



Sneha Murmu

ICAR-Indian Agricultural Statistics
Research Institute
New Delhi
India

Asit Kumar Pradhan

ICAR-National Rice Research Institute
Cuttack
Odisha
India

Himanshushekhari Chaurasia

ICAR-Central Institute for Research on
Cotton Technology
Mumbai
India

Dilip Kumar

ICAR-National Institute of Agricultural
Economics and Policy Research
New Delhi
India

Ipsita Samal

Sri Sri University
Cuttack, Odisha
India

Corresponding Author

Asit Kumar Pradhan
asitpradhan20672@gmail.com
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Impact of Bioinformatics Advances in Agricultural Sciences

Over the past decades, a large amount of scientific data has been generated, especially in the fields of genomics and molecular biology. Bioinformatics, an interdisciplinary scientific field that applies information technology in the form of advanced computational tools, can be effectively used to the processing and management of biological data. Biological and agricultural sciences have evolved into data-driven sciences due to extraordinary technological innovations over the last few decades. The opportunities, challenges and consequences of this revolution are enormous and can only be seen in the long term. Bioinformatics offers greater insight into the underlying biological mechanisms and how biological processes influence the networks of genes, proteins, and metabolites that regulate biological processes in organisms. Extensive omics data such as genomics, proteomics, transcriptomics and metabolomics have been generated from various field of agriculture that includes crop science, livestock, fisheries and horticultural science. Bioinformatics tools and methods can be used in a variety of ways to extract meaning information of such huge collection of data. In this article, we have attempted to highlight the importance and impact of application of bioinformatics advances in agriculture and discuss some of the computational resources relevant to the field of agro-informatics.

INTRODUCTION

Particularly in the areas of genomics and molecular biology, a tremendous amount of scientific data has been produced during the past few decades. Biology, statistics, computer science, physics, and

chemistry are just a few of the fields that are combined in bioinformatics. It played a crucial role in the analysis of data from biological research. According to its definition, bioinformatics is an interdisciplinary scientific subject that uses advanced computational tools and information technology to process and manage biological data. More specifically, genetic content, biological sequence data, and macromolecular structure and function are examined and predicted using bioinformatics. Bioinformatics has already had a significant impact on the fields of agriculture, biotechnology, energy, environment, and human health.

The biological and agricultural sciences, with their extraordinary technological innovations, have evolved into data-driven sciences in the past few decades. The possibilities, challenges, and consequences of this revolution are enormous and can only be seen over the long term. Bioinformatics can provide means to get a deeper insight into the underlying biological mechanisms and reveal how biological processes affect the networks of genes, proteins, and metabolites that regulate the biological processes of an organism. Such efforts will have a significant impact on agricultural productivity, address the impacts of climate change on crops, induce adaptations to biotic and abiotic stresses among organisms. Moreover, bioinformatics analysis can help understand interactions between pathogens and host plants and animals, and control environmental processes, including next-generation crops and biofuels, global carbon management, and remediation of polluted environmental resources.

Research efforts in experimental molecular biology and whole-genome sequencing projects around the world have generated large amounts of nucleotide and protein sequencing data. Traditional molecular biology research is still carried out using sophisticated machines, with an increasing generation of large and diverse datasets that require the use of computational power for effective interpretation. Extensive data have been collected in the fields of genomics, proteomics, transcriptomics and metabolomics. Therefore, the project uses computational techniques to gather biological knowledge from the literature and other public databases to address the challenges of analysis and interpretation. Computer applications are a viable future option for agricultural sciences to track, identify and timely implement today's agricultural problems). By integrating information about the most important biological processes, the long-term goal is to fully understand the biology of an organism. Hence, there are reasons to strengthen the burgeoning field of bioinformatics.

OMICS IN AGRICULTURE

The entire genetic makeup of an organism, or its nuclear DNA content, is represented by its genome. Organelles, like the mitochondrial and chloroplast genomes, can also contain genetic material in addition to the nucleus. Only plants contain chloroplasts. The information found in chromosomal DNA is typically the only information used in the genomic analysis of eukaryotic organisms. Such analysis now includes the sequencing of the genomes of animals and plants for agricultural purposes similarly as human genomes are studied for clinical uses. For instance, efforts in plant genomics research are frequently directed at lowering crop production costs, enhancing the security and quality of the food supply, increasing throughput capacity, and enhancing the efficacy and efficiency of plant breeding procedures.

