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Role of Bioinformatics in Tuber Crop Improvement

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Abstract

Biological informatics' abbreviated to Bioinformatics, uses a massive number of computational approaches for the analysis, management and storage of vast range of biological data. The number of in-silico approaches is helping in generating and analysing the tuber crop data for the crop production enhancement and disease management by sequence alignment and analysis, drug discovery, gene-pathogen interaction and dynamic simulation. Here, in this article we have given a short glance at the role of bioinformatics in tuber crop improvement as well as given some databases containing specific tuber crops related genomic level information.

Introduction

Bioinformatics is presently defined as the structuring of biological data to assign an understanding of natural phenomena. It is crucial in numerous fields of biology, *i.e.*, plant biotechnology, genetics, molecular biology, and physiology. It embraces an assembly of biological information, storage, management of data, and software development for the study of large data sets. Mathematical tools and computer programs like statistics and algorithms are essential for data analysis (Edwards and Batley, 2004). Rapid growth in proteomics and genomics results in vast amount of biological data. These data need sophisticated computational analysis to depict conclusions. The importance of this new field of investigation is expanding due to the rise of vast amounts of proteomic, genomic, and other biological data formation. Due to exponentially increasing data, the need for tools and methods in integration, data management, visualization, modeling, and prediction increases similarly (Kushwaha *et al.*, 2017). Presently, the technologies based on the genomic level have directed the progress of vast amounts of information, resulting in a gradual rise in biological knowledge attained for plant research and numerous areas of biology, specifically the biomedical sciences. With the advent of Next-Generation Sequencing (NGS) techniques and various omics technologies, the application of bioinformatics in plant biotechnology have expanded, thus allowing data integration across various omics platforms to reveal information on proteome, transcriptome, genome, metabolome, and metabolic pathway of different plant species (Edwards and Batley, 2004).

Tuber crops, *i.e.*, sweet potato, yam bean, greater yam and cassava, are considered essential vegetable crops, staple food in some countries, and used as raw materials for some small-scale industries at the global level, especially in less developed tropical countries. The tuber crops have an antiquity of saving human kind in the eras of famine. Specific bioinformatics study is essential to attain sustainable production of tuber crop along with various biotechnological analyses. Thus,

different bioinformatics approaches like proteomics, drug designing and drug development, genomics, metabolomics, and transcriptomics may be used to enhance tuber crop production, thus improving the livelihood of humankind.

Applications of Bioinformatics in Agriculture

Bioinformatics plays a vital role in the growth of the agricultural sector, agricultural by-products utilization, agro-based industries and better management of the environment. Along with the rise of sequencing projects, bioinformatics makes considerable progress in biology by handing scientists access to genomic information. There is an intense that it will take another giant leap in this field in the next decade, where computational methods of systems and broad properties could provide the basis for innovation and experimentation. Agricultural bioinformatics areas that need focus would be our data curation and the need for the use of restricted vocabularies. Bioinformatics, an interface between modern informatics and biology, includes inventions, growth, and application of computational algorithms and software tools that quickly make to understand the biological processes to serve primary agriculture and healthcare sectors with several spin-offs (Kushwaha et al., 2017).

Bioinformatics Approaches for Tuber Crop Improvement

NGS technologies make the extraction of whole genome shotgun DNA sequencing possible. Thus, this technology is now considered one of the preferred genome sequencing technology due to its long-read length, improvised assembly algorithm and considerably reduced cost. Accordingly, a number of advantages is also observed nowadays, i.e., the genomes sequenced the most from crops or non-model plant species and different essential tuber crops. Hence with the help of this technology, innumerable information, which further allows an increased number of applied scientific methodologies for data analysis in the particular crops. The metabolomic and proteomic analysis in sweet potato and cassava leaves have given new insights into how ecotype-specific traits are developed and observed the biochemical processes in the root development of cassava leaves (Shekhar et al., 2016). Fernandez et al. (2021) carried out a genomic study on yam bean species (*P. erosus*). They performed gene annotation and found 37,886 genes and over 10 million SNP's. This analysis will help other researchers during the genomic study of underutilised crop (Fernandez et al., 2021). Thus, the analyzed data may provide a platform for genetic, proteomic, and metabolomic improvement of vital tuber crops (Figure 1). Presently, certain bioinformatic approaches are helping in analysing the pathogens affecting tuber crops. Acharya et al. (2022) worked on the coat protein of Yam Bean Mosaic Virus (YBMV) affecting Yam bean crop.

