Integrating Genomics and Phenomics in Agricultural Breeding: A Comprehensive Review

Abstract

One of the key roles of plant breeders is to improve crop productivity through development of varieties with desirable traits to feed the growing population. The merger of genomics and phenomics - where genomics refer to the study of an organism's entire DNA sequence and phenomonics is the full explanation of observable characteristics has given a new face to breeding strategies. This paper provides information about this technique from beginning up to now, which implicates high-throughput phenotyping, genomic selection, artificial intelligence platform for crop improvement. It seems that coronal genomics and phenotypical imaging results in transgenic or super climate-resilient plants, therefore improving yield under sustainable conditions. Despite its bright future there are certain issues like data standardization, ethical concerns,and resource restraints that need considering. Development later on gets people thinking about technical fields such as inter-disciplinary researches as well as policy supports that have ability to bring these powerful technologies into assurance of food security together with sustainable agriculture initially collaboration doesn't need manufacturing centres of technology including genome and phenome data can help breeders achieve wrists precisions in crops development which will result in having robust agricultural systems able to overcome environmental stressors.

Keywords:*Genomics, Phenomics, Crop Breeding, High-Throughput Phenotyping, and Genome Editing*

1. **Introduction**:

Agricultural breeding is a fundamental practice in enhancing crop productivity and developing varieties with desirable traits to meet the demands of a growing population. Genomics and phenomics play crucial roles in this process by providing insights into the genetic makeup and phenotypic characteristics of plants, respectively.Genomics involves the study of an organism's entire DNA sequence, enabling breeders to identify specific genes associated with traits of interest (Lorenz, 2011). On the other hand, phenomics focuses on the comprehensive study of an organism's observable characteristics, allowing for the assessment of traits related to growth, development, and response to environmental factors (Furbank et al., 2019&Mnzughul et al, 2023).The review aims to explore the integration of genomics and phenomics in agricultural breeding, emphasizing their significance in enhancing breeding strategies and developing improved crop varieties. By leveraging genomic information to understand the genetic basis of traits and utilizing phenotypic data to assess plant performance under different conditions, breeders can make informed decisions in selecting and developing superior cultivars (Crain et al., 2018).

The scope of the review encompasses recent advancements in high-throughput phenotyping methods, genomic selection techniques, and the application of artificial intelligence in crop breeding (Kim et al., 2021). Additionally, it will discuss the challenges and opportunities associated with integrating genomics and phenomics to accelerate the breeding process and address key issues such as biotic and abiotic stresses, yield improvement, and environmental sustainability (Sandhu et al., 2022).Overall, the review will highlight the synergistic relationship between genomics and phenomics in plant breeding, showcasing how these technologies can revolutionize crop improvement efforts and contribute to ensuring food security and sustainable agriculture globally.

2. Historical Evolution of Genomics and Phenomics in Agriculture

Genomics and phenomics have significantly impacted the field of agriculture, revolutionizing crop breeding and enhancing agricultural productivity. The historical evolution of genomics and phenomics in agriculture can be traced through key milestones in genomic research, the development of phenomics, and early breeding techniques.Early breeding techniques laid the foundation for modern agricultural practices by selecting and propagating plants with desirable traits (Bakala et al., 2021). These traditional methods have evolved over time, incorporating advancements in genomics and phenomics to accelerate the breeding process in agriculture and improve crop characteristics better than the existing (Akata&Ikeh, 2018; Hamdan et al., 2022).

Milestones in genomic research have propelled agricultural innovation by enabling the identification of genes associated with important traits in crops (Esposito et al., 2019). Technologies such as genome editing have been instrumental in developing crop varieties with superior qualities and resilience to environmental stresses (Lyzenga et al., 2021). The integration of CRISPR/Cas-based gene editing into crop breeding has advanced domestication and refined crop varieties for diverse applications and growth environments (Rigoulot et al., 2020).Phenomics has emerged as a valuable tool in agriculture, bridging plant phenotypes with genes to enhance crop performance (Pratap et al., 2019). High-throughput phenotyping (HTP) has enabled the efficient assessment of plant traits, facilitating the integration of phenomics with genomics for crop improvement (Rigoulot et al., 2019). Phenomics has the potential to transform agricultural fields by linking genetic information with observable plant characteristics (Razzaq et al., 2021).

