



Bioinformatics: Digital Revolution for Climate Smart Horticulture

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INTRODUCTION

Horticulture, a vital branch of agriculture consisting of fruits, vegetables, flowers, spices & condiments, plantation crops, herbal medicinal and aromatic plants, and ornamentals. The importance of horticultural crops is widely recognized in many aspects of innovation, production, for the uplifting economic condition of farmers, quality maintenance, entrepreneurs and thus plays an important role in ensuring food and nutritional security.

Climate change, associated with global warming, rise in atmospheric temperature, changes in precipitation patterns, excess UV radiation, and higher incidence of extreme weather events like heat, salinity, droughts, floods, increasing incidence of weeds, pests, and pathogens, are strongly influencing major cropping systems and emerges as the major threats for horticulture. The changing climate alters the growth patterns and capabilities for flowering and fruiting of many perennial and annual horticultural plants and due to the highly perishability of Horticulture crops, they are more sensitive to unpredictable climatic changes. Thus, the changing pattern of climate adversely affects the production, productivity, and quality of horticultural products besides worsen abiotic stress.

In this challenging scenario, the concept of the Climate-Smart Horticulture approach has to be implemented to improve food security, livelihoods, and resilience under the realities of climate change. The objective of the National Horticulture Mission is to increase the growth of the horticulture sector by conducting research, technology promotion, post-harvest management, processing, and marketing and improving horticulture production, enhance nutritional security and double the income of farmers. This would only be possible with the development of different strategies that expedite the rate of genetic gains developing new and novel varieties that can be adapted and mitigate climate change.

Therefore, new plant breeding strategies with the biotechnological and digital revolution are urgently required to enable the Climate Smart Horticulture crop.

The advent of newer approaches of omics sciences and sequencing technologies has helped us to understand the physiological, genetic, and molecular mechanisms of plants adapting and responding to climate change and the identification of adaptation traits to variable environmental conditions that are triggered by changing climate. Bioinformatics and computational biology enlarge the pace of scientific invention in life science. It is a rapidly expanding field of research as it is essential to extract knowledge from heterogeneous data. Application of various bioinformatics tools in biological research enables storage, retrieval, analysis, and interpretation of big “omics” data, annotation, and visualization of results, and promotes a better understanding of the biological systems

in fullness. The field of bioinformatics with traditional computational biology and biostatistics is strictly concerned with handling and retrieving information that has profound impacts on different fields. For instance, it plays an important role to detect the metal from Metagenomic sequencing obtains from contaminated soil thus improve nutritional quality and growth in poorer soils (Singh et al., 2011). The 5Gs breeding approaches along with cutting -edge technology and Bioinformatics can accelerate pace to ensure food security for a growing population and changing climate by bringing disruptive changes to crop improvement (Fig. 1). Using in silico genomics technology researchers can identify defense/ disease resistance gene-enzyme with their promoter region and transcription factor which help to enhance the immunity and defense mechanism, thus improve plant resistance against biotic and abiotic stresses.

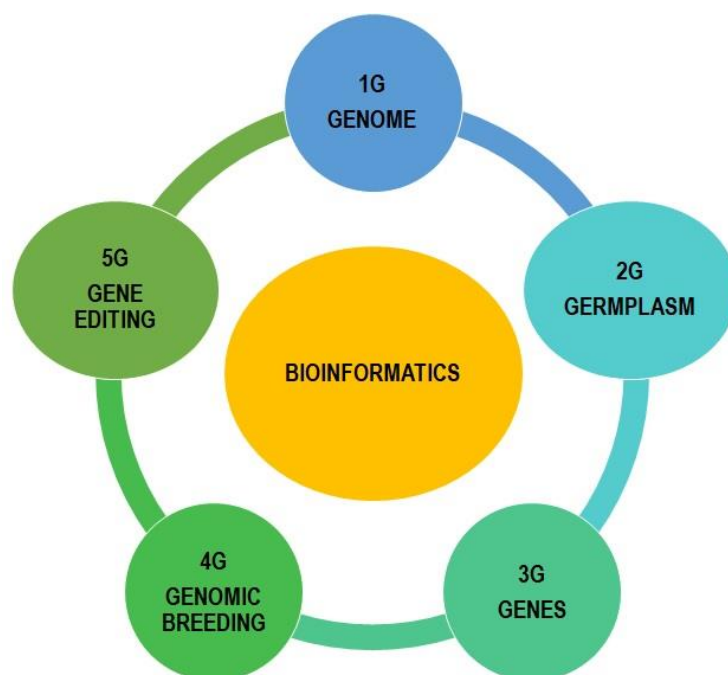


Fig. 1: 5Gs and Bioinformatics for Climate-Smart Agriculture

The rapid development of high throughput sequencing and related technologies, such as PacBio single-molecule real-time (SMRT) sequencing, Oxford Nanopore sequencing, Hi-C, and BioNano optical mapping over the past

10 years have greatly facilitated genome assembly and annotation in most of the horticultural plant species and greatly facilitate horticulture research and breeding (Taranto et al., 2018). The horticultural plants genomes

are highly diverse and complex, with a high degree of heterozygosity and a high ploidy due to long and complex history of evolution and domestication. Horticultural species have contributed significantly to the recent revolution in genomics, with many fruits, vegetables, and nut crops now sequenced. The availability of these genome assemblies makes molecular research, genome editing, and marker-assisted breeding possible in species previously recalcitrant to molecular genetic research and thus provide horticulturists and biologists with valuable new tools to develop new varieties more efficiently and understanding the molecular determinants of key traits unique to horticultural species. Further, the establishment of various online databases provides easy access and interaction with genomic data. These databases help organize genomic resources, facilitate data sharing, and enable genome comparison across different species.

