

- Das G., Rao G.J., Varier M., Prakash A., and Prasad D., 2018, Improved Tapaswini having four BB resistance genes pyramided with six genes/QTLs, resistance/tolerance to biotic and abiotic stresses in rice, *Scientific Reports*, 8(1): 2413.
<https://doi.org/10.1038/s41598-018-20495-x>
- Das G., Patra J.K., and Baek K.H., 2017, Insight into MAS: a molecular tool for development of stress resistant and quality of rice through gene stacking, *Frontiers in Plant Science*, 8: 985.
<https://doi.org/10.3389/fpls.2017.00985>
- Dormatey R., Sun C., Ali K., Coulter J.A., Bi Z., and Bai J., 2020, Gene pyramiding for sustainable crop improvement against biotic and abiotic stresses, *Agronomy*, 10(9): 1255.
<https://doi.org/10.20944/preprints202008.0088.v1>
- Fang Y., Wang L., Sapey E., Fu S., Wu T., Zeng H., Sun X., Qian S., Khan M., Yuan S., Wu C., Hou W., Sun S., and Han T., 2021, Speed-breeding system in soybean: integrating off-site generation advancement, fresh seeding, and marker-assisted selection, *Frontiers in Plant Science*, 12: 717077.
<https://doi.org/10.3389/fpls.2021.717077>
- Gai Y., Liu S., Zhang Z., Wei J., Wang H., Liu L., Bai Q., Qin Q., Zhao C., Zhang S., Xiang N., and Zhang X., 2025, Integrative approaches to soybean resilience, productivity, and utility: a review of genomics, computational modeling, and economic viability, *Plants*, 14(5): 671.
<https://doi.org/10.3390/plants14050671>
- Guo Z., Wang H., Tao J., Ren Y., Xu C., Wu K., Zou C., Zhang J., and Xu Y., 2019, Development of multiple SNP marker panels affordable to breeders through genotyping by target sequencing (GBTS) in maize, *Molecular Breeding*, 39(3): 37.
<https://doi.org/10.1007/s11032-019-0940-4>
- Guo Z., Yang Q., Huang F., Zheng H., Sang Z., Xu Y., Zhang C., Wu K., Tao J., Prasanna B., Olsen M., Wang Y., Zhang J., and Xu Y., 2021, Development of high-resolution multiple-SNP arrays for genetic analyses and molecular breeding through genotyping by target sequencing and liquid chip, *Plant Communications*, 2(6): 100230.
<https://doi.org/10.1016/j.xplc.2021.100230>
- Haque M.A., Rafii M.Y., Yusoff M.M., Ali N.S., Yusuff O., Datta D.R., Anisuzzaman M., and Ikbai M.F., 2021, Recent advances in rice varietal development for durable resistance to biotic and abiotic stresses through marker-assisted gene pyramiding, *Sustainability*, 13(19): 10806.
<https://doi.org/10.3390/su131910806>
- Hasan N., Choudhary S., Naaz N., Sharma N., and Laskar R.A., 2021, Recent advancements in molecular marker-assisted selection and applications in plant breeding programmes, *Journal of Genetic Engineering and Biotechnology*, 19(1): 128.
<https://doi.org/10.1186/s43141-021-00231-1>
- Hassan M.A., Dahu N., Hongning T., Qian Z., Yueming Y., Yiru L., and Shimei W., 2023, Drought stress in rice: morpho-physiological and molecular responses and marker-assisted breeding, *Frontiers in Plant Science*, 14: 1215371.
<https://doi.org/10.3389/fpls.2023.1215371>
- Huang J., Q., Cai Z., Xia Q., Li S., Jia J., Chu L., Lian T., Nian H., and Cheng Y., 2020, Identification and mapping of stable QTLs for seed oil and protein content in soybean [*Glycine max* (L.) Merr.], *Journal of Agricultural and Food Chemistry*, 68(23): 6448-6460.
<https://doi.org/10.1021/acs.jafc.0c01271>
- Huang S., Xia Y., Yang J., Si Y., Chen X., Zhang H., Liu T., Zheng W., Chen X., Zhao Z., Zheng X., Lu Q., Li S., and Xiang F., 2025, A coding SNP in GmPM30 enhances soybean salinity tolerance and yield through the GmLEA1-GmPM30-GmLEC1 module, *Advanced Science*, 12(44): e09391.
<https://doi.org/10.1002/adv.202509391>
- Jarallah M.H., Mouhsan Z.M., and Alamry A.T., 2025, Integration of genetic tools: strategies for combining traditional and modern breeding to combat plant diseases, *European Journal of Ecology, Biology and Agriculture*, 2(4): 79-91.
[https://doi.org/10.59324/ejeba.2025.2\(4\).07](https://doi.org/10.59324/ejeba.2025.2(4).07)
- Jin H., Yang X., Zhao H., Song X., Tsvetkov Y., Wu Y., Gao Q., Zhang R., and Zhang J., 2023, Genetic analysis of protein content and oil content in soybean by genome-wide association study, *Frontiers in Plant Science*, 14: 1182771.
<https://doi.org/10.3389/fpls.2023.1182771>
- Kim D.G., Lyu J.I., Lim Y.J., Kim J.M., Hung N.N., Eom S.H., Kim S., Kim J., Bae C., and Kwon S.J., 2021, Differential gene expression associated with altered isoflavone and fatty acid contents in soybean mutant diversity pool, *Plants*, 10(6): 1037.
<https://doi.org/10.3390/plants10061037>
- Kim J.M., Kim K.H., Jung J., Kang B.K., Lee J., Ha B.K., and Kang S., 2020, Validation of marker-assisted selection in soybean breeding program for pod shattering resistance, *Euphytica*, 216(11): 166.
<https://doi.org/10.1007/s10681-020-02703-w>
- Kumar A., Sandhu N., Dixit S., Yadav S., Swamy B.P.M., and Shamsudin N.A.A., 2018, Marker-assisted selection strategy to pyramid two or more QTLs for quantitative trait-grain yield under drought, *Rice*, 11(1): 35.
<https://doi.org/10.1186/s12284-018-0227-0>
- Kumar B., Yankanchi S., Singh R., P., Sarkar D., Kumar P., Kumar K., Choudhary M., Jat B., and Jat H.S., 2025, Dissecting the genetic architecture of polygenic nutritional traits in maize through meta-QTL analysis, *Food Chemistry: Molecular Sciences*, 10: 100256.
<https://doi.org/10.1016/j.fochms.2025.100256>