

High-throughput Omics Data for mining of important genes/traits linked to Agricultural Productivity: A National Bioinformatics workshop report

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Received: 25 September 2015

Accepted: 26 October 2015

Online: 02 November 2015

ABSTRACT

The emerging advanced technologies facilitate the systematic study of the complex agricultural traits and the regulation underlying the phenotype of the biological organisms. In contrast to the classical research before the post-genomic era, the current agricultural research tends to investigate the behaviour of all system components simultaneously. This strategy intends to reveal how the system components collaborate to regulate the system behaviour rather than an attempt to identify the individual function of a component. In context of the agricultural research, the systems based approaches has been exploited to explore the biological regulation controlling agricultural productivity. This report highlighted the importance of Bioinformatics and systems biology tools in OMICS data analysis for mining of important genes/traits linked to agricultural productivity.

Keywords: Bioinformatics, Systems Biology, Omics, Next-Generation Sequencing, Agricultural Productivity.

1. INTRODUCTION

India, as is known for its great culture, is also known for its vast diversity in all spheres of Agriculture from the time immemorial. The six pillars of Agriculture are **soil, water, climate, seeds, peasants and tools**, believed so from ancient days, are true for ever in scientific terms too. Seed is the central and primary input along with the carrier of the entire genetic factors over generations and **yugas**, which is basic for existence, improvement as well as for propagation of any life on this planet. The seeds have provided everything to human and animals all these years and will continue to provide for ever. The seed is frequently cited as sacred in '**Vedas**' folk literature, '**Sharana Sahitya**' and verses. The importance given to seed management in the ancient Indian agriculture was supreme! Every agricultural family had the tradition of identifying the healthiest and the most productive plants among the standing crop, taking special care of

these and saving the seeds derived from these for sowing the next crop. Utmost care was given to store such elite seeds under special conditions so as to prevent any contamination, infection or deterioration in vigour, germination capacity, etc. In fact, there were families specialized in doing such service and making available quality seeds at the time of planting in each season [1- 2].

Agricultural productivity which includes now both food and nutritional security has become a major challenge given the projected need to increase world food supply by about 70% by 2050. Advent of newer approaches of "omics" sciences and technologies will enable to address several issues and challenges faced by modern agriculture and also ensure food and nutritional security. Exploiting the potential of "omics" technologies for agricultural productivity, plant protection and therapeutic purposes has currently

been receiving a lot of attention; most of the effort has been put into demonstrating the possible applications of various “omics” technologies in agriculture [3-7]. Bioinformatics & Systems Biology could be a valuable approach for a systems level understanding of crop plants systems.

It studies crop plant systems by systematically perturbing them, checking the gene, protein and informational pathway responses; integrating these data; and finally, formulating mathematical models that describe the structure of system and its response to individual perturbations. Consequently systems

biology approaches such as integrative and predictive ones hold immense potential in understanding of molecular mechanism of agriculturally important complex traits linked to agricultural productivity. This has lead to identification of some key genes and proteins involved in networks of pathways involved in input use efficiency, biotic and abiotic stress resistance, photosynthesis efficiency, root, stem and leaf architecture and nutrient mobilization [8-11]. The developments in these fields have made it possible to design smart crops with superior agronomic traits through genetic manipulation of key candidate genes [3].



Figure 1: Inaugural session of the National Bioinformatics Workshop-2015.

In the view of the above facts, a four days National Bioinformatics workshop entitled **“High-throughput Omics Data for mining of important genes/traits linked to Agricultural Productivity”** was organized from 9th-12th September, 2015 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, further will be a starting point for entering in this advanced area of *in silico* Biology. In this 4 days workshop the major objectives that were covered are

- Designing Hi-throughput experimentation work-flow for understanding the molecular basis of agricultural traits linked with agricultural productivity
- Making the sense of big data, data analysis, interpretation and its application in crop improvement programme.
- Transcriptome wide identification, assembly, annotation and Expression analysis.
- Phylogenetic analysis, structural and functional annotation, protein modeling and

molecular docking studies for identification of agrochemicals.

- Modeling & analyzing bio-molecular interaction pathway/networks of agriculturally important traits.

With response to our advertisement we received many applications from various parts of our country. 25 participants were selected based on their keen interest and quest to learn basic paradigms of OMICS platform and their analysis. These participants are from different states of our country such as Uttar Pradesh, Uttarakhand, Gujrat, Punjab, Maharashtra, Andhra Pradesh, and are Faculty members, Ph.D. students and research staff of various national institutions.

Prof. G. K. Garg, Ex-Vice Chancellor, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, Ex-Dean, College of Basic Sciences & Humanities, Pantnagar and founder of the Pantnagar Biotechnology Programme was the Chief Guest who inaugurated the function (Figure 1). Dr. Garg delivered an inaugural address on National training workshop and highlighted the importance of bioinformatics tools in agricultural

Productivity. Dr. Dinesh Kumar, Principal Scientist at Centre for Agricultural Bioinformatics, IASRI, New Delhi was the Guest of Honor described the role of computational tools in management and analysis of genomic data and its utility in biotechnological research for the development of smart crops. After that Dr. Kumar delivered a very informative lecture on topic **“Accelerating genetic gain of agricultural germplasm by computational approach: Global status and Challenges before India”**. After lecture he started the hands on module session and demonstrated various tools and databases developed by his team at IASRI, New Delhi. Dr. Kumar has also provided knowledge about how to use ASHOKA (Advanced Supercomputing hub for omics knowledge in agriculture) from GBPUA&T, Pantnagar.

