



National Agricultural Innovation Project

Establishment of National Agricultural Bioinformatics Grid (NABG) In ICAR



Crop & Horticultural Domain
National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

CCPI: Dr. Soma S. Marla,
CO-PIs: Dr. M. Grover and Dr. S. Archak

National Agricultural Bioinformatics Grid

Introduction

Successful Genome sequencing of several plant species coupled with advances in molecular biology and genetic engineering opened up new opportunities for increasing crop productivity. Crop genomics has witnessed an explosion in genome data and information. A major task of Bioinformatics is to collect and analyze this available information and make it accessible to crop researchers. There is a need to develop databases and Data ware houses to store the crop genome information and design various bioinformatics analysis tools for extracting meaningful inferences accessible to a crop researchers. Software, data analysis pipelines and web based browsers need to be developed for analysis, visualization, mapping and interpretation of the genomic information. Today there are hardly available any robust crop genome computational facilities in the country. In order to support research needs of crop scientists with a robust computational infrastructural facility the National Agricultural Bioinformatics Grid (NABG) has recently established under Indian Council of Agricultural Research (ICAR) availing funding from NAIP. First Supercomputing Hub for Indian Agriculture- ASHOKA (Advanced Super-computing Hub for OMICS Knowledge in Agriculture) has been established at the Centre for Agricultural Bioinformatics (CABin), IASRI and at National Bureau of Plant Genetic resources (NBPGR), New Delhi, National Bureau of Animal Genetic resources (NBAR), Karnal, National Bureau of Fish Genetic Resources (NBFGR), Lucknow, National Bureau of Agriculturally important insects (NBAII), Bangalore and National Bureau of Agriculturally Important Microbes (NBAIM), Mau, U.P. Super Computing Hub (ASHOKA) consists of two super computers This super-computing hub consists of hybrid architecture of high performance computing having 256 nodes Linux cluster, 3072 cores and 38 Tera Flops computing capability. Crop and Horticulture computational domain centre at NBPGR is equipped with a super computer with a Linux cluster (16 nodes), network and parallel file storage system. Embedded with state of art Bioinformatics software packages such as Velvet, Galaxy, Oasis, CLC-Bio Genomics Work bench, Discovery Studio and Schrodinger to provide high performance computational environment for crop genome sequence data analysis. The super computational environment and Bioinformatics software /workflow/pipelines along with National Biological Computing Portal will be made available to plant biologists across the country.



MANDATE

- Establishment of Super computational Facility embedded with NGS softwares
- Collection, Compilation and Analysis Crop Genome data
- Annotation and storage of crop Genome data
- Identification of computational Issues relating to various crop and Horticultural species
- Establish linkages and provide support to various Institutes of ICAR to address problems of crop computation
- Optimization of Genome data analysis employing Next generation sequence analysis (NGS) techniques environment making use of HPC facility
- Design & Development of Crop Databases and Bioinformatics analysis tools
- Capacity building in Human resource development and organization of Bioinformatics training workshops