Thus, the results analysed will further pave the way for researchers to control the YBMV virus affecting yam bean crop (Acharya et al., 2022).

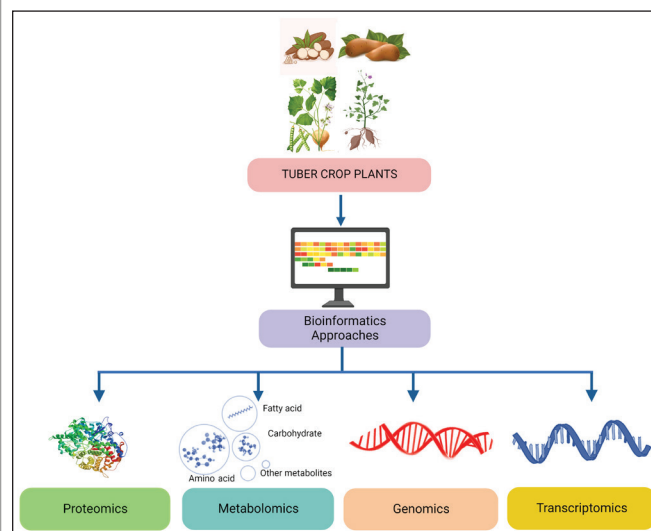


Figure 1: The different approaches of bioinformatics used for tuber crop data analysis

Bioinformatics Databases for Data Repositories

Genomics, one of the bioinformatic approaches, consists of databases that play a crucial role in the tool kit of bioinformatics, which can be described as the organization of biological information to facilitate logical inquiry. Many databases have been created on various platforms and for multiple uses (Table 1). Similarly, several specific databases are generated for genomic data repositories containing genomic level information listed below (Table 2).

Table 1: List of Genomic Databases repositories of different plants and animal species

Name of the Database	Web link
DNA Data Bank of Japan (DDBJ)	http://ddbj.sakura.ne.jp/
autoSNPdb	http://autosnpdb.appliedbioinformatics.com.au/
European bioinformatics institute, EnSEMBL plants	http://plants.ensembl.org/
European Molecular Biology Laboratory (EMBL) nucleotide sequence database	http://www.ebi.ac.uk/embl/
GenBank	http://www.ncbi.nlm.nih.gov/genbank

Table 1: continue...

Name of the Database	Web link
International Crop Information System (ICIS)	http://www.icis.cgiar.org
International Nucleotide Sequence Database Collaboration (INSDC)	http://www.insdc.org
Phytozome	http://www.phytozome.net/
PlantGDB	http://www.plantgdb.org/
Panzea	http://www.panzea.org/
The Plant Ontology Plaza	http://www.plantontology.org/ http://bioinformatics.psb.ugent.be/plaza
PlantsDB	http://mips.helmholtz-muenchen.de/plant/genomes.jsp
SSR taxonomy tree	http://appliedbioinformatics.com.au/projects/ssrtaxonomy/php/
The Crop Expressed Sequence Tag database, CR-EST	http://pgrc.ipk-gatersleben.de/cr-est/
SSR Primer	http://flora.acpfg.com.au/ssrprimer2/
SOL Genomics Network (SGN)	http://solgenomics.net

Table 2: List of databases developed containing specific tuber crops related genomic level information

Name of the crop	Database Name	Web link
Cassava (<i>Manihot esculenta</i>)	cassavabase.org	http://www.istrc.org/links-to-similar-projects/229-root-and-tuber-crops-databases
Greater Yam (<i>Dioscorea alata</i>)	yambase.org	http://www.istrc.org/links-to-similar-projects/229-root-and-tuber-crops-databases
Sweet Potato (<i>Ipomoea batatas</i>)	sweetpotato-base.org	http://www.istrc.org/links-to-similar-projects/229-root-and-tuber-crops-databases
Sweet Potato (<i>Ipomoea batatas</i>)	Sweet potato Genomics Resource	http://sweetpotato.uga.edu
Cassava (<i>Manihot esculenta</i>)	Cassava Genome Hub	https://cassavagenome.org/?q=organism/manihot-esculenta-cassava

Conclusion

In-silico biological approaches are being used to design new techniques, methods, and experiments to enhance plant production by improving the quality of tuber crops. These require statisticians and informatician experts as well as proper complete focus and specific research exposures relating to tuber crops to achieve more valuable data for further analysis to discover its disease management or enhancement in production.

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