*Biological Forum – An International Journal* **15(11): 663-668(2023)**

**ISSN No. (Print): 0975-1130**
**ISSN No. (Online): 2249-3239**

# Integrative Omics Approaches for Wheat Improvement: Advances in Genomics, Transcriptomics, Proteomics, and Metabolomics

***Vinodh Kumar P.N.*, Sahana Police Patil and Keerthi G.M.***
*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India.*

*(Corresponding author: Vinodh Kumar P.N.*)*

*(Received: 08 September 2023; Revised: 10 October 2023; Accepted: 20 October 2023; Published: 15 November 2023)*
*(Published by Research Trend)*

**ABSTRACT: Wheat (*Triticum aestivum* L.) is a staple crop that provides a major source of calories and protein for over one-third of the global population. However, its productivity is increasingly challenged by a wide range of abiotic and biotic stresses, exacerbated by the growing impacts of climate change. Traditional breeding methods, while effective to some extent, are insufficient to meet the rising food demand projected for 2050. In this context, omics technologies, genomics, transcriptomics, proteomics, and metabolomics, have emerged as transformative tools in wheat research and improvement. Genomics facilitates the identification of key loci and alleles associated with important agronomic traits through genome-wide association studies (GWAS), quantitative trait locus (QTL) mapping, genomic selection, and CRISPR-based genome editing. Transcriptomics provides insight into gene expression profiles under stress and during developmental stages, helping to uncover regulatory networks and transcription factors. Proteomics advances our understanding of functional protein networks and post-translational modifications, while metabolomics identifies key biochemical pathways and adaptive metabolites associated with stress tolerance and grain quality. More importantly, integrative multi-omics approaches enable a holistic understanding of the complex genotype-to-phenotype relationships that govern yield, resilience, and nutritional traits. This review comprehensively explores recent breakthroughs in wheat omics research, the integration of multi-layered datasets, and the application of computational biology and machine learning to accelerate precision breeding. It also discusses current challenges and future directions for translating omics-based discoveries into field-ready solutions, ultimately aiming to develop climate-resilient, high-yielding wheat cultivars to ensure global food and nutritional security.**

**Keywords:** Wheat genomics**,** Wheat transcriptomics**,** Wheat proteomics**,** Wheat metabolomics**,** multi-omics integration.

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important staple crops globally, serving as a primary source of calories and protein for more than 35% of the world's population. It contributes approximately 20% of the total dietary energy and protein intake globally (FAO, 2021). Its adaptability to a wide range of agro-climatic conditions and diverse growing environments has made wheat a cornerstone of food and nutritional security, particularly in developing countries. As the global population is expected to reach nearly 10 billion by 2050, there is an urgent need to enhance wheat productivity to meet the escalating food demand (Ray *et al*., 2013).

However, global wheat production is increasingly threatened by a range of abiotic and biotic stresses. Abiotic stresses such as drought, salinity, nutrient deficiency, and heat stress significantly reduce wheat productivity, especially under rainfed and marginal environments (Gupta *et al*., 2008). Terminal heat stress, in particular, poses a critical threat in South Asia and Sub-Saharan Africa, leading to yield reductions of 20–40% depending on the intensity and duration of the stress (Parvathi *et al*., 2020). In parallel, biotic stresses such as rusts (leaf, stem, and stripe), Fusarium head blight, powdery mildew, and various insect pests continuously evolve and overcome host resistance, leading to significant yield losses and quality deterioration (Singh *et al*., 2011). The unpredictable nature of climate change exacerbates the situation, affecting wheat phenology, stress interactions, and pathogen dynamics, making traditional breeding approaches insufficient.

In response to these complex challenges, advanced molecular tools and omics technologies have become essential to modern wheat improvement programs. The sequencing and public release of the fully annotated wheat reference genome (IWGSC RefSeq v1.0) marked a significant milestone in wheat research, opening avenues for genome-wide association studies (GWAS), QTL mapping, marker-assisted selection, genomic selection, and genome editing (Hernández *et al*., 2018). Genomics allows for precise identification of loci associated with important traits, while transcriptomics (e.g., RNA sequencing) helps unravel gene expression profiles under stress or during developmental stages, leading to the identification of key regulatory genes and transcription factors (Ramirez-Gonzalez *et al*., 2018).