The combination of genomics and phenomics has paved the way for next-generation breeding strategies aimed at developing climate-ready crops and enhancing food security. By leveraging modern technologies such as machine learning and precision phenotyping, researchers can identify the genetic basis of traits with unprecedented accuracy, driving advancements in plant breeding (Esposito et al., 2019). The historical evolution of genomics and phenomics in agriculture reflects a journey of continuous innovation and scientific progress. From early breeding techniques to cutting-edge genome editing technologies, the integration of genomics and phenomics has revolutionized crop improvement and paved the way for sustainable agricultural production in the face of changing environmental conditions which stand as hurdle to agricultural production in all parts of the world (Ikeh et al., 2015).

3. Genomics in Agricultural Breeding

Genomic technologies have significantly impacted agricultural breeding practices, providing new tools and methods to enhance crop improvement and food security. Marker-assisted selection and genetic mapping allow breeders to efficiently identify and select desirable traits (Xu & Crouch, 2008). Genome-wide association studies (GWAS) offer insights into the genetic basis of complex traits, aiding in the development of improved crop varieties (Gao, 2021). The emergence of CRISPR and gene editing techniques has further revolutionized agricultural breeding by enabling precise modifications in the plant genome (Fiaz et al., 2021).

Researchers have emphasized the potential of genome editing technologies, like CRISPR/Cas9, in crop enhancement and sustainable agriculture (Turnbull et al., 2021). These technologies present innovative solutions to food insecurity by facilitating the releasing of improve crop varieties with enhanced traits (BONEA, 2022). Despite the promise of gene editing tools in agricultural breeding programs, there are regulatory hurdles that must be overcome to ensure their effective and safe use (Eenennaam et al., 2019).

Consumer acceptance of genetically edited food, particularly among the youth, is influenced by factors such as perceptions of genetically modified organisms and food (Farid et al., 2020&Ikeh et al., 2023). Nevertheless, advancements in genome editing have the capacity to significantly enhance crop breeding in agriculture, offering opportunities to develop improved crops with precision and speed (Sharma et al., 2019). Additionally, the socioeconomic impact of genome editing on agricultural value chains underscores its significance in improving agricultural productivity and sustainability (Maaß et al., 2019).That’s why genomic technologies, encompassing genetic mapping, GWAS, and CRISPR-based gene editing, are propelling innovation in agricultural breeding. These tools hold immense potential for developing improved crop varieties, addressing food security challenges, and advancing sustainable agricultural practices.

4. Phenomics in Agricultural Breeding

Phenomics, the comprehensive study of an organism's phenotypes, plays a crucial role in agricultural breeding by enabling the assessment of dynamic changes in crop characteristics under varying environmental conditions. To enhance agricultural productivity through knowledge-based breeding and the development of crop varieties suited to specific environments, it is essential to leverage high-throughput phenotyping platforms, advanced imaging technologies, and sensors for accurate data collection (Busemeyer et al., 2013).The integration of data obtained from these platforms and technologies is vital for effective analysis and interpretation. By incorporating new knowledge from high-throughput technologies and tools like OMICs, epigenetics, and genome editing techniques, breeders can enhance the efficiency of agricultural practices and design new plant genomes to predict desired phenotypes (Gogolev et al., 2021). This integration of data is crucial for addressing research bottlenecks in crop productivity and supporting informed decision-making in agriculture (Reynolds et al., 2021).Furthermore, the use of smart breeding approaches that consider climate resilience and climate change adaptation is becoming increasingly important. Holistic smart breeding strategies offer promising solutions for developing crop varieties that are better adapted to changing environmental conditions (Bakala et al., 2021). Additionally, the inclusion of plant biodiversity and genetic resources in breeding programs is emphasized to ensure the conservation and utilization of valuable genetic diversity for sustainable crop production (Ebert & Engels, 2020; Maurice and Akata, 2022).

In the context of data integration and analysis, tools like MetaboAnalyst and ConsensusPathDB play a significant role in making metabolomics data more meaningful and providing a comprehensive picture of cell biology by integrating various functional aspects of genes, proteins, and metabolites (Xia et al., 2015; Kamburov et al., 2010). Integrative analysis methods, such as Integrative Biclustering and Sparse Integrative Clustering, enable the simultaneous analysis of multiple omics data sets, facilitating a deeper understanding of complex biological processes (Tomescu et al., 2013; Shen et al., 2013).Overall, the synthesis of data from diverse sources, including genomics, proteomics, metabolomics, and other omics data, is essential for advancing agricultural breeding practices. By leveraging advanced data integration and analysis techniques, researchers can gain valuable insights into crop traits, genetic regulation, and environmental responses, ultimately contributing to the development of climate-ready crops and sustainable agriculture practices.

