

# Addressing the complexity of Stress Biology through Hi-throughput Omics Data Analysis using Bioinformatics Tools: A National Bioinformatics Workshop Report

Anil Kumar<sup>1\*</sup>, Apoorv Tiwari<sup>1</sup>, Rajesh Kumar Pathak<sup>1</sup>, Gohar Taj<sup>1</sup>, A.K. Tewari<sup>2</sup>, Dinesh Pandey<sup>1</sup>, B.R. Singh<sup>1</sup>, Sandeep Arora<sup>1</sup> and N.K. Singh<sup>3</sup>

<sup>1</sup> Department of Molecular Biology & Genetic Engineering, College of Basic Sciences & Humanities, G. B. Pant University of Agriculture & Technology, Pantnagar-263145, Uttarakhand, India.

<sup>2</sup> Department of Plant Pathology, College of Agriculture, G. B. Pant University of Agriculture & Technology, Pantnagar-263145, Uttarakhand, India.

<sup>3</sup> Department of Genetics & Plant Breeding, College of Agriculture, G. B. Pant University of Agriculture & Technology, Uttarakhand, Pantnagar-263145, Uttarakhand, India.

\*Corresponding author: Anil Kumar; email: [anilkumar.mbge@gmail.com](mailto:anilkumar.mbge@gmail.com)

Received: 02 January 2017

Accepted: 06 February 2017

Online: 14 February 2017

## ABSTRACT

Biotic and Abiotic stresses such as drought, temperature extremes and salinity are the major constraints towards the living world more specifically the plant kingdom whose developments as well as crop yield is negatively hampered. Biotechnological approaches, including all the 'omics' have immense potential to help in circumventing biotic and abiotic stress-related issues. Successful application of omics on biotic and abiotic constraints requires advanced knowledge of stress response at molecular level like gene expression to protein or metabolite and its phenotypic effects. Such advances will ensure the availability of the sequenced genomes of model crop plants, along with the possibility of next generation sequencing, thereby increasing the potential to greatly facilitate the 'omics' approaches. Advances in these omics techniques will help in illuminating the genetic structure of plants and thereby allow the full deployment of genetic resources for crop improvement. For instance, a number of bioinformatics and systems biology tools for sequence assembly and annotation, transformation systems, and genomic DNA libraries have been developed following the release of the genome sequences of important model crop plants. In this report, our major emphasis was to acquaint the participants on how to increase stress tolerance in crop plants by using advanced computational technologies and skills in bioinformatics as we progress towards the systemic use of high-throughput sequencing in agricultural research. This will enable to develop the capacity for resolving the complexity of stress biology for enhancing the crop productivity.

**Keywords:** Biotic, Abiotic, Omics data, Gene expression, Assembly, Annotation, Stress Biology.

## 1. INTRODUCTION

Today, in a world of more than 7 billion people, big challenges are faced by agriculture to ensure the food and nutritional security by maintaining high productivity with quality standards [9-10]. The consensus prediction is that the global climate changes

will undermine plant growth conditions and in turn productivity due to severe fluctuations in temperature and erratic weather conditions. These adverse conditions will not only lead to induction of abiotic stresses but also most likely favor the spread of plant pathogens and pests into new geographic areas. Losses

due to pests and diseases in crop plants continue to pose a major threat to agriculture and food security [10]. *In-silico* study to identify and analyze different biochemical molecules like isoflavonoid phytoalexins may improve the plant defense mechanism against pathogen infection [10, 17]. Such a scenario increases the need to develop resistance against biotic as well as abiotic stress in crop plants systems at a speed that cannot be met by breeding alone [2-3]. Addressing these major challenges will require an interdisciplinary and concerted approach. Understanding the molecular mechanisms underlying plant resistance or tolerance helps us to develop fruitful agricultural strategies [10]. The creation of modern systems biology comes from the need to gather information from genome-scale studies and being able to present them in biological interpretations [1-4, 6-7, 15-16,].