Chen et al. 2019 and Li et al. 2021 reported the sequenced genomes of 181 horticultural species that include 4 beverages, 47 fruit, 44 medicinal, 44 ornamental, and 42 vegetable plants. Most of them are the Rosaceae family, including many popular fruit-bearing and ornamental plants. Genome Database for Rosaceae (GDR) (www.rosaceae.org) is, by far, the best resource hub for Rosaceae research. It hosts the most comprehensive and up-to-date collection of genome assembly and annotation versions for widely studied genera, *Fragaria*, *Malus*, *Prunus*, *Potentilla*, *Pyrus*, *Rosa*, and *Rubus*. For cucurbits, the Cucurbit Genomics Database (CuGenDB; <http://cucurbitgenomics.org>), a central portal for the cucurbit research and breeding community, has been developed using the Tripal toolkit (Zheng et al., 2019). The database contains all available genome and expressed sequence tag (EST) sequences, genetic maps, and transcriptome profiles for cucurbit species, as well as sequence annotations, biochemical pathways,

and comparative genomic analysis between different cucurbit species.

The first citrus-specific comprehensive database, the citrus genomic variation database (CitGVD, <http://citgvd.cric.cn/home>) was developed dedicated to genome-wide variations including single nucleotide polymorphisms (SNPs) and insertions/deletions (INDELs). CitGVD integrates closely related information on genomic variation, related gene annotations, and details about the organisms, that can be used for genetic structure analysis (Li et al., 2020).

Chauhan et al. 2014 reported the development of the Fruit Crops Diseases Database (FCDD) (<http://www.fruitcropsdd.com/>) that helps to develop strategies to improve fruit crops diseases productivity. The FCDD is a unique bioinformatics resource that assembles information about 162 details on fruit crops diseases, diseases type, its causal organism, images, symptoms, and their control. The FCDD contains 171 phytochemicals from 25 fruits, their 2D images, and their 20 possible sequences.

Moyle et al. 2005 reported the development of the Pineapple DB database (<http://www.pgcl.com.au>) that provides integrated access to annotated expressed sequence tag (EST) data for cDNA clones isolated from pineapple fruit, root, and nematode infected root gall vascular cylinder tissues. The database currently consists of 5600 EST sequences, 3383 contig consensus sequences, and data on splice variants, Arabidopsis homologs, both MIPS-based and Gene Ontology functional classifications, and clone distributions. The online pineapple bioinformatics resource provides the research community with access to pineapple fruit and root/gall sequence and bioinformatic data in a user-friendly format. The search tools enable efficient data mining and present a wide spectrum of bioinformatics and functional classification information.

Yue et al. 2015, reported the development of FR database 1.0 (<http://www.fruitech.org/>), using manual curation from 38 423 articles published before 1 April 2014, and integrating protein interactomes and several transcriptome datasets. This database gives information of 904 genes derived from 53 organisms that participate in fleshy fruit development and ripening. Genes from climacteric and non-climacteric fruits are also annotated, with several interesting Gene Ontology (GO) terms being enriched for these two gene sets and seven ethylene-related GO terms found only in the climacteric fruit group. Furthermore, protein-protein interaction analysis by integrating information from the FR database presents the possible function network that affects fleshy fruit size formation.

CONCLUSION

In the 21st century, agriculture and horticulture face new challenges, largely due to the need to increase global food supply under the declining availability of arable lands and increasing threats from climate change. Therefore, new breeding strategies are required to develop cultivars resilient to climate change. Since, in recent decades, a large amount of transcriptomics, genomics, genetic and breeding data of the horticultural crops has been generated. Thus, the structuring and digitalization, analysis, and interpretation of these big “omics” data provide support to the breeders and agricultural biotechnologists. Such coordination of information along with data exchange, data transfer, and improved analytical capacity help to develop Climate-Smart Horticulture, enabling the ability to cope with food security while facing the challenges of climate change in the near future.

REFERENCES

- Chauhan, R., & Jasrai, Y. (2014). FCDD: A Database for Fruit Crops Diseases. *Bioinformation* 10(9), 595-598.
- Chen, F. (2019). Genome sequences of horticultural plants: past, present, and future. *Horticulture Research*. 6, 112.
- Li, M., Xiao, Y., Mount, S., & Liu, Z. (2021). An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. *Frontiers in Plant Science*. doi: 10.3389/fpls.2021.644881.
- Li, Q. (2020). CitGVD: a comprehensive database of citrus genomic variations. *Horticulture Research*. 7, 12.
- Moyle, R. L., Mark, L., & Crowe, M. L. (2005). PineappleDB: An online pineapple bioinformatics resource. *BMC Plant Biology*. 5(21). doi: 10.1186/1471-2229-5-21.
- Singh, V. K., Singh, A. K., Chand, R., & Kushwaha, C. (2011). Role of Bioinformatics in Agriculture and Sustainable Development. *International Journal of Bioinformatics Research*. 3(2), 221-226.
- Taranto, F., Nicolia, A., Pavan, S., De Vita, P., & D'Agostino, N. (2018). Biotechnological and Digital Revolution for Climate-Smart Plant Breeding. *Agronomy* 8, 277.
- Yue, J., & Ma, X. (2015). FR database 1.0: a resource focused on fruit development and ripening. Database 1–8. doi: 10.1093/database/bav002.
- Zheng, Y. (2019). Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. *Nucleic Acids Research*. 47, 1128–1136.