5. Integrating Genomics and Phenomics: Methodologies and Approaches

Integrating genomics and phenomics involves the convergence of various methodologies and approaches to extract meaningful insights from the vast amount of genomic and phenotypic data available. One key aspect is the development of frameworks for integration (Houle et al., 2010). Phenomics, as an emerging discipline, plays a crucial role in this integration by enabling high-throughput and high-dimensional phenotyping (Houle et al., 2010). However, challenges exist in phenomics due to the rapid advancements in genomic data collection compared to phenomic data (Eliason et al., 2019). To address this, the field requires effective data management and bioinformatics tools (Deans et al., 2015; Bhave et al., 2007) to handle the integration of genomic and phenomic data efficiently.

Machine learning and artificial intelligence (AI) applications are pivotal in leveraging integrated genomics and phenomics data. These technologies have a significant impact on genomics, enabling the identification of associations between genotype and phenotype through methods like genome-wide association studies (GWAS) and phenome-wide association studies (PheWAS) (Jiang & Ngiam, 2023). AI-based technologies are increasingly being utilized to predict complex phenotypic traits by prioritizing informative genes for analysis and selecting genomic features for machine learning algorithms (Pal, 2023). Furthermore, the application of AI in phenomics is expanding, with ongoing efforts to integrate AI into plant phenotyping Tripodi et al. (2022) and to predict phenotypic traits based on genetic markers and environmental data (Danilevicz et al., 2022).

Case studies showcasing integrated approaches in genomics and phenomics highlight the practical implications of these methodologies. For instance, aligning the human interactome with the phenome has been shown to identify causative genes and networks underlying disease families (Wu et al., 2008). Additionally, the development of metrics like the Pleiotropic Variability Score (PVS) aids in quantifying phenomic associations of genomic variants based on semantic reasoning algorithms (Shameer et al., 2021). The integration of genomics and phenomics requires robust frameworks, advanced data management tools, and the application of machine learning and AI technologies. Case studies demonstrate the effectiveness of these integrated approaches in identifying genetic associations with phenotypic traits. As the field continues to evolve, addressing challenges in phenomics and enhancing the usability and accuracy of machine learning models remain critical areas for further research and development.

6. Benefits of Integrating Genomics and Phenomics

Integrating genomics and phenomics in agricultural breeding offers a multitude of benefits that can revolutionize crop improvement strategies. By combining genomic information with high-throughput phenotypic data, breeders can achieve enhanced precision in breeding, accelerated breeding cycles, and improved crop traits and yield, ultimately contributing to sustainability and food security (Tardieu et al., 2017; Rahaman et al., 2015; Furbank et al., 2019; Bezouw et al., 2019; Crossa et al., 2021; Sandhu et al., 2022).Phenomics involves the comprehensive analysis of physical and biochemical traits of organisms, playing a crucial role in crop breeding by enabling breeders to select materials for crossing based on physiological traits and mechanistic science, leading to genetic gain (Furbank et al., 2019; Bezouw et al., 2019). This approach allows for the identification of favorable genes and the production of site-specific sequence changes that enhance agronomic traits (Xu et al., 2020). Furthermore, high-throughput phenotyping technologies can generate large volumes of data at low costs, facilitating the indirect prediction of yield and enabling the assessment of dynamic genetics of complex traits (Lane et al., 2020; Busemeyer et al., 2013).

The integration of genomics and phenomics not only optimizes breeding pipelines but also supports the development of cultivars resilient to climate change and various stresses, ensuring robust yields under challenging environmental conditions (Crossa et al., 2021). This integration allows for the generation of high-quality quantitative data, effective characterization of breeding populations, and rapid development of improved crop varieties (Sandhu et al., 2022; Pratap et al., 2019). The synergy between genomics and phenomics in agricultural breeding holds great promise for enhancing breeding efficiency, accelerating genetic gains, and addressing global food security challenges. By leveraging advanced technologies and data-driven approaches, breeders can unlock the full potential of crop improvement strategies, ultimately contributing to sustainable agricultural production.

7. Challenges and Limitations

Integrating genomics and phenomics in agricultural breeding presents various challenges and limitations that need to be addressed for successful implementation. Technical and operational barriers encompass the complexities of the breeding process, leading to a heterogeneous genomic landscape with peaks and troughs of differentiation and divergence (Ravinet et al., 2017). Data standardization and interoperability are crucial issues that must be overcome to ensure seamless integration of genomics and phenomics data in breeding programs (Arend et al., 2016). Ethical and regulatory considerations play a significant role, especially in genetically modified and genome-edited organisms, where concerns about animal welfare, ecological impacts, and regulatory frameworks need to be carefully navigated (May, et al, 2012; Eriksson et al., 2018; Farstad, 2018 and Lassoued et al., 2021).

