Available online at www.climatechangejournal.org

DOI: http://dx.doi.org/10.18782/2583-4770.118

ISSN (E): 2583 – 4770

Emrg. Trnd. Clim. Chng. (2023) *2*(1), 1-6

Review Article

Emerging Trends in Climate Change

Peer-Reviewed, Refereed, Open Access Journal

The Use of Genomics and Bioinformatics to Hasten Agricultural Improvement in Response to Climate Change

S Rehan Ahmad*

Assistant Professor, Hiralal Mazumdar Memorial College for Women, Kolkata, W.B, India

*Corresponding Author E-mail: zoologist.rehan@gmail.com

Received: 13.1.2023 | Revised: 26.03.2023 | Accepted: 5.04.2023

ABSTRACT

Pressure on our ability to produce enough food will increase due to the changing environment and expanding world population. Breeding new crops and adapting existing crops to the new environment is necessary to ensure continuing food production. The development of genomics has the potential to speed up crop plant breeding using genomics. It is still extremely difficult to integrate genomic data into agronomic qualities related to climate for use in breeding, and doing so will necessitate the collaboration of many different skills and specialities. By accelerating the production of climate-ready crops, bioinformatics and genomics have the potential to sustain food security in the face of climate change.

Keywords: *Climate Change, Bioinformatics, Genomics.*

INTRODUCTION

The idea that the global climate is changing and that these changes are caused by human activity, particularly the burning of fossil fuels and the associated rises in atmospheric carbon dioxide concentration, is becoming more widely accepted (IPPC: Climate change, 2014). The precise changes that are anticipated to take place and their effects on agriculture are still up for debate. Accurate climate change prediction is difficult due to the complexity of climate control processes (Asseng et al., 2013). But there is broad agreement that global warming will bring about changes in rainfall patterns, and these changes in rainfall are expected to have a considerable influence on agriculture.

Not every expected change in the climate will be detrimental right away. By extending the growing season, warmer temperatures may boost agricultural productivity in some temperate zones. A net gain in yield may result from higher carbon dioxide concentrations because they may improve photosynthetic efficiency, decrease water loss through transpiration, and enhance yield. However, the frequency and intensity of droughts are anticipated to rise, negating these beneficial aspects in many agricultural regions, especially at low to mid-latitudes.

Cite this article: Ahmad, S. Rehan (2023). The Use of Genomics and Bioinformatics to Hasten Agricultural Improvement in Response to Climate Change, *Emrg. Trnd. Clim. Chng. 2*(1), 1-6. doi: http://dx.doi.org/10.18782/2583-4770.118

Action must be taken immediately to maintain global food security because the anticipated climatic changes will likely disrupt the world's food resources. There is a need for novel crops and types that are tolerant to abiotic stress, resistant to pests and diseases, and exhibit improved nutrient usage efficiency (Abberton et al., 2015) in addition to ongoing monitoring of the climate and its effects on food crops. While enhancements to current key crops will predominate, new species that were not previously thought of for domestication may also be adopted.

Climate Change Traits

While it is challenging to forecast how climate change will affect a specific location, several broad trends regarding crop adaptability are evident. These include strengthened resilience to high and low-temperature extremes, increased resistance to pests and disease, and improved ability to sustain yield under drought or flooding. The increase in atmospheric CO_2 concentration, one of the more noticeable climate changes, is anticipated to have a net beneficial impact on crop development because CO_2 is a crucial nutrient for plant growth (Lawlor et al., 1991). For C3 plants, like wheat and rice, the effects of rising CO_2 will be more severe than for C4 plants, like maize, which have developed mechanisms to maximize CO_2 efficiency.

Because more efficient gas exchange occurs with fewer stomatal openings, higher CO_2 concentrations also increase water use efficiency. This is significant since more frequent and severe droughts and floods are predicted to occur in many locations due to climate change (Mackill et al., 2012). The ability to survive and maintain output under drought stress and better water usage efficiency will become increasingly significant features, even though crops cannot be grown without water. Although there will not be a "magic bullet," crop breeders should focus on selection for enhanced adaptability to drier circumstances while preserving yield. Drought tolerance and water usage efficiency are complicated traits with strong environmental interactions (Xu KN et al., 2006).

The nutritional value of food is projected to be impacted by increased plant growth and decreased transpiration brought on by rising atmospheric CO_2 levels, with a decrease in nitrogen content in some species (Cotrufo et al., 1998). The underdeveloped world, where dietary nutrition is already frequently subpar, might be where this has the biggest influence. The overall yield is usually prioritized over the selection of quality features, and maintaining yield and quality will be harder under forecasted climate change scenarios.