Bioinformatics is playing a key role to establish a link between the information encoded in genomic sequences to the observed behavior of living organisms. Bioinformatics web resources and tools are capable of recognizing the hidden biological information [6-8, 11-15, 18]. A major goal of this four-day workshop is to appreciate the harnessing of the potential of huge genomics data by the professionals and exchange their scientific ideas to develop new research avenues to sort out these challenges [9]. Besides, it had also provided a platform to young professionals for presenting new strategies for addressing the complexity of stress biology through hi-throughput OMICS data analysis using modern bioinformatics tools [5, 10, 18-24].

With the above background, National Bioinformatics training workshop entitled “Addressing the complexity

of Stress Biology through Hi-throughput Omics Data Analysis using Bioinformatics Tools” was organized from 04<sup>th</sup>-07<sup>th</sup> October 2016 to give exposure to the participants with a theoretical and practical understanding of high-throughput OMICS data analysis and its interpretation through Bioinformatics and Systems Biology tools. The contents of training were planned with the intention that it can be a starting point for participants to enter in this advanced area of *in silico* Biology [10, 12].

The major objectives of the workshop were centered around to understand the complexity of stress biology in order to cope up with the simultaneously challenged by different biotic, as well as abiotic stresses. In this 4 days national workshop the major objectives that were covered are

1. Demonstration of Various OMICS-based Instruments used in Stress Biology for decoding the intricacy of Host-pathogen Interaction and provides raw data for Bioinformatics investigations.
2. Hands-on exercise of Assembly & annotation of sequencing data for identification of resistance genes for molecular breeding and genetic manipulation.
3. Protein Structure Prediction, Validation, Visualization and Molecular docking studies for Identification of agriculturally important molecules for the protection of Crop Plants.
4. Pathway modeling, Network analysis and simulation studies to predict the behaviour of Biological systems during stress conditions for management of agriculturally important diseases.



**Figure 1: Inaugural Function of the National Bioinformatics Training/Workshop-2016. (A)** Lightening by Dr. R.S. Chauhan, Chief Guest of the function. **(B & C)** Lightening by Dr. Anil Kumar, Head MBGE, and Dr. A.K. Shukla, Acting Dean CBSH. **(D)** Inaugural speech by Dr. Anil Kumar.

With response to our advertisement, we received many applications from various parts of our country. Total 27 participants were selected based on first come first serve basis. These participants are from different states of our country such as Uttar Pradesh, Uttarakhand, Madhya Pradesh, Punjab, Haryana, Tamil Nadu, New Delhi, Kerala, and Jammu & Kashmir and are Faculty

members, Ph.D. students and research staff of various national institutions. Prof. R.S. Chauhan, Dean (Biotechnology) Prof. & Head Biotechnology & Bioinformatics at Jaypee University of Information Technology, Wanknaghat, Solan, HP was the Chief Guest who inaugurated of the national Training Workshop. Dr. Chauhan delivered an Inaugural address of

workshop and highlighted the importance of bioinformatics tools and high-throughput genomics to unravel the complexity of host-pathogen interactions. He described briefly about the comparative genomics, cloning and functional characterization of genes controlling disease resistance in rice blast an important fungal pathogen.

Later our Research Fellows Dr. Manoj Singh, Dr. Supriya Gupta and Dr. Pallavi Shah demonstrated the various instruments of OMICS such as Genomics, Proteomics, Transcriptomics and Metabolomics and its application in Stress Biology. In the afternoon, Dr. Anil Kumar, Professor and Head Molecular Biology and Genetic Engineering, delivered a lecture on topic "Addressing the complexity of Stress Biology through Hi-throughput Omics data analysis by utilizing the power of Bioinformatics and Systems Biology Tools" and addressed the fundamental concepts of stress biology and use of Omics technology, computational tools for experimentation and interpretation of the biological data in context of stress biology. He had discussed various key concepts related to Omics-based bottom up and top down technology and its application in defining systems biology for a better understanding of biological systems with respect to biotechnological research for improving agricultural productivity.

In the 2nd day of the workshop, Dr. A.K. Tewari, Professor, Plant pathology, College of Agriculture, GBPUA&T, Pantnagar delivered a lecture on "Disease Menace: A challenge before biologist for their detection and management". Dr. Tewari highlighted techniques used for plant disease management using diagnostics & remedial treatment by the development of new regimens of biocides. He described how to enhance the production of reactive oxygen species and why Plant disease management is necessary?.