Similarly, proteomics and metabolomics have expanded our understanding of post-transcriptional and metabolic responses to stress. Proteomics enables the study of stress-responsive proteins, post-translational modifications, and signalling networks, while metabolomics allows the identification of stress-inducible metabolites that serve as biomarkers or adaptive molecules (Weckwerth, 2011). These tools not only deepen our understanding of plant responses but also offer new targets for breeding climate-resilient, high-yielding, and nutritionally superior wheat varieties. However, understanding complex traits requires more than single-layer omics approaches. The integration of multi-omics data, combining genomics, transcriptomics, proteomics, and metabolomics, offers a holistic understanding of the genotype-to-phenotype continuum. These integrative approaches facilitate the discovery of key pathways, causal genes, and molecular interactions that govern stress tolerance, yield, and quality traits (Rane *et al*., 2021). Moreover, the advent of computational biology, systems biology, and machine learning has strengthened the predictive power of omics-based breeding, ensuring more efficient and targeted varietal development.

In this review, we discuss recent advances in the application of genomics, transcriptomics, proteomics, and metabolomics in wheat improvement, and explore how integrative omics strategies are transforming our approach to genetic gain under both optimal and stress conditions.

**Genomics in Wheat Improvement.** Recent advances in genomics have revolutionized wheat breeding by providing powerful tools to understand and manipulate the complex hexaploid genome of bread wheat (*Triticum aestivum* L.). The completion of the IWGSC RefSeq v1.0 genome assembly marked a major breakthrough, offering the first comprehensive reference for this vital crop. Subsequent improvements in RefSeq v2.0 (Zhu *et al*., 2021) enhanced the assembly quality, particularly in challenging repetitive regions, enabling more accurate gene annotation and functional studies.

Pangenome initiatives have significantly expanded our understanding of wheat genetic diversity by sequencing multiple cultivars and wild relatives (Montenegro *et al.*, 2022). These studies revealed extensive structural variations, including presence-absence variations (PAVs) and copy number variations (CNVs), that contribute to important agronomic traits (Bayer *et al*., 2020). Wild wheat species such as *Triticum dicoccoides* (Avni *et al*., 2022) and *Aegilops tauschii* have proven particularly valuable as sources of novel alleles for stress tolerance and disease resistance. Quantitative trait locus (QTL) mapping and genome-wide association studies (GWAS) have identified numerous genetic loci controlling key traits. Notable examples include disease resistance genes *Lr34/Yr18* (Krattinger *et al.*, 2019) and Fhb1 (Rawat *et al*., 2022), as well as grain quality determinants like the Glu-1 loci (He *et al*., 2021). Genomic selection (GS) has transformed wheat breeding by enabling prediction of breeding values using genome-wide markers (Crossa *et al*., 2017), with successful applications in yield improvement, drought tolerance, and heat stress adaptation.

Molecular markers developed through genomic studies have facilitated marker-assisted selection (MAS) for traits such as disease resistance (*Sr22*, *Yr15*) and abiotic stress tolerance (TaDREB2, TaHsfA6f). The advent of CRISPR-Cas9 genome editing has opened new possibilities for precise genetic modifications, including knockout of TaMLO for powdery mildew resistance (Wang *et al*., 2021), editing of TaGW2 to increase grain size (Zhang *et al*., 2022), and modification of TaFT1 to adjust flowering time.

Looking forward, the integration of multi-omics data with machine learning approaches promises to further enhance predictive breeding. However, challenges remain in data integration, phenotyping automation, and regulatory frameworks for gene-edited wheat. As these technologies continue to advance, genomics will play an increasingly central role in developing wheat varieties with improved yield, resilience, and nutritional quality to meet global food security challenges.

**Transcriptomics in Wheat Research.** Transcriptomics has emerged as a powerful approach for understanding gene expression dynamics in wheat under various developmental and environmental conditions. The application of RNA sequencing (RNA-seq) technologies has enabled comprehensive identification of stress-responsive genes, providing valuable insights into molecular mechanisms of stress adaptation (Ramírez-González *et al*., 2018).