Increased virulence and abundance of pests and diseases are predicted as a result of climate change (Garrett et al., 2006; & Gregory et al., 2009), and a better understanding of host resistance mechanisms and disease virulence is likely to lessen the impact of pests and pathogens on important crops and developed countries.

The Role of Genomics

The fields of genomics and bioinformatics are quickly developing due to the ongoing advancement and declining cost of DNA genotyping and sequencing (Edwards et al., 2010; & Edwards et al., 2013). While many of the early genetics research fields centred on advancing our fundamental understanding of biology, the use of genomics in agriculture has grown more recently. The application of genetics to bettering human nutrition and health will significantly impact society in industrialized and developing nations.

The rising use of genomics in agriculture is important since it occurs at a time when food production must simultaneously contend with tremendous population growth and climate change. The DivSeek and African orphan crops initiatives (http://www.divseek.org;.http://africanorphancrops.org/) aim to promote and coordinate the capture of crop genomic diversity for use in crop improvement. Draught genome assemblies are now available for many of the major crops as well as an increasing number of their wild relatives (Brozynska et al., 2015).

The variety within a species, which is exploited for selection and breeding, is not represented by one reference genome sequence, even though it offers valuable information. Single nucleotide polymorphisms (SNPs) and structural variations, such as copy number or presence/absence variations (CNVs/PAVs), are the main kinds of heritable genomic variety. The resolution of molecular markers created by SNPs is one nucleotide, and they are widely distributed across genomes (Edwards et al., 2007). Genome resequencing may be used to find them in great quantities, and they can be measured using a variety of techniques (Imelfort et al., 2009). Only recently has the significance of structural variation been recognized for both genomic and phenotypic diversity, with up to 20% of genes in some plant species displaying missing in some individuals (Li et al., 2014; Lin et al., 2014; & Springer et al., 2009). The hybrid vigour seen when two diverse individuals are crossed is likely due to the interaction between gene sequence variety and the presence of variable genes (Miller et al., 2015; & Voss-Fels K et al., 2015).

With the transition away from PCR-based single markers as simple sequence repeats and towards highly parallel SNP-based markers using genotyping arrays from suppliers like Illumina and Affymetrix, or more recently, genotyping-by-sequencing (GBS) approaches, population genotyping has also undergone a revolution in the last ten years (Poland et al., 2012; & Elshire et al., 2011). GBS technologies, particularly resequencing or skimGBS-based methods (Voss-Fels et al., 2015; & Bayer et al., 2015), are anticipated to dominate the future of agricultural genotyping as the cost of producing DNA sequence data continues to decline.

The creation of appropriate phenotypic data for trait association has been one of the trait association's bottlenecks (Fahlgren et al., 2015). High-throughput automated glasshouse phenotyping is being used to remedy this, and the use of adapted drones to view and evaluate crops is expanding quickly (Liebisch et al., 2015). These drones are being used more frequently for normal on-farm crop growth evaluation. Expanding remote monitoring as a routine agricultural practice is possible to enable cultivar assessment under various geographic and environmental situations.

The Role of Bioinformatics

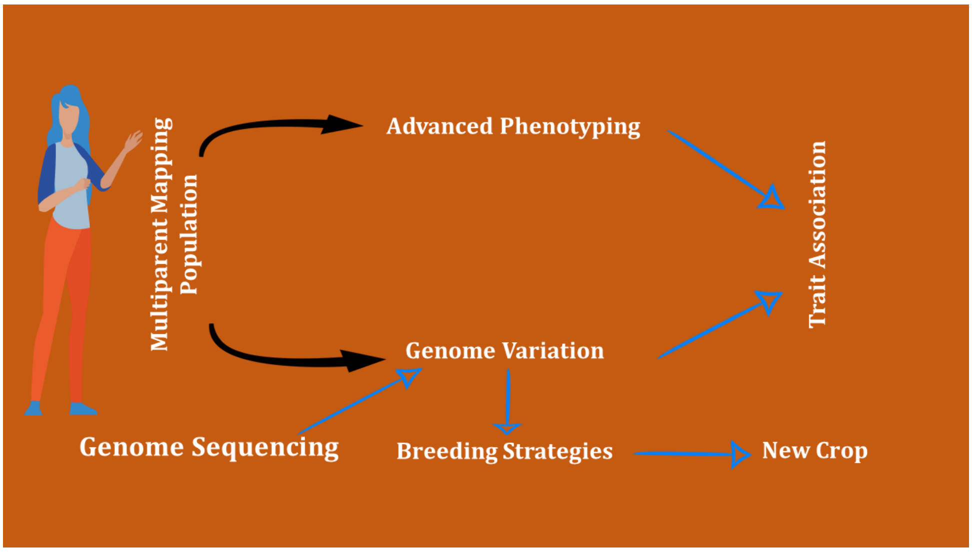
Applying this knowledge for practical crop development is challenging due to the deluge of data from genome diversity research, phenotypic tests, gene expression, proteomics, metabolomics, epigenetics, and other related investigations. The integrated breeding platform (https://www.integrated breeding.net/) and the Triticeae toolbox (https://triticeaetoolbox.org) are two database systems created to manage this information for crop improvement; however, they do not capture the full range of relevant public information, and information related to historical published experiments or genes from related species is particularly absent.