Mr. Apoorv Tiwari, Senior Research Fellow in Sub-DIC Bioinformatics Centre at GBPUA&T, Pantnagar demonstrated and taking a hands-on practical module on "Bioinformatics analysis of Transcriptome data for identification and annotation of genes" using Standalone BLAST tool. After that our research fellow Mr. Ravendra P. Chauhan organized a hands-on module on CyVerse a platform for NGS data analysis.

Dr. Praveen Kumar Verma, Senior Scientist at NIPGR, New Delhi had delivered a very informative lecture on topic "Potential of fungal genomics for deciphering effectors functions involved in Pathogenesis" and described that how fungal pathogens manipulate themselves as well as plant cells to proliferate in a hostile environment. This aspect, he described the novel fungal effectors (Effectoromics) and the genes that counteract host-generated oxidative stress during hypersensitive response and characterization of the genes involved in resistance/or susceptibility, downstream signaling, and characterization of fungal effectors and their mechanism for searching novel targets for the development of new fungicides was also

harnessing. Potential of fungal genomics for deciphering effectors functions involved in pathogenesis by using different computational tools. In afternoon session, Mr. Rajesh Kumar Pathak, from Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi started a practical session on Protein Structure Prediction, visualization, and analysis, and identification of defense inducer/agriculturally important molecule(s) through molecular docking.

The 3rd-day session included a very informatics lecture on topic "Amelioration of Abiotic stresses: Using plant breeding approaches" and delivered by Dr. N.K. Singh, Professor, Genetics & Plant Breeding, College of agriculture, GBPUA&T, Pantnagar. He briefly described how stress biology is important for breeding purposes and enhances the crop productivity.

After that, Ms. Divya Sharma, Mr. Apoorv Tiwari, and Mr. Rajesh Kumar Pathak performed hands on the module on "Genotyping-by-sequencing data analysis: Phylogenetic by TASSEL and Population Structure by STRUCTURE software" [8] and "Modeling of Metabolic and Gene-regulatory pathway using CellDesigner software" respectively.

Dr. Charu Lata, Scientist from National Botanical Research Institute, Lucknow and alumni our MBGE department presented an interesting talk as well as hands-on module on "Application of High-throughput omics data derived from Next Generation Sequencing /Transcriptome analysis in agricultural: An emphasis on abiotic Stresses" and discussed various computational biology approaches for mining of traits linked with stress biology for improving agricultural productivity.

During the workshop, Dr. Rohit Saluja, Scientist (Ramalingaswami Fellow) at AIIMS Bhopal, presented a thought-provoking lecture and organized a hands session on topic "Integration of metabolic signaling, energy transduction, and transcriptional regulation upon exposure to oxidative stresses: A panorama of system biology approaches". Dr. Saluja was taking different hands-on module of basic bioinformatics approaches like ORF prediction, intron and exon prediction in a gene and secondary structure prediction by CFSSP server, etc. In the evening session, Mr. Rajesh Kumar Pathak started a hands-on module on Visualization and analysis of metabolic and gene regulatory network using Cytoscape and provide a key concept to participants for integration and visualization of experimental data generated in past decades to decipher the intricacy of complex diseases in crop plant with example of his studies on *Alternaria* blight: A recalcitrant disease of Brassica crop.

In the 4 days, national training workshop a total of 7 lectures and 8 practical modules equivalent to credit hours of 25 were covered to provide directional flow of information in stress biology.



**Figure 2: Valedictory Function (A)** Dr. Uma Melkania, Dean, CBSH presented a bouquet to Dr. Gulshan Wadhwa, Joint Director, DBT, New Delhi. **(B)** Dr. Anil Kumar, Coordinator Bioinformatics Centre, and Head MBGE presented Workshop report. **(C)** Guest Speaker Dr. Rohit Saluja, Scientist, AIIMS, Bhopal and other Faculty members (Left to Right). **(D)** Participants from 9 different States of India.

