Plant Bulletin Vol 2, (2) 2023: 88-92 ISSN: 2959-3379 (Print), 2959-3387 (Online)

Review Article

The application of genomics and bioinformatics tools to recognize soybean pathogen interaction in a changing climate

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ABSTRACT

The changing climate and continuously increasing global population has posed immense pressure on plant scientists to ensure per capita availability of food under scarcity of natural resources. The present circumstances also enforce to understand how rising CO2 level caused greenhouse effect in the environment which causes rise in the temperature and consequently influence the development of plant disease epidemic, to predict the genomic-based models under changing environmental conditions and to ensure continued food production. The application of genomics and bioinformatics tools are the innovative approaches to understand plant pathogen interaction and prediction that offers unique opportunities to enhance plant yield, stability in quality and production, boost the resilience of soybean to integrate resistance genes in present cultivars to sustain yield under epidemic disease conditions in abruptly changing climate. However, genomics data can be used for genomic based selections and advanced bioinformatics tools can be used to make predictions for genotype by pathogen interaction whereas it had ever been remained a great challenge to homogenize the diverse genomic data to which advanced skills and expertise are required in handling bioinformatics tools. Bioinformatics and genomics have the potential to sustain yield for food security by selection of tolerant or resistant genetic combination for disease sensitive environments as well as to facilitate for maintaining food security and mitigate the effect of inversely changing climatic conditions.

Keywords: Genomics, bioinformatics, plant pathogen interaction, climate change

INTRODUCTION

The world is facing an abrupt change in the climatic conditions that is resulting variation in the human activities that include, burning of fossil fuel, rise in carbon dioxide and chlorofluorocarbon accumulation due to frequent use of cooling appliances [1]. Apart from variation in the normal profile of atmosphere, the climate change is also having a significant impact on the host-pathogen interaction and the accurate prediction of change are much difficult to quantify due to complexity of the factors [2]. The changing climatic conditions are continuously influencing the rainfall patterns that will lead to shift in the cropping patterns of specific regions and hence will have unquantifiable impact on the plant pathogen interaction [3].

All the predicted fluctuations in the climate will not have spontaneous negative impact on crop productivity but increased carbon dioxide and chlorofluorocarbons concentrations may stimulate photosynthetic efficiency, diminish water loss by transpiration and may lead to increase net productivity [4].

With the passage of time, the unpredictable spontaneous changes in the climatic conditions are likely to disrupt global food supplies, consequently the immediate actions are required to ensure global food security. In addition to abruptly changing climate, new varieties/ germplasm is urgently required which exhibit tolerance to biotic and abiotic stresses and demonstrate greater nutrient use efficiency [5].

Article History
Received: September 12, 2023, Accepted: December 11, 2023, Published: December 30, 2023

Advances will predominantly be occurred by improving resistance in soybean through adopting genomics and bioinformatics approaches as well as adoption of new plant species which have not previously been considered for domestication [6].

Soybean Status in Pakistan

The consumption of oilseed crops is increasing tremendously owing to the increase in the global population, but under the prevailing circumstances it is difficult to fulfill the needs. Consequently, the import bill for oilseed crops has enhanced to over 192.00 billion rupees during 2015-16 in Pakistan. Soybean (Glycine max L.) is a crop of economic significance in the world under the production of 282.4 million tons [7]. In Pakistan, total oilseeds production was 4.3 million metric tons during 2016-17 (USDA Foreign Agency, 2018). Soybean has high nutritional value as it contains Lipids (19.40%), proteins (39.40%), Ash (4.05%), crude fiber (6.70%), carbohydrates (25.15%) and moisture (5.3%) per 100 grams [8].

Successful production of soybeans is facing numerous constraints of fungal, bacterial and viral diseases owing to non-availability of disease-free seeds. Among these constraints, brown leaf spot of soybean, caused by Septoria glycine, is the most destructive disease in Pakistan which is deteriorating the quality and quantity of Soybean. In the world an estimated annual loss owing to this disease is US$ 220 billion while in Pakistan, the disease has significantly reduced the production of soybean and caused yield loss of 10-60%, with disease incidence of 50-70% under humid conditions [9].

The appearance of fungal brown spots on leaves, decaying and stunting are the characteristic symptoms of brown leaf spot of soybean. The whole plant appears to be chlorotic and undergoes premature defoliation of leaves, it has brown to blackish spots, reduced photosynthetic area and consequently there is death of the plant [10].