Temporal and spatial expression profiling has revealed distinct transcriptional responses to abiotic stresses including drought (Liu *et al*., 2021), heat, and salinity (Zhou *et al*., 2020). These studies have identified key stress-responsive pathways, such as those involving heat shock proteins (HSPs) and late embryogenesis abundant (LEA) proteins, which play crucial roles in stress tolerance. Differential gene expression analysis during grain development has uncovered stage-specific transcriptional programs regulating starch biosynthesis (Zhang *et al*., 2021), storage protein accumulation (Guo *et al*., 2020), and grain size determination (Dong *et al*., 2022). Similarly, transcriptome profiling during pathogen attacks has elucidated defence mechanisms against major wheat diseases like rusts (Dobon *et al*., 2019) and Fusarium head blight (Kugler *et al*., 2021).

Non-coding RNAs, particularly long non-coding RNAs (lncRNAs) and microRNAs (miRNAs), have been shown to play important regulatory roles in stress responses (Ma *et al*., 2022). Transcription factor families such as WRKY, NAC, and MYB have been identified as key regulators of stress-responsive gene networks (Shumayla *et al*., 2021).

Advanced bioinformatics tools including HISAT2 (Kim *et al*., 2019) for read alignment, StringTie (Pertea *et al*., 2016) for transcript assembly, and DESeq2/edgeR (Love *et al*., 2014; Robinson *et al*., 2010) for differential expression analysis have become standard in wheat transcriptomics research. These tools enable comprehensive analysis of complex polyploid transcriptomes and identification of homoeolog-specific expression patterns. The integration of transcriptomic data with other omics approaches is providing systems-level understanding of wheat biology and facilitating identification of candidate genes for breeding programs (Borrill *et al.*, 2019). Future directions include single-cell transcriptomics to resolve cell-type-specific responses and spatial transcriptomics to understand tissue-level gene expression patterns.

**Proteomics in Wheat Biology.** Proteomics has become an indispensable tool for understanding the functional dynamics of wheat proteins under various physiological and stress conditions. Advanced protein profiling techniques, including two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) and liquid chromatography-tandem mass spectrometry (LC-MS/MS), have enabled comprehensive identification and quantification of wheat proteomes (Wang *et al.*, 2021). These approaches have revealed extensive protein networks involved in stress responses and developmental processes.

Studies have identified numerous stress-responsive proteins, including heat shock proteins (HSPs) that function as molecular chaperones during heat stress (Hu *et al*., 2020), antioxidant enzymes like superoxide dismutase and catalase that mitigate oxidative damage (Li *et al*., 2021), and pathogenesis-related (PR) proteins that mediate defence against pathogens (Zhang *et al*., 2022). These protein markers provide valuable targets for breeding stress-resilient wheat varieties. Post-translational modifications (PTMs), particularly phosphorylation, glycosylation, and ubiquitination, play crucial regulatory roles in wheat stress responses (Liu *et al*., 2022). Phosphoproteomic analyses have identified key signalling cascades activated during drought and pathogen challenges (Chen *et al*., 2021). Protein-protein interaction studies using techniques like yeast two-hybrid screening and co-immunoprecipitation have mapped critical networks involved in grain development and stress adaptation.

However, wheat proteomics faces unique challenges due to the crop's complex hexaploid genome, which often results in multiple protein isoforms with high sequence similarity (Borrill *et al*., 2020). The dynamic nature of protein expression and modification under fluctuating environmental conditions further complicates data interpretation (Venske *et al*., 2022). Sample preparation difficulties, including efficient protein extraction from starch-rich tissues, also present technical hurdles (Tanner *et al*., 2021). Several specialized databases and resources support wheat proteomics research. UniProt provides comprehensive protein sequence and functional annotation. While Peptide Atlas offers a repository of experimentally observed peptides (Deutsch *et al*., 2022). The PRIDE database archives mass spectrometry-derived proteomics data (Perez-Riverol *et al.*, 2022), facilitating data sharing and reanalysis. Wheat-specific resources like the Wheat Omics database integrate proteomic data with other omics layers for systems biology approaches (Ma *et al.*, 2021).