ACHIEVEMENTS

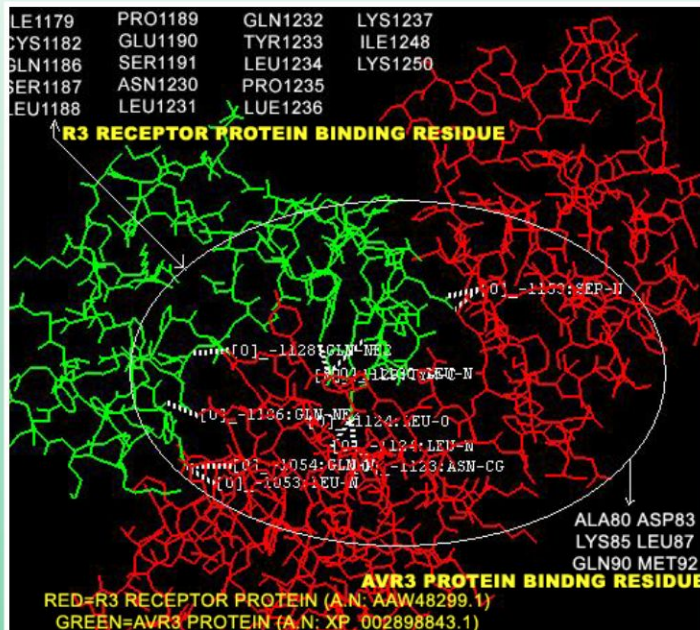
- A robust Super computational facility (40 TB, 16 node) has been established at NBPGR, New Delhi.
- Computational environment has been optimized for analysis of crop genome data generated from different sequencing platforms, employing NGS techniques and software packages such as CLC-Bio Work bench, Velvet, Oasis, Discovery Studio and Schrodinger.
- The facility is being actively utilized for analysis of crop genome data and to discover genes of agronomic importance in Pigeon pea, Sesame and Musk melon.
- Employing Next Generation sequencing Techniques, resistance gene analogues have been predicted for Fusarium wilt disease in Pigeon pea.
- Organized six National Training workshops attended by 140 crop researchers from various State Agricultural Universities and ICAR institutes imparting bioinformatics skills in crop genome data analysis.
- Developed Bioinformatics analysis tools (DPPrimer and EST analysis pipeline) and three crop databases (LabManager), which are available in public online domain for use by crop biotechnology researchers.
- A total of nine research papers are published in various National & international Scientific journals.

IMPORTANT LINKS:

National Agricultural Bioinformatics Grid	http://nabg.iasri.res.in/
DPPrimer- A Degenerate PCR Primer Design Tool	http://202.141.12.147/DGEN_tool/index.html
Plant Pathogen Genome browser	http://www.bioinfo.de/isb/2007/07/0038/).
Lab Companion, A Tool for Organization of Mol Biol. Lab Repository	http://www.ijcse.com/docs/IJCSE10-01-04-21.pdf
Allergen Domain Online: -A database for domains occurring in the allergens	http://nabg.iasri.res.in/allergen/

3-D Modeling of Predicted Avr Proteins and their Docking to Host Potato R Proteins.

Workshop on Gene Expression Data Analysis and Structural Bioinformatics, March, 1-11, 2011



DPPrimer- A Degenerate PCR Primer Design Tool:
 Availability: http://202.141.12.147/DGEN_tool/index.html

DEGEN Tool: Degenerate Primer Design Tool

[Download Contacts](#)

Select input type Protein sequence in fasta format

Enter NCBI protein ID or protein sequence

Job Title

[Optional: Enter a descriptive title for your Degenerate primer search, e.g. Design degenerate primers for SHP1 protein]

Domain Search

This will search domain in your protein sequence using Interproscan tool
[Interproscan scans a given protein sequence against the protein signatures of the InterPro member databases (PROSITE, PRINTS, Pfam, ProDom, SMART, TIGRFAMMs)]

Parameter Selection

[Following are the default parameters. If you want to change parameters, you can change value of parameters]

BLAST sequence identity threshold

Consensus sequence identity threshold

Product size

Tm Difference

Degeneracy

Bioinformatics Lab, National Bureau of Plant Genetic Resources (ICAR), New Delhi

For more information Contact:

Director,
 NBPGR,
 Pusa campus, New Delhi.12
director@nbpgr.ernet.in

Dr. Soma S. Marla
 Principle scientist,
 Division of Genomic resources
 CCPI, NABG NBPGR, New Delhi.12
 Web: <http://www.nbpgr.ernet.in/Personnel/Scientists/tabid/4226/sid/118/Default.aspx>
 Email: soma.marla@nbpgr.ernet.in

Dr. Anil Rai
 Principle Investigator
 NABG, CABI,
 IASRI, New delhi.12
anilrai@iasri.res.in