Cost and resource constraints pose practical challenges in the large-scale application and integration of advanced technologies like CRISPR/Cas9 genome editing in agricultural breeding schemes (Rodríguez-Leal et al., 2017; Khatodia et al., 2016). Additionally, the global regulation of genetically modified crops amidst the gene-edited crop boom presents a complex landscape with varying regulatory schemes worldwide, ranging from moratoriums to unified regulatory frameworks (Turnbull et al., 2021; Whelan et al., 2020). The need for improved oversight and regulation of genetically engineered crops is emphasized to ensure food security and address concerns related to genetic modification (Herman et al., 2020).So the future of agricultural breeding lies in the successful integration of genomics and phenomics, but this endeavor is met with technical, operational, ethical, regulatory, and resource-related challenges that necessitate careful consideration and strategic solutions to realize the full potential of these advancements in agriculture.

8. Future Directions and Emerging Trends

The integration of genomics and phenomics represents a significant advancement in agricultural breeding, offering promising future directions and emerging trends. By combining genomic information with phenotypic data, researchers can gain a comprehensive understanding of plant traits and their underlying genetic mechanisms, leading to more precise and efficient breeding strategies (Dutta et al., 2022). This integration is particularly crucial for enhancing genetic gain through genomic selection, which has the potential to revolutionize breeding practices in both livestock and plant species (Xu et al., 2020).Moreover, the application of advanced technologies such as bioinformatics and genomic tools is playing a pivotal role in accelerating crop improvement (Hu et al., 2018). These tools provide opportunities to enhance breeding efficiency, reduce the phenotype gap, and ultimately contribute to the development of superior crop varieties (Hu et al., 2018). Additionally, the successful application of phenotyping technologies is expected to further increase agricultural productivity by enabling the rapid and accurate assessment of plant traits (Casto et al., 2021).

Collaborative and interdisciplinary research approaches are essential for driving innovation in agricultural breeding. By fostering partnerships between different scientific disciplines, such as agronomy, plant physiology, and ecology, researchers can gain a holistic understanding of crop interactions and environmental factors that influence breeding outcomes (Brooker et al., 2014). Interdisciplinary learning opportunities in agriculture and natural resources are crucial for preparing scholars and faculty to address complex agricultural challenges through a multidisciplinary lens (McKim et al., 2018).Policy and funding opportunities are critical for supporting agricultural research and innovation, especially in the context of smallholder farmers and developing regions. Governments all levels are increasingly recognizing the importance of developing adaptation policies to address the impacts of climate change on agriculture, with a particular focus on supporting smallholder farmers (Donatti et al., 2018). Additionally, the establishment of open-source breeding networks and the protection of germplasm through innovative licensing approaches can facilitate the free exchange of genetic resources and stimulate plant breeding efforts (Kotschi&Horneburg, 2018).

Conclusion

In summary, the blend of genomics and phenomics in agribusiness leads to a paradigm shift which affects all aspects of crop production, sustainable agriculture and food security. The techniques involved in this combination are high-throughput phenotyping, genomic selection and artificial intelligence that help you speed up breeding cycles, increase accuracy as well as develop crops that are climate-resilient. Yet, moving from current state to fully implemented framework is hampered by technicalities that require careful and innovative solutions. The past one including CRISPR-Cas genome editing technologies is a major turning point in the history of crop breeding since it permits very precise genetic modifications for the betterment of plants' productivity. On the same time, development of phenomics through analyzing plant traits holistically has made the integration of genetic data with observable traits possible for optimization of breeding outcomes. New directions in this area draw attention to the significance of data harmonization and analysis in terms of bioinformatics and AI technology for efficient and accurate prediction of trait values. The researches should be collaborative, interdisciplinary as well as publicly supported for addressing agricultural problems which are complex and require innovative approaches towards climate change mitigation. As a result implementation of such approach will lead to significant improvement in crop productivity will increase their resistance to biotic/abiotic stresses and promoting more effective breeding pipelines. Nevertheless, there are certain obstacles on the way to standardization such as ethical concerns about data sharing or cost constraints which must be addressed before full benefits can be realized.The future development of agricultural practices will be continuously pushed as the genomics and phenomics fields grow and interact more with each other. The results will be felt in the various crop improvement approaches spurring this development. Finally, let me mention that it goes without saying that the above-mentioned all will be directly connected to a better and safer future concerning our daily diet.