The emerging field of OMICS science encompasses genomics, transcriptomics, proteomics, and metabolomics and seeks to combine all segmented sciences into a holistic biological approach called systems biology. Plant, animal, fish, and microbial whole-genome sequencing projects are on the rise, as are proteomics and transcriptomics-related projects.

BIOINFORMATICS IN AGRICULTURE

Bioinformatics is becoming more and more crucial in the field of agricultural genomics for the gathering, storage, and analysis of a wide range of omics data. There are numerous applications for bioinformatics tools and techniques in agriculture. Increasing plant tolerance to biotic and abiotic stresses and enhancing the nutritional quality of nutrient-poor soils are its main uses. The application of bioinformatics in agriculture has been collectively termed agro-informatics.

In addition to these objectives, genetic discovery using computer software has enabled researchers to improve seed quality, incorporate micronutrients into plants to improve human health, and develop plants with phytoremediation capabilities.

PLANT PROTECTION

Insect genomics must be taken into account, in addition, to plant genome organization when researching insect-plant interactions since it is crucial for determining the mechanisms underlying both bio-resistance and prospective targets in plants. For instance, the genome of the bacterial species *Bacillus thuringiensis*, which is frequently found in soil, has attracted attention because it generates proteins that are poisonous to some insects. Crops including cotton, maize, and potatoes have benefited from the introduction of several isolated genes from the *Bacillus thuringiensis* in order to strengthen plant defenses against insect attack and minimize or do away with the need for some chemical treatments. Different genetic strategies have been utilized to enhance plant defenses against abiotic stress in addition to using genomics to increase plant tolerance to biotic stress. The capacity of plant roots to endure the negative impacts of abiotic stress is principally responsible. If the soil around their roots is healthy and biologically varied, plants have a better chance of surviving harsh situations. They may not be able to respond to this kind of stress rapidly enough because they are extremely sensitive to environmental changes, such as excessive heat or cold. Computational methods and in-silico genomics approaches must be combined with research on transcription factors, promoter areas, and genetic enzyme disease resistance in order to protect plants from these kinds of situations. By boosting particular genes linked to higher resistance mechanisms, researchers may be able to improve plant immunity by finding these genetic patterns.

NUTRIGENOMICS

Nutrition genomics, commonly referred to as nutrigenomics, is the study of the human genome and how nutrition and health are related to it. Nutrigenomics is used by the agricultural sector to identify genes in certain plant species that can be used as dietary disease therapies. The introduction of genes that can raise iron, micronutrient, and vitamin A levels in rice is one example of how nutrigenomics is used in agriculture. Individuals may experience psychological repercussions from anemia brought on by iron insufficiency and blindness brought on by vitamin A deficiency, respectively. As a preventive measure, rice with higher nutritional content can be beneficial.

IMPROVING SOIL QUALITY

In addition to assisting researchers in enhancing the nutritional value of crops meant for human consumption, bioinformatics may also offer details regarding the presence of particular toxins in the soil. The majority of soils have extremely complex microbial communities that are made up of various gene sequences. Metagenomics sequencing can be used to identify enzymes with the potential to degrade harmful elements with the aim of eventually removing these components from the soil.

COMPUTATIONAL RESOURCES IN AGRO-INFORMATICS

The collection, storing, and analyzing of omics-based data are the main focuses of bioinformatics used in plant and animal biology. Numerous resources have been developed by various research groups for plant and animal study. Some of them are mentioned in Table 1.

Table 1. Bioinformatics resources for different domains of agriculture that includes crop science, fisheries, horticultural science, and animal science.