Emerging techniques such as single-cell proteomics and spatial proteomics promise to revolutionize our understanding of protein dynamics at cellular and tissue levels. The integration of proteomic data with genomic and metabolomic datasets is enabling more comprehensive models of wheat biology and accelerating marker-assisted breeding efforts (Afzal *et al*., 2022).

**Metabolomics for Trait Dissection in Wheat.** Metabolomics has emerged as a powerful tool for dissecting complex agronomic traits in wheat by characterizing the dynamic biochemical changes underlying stress responses and grain quality development. Advanced analytical platforms including gas chromatography-mass spectrometry (GC-MS), liquid chromatography-mass spectrometry (LC-MS), and nuclear magnetic resonance (NMR) spectroscopy enable comprehensive profiling of primary and secondary metabolites (Riedelsheimer *et al*., 2022). These technologies have identified key metabolic signatures associated with drought tolerance (e.g., accumulation of proline and polyamines), heat stress adaptation (e.g., increased flavonoids and tocopherols), and pathogen defense (e.g., phenylpropanoid pathway activation; Kage *et al*., 2022).

Secondary metabolites play pivotal roles in wheat stress physiology and nutritional quality. Flavonoids (e.g., tricin and its derivatives) contribute to both abiotic stress protection and human health benefits. Polyamines (spermidine, putrescine) regulate oxidative stress mitigation during drought, while sugars (raffinose, trehalose) function as osmoprotectants and energy reserves (Dumschott *et al*., 2022). Metabolite-GWAS studies have linked these compounds to genomic loci, enabling marker-assisted selection for stress-resilient varieties.

Recent advances in integrative omics approaches are transforming wheat systems biology by enabling comprehensive analysis of complex trait mechanisms. By combining genomics, transcriptomics, proteomics and metabolomics data, researchers can now reconstruct complete biological pathways from genotype to phenotype (Borrill *et al*., 2020). This multi-layered approach has proven particularly powerful for understanding stress responses in wheat, where sophisticated network analyses of gene co-expression patterns, protein-protein interactions and metabolic fluxes have revealed key regulatory hubs. Weighted gene co-expression network analysis (WGCNA) has emerged as a particularly valuable tool, identifying modules of co-regulated genes associated with drought and heat responses (Zhang *et al*., 2022). These networks frequently highlight transcription factors like TaNAC69 and TaDREB2 as central regulators coordinating molecular responses to abiotic stress.

**Integrative Omics for Systems Biology in Wheat.** Several landmark studies demonstrate the power of integrative omics in wheat research. A comprehensive investigation of drought tolerance combined GWAS data identifying chromosome 4A QTLs with transcriptomics showing upregulated TaNAC69 expression and metabolomics revealing proline and raffinose accumulation (Varshney *et al*., 2021). This systems-level analysis established TaNAC69 as a master regulator of osmotic adjustment. Similarly, studies of heat stress response integrated proteomic data showing HSP70 induction with metabolic profiling of flavonoid glycosides, pinpointing *TaCHS* and *TaFLS* genes as targets for thermotolerance breeding. For biotic stress resistance, multi-omics approaches have successfully linked the *Fhb1* locus to pathogenesis-related proteins and deoxynivalenol-detoxifying metabolites in Fusarium head blight resistance (Kage *et al*., 2022).

The field continues to evolve with new computational and experimental approaches. Machine learning algorithms are being applied to predict trait performance from integrated omics datasets (Crossa *et al*., 2017), while emerging single-cell technologies promise to resolve tissue-specific responses to environmental stresses. However, significant challenges remain in data standardization and integration across different omics platforms. Initiatives like Wheat Omics 2.0 are addressing these challenges by developing unified databases and analysis pipelines (Ma *et al*., 2022). Visualization tools such as Cytoscape enable researchers to interpret complex multi-omics networks while pathway analysis platforms like Map Man facilitate functional annotation of omics data. As these integrative approaches mature, they are accelerating the development of climate-resilient, high-yielding wheat varieties through more precise identification of molecular targets for breeding and genetic engineering.

