A., Xiao, Y., Sun, K. and Feng, J. (2023). Diversifying selection and climatic effects on major histocompatibility complex class II gene diversity in the greater horseshoe bat. *Evolutionary Applications*. **16(3):** 688-704.

Li, W., Wang, D., Li, H. and Liu, S. (2017). Urbanization-induced site condition changes of peri-urban cultivated land in the black soil region of northeast China. *Ecological Indicators*. **80:** 215-223.

Liao, C., Yan, W., Chen, Z., Xie, G., Deng, X.W. and Tang, X. (2021). Innovation and development of the third-generation hybrid rice technology. *The Crop Journal*. **9(3):** 693-701.

Liu, Y., Wang, W., Li, Y., Liu, F., Han, W. and Li, J. (2021). Transcriptomic and proteomic responses to brown plant hopper (*Nilaparvata lugens*) in cultivated and Bt-transgenic rice (*Oryza sativa*) and wild rice (*O. rufipogon*). *Journal of Proteomics*. **232:** 104051.

Liu, J.J.J., Krenz, D.C., Galvez, A.F. and de Lumen, B.O. (1998). Galactinol synthase (GS): Increased enzyme activity and levels of mRNA due to cold and desiccation. *Plant Science*. **134(1):** 11-20.

Long, W., Li, N., Jin, J., Wang, J., Dan, D., Fan, F., Gao, Z. and Li, S. (2023). Resequencing-based QTL mapping for yield and resistance traits reveals great potential of *Oryza longis-taminata* in rice breeding. *The Crop Journal*. **11(5):** 1541-1549.

Lv, S., Wu, W., Wang, M., Meyer, R. S., Ndjiondjop, M. N., Tan, L., Zhou, H., Zhang, J., Fu, Y., Cai, H. and Sun, C. and Zhu, Z. (2018). Genetic control of seed shattering during African rice domestication. *Nature Plants*. **4(6):** 331-337.

Malik, R.S. (2018). Educational challenges in 21st century and sustainable development. *Journal of Sustainable Development Education and Research*. **2(1):** 9-20.

Mohapatra, P.K. and Sahu, B.B. (2021). Panicle Architecture of Rice and its Relationship with Grain Filling. Springer Nature.

Nair, R.J. and Pandey, M.K. (2024). Role of molecular markers in crop breeding: A review. *Agricultural Reviews*. **45(1):** 52-59. doi: 10.18805/ag.R-2322.

Nautiyal, A.K., Ahuja, V., Kshirsagar, S. and Dasgupta, D. (2021). Recent advancement in NGS technologies. *Bioinformatics in Rice Research: Theories and Techniques*. pp. 585-609.

Peng, X., Xie, J., Li, W., Xie, H., Cai, Y. and Ding, X. (2021). Comparison of wild rice (*Oryza longistaminata*) tissues identifies rhizome-specific bacterial and archaeal endophytic microbiomes communities and network structures. *Plos One*. **16(2):** e0246687.

Panda, S., Majhi, P.K., Anandan, A., Mahender, A., Veludandi, S., Bastia, D., Guttala, S.B., Singh, S.K., Saha, S. and Ali, J. (2021). Proofing direct-seeded rice with better root plasticity and architecture. *International Journal of Molecular Sciences*. **22(11):** 6058.

Peng, K., He, X. and Xu, C. (2023). Coupling coordination relationship and dynamic response between urbanization and urban resilience: Case of Yangtze River delta. *Sustainability*. **15(3):** 2702.

Peng, S., Tang, Q. and Zou, Y. (2009). Current status and challenges of rice production in China. *Plant Production Science*. **12(1):** 3-8.

Qi, Y., Zhang, D., Zhang, H., Wang, M., Sun, J., Wei, X. and Li, Z. (2006). Genetic diversity of rice cultivars (*Oryza sativa* L.) in China and the temporal trends in recent fifty years. *Chinese Science Bulletin*. **51:** 681-688.

Qin, H., Li, Y. and Huang, R. (2020). Advances and challenges in the breeding of salt-tolerant rice. *International Journal of Molecular Sciences*. **21(21):** 8385.

Rana, N., Rahim, M.S., Kaur, G., Bansal, R., Kumawat, S., Roy, J., Deshmukh, R., Sonah, H. and Sharma, T.R. (2020). Applications and challenges for efficient exploration of omics interventions for the enhancement of nutritional quality in rice (*Oryza sativa* L.). *Critical Reviews in Food Science and Nutrition*. **60(19):** 3304-3320.

Sangeetha, J., Habeeb, J., Thangadurai, D., Alabhai, J.M., Hospet, R., Maxim, S.S., Pandhari, R. and Kushwaha, U.K.S. (2020). Potentiality of wild rice in quality improvement of cultivated rice varieties. *Rice Research for Quality Improvement: Genomics and Genetic Engineering: Breeding Techniques and Abiotic Stress Tolerance*. **1:** 61-85.

Shabir, G., Aslam, K., Khan, A.R., Shahid, M., Manzoor, H., Noreen, S. and Arif, M. (2017). Rice molecular markers and genetic mapping: Current status and prospects. *Journal of Integrative Agriculture*. **16(9):** 1879-1891.

Shamim, M., Sharma, D., Bisht, D., Maurya, R., Kaashyap, M., Srivastava, D., Mishra, A., Kumar, D., Kumar, M., Juturu, V.N. and Singh, K.N. (2022). Proteo-molecular investigation of cultivated rice, wild rice and barley provides clues of defense responses against *Rhizoctonia solani* infection. *Bioengineering*. **9(10):** 589.