Aiming to compile genomic data and convert it for practical crop improvement are crop-specific information consortia like the wheat information system (http://wheatis.org/) and the rice informatics consortium (http://iric.irri.org/). The normal tabular design of conventional databases cannot effectively manage the numerous connections between data or permit broad queries, which is one of the difficulties of maintaining and integrating such huge and diverse information. Systems like Index (Ko¨hler et al., 2006) and Neo4j (Miller et al., 2013) bring up the possibility to investigate and mine varied data interactions, including historically published data on related species that may be relevant to the crop. New innovations in graph database design give chances to alleviate this constraint.

Although the use of graph databases in genomics is still in its early stages, as they advance and become more complex, they are anticipated to find widespread adoption for both understanding the basics of biology and for creating useful breeding tools.

Global Impact of Climate Change

It is obvious that different parts of the world will see different effects of climate change on agriculture, both in terms of how crops will fare and how well communities will be able to adjust to the changing climate. The intensification of agriculture practised in rich nations has not been seen by many emerging nations, and many regions still rely on subsistence farming of a small number of crop species. Without funding for specific crops and assistance to increase agricultural intensification and related food storage and distribution networks, these regions, which are particularly vulnerable to climate change, are unlikely to greatly benefit from the advances in genomics seen in more mainstream crops. However, when these more extensive changes to agricultural methods are implemented, there will be a chance to quickly progress crops that currently have little investment in reducing breeding cycles and enhancing genetic gain. As established industries invest in and compete for their share of the seed market, varieties for yield, quality, and climatic resilience will continue to advance, which will benefit countries with intensive agricultural production the most in the short term (Picture 1).



Picture – 01

CONCLUSION

Without concerted action to support food security, there is a risk that climate change might cause severe food shortages and widen the global wealth and well-being gap. The development of better crops could be accelerated thanks to developments in genetics and bioinformatics, enhancing global food security in the face of climate change.

Declarations:

Ethics approval and consent: This study has nothing to do with human and animal testing.

Consent for Publication: All the authors consent to publish the current manuscript.

Competing Interest: The authors declare that they have no conflict of interest.

Funding Declaration: It hereby declares that any agency did not fund the current project.

ORCID id: https://orcid.org/0000-0003-0796-5238

REFERENCES

Abberton, M., Batley, J., Bentley, A., Bryant, J., Cai, H., Cockram, J., Costa de Oliveira, A., Cseke, L. J., Dempewolf, H., & De Pace, C. (2015). Global agricultural intensification during climate change: a role for genomics. *Plant Biotechnol J.*

Asseng, S., Ewert, F., Rosenzweig, C., Jones, J. W., Hatfield, J. L., Ruane, A. C., Boote, K. J., Thorburn, P. J., Rotter, R. P., & Cammarano, D. (2013).Uncertainty in simulating wheat yields under climate change. *Nat Clim Change 3*, 827-832.

Bayer, P. E., Ruperao, P., Mason, A. S., Stiller, J., Chan, C. K. K., Hayashi, S., Long, Y., Meng, J., Sutton, T., & Visendi, P. (2015). High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in Cicer arietinum and Brassica napus. *Theor Appl Genet 128*, 1039-1047.

Brozynska, M., Furtado, A., & Henry, R. J. (2015). Genomics of crop wild relatives: expanding the gene pool for crop improvement. *Plant Biotechnol J* http://dx.doi.org/10.1111/pbi.12454.

Cotrufo, M. F., Ineson, P., & Scott, A. (1998). Elevated CO_2 reduces the nitrogen concentration of plant tissues. *Global Change Biol 4*, 43-54.

Edwards, D., Forster, J. W., Chang, D., & Batley, J. (2007). What are SNPs? In Association Mapping in Plants. Edited by Oraguzie, N. C., Rikkerink, E. H. A., Gardiner, S. E., & De Silva, H. N. Springer; 41-52.

Edwards, D., & Batley, J. (2010). Plant genome sequencing: applications for crop improvement. *Plant Biotechnol J 8*, 2-9.

