LETTER TO THE EDITOR

The Plant Genome special section: Grain quality and nutritional genomics for breeding next-generation crops

By 2050, the world's population is expected to reach 9.8 billion according to United Nations predictions (https://www.un.org/en/desa/world-population-projected-reach-98-billion-2050-and-112-billion-2100). As a result, crop yields must roughly double in order to feed an expanding global population while still satisfying consumer demands for grain quality and nutrition. In addition to enhancing the nutritional value of food crops, making available affordable, nutrient-dense food, especially to those who are economically disadvantaged, will be a central pillar to address food and nutritional security. The strategy for improving grain quality and nutritional traits in breeding programs has been prioritized with the recent advancements in phenotyping of seeds and grains (metabolomics, mineral and vitamins, assessing the quality of starch, proteins and lipids, and capturing consumer preferred traits), sequencing technologies to do high-throughput genotyping, functional genomics aided gene discovery, high-resolution trait mapping and superior haplotype discovery, as well deploying genomic selection tools in a variety of crops (Pandey et al., 2016; Varshney et al., 2019). To improve population dietary patterns, a new generation of foods and ingredients with improved intrinsic nutritional quality and preferred grain quality attributes needs to be generated through advanced breeding methods. This will help to improve public health by increasing nutritional density and optimizing the quality of complex carbohydrates, proteins, and lipids. By utilizing and integrating both modern and traditional breeding techniques, it is possible to hasten the production of new crop types with improved yield, grain, and nutritional quality. This special issue highlights the most significant findings, which cover developments in high-throughput genomics, including genomic prediction of traits related to grain quality, and enhancement of nutritive traits in cereals (rice, wheat, maize, and oat) as well as legume crops like groundnut. Overall, this special issue includes a collection of studies deciphering genetic mechanisms of micronutrients covering minerals such as grain iron (Fe), zinc (Zn), and vitamin enrichment (tocochromanols), pigmented

bioactives, amino acids, dietary fiber, fatty acid composition, food safety, and end user grain quality traits in cereals and selected legumes.

The genetic mapping approach for identifying genetic regions controlling key grain quality and nutrition traits has been the most successful approach and has contributed significantly to marker discovery and use in crop breeding programs (Cockram & Mackay, 2018). High concentrations of essential amino acid such as lysine and limiting the high concentrations of free asparagine to prevent acrylamide during bread formation enhance the nutritional value of wheat grain. The article by Oddy et al. (2023) used this approach for understanding genetic control of grain amino acid composition in a UK soft wheat mapping population with major emphasis on lowering free asparagine and higher lysine content. This article used the multivariate analysis showing these traits largely independent of one another, with the largest effect on amino acids being from the environment. This study also identified quantitative trait loci (QTLs) controlling asparagine content, which may prove useful in applying appropriate strategies to reduce free asparagine in wheat breeding programmes. Using the same genetic mapping approach in groundnut, Parmar et al. (2023) identified co-localized major main effect quantitative trait loci and candidate genes for high iron content and Zn content. This study reports identification of six main-effect QTLs for Fe content and five main effect QTLs for Zn content. Interestingly, this study also identified three co-localized QTLs for Fe and Zn content as well as candidate genes that may further facilitate fine mapping and diagnostic marker development in groundnut. Using pooled sequencing-based genomic region identification approach from a biparental population in groundnut, Gangurde et al. (2022) used QTL-Seq approach for the discovery of candidate genes and development of markers for seed weight. This study successfully identified five associated genomic regions for seed weight and identified 182 SNPs in genic and intergenic regions. Although this study has identified multiple important candidate genes from these genetic regions, the

identification of gene *Ulp proteases* and *BIG SEED locus* genes is very important because of its detection in other crops as well. More importantly to breed groundnut varieties with bigger seed size, gene-specific Kompetitive allele-specific PCR markers were developed and successfully validated.

It is vital to determine Meta-QTLs as well as superior haplotypes for nutritional target traits, as numerous studies found several related genomic areas in the form of QTLs that influence mineral content in the grain. The study by Joshi et al. (2023) addresses this aspect in the paper for Zn biofortification of rice by performing meta-analysis of 155 Zn QTLs followed by identification of 57 MQTLs with reduced confidence intervals. More importantly, this study not only detected the co-localization of major metal homeostasis genes with MQTLs but also found involvement of network of genes in metal homeostasis through in silico expression and co-expression analyses. Furthermore, this study also detected superior haplotypes for efficient rice Zn biofortification. Another study led by Diers et al. (2023) presented results on genetic architecture of concentration of seed protein, oil, and meal protein using soybean nested association mapping population and reported the identification of 107 marker-trait associations (MTAs) for the above-mentioned three traits. Interestingly, few MTAs for the three traits were mapped within 5 cM intervals and most (94%) significant effects matched correlation between these traits. Although this study reported candidate genes linked to MTAs but suggested that genomic prediction would be more effective in improving these traits because of the large number of small effect MTAs for the composition traits. The study led by Derbyshire et al. (2023) utilized the soybean pangenome developed based on thousands of soybean lines to identify new alleles that may be involved in fatty acid biosynthesis. The study detected three possible instances of a gene missing in wild soybean, including *FAD8* and *FAD2-2D* involved in oleic and linoleic acid desaturation, respectively. This article also reported significantly reduced frequency of missense alleles in fatty acid biosynthesis genes, which could be because of selection during domestication.