Later our research fellows Dr. Manoj Singh, Dr. Pallavi Shah, Mr. Manu Gaur Ms. Bhawana Negi and Mr. Mohd. Tasleem demonstrated various instruments of *OMICS* such as Genomics, Proteomics and Metabolomics and its application in crop improvement program.

In the 2nd day of workshop, Mr. Ashvani Kumar Mishra from NXGenBio Life Sciences, New Delhi delivered a lecture on **“Genotype by Sequencing (GBS)”** Mr. Mishra highlighted the Next generation sequencing technology for identification and characterization of important agricultural traits and GBS data analysis for

SNP discovery. After that he started practical modules on Tassel software.

Dr. Mahendra P. Darokar, Principal Scientist and Head, Molecular Bioprospection Department, CSIR-CIMAP, Lucknow could not come due to some health problem. However, in his place Prof. Anil Kumar, Coordinator Bioinformatics and Head, Department of Molecular Biology & Genetic Engineering has interacted with participants to highlight about the role of metabolome and metabolic engineering.

Later Dr. Vikram Singh Gaur, alumni of this University and did his Ph.D. from Department of Molecular Biology & Genetic Engineering and currently working as Assistant Professor of Agricultural Biotechnology at College of Agriculture, Balaghat, Madhya Pradesh started practical modules on **“Bioinformatics analysis of Transcriptome data for identification, assembly, annotation and expression analysis of agriculturally important traits”**.

On 3rd day Prof. Anil Kumar, Coordinator Bioinformatics and Head, GBPUA&T, Pantnagar delivered a lecture on topic **“Proteomics: From wet lab to computer”** and provided fundamental concepts of proteomics based experimentation and how to analyze and interpreted these data through computational tools.



Figure 2: A group photo of participants along with organizers in the National Bioinformatics Workshop-2015.

After that Dr. Avinash Mishra from Supercomputing facility for Bioinformatics and Computational Biology IIT, Delhi delivered an informative lecture on **“Prediction of native protein structure amongst decoys of proteins”** and briefly described basic concept of modeling, visualization and analysis of

protein from sequence to structure. Dr. Mishra started a demonstration on **“Protein Structure Modeling, Analysis, validation and molecular docking studies using INVENTUS™(Drug Discovery Software)”** for identification of agriculturally important molecules for crop plant protection.

Later Dr. Mukesh Jain Scientist from National Plant Genome Research Institute, New Delhi presented a very informative talk on “**Next Generation Genomics for Mining Genes/Alleles Associated with Agronomic Traits**” and discussed various computational biology approaches for mining of traits linked with agricultural productivity.

In 4th day of workshop Prof. Anil Kumar, Coordinator Bioinformatics and Head, Department of Molecular Biology & Genetic Engineering, GBPUA&T, Pantnagar tried to elaborate the need of “**Systems Biology in Agriculture: Filling the gaps between genotypes to phenotypes for important and complex traits linked with agricultural productivity**” and provided key concepts of omics based bottom up and top down technology and its application in defining systems biology for better understanding of biological systems with respect to biotechnological research and agricultural productivity.

Nonetheless, the practical hands on modules by the researchers of the bioinformatics centre (Sub DIC) on GBS data analysis, Phylogenetic analysis, structural and functional analysis of proteins sequences, modeling of metabolic and gene regulatory pathway, visualization and its analysis by Mr. Rajesh Kumar Pathak, Mr. Apoorv Tiwari and Mr. Himanshu Avashthi along with Mr. Ram Pratap Singh and Mr. Ganga Dutt Sharma DPAs of the centre was also well taken by the target group and responded with a token of appreciation.

The 4 day national training workshop has conducted a total of 7 lectures and 9 practical modules. The certificate of participation, lectures and modules are also distributed to all participants (Figure 2). The Valedictory function was presided by Dean, College of Basic Sciences & Humanities, Dr. Uma Melkania and gave her concluding remarks on behalf of our Hon'ble Vice-Chancellor, Dr. Mangala Rai.

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/>.

2. 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. NXGenBio Life Sciences, New Delhi, Novo Informatics Pvt. Ltd. New Delhi as well as G. B. Pant University of Agriculture & Technology, Pantnagar are also duly acknowledged for providing all necessary facilities for the organization of this national training workshop.

3. REFERENCES

1. Ramaswami B. (2002) Understanding the Seed Industry: Contemporary Trends and Analytical Issues. Indian Journal of Agricultural Economics. 57: 417-429
2. Mahadevappa M. (2005) Seed Industry - Meeting the increased demand, The Hindu Survey of Indian Agriculture, 183-187
3. 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: A Journal of Integrative Biology. 19: 581-601
4. Kumar A et al. (2014) De Novo Assembly and Characterization of Developing Spikes Transcriptome of Finger Millet (*Eleusine coracana*): a Minor Crop Having Nutraceutical Properties. Plant Molecular Biology Reporter. 1-18
5. Pathak RK 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
6. Goel et al. (2012) *In silico* analysis of expression data for identification of genes involved in spatial accumulation of calcium in developing seeds of rice. OMICS: A Journal of Integrative Biology. 16: 402-413
7. Avashthi H 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: 454-459
8. 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
9. Singh UM et al. (2015) Identification and characterization of calcium transporter gene family in finger millet in relation to grain calcium content. Gene 566: 37-46
10. Gupta et al. (2013) Nitrate signals determine the sensing of nitrogen through differential expression of genes involved in nitrogen uptake and assimilation in finger millet. Functional & integrative genomics. 13: 179-190
11. Singh UM et al. (2014) Transcriptome wide identification and validation of calcium sensor gene family in the developing spikes of finger millet genotypes for elucidating its role in grain calcium accumulation. PLoSOne. 9: e103963.

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