Lawlor, D. W., & Mitchell, R. A. C. (1991). The effects of increasing CO_2 on crop photosynthesis and productivity—a review of field studies. *Plant Cell Environ 14*, 807-818.

Mackill, D. J., Ismail, A. M., Singh, U. S., Labios, R. V., & Paris, T. R. (2012). Development and rapid adoption of submergence-tolerant (Sub1) rice varieties. *Adv Agron 115*.

Xu, K. N., Xu, X., Fukao, T., Canlas, P., Maghirang-Rodriguez, R., Heuer, S., Ismail, A. M., Bailey-Serres, J., Ronald, P. C., & Mackill, D. J. (2006). Sub1A is an ethylene-response-factor-like gene that confers submergence tolerance to rice. Nature (London) 442.

Garrett, K. A., Dendy, S. P., Frank, E. E., Rouse, M. N., & Travers, S. E. (2006). Climate change effects on plant disease: genomes to ecosystems. *Annu Rev Phytopathol 44*, 489-509.

Gregory, P. J., Johnson, S. N., Newton, A. C., & Ingram, J. S. I. (2009). Integrating pests and pathogens into the climate change/food security debate. *J Exp Bot 60*, 2827-2838.

Edwards, D., Batley, J., & Snowdon, R. J. (2013). Accessing complex crop genomes with next-generation sequencing. *Theor Appl Genet 126*, 1-11.

Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., Buckler, E. S., & Mitchell, S. E. (2011). A robust simple genotyping-by sequencing (GBS) approach for high diversity species. PLoS One 6.

Fahlgren, N., Gehan, M. A., & Baxter, I. (2015). Lights, camera, action: high-throughput plant phenotyping is ready for a close-up. *Curr Opin Plant Biol 24*, 93-99.

IPPC: Climate change 2014: impacts, adaptation, and vulnerability, Part A: global and sectoral, aspects. In Contribution of Working Group II to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change. Edited by Field, C. B., Barros, V. R., Dokken, D. J., Mach, K. J., Mastrandrea, M. D., Bilir, T. E., Chatterjee, M., Ebi, K. L., Estrada, Y. O., Genova, R. C., Girma, B., Kissel, E. S., Levy, A. N., MacCracken, S., Mastrandrea, P. R., & White, L. L. Cambridge, United Kingdom and New York, NY, USA: Cambridge University Press; 2014.

Imelfort, M., Duran, C., Batley, J., & Edwards, D. (2009). Discovering genetic polymorphisms in next-generation sequencing data. *Plant Biotechnol J 7*, 312-317.

Ko¨ hler, J., Baumbach, J., Taubert, J., Specht, M., Skusa, A., Ru¨ egg, A., Rawlings, C., Verrier, P., & Philippi, S. (2006). Graph-based analysis and visualization of experimental results with ONDEX. *Bioinformatics 22*, 1383-1390.

Liebisch, F., Kirchgessner, N., Schneider, D., Walter, A., & Hund, A. (2015). Remote aerial phenotyping of maize traits with a mobile multisensor approach. *Plant Methods 11*.

Li, Y. H., Zhou, G. Y., Ma, J. X., Jiang, W. K., Jin, L. G., Zhang, Z. H., Guo, Y., Zhang, J. B., Sui, Y., & Zheng, L. T. (2014). De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. *Nat Biotechnol 32*, 1045.

Lin, K., Zhang, N., Severing, E., Nijveen, H., Cheng, F., Visser, R., Wang, X., de Ridder, D., & Bonnema, G. (2014). Beyond genomic variation—compare.son and functional annotation of three Brassica rapa genomes: a turnip, a rapid cycling and a Chinese cabbage. *BMC Genomics 15*, 250.

Miller, J. J. (2013). Graph database applications and concepts with Neo4j. In Proceedings of the Southern Association for Information Systems Conference; March 23rd–24th, Atlanta, GA, USA.

Miller, M., Song, Q. X., Shi, X. L., Juenger, T. E., & Chen, Z. J. (2015). Natural variation in timing of stress-responsive gene expression predicts heterosis in intraspecific hybrids of Arabidopsis. *Nat Commun 6*.

Poland, J. A., Brown, P. J., Sorrells, M. E., & Jannink, J. L. (2012). Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *PLoS One 7*, e32253.

Springer, N. M., Ying, K., Fu, Y., Ji, T. M., Yeh, C. T., Jia, Y., Wu, W., Richmond, T., Kitzman, J., & Rosenbaum, H. (2009). Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. *PLoS Genet 5*.

Voss-Fels, K., & Snowdon, R. J. (2015). Understanding and utilizing crop genome diversity via high-resolution genotyping. *Plant Biotechnol J* http://dx.doi.org/10.1111/pbi.12456.