

Functional Genomics: Application in Crop Improvement

Amaresh¹ and Aswini Nunavath²

¹Ph.D Scholar, Division of Genetics, Indian Agricultural Research Institute, New Delhi

²Ph.D Scholar, Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agricultural University, Hyderabad

SUMMARY

Functional genomics is branch of genomics which describes the function, interactions of gene(s), proteins and metabolites in an organism. Functional genomics have three branches namely, Transcriptomics, Proteomics and Metabolomics. Various techniques and databases are available currently which deals with functional genomics. Functional genomics have several applications in crop improvement which plays important role in developing stress tolerance crops with higher yield.

INTRODUCTION

Functional genomics is the branch of genomics deals with function of gene, gene product and interaction of gene product. It characterize the function of sequences determined by structural genomics. Functional genomics is a trait wise study. Knowing the precise sequence and location of all the genes of a given plant is the first step to understanding how all the parts of a biological system work. In this regard functional genomics is the significant method to converting quantity into quality to crop improvement. Functional genomics is a universal method to understanding how the genes of a creature work together by assigning particular functions to unknown gene(s). There three branches, namely, Transcriptomics, Proteomics and Metabolomics.

Transcriptomics:

Includes set of rRNA, tRNA, mRNA, miRNA, lncRNA, snoRNA, etc. produced in one or more population. It varies with tissue, Environment, Splicing and editing.

The transcriptome of an organism is defined as:

- All the mRNAs and other RNAs expressed throughout the life cycle of the organism.
- All mRNAs and other RNAs expressed in each cell or tissues of an organism.
- All mRNAs and other RNAs expressed under all conditions in an organism.
- All mRNAs and other RNAs expressed in all tissues of an organism

Transcriptomics or transcriptome Analysis the is the investigation of all RNA sequences made by an organism defining when and where in an organism each one is made. As such, quantitatively measuring the level of every mRNA the organism makes in every tissue, and in response to various environmental signals are major goals of transcriptomics

Techniques of transcriptomics

- Northern hybridization
- EST development
- RT-PCR
- RNA-seq
- Micro-array
- RACE
- qRT-PCR

Proteomics:

Branch of functional genomics which deals with characterization of proteins which includes,

- Protein identification and quantification
- Studying protein-protein interaction
- Studying post translational modification

Proteomics refers to all of the proteins expressed in organisms, their structure, and when and where they function in the organism and in cells.

Proteomics could be considered:

- A catalog of all proteins expressed throughout the life cycle of the organism.

- A catalog of all proteins expressed in each cell or tissues of an organism.
- A catalog of all proteins expressed under all conditions in an organism.
- A catalog of all proteins expressed in all tissues of an organism.
- Understanding the structural properties of proteins.
- Analyze the function of all proteins in an organism
- To understand how proteins of an organism interact with each other.
- To understand how proteins of an organism are modified & regulated

Techniques for Proteomics

- MALDI-TOF
- 2D-Gel electrophoresis
- Yeast two hybrid system
- Protein micro-array

Metabolomics:

The metabolome is the total metabolite pool in an organism, which can be measured to characterize genetic or environmental variations. Involves identifying and quantifying of metabolites and chemical footpaths of cellular regulatory processes in different biological organisms. Metabolomics plays a important role in exploring environment–gene interactions, mutant characterization, phenotyping, identification of biomarkers. Metabolomics is a auspicious method to decipher various metabolic networks that are linked with biotic and abiotic stress tolerance in plants. In this situation, metabolomics-assisted breeding enables effective screening for yield and stress tolerance of crops.

Techniques for metabolomics

- Nuclear magnetic resonance spectroscopy (NMR)
- Liquid chromatography mass-spectroscopy (LC-MS)
- Gas chromatography-mass spectrometry (GC-MS)
- High performance liquid chromatography (HPLC)
- Direct flow injection (DFI) mass spectrometry

Tools for functional genomics in crop plants

- NCBI BLAST: To search homology between sequences. It compares nucleotide or protein-protein sequences to sequence databases (<http://www.ncbi.nlm.nih.gov/projects/mapview/>)
- EMBL (European molecular biology lab): Used for Nucleotide sequence.
- Gene Bank: For Nucleotide Sequence.
- GenMAPP: To visualize gene expression and other genomic data on maps representing biological pathways and grouping of genes.
- GRAMENE Data base: Gramene is a curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species (<http://www.gramene.org>)
- AgBase: Functional genomics resource for agriculture (<http://www.agbase.msstate.edu/>)
- PFGD: Functional genomics of phytophthora–plant interactions (<http://www.pfgd.org>)
- PlantsT: A functional genomics database for plant transport proteins (<http://plantst.sdsc.edu>)
- RAP-DB: Rice annotation project database (<http://rapdb.dna.affrc.go.jp/>)
- SFGD: Soybean functional genomics database (<http://bioinformatics.cau.edu.cn/SFGD/>)
- TFGD: Tomato functional genomics databases (<http://ted.bti.cornell.edu/>)

Application of functional genomics in crop improvement

- Differential gene expression analysis
- Transcriptional profiling
- Identification of splice variants (Isoforms)

- Novel gene identification
- Transcriptome assembly- Map of exon, intron boundaries
- SNP finding
- Genome wide regulatory networks to improve Traits
- Diversity analysis
- Evolutionary relationship
- Gene fusion
- Alternative splicing
- Novel transcribed regions
- Allele-specific expression
- RNA editing
- Transcriptome for non-model organism
- Gene interaction study
- Study co-expression of genes
- Protein identification and quantification
- Studying protein-protein interaction
- Studying post translational modification
- Discovery of gene(s),proteins and metabolites responsible for tolerance to various stresses
- Environment–gene interactions
- Identification of biomarkers

CONCLUSION

With ever increasing population, decreasing arable land functional genomics tools are important which play significant role in developing crops which withstand to adverse conditions with higher yield.

REFERENCES

- Bunnik, E. M., & Le Roch, K. G. (2013). An introduction to functional genomics and systems biology. *Advances in wound care*, 2(9), 490-498.
- Maghuly, F., Myśków, B., & Till, B. J. (2021). Functional Genomics for Plant Breeding. *International Journal of Molecular Sciences*, 22(21), 11854.
- Mittler, R., & Shulaev, V. (2013). Functional genomics, challenges and perspectives for the future. *Physiologia plantarum*, 148(3), 317-321.