Sl.No.	Resources	Description	Available at URL
Crop Science			
1	TamiRPred	A web server to predict putative miRNA in wheat	http://webtom.cabgrid.res.in/tamirpred/
2	VISTa	A variety identification system for wheat	http://webtom.cabgrid.res.in/vista/
3	CbLncRNAdb	This database contains information related long non-coding RNAs of cluster bean and miRNAs with which it interacts.	http://cabgrid.res.in/cblncrnadb/
4	GinMicrosatDb	It consists of huge number of SSRs, their distribution on linkage groups, five sets of primers along with their flanking sequences and physical map.	http://backwin.cabgrid.res.in:8080/Gingelly7/
5	Pipemicrodb	This database contains microsatellites marker information of pigeon pea.	http://webapp.cabgrid.res.in/pigeonpea/
6	VmTDB	It provides the extensive transcriptome information of moong (<i>Vigna mungo</i>).	http://webtom.cabgrid.res.in/vmtdb/
7	VigSatDB	This database includes in-silico identified microsatellite markers that were extracted from seven assemblies of three <i>Vigna</i> species <i>Vigna radiata</i> , <i>Vigna angularis</i> , and <i>Vigna unguiculata</i> .	http://webtom.cabgrid.res.in/vigna_ssr/
8	WDRoTDb	It provides the transcriptome characterizations of NI5439 (drought resistant) and WL711 (drought susceptibility) genotypes of wheat.	http://webtom.cabgrid.res.in/wdrotdb/
Fisheries			
1	Fish Karyome	It provides collection of cytogenetic information of fish besides other aquatic organisms. The information includes morphology, chromosome number, sex chromosomes, karyotyping, and cytogenetic markers.	https://mail.nbfgr.res.in/Fish_Karyome/
2	FMiR	It is a comprehensive and curated database of complete mitochondrial genome of fishes belonging to different ecosystems that includes precise tools for data analysis and retrieval of information on taxonomy, habitat, distribution,	https://mail.nbfgr.res.in/fmir/

		occurrence and conservation status of fishes.	
3	FishMicrosat	It is a fish and shellfish microsatellite database.	https://mail.nbfgr.res.in/fishmicrosat/
4	FBIS	It is a platform that supports and manages the collection, storage, analysis, and exploration of DNA barcode records of fish and other aquatic organisms for identifying the diseases, taxonomic ambiguity resolution, and molecular genetic analysis. purpose.	https://mail.nbfgr.res.in/fbis/
5	FishAMP	Antimicrobial Peptide Prediction Server for Fish.	http://webapp.cabgrid.res.in/fishamp/
6	LrSATdb	It is transcriptome database of genes associated with seasonality in carp fish, Labeo rohita (Rohu).	http://webtom.cabgrid.res.in/lrsatdb/
Horticultural Science			
1	BANSATDB	This database contains information related to Banana microsatellites marker.	http://webtom.cabgrid.res.in/bansatdb/
2	MangoSNPs	This database contains SNPs (Single Nucleotide Polymorphisms) marker of mango.	http://webtom.cabgrid.res.in/mangosnps/
3	The Onion Genomic Resource	It is a comprehensive information on genomic resources of onion.	http://webtom.cabgrid.res.in/ogr/
4	Small Cardamom Mosaic Virus Transcriptome Database (SCMVTDB)	It contains the transcriptomic information of small cardamom mosaic virus.	http://webtom.cabgrid.res.in/scmvtdb/
5	Sugar Beet Microsatellite Database	It is a database of microsatellite marker of sugar beet whole genome.	http://webapp.cabgrid.res.in/sbmdb/
6	TomSatDB	This database contains microsatellites present in the whole genome sequence of tomato. The microsatellite marker consists of simple and compound.	http://webapp.cabgrid.res.in/tomsatdb/
7	CnTDB	It is transcriptome database of seasonality associated genes in coconut.	http://webtom.cabgrid.res.in/cntdb/
Animal Science			
1	BIScattle	Breed Identification Server for Cattle	http://webapp.cabgrid.res.in/biscattle/
2	GOMI	Goat Microsatellite web server for prediction of Indian goat breeds	http://webapp.cabgrid.res.in/gomi/
3	CattleAMP	Antimicrobial Peptide Prediction Server for Cattle	http://webapp.cabgrid.res.in/amp/
4	SNPRBb	Trait Specific SNP Resources of Bubalus bubalis	http://cabgrid.res.in:8080/snprbb/home.php

5	Bufsatdb	Buffalo Microsatellite marker Databse	http://webapp.cabgrid.res.in/buffsatdb/
6	Livestock Epigenetic Database	This database can be used to analyze data of different mechanisms in livestock species viz., cattle, goat, sheep, buffalo and camel.	http://bioinformatics.iasri.res.in/edil/histone_proteins.html

CONCLUSION

The potential of bioinformatics in other fields of fundamental cell biology is also clear, as is its influence on the development of omics in plants, animals, and aquatic life. Recent research has examined their contributions to the growth of allied sectors like crop protection. The need to extend omics from models to agriculturally significant species will present the challenge for the agricultural research community in the next years. The integration of multiple omics data is very important. The creation and use of systems that allow for flexible access to a wide range of biological data will speed up the rate at which bioinformatics can be used to characterize, contrast, and analyse omics data that is crucial to agriculture.