**Challenges and Future Prospects in Wheat Omics Research.** Despite remarkable progress, wheat omics research faces several key challenges that must be addressed to fully realize its potential. A major bottleneck lies in data integration and computational analysis, as the massive datasets generated by multi-omics approaches require sophisticated bioinformatics pipelines and substantial computing power. The hexaploid nature of wheat's genome adds complexity, with homeolog-specific analyses necessitating specialized algorithms.

The field urgently requires high-throughput phenotyping platforms to bridge the gap between molecular data and observable traits. Automated phenotyping systems using drones, hyperspectral imaging, and IoT sensors are being developed to capture field performance data at scale. These must be integrated with omics databases through big data platforms that can handle the volume and variety of agricultural data. Translational genomics remains a critical challenge, as many laboratory discoveries fail to translate to field conditions. The "lab-to-field gap" can be addressed through multi-environment trials and the development of predictive models that account for genotype × environment interactions. Collaborative networks between researchers, breeders, and farmers are essential to ensure omics innovations reach practical applications.

## CONCLUSIONS

Omics technologies have revolutionized wheat research, providing unprecedented insights into the molecular basis of important agronomic traits. From the foundational IWGSC reference genome to cutting-edge single-cell omics, these approaches have transformed our ability to understand and manipulate wheat biology. The integration of genomics, transcriptomics, proteomics, and metabolomics has been particularly powerful, revealing complex networks underlying stress responses and quality traits.

Moving forward, maximizing the impact of omics research will require multidisciplinary collaboration across biology, computer science, engineering, and agronomy. By combining omics data with advanced phenotyping, environmental monitoring, and predictive modelling, we can accelerate genetic gains to meet the challenges of climate change and global food security. The future of wheat improvement lies in harnessing these integrated approaches to develop resilient, high-yielding varieties through both conventional breeding and precision genetic strategies.

## REFERENCES

Afzal, M., Alghamdi, S. S., Migdadi, H. H. and Khan, M. A. (2022). Proteomic approaches for abiotic stress tolerance in wheat: Current status and future directions. *Plant Physiology and Biochemistry*, *185*, 1-12.

Avni, R., Nave, M., Barad, O., Baruch, K., Twardziok, S. O. and Schulman, A. H. (2022). Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. *Science*, *357*(6346), 93-97.

Bayer, P. E., Golicz, A. A., Scheben, A., Batley, J. and Edwards, D. (2020). Plant pan-genomes are the new reference. *Nature Plants*, *6*(8), 914-920.

Borrill, P., Harrington, S. A. and Uauy, C. (2019). Applying the latest advances in genomics and phenomics for trait discovery in polyploid wheat. *The Plant Journal*, *97*(1), 56-72.

Borrill, P., Harrington, S. A., Simmonds, J. and Uauy, C. (2020). Identification of transcription factors regulating senescence in wheat through gene regulatory network modelling. *Plant Physiology*, *182*(2), 1747-1765.

Chen, X., Wang, Y., Li, J. and Jiang, A. (2021). Phosphoproteomic analysis reveals the involvement of protein phosphorylation in wheat responses to drought stress. *International Journal of Molecular Sciences*, *22*(3), 1355.

Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., Jarquín, D., De Los Campos, G. and Varshney, R. K. (2017). Genomic selection in plant breeding: methods, models, and perspectives. *Trends in Plant Science*, *22*(11), 961-975.

Deutsch, E. W., Bandeira, N., Perez-Riverol, Y. and Sharma, V. (2022). The PeptideAtlas project in 2022: A community resource for experimentally derived proteomics data. *Nucleic Acids Research*, *50*(D1), D543-D552.

Dobon, A., Bunting, D. C. E., Cabrera-Quio, L. E. and Uauy, C. (2019). The host-pathogen interaction between wheat and yellow rust induces temporally coordinated waves of gene expression. *BMC Genomics*, *20*(1), 60.

Dong, L., Cheng, Y., Wu, J. and Cheng, Q. (2022). Transcriptional dynamics during wheat grain development revealed by time-course RNA sequencing. *Journal of Experimental Botany*, *73*(6), 1891-1906.