### Feedback analysis and conclusions

The workshop drew 27 participants (Fig.3) representing academia, industry, and research organizations from across India. The participants represented 9 different States of India. Participants' feedback was collected from a questionnaire to evaluate the outcome of the workshop. The questionnaire consisted of 15 items divided into sub-domains, ranging from technical expertise to learning experience to hands-on training to hospitality rendered. The domains were titled as overall workshop assessment; talks on bioinformatics, systems biology; technical acumen of trainers; hands-on training; workshop hand-outs; workshop conduct; logistics; outcome evaluation; improvements for future workshops and overall impressions, comments, and suggestions. A scoring system was used to evaluate responses with the ratings accordingly like Need to be relaxed, adequate, somewhat adequate, inadequate,

satisfactory or poor and participants replied positively to all domains. The organizers were gratified by participants' self-analysis of their knowledge, skills, and confidence with respect to combining laboratory exercises with the use of different systems biology during the workshop. Thus, it was clear from the feedback evaluation that the workshop was a considerable success, even with the limitations of long hours required to cover a broad range of material in limited days. This report highlights the recent workshop on "Addressing the complexity of Stress Biology through Hi-throughput Omics Data Analysis using Bioinformatics Tools". Gradual increase in the high-quality hi-throughput data and mathematical modeling of biological processes by using different bioinformatics tools will lead to better strategies to researchers for development of crop varieties for robust agricultural productivity and sustainability.



**Figure 3:** Group photograph of all participants and Organizers with the Dr. J. Kumar Vice Chancellor GBPUA&T, Pantnagar & Dr Gulshan Wadhwa, Joint Director, BTISNET, DBT, New Delhi.

The details about the organization of 'National training workshop' and report along with photographs can be found at the URL <http://www.gbpuat.ac.in/> and <http://www.gbpuat-cbsh.ac.in/>.

## ACKNOWLEDGEMENTS

Authors are grateful to Biotechnology Information System Network (BTISNet), Department of Biotechnology, Government of India, New Delhi for providing financial assistance to Bioinformatics Sub-DIC for conducting quality teaching, training, and research in emerging area of Bioinformatics at Pantnagar.