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References:

Akata, O.R., and Ikeh, A.O. (2021) Rsponse of Groundnut (*Arachis hypogaea* L.) varieties to intra-Row spacing in Rainforest zone of Southeastern Nigeria. *Nigeria Journal of Agriculture, Food and Environment*, 17 (1 & 2) 57 – 64.

Arend, D., Junker, A., Scholz, U., Schüler, D., Wylie, J., & Lange, M. (2016). Pgp repository: a plant phenomics and genomics data publication infrastructure. Database, 2016, baw033. https://doi.org/10.1093/database/baw033

Bakala, H., Singh, G., & Srivastava, P. (2021). Smart breeding for climate resilient agriculture.. https://doi.org/10.5772/intechopen.94847

Bezouw, R., Keurentjes, J., Harbinson, J., & Aarts, M. (2019). Converging phenomics and genomics to study natural variation in plant photosynthetic efficiency. The Plant Journal, 97(1), 112-133. https://doi.org/10.1111/tpj.14190

Bhave, S., Hornbaker, C., Phang, T., Saba, L., Lapadat, R., Kechris, K., … &Tabakoff, B. (2007). The phenogen informatics website: tools for analyses of complex traits. BMC Genetics, 8(1). https://doi.org/10.1186/1471-2156-8-59

Bonea, D. (2022). Applications of the crispr/cas9 technique in maize and wheat breeding. Annals of the University of Craiova - Agriculture Montanology Cadastre Series, 52(1), 51-58. https://doi.org/10.52846/aamc.v52i1.1313

Brooker, R., Bennett, A., Cong, W., Daniell, T., George, T., Hallett, P., … & White, P. (2014). Improving intercropping: a synthesis of research in agronomy, plant physiology and ecology. New Phytologist, 206(1), 107-117. https://doi.org/10.1111/nph.13132

Busemeyer, L., Ruckelshausen, A., Möller, K., Melchinger, A., Alheit, K., Maurer, H., … &Würschum, T. (2013). Precision phenotyping of biomass accumulation in triticale reveals temporal genetic patterns of regulation. Scientific Reports, 3(1). https://doi.org/10.1038/srep02442

Casto, A., Schuhl, H., Tovar, J., Wang, Q., Bart, R., & Fahlgren, N. (2021). Picturing the future of food. The Plant Phenome Journal, 4(1). https://doi.org/10.1002/ppj2.20014

Crain, J., Mondal, S., Rutkoski, J., Singh, R., & Poland, J. (2018). Combining high□throughput phenotyping and genomic information to increase prediction and selection accuracy in wheat breeding. The Plant Genome, 11(1). https://doi.org/10.3835/plantgenome2017.05.0043

Crossa, J., Fritsche□Neto, R., Montesinos□López, O., Costa□Neto, G., Dreisigacker, S., Montesinos□López, A., … & Bentley, A. (2021). The modern plant breeding triangle: optimizing the use of genomics, phenomics, and enviromics data. Frontiers in Plant Science, 12. https://doi.org/10.3389/fpls.2021.651480

Danilevicz, M., Gill, M., Anderson, R., Batley, J., Bennamoun, M., Bayer, P., … & Edwards, D. (2022). Plant genotype to phenotype prediction using machine learning. Frontiers in Genetics, 13. https://doi.org/10.3389/fgene.2022.822173

Deans, A., Lewis, S., Huala, E., Anzaldo, S., Ashburner, M., Balhoff, J., … & Mabee, P. (2015). Finding our way through phenotypes. Plos Biology, 13(1), e1002033. https://doi.org/10.1371/journal.pbio.1002033

Donatti, C., Harvey, C., Martínez□Rodríguez, M., Vignola, R., & Rodriguez, C. (2018). Vulnerability of smallholder farmers to climate change in central america and mexico: current knowledge and research gaps. Climate and Development, 11(3), 264-286. https://doi.org/10.1080/17565529.2018.1442796

Dutta, C., Behera, P., & Sarma, R. (2022). Applied genetics and plant breeding in 21st century for crop improvement – status and prospects. International Journal of Environment and Climate Change, 252-264. https://doi.org/10.9734/ijecc/2022/v12i1130970

Ebert, A. and Engels, J. (2020). Plant biodiversity and genetic resources matter!. Plants, 9(12), 1706. https://doi.org/10.3390/plants9121706