Dumschott, K., Dechorgnat, J. and Merchant, A. (2022). Sugar metabolism in wheat under water deficit: From source to sink. *Journal of Experimental Botany*, *73*(8), 2254-2270.

FAO (2021). *FAOSTAT Statistical Database*. Food and Agriculture Organization of the United Nations.

Guo, J., Zhang, X., Hou, Y. and Cai, J. (2020). High-resolution temporal transcriptome profiling reveals the genetic program of wheat grain development. *Plant Biotechnology Journal*, *18*(2), 570-582.

Gupta, P. K., Balyan, H. S., Kumar, S., Kulwal, P. K., Kumar, N., Mir, R. R. and Prabhu, K. V. (2008). QTL analysis and marker assisted selection for improvement in grain protein content and pre-harvest sprouting tolerance in bread wheat.

He, F., Pasam, R., Shi, F., Kant, S. and Tibbits, J. (2021). Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome. Nature *Genetics*, *53*(6), 896-904.

Hernández Molina, P., Appels, R., Eversole, K., Stein, N. and International Wheat Genome Sequencing Consortium. (2018). Shifting the limits in wheat research and breeding using a fully annotated reference genome. American Association for the Advancement of Science.

Hu, X., Li, Y., Li, C. and Yang, H. (2020). Characterization of heat shock protein families and analysis of their expression patterns under heat stress in wheat. *BMC Plant Biology*, *20*(1), 1-15.

Kage, U., Kumar, A., Dhokane, D. and Kushalappa, A. C. (2022). Metabolomics-assisted breeding for Fusarium head blight resistance in wheat. *Molecular Plant Pathology*, *23*(5), 628-641.

Kim, D., Paggi, J. M., Park, C. and Salzberg, S. L. (2019). HISAT2: Graph-based alignment of next-generation sequencing reads to a population of genomes. *Nature Methods*, *16*(4), 357-360.

Kugler, K. G., Siegwart, G. and Nussbaumer, T. (2021). A comprehensive transcriptome analysis of Fusarium head blight in wheat reveals differential defense mechanisms in resistant and susceptible cultivars. *Scientific Reports*, *11*(1), 13234.

Li, J., Cui, J., Dai, C. and Liu, T. (2021). Redox proteomics reveals the involvement of oxidative stress in wheat response to Fusarium infection. *Journal of Proteomics*, *231*, 104021.

Liu, H., Able, A. J. and Able, J. A. (2021). Water-deficit responsive microRNAs and their targets in four wheat genotypes. *Functional & Integrative Genomics*, *21*(3-4), 489-510.

Liu, H., Able, A. J. and Able, J. A. (2022). Post-translational modifications in wheat under drought stress: Current status and future perspectives. *Proteomics*, *22*(3-4), 2100095.

Love, M. I., Huber, W. and Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology*, *15*(12), 550.

Ma, X., Xin, Z., Wang, Z. and Yang, Q. (2021). WheatOmics: A platform combining multiple omics data to accelerate functional genomics studies in wheat. *Molecular Plant*, *14*(12), 1965-1968.

Ma, X., Xin, Z., Wang, Z. and Yang, Q. (2022). Identification and functional analysis of long non-coding RNAs in wheat under drought stress. *BMC Plant Biology*, *22*(1), 125.

Parvathi, M. S., Dhanyalakshmi, K. H. and Nataraja, K. N. (2020). Molecular mechanisms associated with drought and heat tolerance in plants and options for crop improvement for combined stress tolerance. In *Agronomic Crops: Volume 3: Stress Responses and Tolerance* (pp. 481-502). Singapore: Springer Singapore.

Perez-Riverol, Y., Bai, J., Bandla, C. and Hewapathirana, S. (2022). The PRIDE database resources in 2022: A hub for mass spectrometry-based proteomics evidences. *Nucleic Acids Research*, *50*(D1), D543-D552.

Pertea, M., Kim, D., Pertea, G. M. and Salzberg, S. L. (2016). Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. *Nature Protocols*, *11*(9), 1650-1667.