Interaction of disease under changing climatic conditions.

Diseases in plants occur due to interaction of the susceptible host plant, virulent pathogen, and compatible environmental conditions. The significance of the environmental conditions on the development of plant diseases is known from two thousand years ago when Theophrastus (370-286 B.C.) observed that plants grown in higher altitude with direct exposure to wind, exhibited minimum disease incidence as compared to plants cultivated in lower altitude regions [11].

As a consequence of abrupt environmental changes, the average global surface temperature has increased by 0.2°C per decade in the past 30 years [12]. A continuously changing environment influences atmospheric CO2 level, relative humidity, wind velocity, rainfall, susceptibility/ resistance of host plant, pathogen reproduction, dispersal, survival and the plant-pathogen interaction. An increase in global atmospheric CO2 level subsequently influences plant growth, transpiration rate and nutritional value of food, as well as reducing nitrogen content. Similarly, temperature and relative humidity pose direct impacts on production, germination and survival of thermophilic pathogen propagules whereas leaf wetness also accelerates the growth of foliar pathogens, along with other environmental factors [14].

Temperature requirements for infection and disease development differ extensively among pathogen species. In general, prolonged temperature, precipitation, and humidity lead towards disease epidemics [15].

One often overlooked dreadful impact of climate change is the unpredictable fluctuation in the resistance and virulence of soybean pathogen interaction. A greater understanding of pathogen virulence and host resistance mechanism is likely to reduce the impact of pathogens in soybean and developed countries. The sudden changes in global climate enforce research to investigate the impact of environmental factors on the emergence of disease and plant pathogen interaction to ensure global food security [16].

The Application of Genomics

The ever-increasing population and climate change is creating numerous problems, particularly food shortage and plant diseases. A yield increase of 11 -13% in major crops is most importantly required to feed the world and alleviate hunger in 2050 (Fischer et al., 2009). Consequently, the evolution in biological research is exploring new tools and opportunities which are instigating researchers to conduct experiments on such aspects that were previously unimaginable i.e. genomics. In novel discoveries of genomics, numerous genes on a whole genome are studied simultaneously. A whole genome sequencing provides valuable information to identify locus linked with disease resistance and crop breeding. Applications of genomics can be used for genomic selection and genome wide associations-based approaches provides opportunities to identify resistant genes associated with specific lines or genotypes that can be used as parents for breeding and integration of resistance genes in the present cultivars. Resistance genes provide resistance against diseases and help to sustain yield inducing a hypersensitive response [17].

The constantly increased application and adaptation of genomics in every field of life, specifically in agriculture, is timely, appearing when world food production is facing the dual challenges of unexceptional population growth and abrupt climate change. Whole genome sequencing and genome wide association studies are very useful for crop improvement. Whereas genomic selections are very crucial for breeding and selection. The major types of heritable genomic diversity include structural variation and single nucleotide polymorphisms (NSPs) that are more commonly used for the marker assisted selection. The molecular markers that are developed from SNPs possess the resolution of single nucleotide and are much abundant across the genomes [18].

Mapping of traditional traits can be performed on pairwise progeny crosses which have comparatively low resolution owing to inadequate recombination and have insufficient ability to measure broader effects of multi-gene interactions. The most recent trait mapping methods have been applied to multi parent populations namely nested association mapping (NAM) and magic (multiparent advanced generation intercross) populations. These populations have provided greater resolution because of the higher frequency of recombination captured [19].

The revolution and evolution has also occurred in genotyping population from the last decade which has gone from PCR based single markers like simple sequence repeats to highly parallel SNP based markers by using genotyping arrays through providers namely Ilumina and Affymetrix as well as the most currently genotyping by sequencing (GBS) approaches [20]. These approaches such as GBS and mainly resequencing or skinGBS based methods have dominated the future of crop genotyping and reduced the cost of generating DNA sequencing data [21].

One of the most pivotal ways for trait association is the production of proper phenotypic information for trait association [22]. It is being addressed by using the high throughput automated glasshouse phenotyping and the rapid enhancement is the utilization of modified drones to observe and evaluate the crops [23]. The use of these drones is rising tremendously in agriculture, especially in soybean at Iowa state university for assessing the crop growth and remote monitoring to assess the cultivars grown under diverse geographical and climatic conditions [24].