## 5. REFERENCES

1. Avashthi A., Gautam B., Jain P.A., Tiwari A. et al. (2014). In silico identification of MAPK3/6 substrates in WRKY, bZIP, MYB, MYB-related, NAC and AP-2 transcription factor family in *Arabidopsis thaliana*. *International Journal of Computational Bioinformatics and In Silico Modeling*. 3(4): 454-459.
2. Borges A et al. (2014). Priming crops against biotic and abiotic stresses: MSB as a tool for studying mechanisms. *Frontiers in Plant Science* 5:642.
3. Chang F et al (2012). Reverse engineering biomolecular systems using omics data: challenges, progress and opportunities. *Briefings in Bioinformatics*. 13: 430-445.
4. D. Srinivas Reddy et al. (2012). Grain Legumes (Soybean, Chickpea, and Peanut): Omics Approaches to Enhance Abiotic Stress Tolerance. *Improving Crop Resistance to Abiotic Stress*, First Edition.
5. Garg V.K., Avashthi H, Tiwari A., et al, (2016). MFPPi – Multi FASTA ProtParam Interface. *BIOINFORMATION* 12(2): 74-77.
6. Jian Xue, et al. *BIOINFORMATICS AND ITS APPLICATIONS IN AGRICULTURE*. college of Biological and Agricultural Engineering, Jilin University, Changchun, China.
7. Jing Zhuang, Jian Zhang, Xi-Lin Hou, Feng Wang & Ai-Sheng Xiong (2014). Transcriptomic, Proteomic, Metabolomic and Functional Genomic Approaches for the Study of Abiotic Stress in Vegetable Crops, *Critical Reviews in Plant Sciences*, 33:2-3, 225-237, DOI: 10.1080/07352689.2014.870420.
8. Keyura Katam et al. (2015). Advances in Proteomics and Bioinformatics in Agriculture Research and Crop Improvement. *Proteomics Bioinform* 2015, 8:3.
9. Kumar A et al. (2015). High-throughput Omics Data for mining of important genes/traits linked to Agricultural Productivity: A National Bioinformatics workshop report. *Int J Comput Bioinfo In Silico Model* 4: 749-752.
10. Kumar A, Pathak RK et al. (2015) Systems Biology for Smart Crops and Agricultural Innovation: Filling the Gaps between Genotype and Phenotype for Complex Traits Linked with Robust Agricultural Productivity and Sustainability. *OMICS*. 19: 581-601.
11. Kumar A, Sharma D, Tiwari A, Jaiswal JP, Singh NK, Sood S. (2016). Genotyping-by-Sequencing Analysis for Determining Population Structure of Finger Millet Germplasm of Diverse Origins. *Plant Genome*. Jul;9(2). doi: 10.3835/plantgenome2015.07.0058.
12. Kumar A., et al. (2016). Genotyping-by-Sequencing Analysis for Determining Population Structure of Finger Millet Germplasm of Diverse Origins. *Plant Genome* 9. doi:10.3835/plantgenome2015.07.0058.
13. Mohammad MS Al-Haggar et al (2013). Bioinformatics in High Throughput Sequencing: Application in Evolving Genetic Diseases. *J Data Mining Genomics Proteomics* 2013, 4:3.
14. Pankaj Barah et al (2014). Multidimensional approaches for studying plant defence against insects: from ecology to omics and synthetic biology. *Journal of Experimental Botany*.
15. Pathak RK, Giri P, Taj G et al. (2013). Molecular Modeling and Docking approach to predict the potential interacting partners involved in various biological processes of MAPK with downstream WRKY transcription factor family in *Arabidopsis thaliana*. *International Journal of Computational Bioinformatics and In Silico Modeling*. 2: 262-268.
16. Pathak RK, Taj G et al. (2013). Modeling of the MAPK machinery activation in response to various abiotic and biotic stresses in plants by a system biology approach. *Bioinformation*. 9: 443-449.
17. Pathak RK, Taj G et al. (2016). Molecular modeling and docking studies of phytoalexin (s) with pathogenic protein (s) as molecular targets for designing the derivatives with anti-fungal action on *Alternaria* spp. of Brassica. *Plant Omics*, 9:172.
18. Rupesh Deshmukh et al. (2012). Integrating omics approaches for abiotic stress tolerance in soybean. *Frontiers in Plant Science, Plant Genetics and Genomics June2014|Volume5|Article244 | 2*.
19. Sarvajeet Singh Gill, Narendra Tuteja (2010). Reactive oxygen species and antioxidant machinery in abiotic stress tolerance in crop plants. *Plant Physiology and Biochemistry* 48 (2010) 909e930.
20. Singh V.K. et al (2011). Role of Bioinformatics in Agriculture and Sustainable Development. *International Journal of Bioinformatics Research* ISSN: 0975-3087, E-ISSN: 0975-9115, Vol. 3, Issue 2, pp-221-226.
21. Syeda Fatma Hasan Bukhari et al (2015). Omics approaches and abiotic stress tolerance in legumes. Chapter 13, *Legumes under Environmental Stress: Yield, Improvement and Adaptations*, First Edition.
22. Tiwari A., et al. (2016). Insights using the molecular model of Lipoxxygenase from Finger millet (*Eleusine coracana* (L.)) *Bioinformation* 12(3): 156-164.
23. Vemanna S. Ramu et al, (2016). Transcriptome Analysis of Sunflower Genotypes with Contrasting Oxidative Stress Tolerance Reveals Individual- and Combined-Biotic and Abiotic Stress Tolerance Mechanisms. *PLOS ONE* | DOI:10.1371/journal.pone.0157522.
24. Yadav N., Tiwari A., Garg V.K. (2016). Multiple Sequence Alignment of Model Plants Using Bioinformatics Approach. *International Journal of Agriculture Innovations and Research*. 4(5), 2319-1473.

© 2017; AIZEON Publishers; All Rights Reserved

This is an Open Access article distributed under the terms of the Creative Commons Attribution License which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

\*\*\*\*\*