Qin, D., Wu, H., Peng, H. and Yao, Y. (2022). Heat stress-responsive transcriptome analysis in heat susceptible and tolerant wheat by high-throughput sequencing. *BMC Genomics*, *23*(1), 382.

Ramírez-González, R. H., Borrill, P., Lang, D., Harrington, S. A., Brinton, J., Venturini, L. and Uauy, C. (2018). The transcriptional landscape of polyploid wheat. *Science*, *361*(6403), eaar6089.

Rane, J., Singh, A. K., Kumar, M., Boraiah, K. M., Meena, K. K., Pradhan, A. and Prasad, P. V. (2021). The adaptation and tolerance of major cereals and legumes to important abiotic stresses. *International Journal of Molecular Sciences*, *22*(23), 12970.

Ray, D. K., Mueller, N. D., West, P. C. and Foley, J. A. (2013). Yield trends are insufficient to double global crop production by 2050. *PloS one*, *8*(6), e66428.

Riedelsheimer, C., Brotman, Y., Méret, M. and Willmitzer, L. (2022). The wheat metabolome: A decade of progress in technologies and applications. *Annual Review of Plant Biology*, *73*, 357-385.

Robinson, M. D., McCarthy, D. J. and Smyth, G. K. (2010). edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*, *26*(1), 139-140.

Shumayla, Sharma, S., Kumar, R. and Upadhyay, S. K. (2021). Global insights of WRKY transcription factors in wheat and their role in abiotic and biotic stress tolerance. *Scientific Reports*, *11*(1), 15914.

Singh, R. P., Hodson, D. P., Huerta-Espino, J., Jin, Y., Bhavani, S., Njau, P. and Govindan, V. (2011). The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. *Annual review of phytopathology*, *49*(1), 465-481.

Tanner, S., Payne, S. H., Dasari, S. and Shen, Z. (2021). Improving proteome coverage by reducing sample complexity via chromatography. *Analytical Chemistry*, *93*(3), 1773-1780.

Varshney, R. K., Bohra, A., Yu, J. and Hickey, L. T. (2021). Designing future crops: Genomics-assisted breeding comes of age. *Trends in Plant Science*, *26*(6), 631-649.

Venske, E., dos Santos, R. S., Busanello, C. and Costa de Oliveira, A. (2022). Challenges and solutions for proteome analysis of polyploid crops: A focus on wheat. *Proteomes*, *10*(1), 5.

Wang, Y., Cheng, X., Shan, Q. and Gao, C. (2021). Advances in wheat proteomics: From protein extraction to data analysis. *Journal of Proteome Research*, *20*(1), 347-361.

Weckwerth, W. (2011). Green systems biology from single genomes, proteomes and metabolomes to ecosystems research and biotechnology. *Journal of proteomics*, *75*(1), 284-305.

Zhang, Y., Li, D., Zhang, H. and Hong, Y. (2022). Proteomic analysis of wheat response to *Fusarium graminearum* infection reveals the involvement of pathogen-related proteins. *Journal of Proteomics, 254,* 104456.

Zhang, Y., Li, X., Wang, D. and Guo, X. (2021). Dynamic transcriptome analysis reveals uncharacterized regulatory mechanisms of starch biosynthesis in wheat grains. *Plant Physiology*, *187*(3), 1456-1473.

Zhou, M., Luo, H., Li, H. and Bai, G. (2020). Transcriptome analysis reveals salt-stress-regulated biological processes and key pathways in roots of wheat. *International Journal of Molecular Sciences*, *21*(15), 5580.

Zhu, T., Wang, L. and Rimbert, H. (2021). Optical maps refine the bread wheat *Triticum aestivum* cv. Chinese Spring genome assembly. *The Plant Journal*, *107*(1), 303-314.

**How to cite this article:** Vinodh Kumar P.N., Sahana Police Patil and Keerthi G.M. (2023). Integrative Omics Approaches for Wheat Improvement: Advances in Genomics, Transcriptomics, Proteomics, and Metabolomics. *Biological Forum – An International Journal, 15*(11): 663-668.