The role of Bioinformatics

Bioinformatics is an organized information system for molecular biology as well as an application of numerous techniques derived from mathematics, statistics, biochemistry, and computer sciences. It provides complicated information for structural, functional, and comparative genomics. The amount of DNA sequencing and bulk quantitative data is exponentially increasing so, it is considerably more difficult to store, manage and exploit huge data without the application of bioinformatics. Thus, bioinformatics tools help to make predictions from the available data [25].

Bioinformatics tools are essential in analyzing and interpreting genome data to make predictions about phenotypes, contributing significantly to this process such as Sequence Alignment and Assembly, Variant Calling, Functional Annotation, Pathway Analysis, Phenotype Prediction, Structural Variant Analysis, Comparative Genomics, Epigenomics Analysis, Phylogenetic Analysis etc. Bioinformatics tools enable researchers to analyze genome data, providing insights into genetic basis of phenotypes and disease management advancements [26]. Genomic prediction or genomic selection uses high-throughput phenotypic data to predict an individual's genetic merit, useful for breeding and agriculture, using statistical models like, Collect High Throughput Phenotypic Data, Generate Genomic Data, Data Preprocessing, Genomic Prediction models, Training the model, Validation, Genomic Prediction and Selection Decisions etc. [25]. Bioinformatics plays a critical role in identifying and developing disease-resistant traits in soybeans through Genomic Sequencing, Identification of Candidate Genes, Comparative Genomics, Functional Annotation, Marker-Assisted Selection (MAS), Genome-Wide Association Studies (GWAS), Pathogen Genomics, Expression Profiling, Network Analysis, CRISPR/Cas9 Technology and Data Integration. Likewise, Bioinformatics aids in genomic selection, a process that uses statistical models to predict the genetic merit of individuals based on their genomic information like, Genomic data generation, Data preprocessing, Genomic prediction models (Genomic Best linear unbiased prediction (GBLUP) Bayesian methods, Machine learning models), Training the genomic prediction model, Validation, Marker contribution analysis, Optimizing model parameters and Application in Breeding programs [27].

Future Perspectives of Bioinformatics and Genomics

Bioinformatics is becoming the most essential interdisciplinary scientific field for analyzing “omes” data. There is need of well qualified and integrated software knowledge for new generation scientist with multilingual abilities as well as cross field experiences who are fully capable of handling sophisticated operating system, softwares and algorithms, databases/ networking technologies for handling analyzing and interpreting complicated biological data [28]. The goals related to bioinformatics information dissemination can be accomplished through globally coordinated institutions of bioinformatics courses, online trainings, web based educational platforms, research conferences, workshops and providing online materials in developing countries with innovative platforms, training techniques, providing better funding opportunities, web and network access, and high-performance based computing systems [29].

The tools of bioinformatics need to be developed for analysis of pan genomics, metagenomics, metabolomics and proteomics data in biological research. Similarly, it is also dire need for "effective bioinformatics tools" to perform adequate genome assembly and annotation with high accuracy which requires improved quality sequenced genomes without gaps, sub-genomes, sequence of additional genome representatives, genomes of single cells, polyploidy species as well as some tissues that would produce information to work, amend and proper bioinformatics algorithms along with programming approaches [30].

Similarly, there is also need to integrate and prepare sequenced genome data much functional by constructing an organized, user friendly, metabolic pathways and cell wide biological networks with superior visualization effects, knowledge based construction and graphics outputs, but high throughput phenotyping and real-time imaging systems are required that would help to determine the meaningful biological associations between genomics and phenotypic data, advancement in the translational sciences and personalized medicine and/or agriculture [31].

Conclusion

The resistances/ susceptibility in soybean and virulence in pathogens is adversely affecting the production and consumption due to global climate change which desperately created health implications in developing countries due to unavailability of balanced nutritious diet. Novel approaches in genomics and bioinformatics retain the potential to accelerate the production by understanding the accurate plant pathogen interaction and improving the global food security in the situation of abrupt climate change. SoyXpress is designed for this purpose to explore the transcriptomic differences in genotypes. Similarly, soybeans EST sequences, microarray and pathway data and searchable as well as browsable gene ontology is also integrated and presented to face the current challenges under global climate change.

Acknowledgement

The author acknowledges the Agriculture Department, Government of Punjab, Pakistan for providing adequate funding for promotion of oilseed crop under climate change scenario and Dr. Muhammad Atiq, Assistant Professor Department of Plant Pathology for positive criticism, co-operation and instigation in write up of the current review.

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