Shi, J., An, G., Weber, A.P. and Zhang, D. (2023). Prospects for rice in 2050. *Plant, Cell and Environment*. **46(4):** 1037-1045.

Singh, G., Kaur, N., Khanna, R., Kaur, R., Gudi, S., Kaur, R. and Mangat, G.S. (2022). 2Gs and plant architecture: Breaking grain yield ceiling through breeding approaches for next wave of revolution in rice (*Oryza sativa* L.). *Critical Reviews in Biotechnology*. pp. 1-24.

Thakur, K. and Sarma, M.K. (2023). Genetic diversity and principal component analysis in cultivated rice (*Oryza sativa*) varieties of Assam. *The Indian Journal of Agricultural Sciences*. **93(2**): 145-150.

Varshney, R.K., Bohra, A., Yu, J., Graner, A., Zhang, Q. and Sorrells, M.E. (2021). Designing future crops: Genomics-assisted breeding comes of age. *Trends in Plant Science*. **26(6):** 631-649.

Wambugu, P.W. and Henry, R. (2022). Supporting in situ conservation of the genetic diversity of crop wild relatives using genomic technologies. *Molecular Ecology*. **31(8):** 2207-2222.

Wang, X., Bai, J., Xie, T., Wang, W., Zhang, G., Yin, S. and Wang, D. (2021). Effects of biological nitrification inhibitors on nitrogen use efficiency and greenhouse gas emissions in agricultural soils: A review. *Ecotoxicology and Environmental Safety*. **220:** 112338.

Xie, H., Chen, Q., Wang, W. and He, Y. (2018). Analyzing the green efficiency of arable land use in China. *Technological Forecasting and Social Change*. **133:** 15-28.

Xu, Z., Du, Y., Li, X., Wang, R., Chen, Z., Zhao, X. and Zhang, H. (2022). Identification and fine mapping of a fertility restorer gene for wild abortive cytoplasmic male sterility in the elite indica rice non-restorer line 9311. *The Crop Journal*. **11(3):** 887-894.

Yao, Z., Chen, Y., Luo, S., Wang, J., Zhang, J., Zhang, J., Tian, C. and Tian, L. (2022). Culturable screening of plant growth-promoting and biocontrol bacteria in the Rhizosphere and Phyllosphere of wild Rice. *Microorganisms*. **10(7):** 1468.

Yu, H., Lin, T., Meng, X., Du, H., Zhang, J., Liu, G Chen, M., Jing, Y., Kou, L., Li, X. and Gao, Q. (2021). A route to de novo domestication of wild allotetraploid rice. *Cell*. **184(5):** 1156-1170.

Yu, H., Shahid, M.Q., Li, R., Li, W., Liu, W., Ghouri, F. and Liu, X. (2018). Genome-wide analysis of genetic variations and the detection of rich variants of NBS-LRR encoding genes in common wild rice lines. *Plant Molecular Biology Reporter*. **36:** 618-630.

Zhang, J., Yu, H. and Li, J. (2023). De novo domestication: Retrace the history of agriculture to design future crops. *Current Opinion in Biotechnology*. **81:** 102946.

Zhang, L., Shivute, F.N., Shahid, M.Q., Kamara, N., Wu, J. and Liu, X. (2019). *In vitro* induction of auto-allotetraploid in a newly developed wild rice line from Oryza alta Swallen. *Plant Cell, Tissue and Organ Culture (PCTOC)*. **139:** 577-587.

Zhai, H., Lv, C., Liu, W., Yang, C., Fan, D., Wang, Z. and Guan, Q. (2021). Understanding spatio-temporal patterns of land use/land cover change under urbanization in Wuhan, China, 2000-2019. *Remote Sensing*. **13(16):** 3331.

Zhang, M., Yao, Y., Tian, Y., Ceng, K., Zhao, M., Zhao, M. and Yin, B. (2018). Increasing yield and N use efficiency with organic fertilizer in Chinese intensive rice cropping systems. *Field Crops Research*. **227:** 102-109.227.

Zhang, Y., Liu, H. and Yan, G (2021). Characterization of near-isogenic lines confirmed QTL and revealed candidate genes for plant height and yield-related traits in common wheat. *Molecular Breeding*. **41:** 1-17.

Zhang, Z., Gao, S. and Chu, C. (2020). Improvement of nutrient use efficiency in rice: Current toolbox and future perspectives. *Theoretical and Applied Genetics*. **133:** 1365-1384.

Zheng, W., Ma, Z., Zhao, M., Xiao, M., Zhao, J., Wang, C. and Sui, G. (2020). Research and development strategies for hybrid japonica rice. *Rice*. **13(1):** 1-22.

Zheng, W. and Walsh, P.P. (2019). Economic growth, urbanization and energy consumption-A provincial level analysis of China. *Energy Economics*. **80:** 153-162.

Zhou, D., Lin, Z., Ma, S., Qi, J. and Yan, T. (2021). Assessing an ecological security network for a rapid urbanization region in Eastern China. *Land Degradation and Development*. **32(8):** 2642-2660.

Zhou, J., Yang, Y., Lv, Y., Pu, Q., Li, J., Zhang, Y. and Tao, D. (2022). Interspecific hybridization Is an important driving force for origin and diversification of asian cultivated rice *Oryza sativa* L. *Frontiers in Plant Science*. **13:** 2027.

Zsögön, A., Peres, L.E., Xiao, Y., Yan, J. and Fernie, A.R. (2022). Enhancing crop diversity for food security in the face of climate uncertainty. *The Plant Journal*. **109(2):** 402-414.