Eenennaam, A., Wells, K., & Murray, J. (2019). Proposed u.s. regulation of gene-edited food animals is not fit for purpose. NPJ Science of Food, 3(1). https://doi.org/10.1038/s41538-019-0035-y

Eliason, C., Edwards, S., & Clarke, J. (2019). Phenotools: an r package for visualizing and analysing phenomic datasets. Methods in Ecology and Evolution, 10(9), 1393-1400. https://doi.org/10.1111/2041-210x.13217

Eriksson, S., Jonas, E., Rydhmer, L., &Röcklinsberg, H. (2018). Invited review: breeding and ethical perspectives on genetically modified and genome edited cattle. Journal of Dairy Science, 101(1), 1-17. https://doi.org/10.3168/jds.2017-12962

Esposito, S., Carputo, D., Cardi, T., & Tripodi, P. (2019). Applications and trends of machine learning in genomics and phenomics for next-generation breeding. Plants, 9(1), 34. https://doi.org/10.3390/plants9010034

Farid, M., Cao, J., Lim, Y., Arato, T., & Kodama, K. (2020). Exploring factors affecting the acceptance of genetically edited food among youth in japan. International Journal of Environmental Research and Public Health, 17(8), 2935. https://doi.org/10.3390/ijerph17082935

Farstad, W. (2018). Ethics in animal breeding. Reproduction in Domestic Animals, 53(S3), 4-13. https://doi.org/10.1111/rda.13335

Fiaz, S., Ahmar, S., Saeed, S., Riaz, A., Mora-Poblete, F., & Jung, K. (2021). Evolution and application of genome editing techniques for achieving food and nutritional security. International Journal of Molecular Sciences, 22(11), 5585. https://doi.org/10.3390/ijms22115585

Furbank, R., Berni, J., George□Jaeggli, B., Potgieter, A., & Deery, D. (2019). Field crop phenomics: enabling breeding for radiation use efficiency and biomass in cereal crops. New Phytologist, 223(4), 1714-1727. https://doi.org/10.1111/nph.15817

Furbank, R., Berni, J., George□Jaeggli, B., Potgieter, A., & Deery, D. (2019). Field crop phenomics: enabling breeding for radiation use efficiency and biomass in cereal crops. New Phytologist, 223(4), 1714-1727. https://doi.org/10.1111/nph.15817

Gao, C. (2021). Genome engineering for crop improvement and future agriculture. Cell, 184(6), 1621-1635. https://doi.org/10.1016/j.cell.2021.01.005

Gogolev, Y., Ahmar, S., Akpinar, B., Budak, H., Kiryushkin, A., Gorshkov, V., … & Korzun, V. (2021). Omics, epigenetics, and genome editing techniques for food and nutritional security. Plants, 10(7), 1423. https://doi.org/10.3390/plants10071423

Hamdan, M., Karlson, C., Teoh, E., Lau, S., & Tan, B. (2022). Genome editing for sustainable crop improvement and mitigation of biotic and abiotic stresses. Plants, 11(19), 2625. https://doi.org/10.3390/plants11192625

Herman, R., Gaffney, J., & Storer, N. (2020). Enlightened oversight of genetically engineered crops for the next generation. Agricultural & Environmental Letters, 5(1). https://doi.org/10.1002/ael2.20004

Houle, D., Govindaraju, D., & Omholt, S. (2010). Phenomics: the next challenge. Nature Reviews Genetics, 11(12), 855-866. https://doi.org/10.1038/nrg2897

Hu, H., Scheben, A., & Edwards, D. (2018). Advances in integrating genomics and bioinformatics in the plant breeding pipeline. Agriculture, 8(6), 75. https://doi.org/10.3390/agriculture8060075

Ikeh A. O., Ndaeyo N. U., Akata, O. R., Udoh E. I., Akpan E. A. and Esang D. M. (2023).Effects of Genotypes and Harvesting Time on Yield and Organoleptic Qualities of Pro-Vitamin A Cassava (*Manihotesculenta*Cratz) Garri. *UAES Journal of Innovative Sciences and Technology for Development (UJISTD)*, 1:2: 12-28.

Ikeh, A. O. Essien B. A., Akata O.R., and Akpan, E. A., (2015). Dessert Encroachment Impacts on Food Production of Okigwe Local Government Area, Imo State Nigeria. *Journal of Forestry, Environment and Sustainable Development*, 1:2: 58-63.