The genome-wide association study (GWAS) is an alternate approach for trait mapping and gene discovery and has been more useful in plant species to rely on the genetic variation of various core collections, instead of developing biparental populations (Gangurde et al., 2022; Sushmitha et al., 2023). The paper by Panahabadi et al. (2023) uses this approach to identify associated genomic regions and genes for monosaccharides contents in rice. Monosaccharides are the building blocks for the synthesis of polymers or complex carbohydrates. This study has reported identification of 49 MTAs housed in 17 genomic regions (QTLs) located on seven chromosomes of rice associated with monosaccharides contents of whole grain, all of which are novel. Multiple promising candidate genes are being identified with further

potential of validation and its use in breeding. The next paper led by Mbanjo et al. (2023) performs GWAS in rice and identified marker trait associations linking nutritional value with pigmentation in rice seed. This study reported >280 significant SNPs, and many of these were found associated with more than one trait of secondary metabolite accumulation and rice pigmentation. Further, the targeted association analysis identified 67 SNPs in 52 candidate genes, which showed association with 24 traits. This study also reports discovery of six haplotypes from the significant SNPs within the genes *Rc/bHLH17* and *OsIPT5* genes important for regulation of a wide range of phenolic compounds in addition to color. The information made available through this article may be further exploited for gene validation and deployment in rice-breeding program.

Genomic selection has emerged as one of the most powerful approach to facilitate genomic prediction-based selection of promising plant progenies in crop-breeding programs even in early generation, therefore, saving the resources, time, and also increasing the precision are added advantage. There are plenty of studies on testing of a range of statistical models for genomic prediction as well as successful deployment of genomic selection in maize and wheat. By now, huge information is available on training population size and constitution, appropriate genotyping platforms, and statistical models for genomic prediction keeping in mind the genotype interaction with environment and soil, as well as possibilities for multiple trait selection. There are multiple case studies published in this emerging area of genomic selection. Research led by Tibbs-Cortes et al. (2022) provided exciting results on the genomic prediction in exotic-derived maize for tocochromanols (vitamin E), which is essential micronutrients in human diet. As expected, the prediction accuracies were achieved higher when predicting within each population but it decreased when performed in diversity panel training set. This study provided strength to the hypothesis for optimal designing of training population to efficiently incorporate new exotic germplasm into a plant breeding program. Tanaka et al. (2022) worked on the same trait and provided sound data support for the hypothesis that prior major QTL contributing regions and candidate causal genes conferring biological knowledge to elevate vitamin E content improves prediction based on analysis deploying multi-trait prediction model in two panels of maize inbred lines. Next, research by Brzozowski et al. (2023) on genomic selection was in oat targeting seed nutritional traits in biparental populations by testing multiple genomic prediction methods for 12 seed fatty acid content traits. The results indicated more variability for prediction accuracy within family as compared to the unrelated panel. Further, families that had half-sib families in the training set had higher prediction accuracy than those without it, suggesting use of related germplasm panels as training populations is more effective approach.

The next article led by Meher et al. (2023) tested eight Bayesian genomic prediction models for three micro-nutrient traits including seed Zn, seed Fe, and β-carotenoid concentrations in bread wheat, and the results showed that the Bayesian ridge regression model is the most reliable and superior method for genomic selection. This study also revalidated the hypothesis that the reliability of genomic selection increases with increase in the size of training population and the BLUE values being the most appropriate for use as response variables for better genomic selection. Fradgeley et al. (2023) summarized maintenance of UK Bread Baking Quality trends in wheat quality traits over 50 years of breeding and potential for future application of genomic-assisted selection. This article showed no subsequent net loss of genetic diversity and increase in genetic gain due to breeders' selection, despite significant genetic gain for both yield and quality traits being achieved during this time. This study also proposed that despite reduction in protein, the selection for increased gluten quality in combination with changes in the industrial bread baking process has enabled the large increases in yield and quality of wheat achieved through breeding in recent decades. Most importantly, testing multiple and diverse genomic prediction models with varied statistical hypothesis and algorithm provided no clarity on the best performing models, and therefore, best model can be selected in realistic breeding prediction scenarios and traits. The next article on genomic selection led by Gill et al. (2023) presented results on implementing multi-trait genomic selection to improve the prediction accuracy of processing and end-use quality traits in hard winter wheat. This article showed that the multi-trait genomic prediction (MTGP) model outperformed the single trait model with up to a twofold increase in prediction accuracy. This study also suggests to use the MTGP models together with flour protein and sedimentation weight value evaluated from earlier generations to predict baking traits in earlier generations.

In this special issue, two review articles are being published focusing on mineral nutrients in plants led by Khan et al. (2023) and another one on allergens in food crops led by Parmar et al. (2023). The article on mineral nutrients in plants under changing environments provided information on role of mineral nutrients in plants under stressful environments and biotechnological strategies for optimization of nutrient acquisition, transport, and distribution in plants. This article also provides recent advancements in bio-fortification breeding to optimize yield and grain mineral concentrations under stress conditions to address food and nutritional security. The article by Parmar et al. (2023) emphasizes about the increasing concerns about food safety and the need to protect consumer health from the negative effects of food-born allergies. This article provides current updates on research and predicts future prospects for developing allergen-depleted food crops. This article discussed in detail how the recent advances in molecular breeding, genetic engineering, and genome editing may facilitate developing potentially allergen-depleted food crops to protect consumer health.

AUTHOR CONTRIBUTIONS
Manish K. Pandey: Conceptualization; investigation; methodology; project administration; resources; supervision; writing—original draft; writing—review and editing. **Reyazul Rouf Mir**: Conceptualization; investigation; project administration; writing—review and editing. **Nese Sreenivasulu**: Conceptualization; investigation; project administration; writing—review and editing.

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