Jiang, L. and Ngiam, K. (2023). How data science and ai-based technologies impact genomics. Singapore Medical Journal, 64(1), 59. https://doi.org/10.4103/singaporemedj.smj-2021-438

Kamburov, A., Pentchev, K., Galicka, H., Wierling, C., Lehrach, H., & Herwig, R. (2010). Consensuspathdb: toward a more complete picture of cell biology. Nucleic Acids Research, 39(suppl_1), D712-D717. https://doi.org/10.1093/nar/gkq1156

Khatodia, S., Bhatotia, K., Passricha, N., Khurana, S., & Tuteja, N. (2016). The crispr/cas genome-editing tool: application in improvement of crops. Frontiers in Plant Science, 7. https://doi.org/10.3389/fpls.2016.00506

Kim, M., Lee, C., Hong, S., Kim, S., Baek, J., & Kim, K. (2021). High-throughput phenotyping methods for breeding drought-tolerant crops. International Journal of Molecular Sciences, 22(15), 8266. https://doi.org/10.3390/ijms22158266

Kotschi, J. and Horneburg, B. (2018). The opensource seed licence: a novel approach to safeguarding access to plant germplasm. Plos Biology, 16(10), e3000023. https://doi.org/10.1371/journal.pbio.3000023

Lane, H., Murray, S., Montesinos‐López, O., Montesinos‐López, A., Crossa, J., Rooney, D., … & Morgan, C. (2020). Phenomic selection and prediction of maize grain yield from near‐infrared reflectance spectroscopy of kernels. The Plant Phenome Journal, 3(1). https://doi.org/10.1002/ppj2.20002

Lassoued, R., Phillips, P., Macall, D., Hesseln, H., & Smyth, S. (2021). Expert opinions on the regulation of plant genome editing. Plant Biotechnology Journal, 19(6), 1104-1109. https://doi.org/10.1111/pbi.13597

Lorenz, A. (2011). Genomic selection in plant breeding., 77-123. https://doi.org/10.1016/b978-0-12-385531-2.00002-5

Lyzenga, W., Pozniak, C., &Kagale, S. (2021). Advanced domestication: harnessing the precision of gene editing in crop breeding. Plant Biotechnology Journal, 19(4), 660-670. https://doi.org/10.1111/pbi.13576

Maaß, O., Consmuller, N., & Kehlenbeck, H. (2019). Socioeconomic impact of genome editing on agricultural value chains: the case of fungal-resistant and coeliac-safe wheat. Sustainability, 11(22), 6421. https://doi.org/10.3390/su11226421

Maurice, B. P., &Akata, O. (2022). Evaluation of Genetic Variations and Agronomic Performance of Some Cultivars of White Yam (Dioscorea rotundata) in Obio Akpa, Nigeria. *International Journal of Innovative Research and Development, 11*(7)

May, B.I., Ikeh, A. O, Uduak, G. I., Udoh, E. I. and Etokeren, U. E. (2012). The Roles of Urban Forestry in Mitigating Climate Change. *Agricultural Economics and Extension Research Studies,* 1:2:26-30.

McKim, A., Pauley, C., Velez, J., & Sorensen, T. (2018). Interdisciplinary learning opportunities in agriculture, food, natural resources, and science: the role of the teacher. Journal of Agricultural Education, 59(2), 179-196. https://doi.org/10.5032/jae.2018.02179

Mnzughul, N.S., Esang, D.M and Ikeh,A.O. (2023).Variability of elite maize (Zea mays L.) varieties at different row spacing in Guinea Savannah Region of Nigeria. *Open Global Scientific Journal*, 02 (02): 81-93 2023.

Pal, D. (2023). Post-gwas prioritization of genome-phenome associations in sorghum. https://doi.org/10.1101/2023.12.05.570238

Pratap, A., Gupta, S., Nair, R., Gupta, S., Schafleitner, R., Basu, P.& Baek, K. (2019). Using plant phenomics to exploit the gains of genomics. Agronomy, 9(3), 126. https://doi.org/10.3390/agronomy9030126

Rahaman, M., Chen, D., Gillani, Z., Klukas, C., & Chen, M. (2015). Advanced phenotyping and phenotype data analysis for the study of plant growth and development. Frontiers in Plant Science, 6. https://doi.org/10.3389/fpls.2015.00619

Ravinet, M., Faria, R., Butlin, R., Galindo, J., Bierne, N., Rafajlović, M., … &Westram, A. (2017). Interpreting the genomic landscape of speciation: a road map for finding barriers to gene flow. Journal of Evolutionary Biology, 30(8), 1450-1477. https://doi.org/10.1111/jeb.13047

Razzaq, A., Kaur, P., Akhter, N., Wani, S., & Saleem, F. (2021). Next-generation breeding strategies for climate-ready crops. Frontiers in Plant Science, 12. https://doi.org/10.3389/fpls.2021.620420

Reynolds, M., Atkin, O., Bennett, M., Cooper, M., Dodd, I., Foulkes, J., … & Wittich, P. (2021). Addressing research bottlenecks to crop productivity. Trends in Plant Science, 26(6), 607-630. https://doi.org/10.1016/j.tplants.2021.03.011

Rigoulot, S., Schimel, T., Lee, J., Brabazon, H., Meier, K., Schmid, M., … & Stewart, C. (2019). Fluorescence-based whole plant imaging and phenomics.. https://doi.org/10.1101/865428

Rigoulot, S., Schimel, T., Lee, J., Sears, R., Brabazon, H., Layton, J., … & Stewart, C. (2020). Imaging of multiple fluorescent proteins in canopies enables synthetic biology in plants. Plant Biotechnology Journal, 19(4), 830-843. https://doi.org/10.1111/pbi.13510

Rodríguez-Leal, D., Lemmon, Z., Man, J., Bartlett, M., & Lippman, Z. (2017). Engineering quantitative trait variation for crop improvement by genome editing. Cell, 171(2), 470-480.e8. https://doi.org/10.1016/j.cell.2017.08.030

Sandhu, K., Merrick, L., Sankaran, S., Zhang, Z., & Carter, A. (2022). Prospectus of genomic selection and phenomics in cereal, legume and oilseed breeding programs. Frontiers in Genetics, 12. https://doi.org/10.3389/fgene.2021.829131

Shameer, K., Glicksberg, B., Badgeley, M., Johnson, K., & Dudley, J. (2021). Pleiotropic variability score: a genome interpretation metric to quantify phenomic associations of genomic variants.. https://doi.org/10.1101/2021.07.18.452819

Sharma, S., Lee, S., & Huo, H. (2019). Current status of research, regulations, and future challenges for crispr gene-editing in crop improvement. Edis, 2019(4), 4. https://doi.org/10.32473/edis-hs1334-2019

Shen, R., Wang, S., & Mo, Q. (2013). Sparse integrative clustering of multiple omics data sets. The Annals of Applied Statistics, 7(1). https://doi.org/10.1214/12-aoas578

Tardieu, F., Cabrera□Bosquet, L., Pridmore, T., & Bennett, M. (2017). Plant phenomics, from sensors to knowledge. Current Biology, 27(15), R770-R783. https://doi.org/10.1016/j.cub.2017.05.055

Tomescu, O., Mattanovich, D., &Thallinger, G. (2013). Integrative analysis of -omics data: a method comparison. Biomedical Engineering / Biomedizinische Technik. https://doi.org/10.1515/bmt-2013-4311

Tripodi, P., Nicastro, N., & Pane, C. (2022). Digital applications and artificial intelligence in agriculture toward next-generation plant phenotyping. Crop and Pasture Science, 74(6), 597-614. https://doi.org/10.1071/cp21387

Turnbull, C., Lillemo, M., &Hvoslef-Eide, T. (2021). Global regulation of genetically modified crops amid the gene edited crop boom – a review. Frontiers in Plant Science, 12. https://doi.org/10.3389/fpls.2021.630396

Whelan, A., Gutti, P., & Lema, M. (2020). Gene editing regulation and innovation economics. Frontiers in Bioengineering and Biotechnology, 8. https://doi.org/10.3389/fbioe.2020.00303

Wu, X., Liu, Q., & Jiang, R. (2008). Align human interactome with phenome to identify causative genes and networks underlying disease families. Bioinformatics, 25(1), 98-104. https://doi.org/10.1093/bioinformatics/btn593

Xia, J., Sinelnikov, I., Han, B., & Wishart, D. (2015). Metaboanalyst 3.0—making metabolomics more meaningful. Nucleic Acids Research, 43(W1), W251-W257. https://doi.org/10.1093/nar/gkv380

Xu, Y. and Crouch, J. (2008). Marker□assisted selection in plant breeding: from publications to practice. Crop Science, 48(2), 391-407. https://doi.org/10.2135/cropsci2007.04.0191

Xu, Y., Liu, X., Fu, J., Wang, H., Wang, J., Huang, C.,& Zhang, A. (2020). Enhancing genetic gain through genomic selection: from livestock to plants. Plant Communications, 1(1), 100005. https://doi.org/10.1016/j.xplc.2019.100005