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Application of functional genomics in agriculture

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Abstract

Area of genomics revolves around the study of genes and gene functioning. It is broadly sub categorized as structural genomics, functional genomics, comparative genomics, epigenomics, translational genomics and pharmacogenomics. Functional genomics, highlighted in this account, links the organism's genome to its function and phenotype. It could be further subdivided into proteomics, transcriptomics and metabolomics and could be studied by reverse genomic techniques like RNAi and mutagenesis. In agriculture, functional genomics finds its application in generation of crop plants with highly improved agronomic traits so that the exponentially increasing population is well fed, today and in near future. With high through-put and next generation approaches, functional genomics might help in circumventing hindrance in achieving food security. Though crucial, this approach involves meticulous planning and efficient policy making along with brotherhood from whole scientific fraternity in achieving the marvels in agriculture field, of which this technology is very well capable of.

Keywords: Functional Genomics, Agriculture, Crop Improvement, Food Security, Major concerns

Introduction

Over the past decade, invention of high-throughput technologies for DNA and protein analysis has revolutionized the ways in which cells could be investigated. Within a relatively short time frame, research has leaped from studying individual genes and proteins to analyzing entire genomes and proteomes. The integration of information extracted from studying the various processes that occur within a cell provide a wholesome picture of how genes give rise to biological functions, and aids in understanding the biology of organisms, in both healthy and diseased state.

Genomics deals with the study of full genetic complement of an organism, differentiating it from genetics, study of the composition and activity of single gene^[1]. The aim of genomics is to discover genes that code for Mendelian and complex traits, and to utilize the knowledge gained from such studies to address problems in fundamental (e.g. biochemical and developmental biology) and applied biology (e.g. agricultural, industrial, medical and environmental applications) as well as in product development^[2]. Genomics bifurcates broadly into structural genomics (deciphering of the nucleotide base composition of gene sequences) and functional genomics (regulation and expression of genes, at the level of DNA, RNA (transcriptome) and protein (proteome))^[3].

The field of functional genomics, per se, deals with description of the functions and interactions of genes and proteins in an organism by making use of genome-wide approaches such as genome and RNA sequencing, as opposed to the gene-by-gene approach of classical molecular biology techniques. It includes a systematic analysis of mRNA and protein expression, exploration of gene product interactions and their influence on different phenotypical traits to define gene functions. It combines data derived from the various processes related to DNA sequence, gene expression, and protein function, such as coding and non-coding transcription, protein translation as well as protein-DNA, protein-RNA, and protein-protein interactions. Together, these data are compiled into numerous databases which are used to model interactive and dynamic networks that regulate gene expression, cell differentiation and cell cycle progression^[4].

Functional Genomics and Agriculture

The goal of agriculture is to improve crop productivity and quality of agricultural produce and simultaneously keeping the ecological balance. Methods and techniques developed in molecular biology have offered a commendable support to various aspects of agriculture like agronomy, crop breeding, etc.

Adoption of approaches *viz.* structural and functional genomics will help in designing new and effective engineering techniques for crop improvement and addressing food security, eventually [5].

Whole genome sequencing of a number of important plant species started from *Arabidopsis thaliana* (2000), ranging from rice (2002) to chickpea (2013) and presently has reached till sequencing of diploid ancestors of peanut (2016), holds a pivotal role in accomplishing huge success in crop improvement programs observed in recent decades [4, 6]. These reference genomes serve as the basis for comparative studies within or among species and as a framework for a wide variety of functional genomics approaches. In addition, projects like 'DBT propelled project to create mutant resources for functional genomics in rice' [7] might be crucial in availing a better understanding of inter and intra-specific variations in a crop's genome.

Recent biotechnological advances are commoditizing functional genomics platforms, enabling researchers to apply high throughput, whole genome studies to an increasing range of species. This means that in a relatively short period of time these techniques, once limited to a handful of species though with complete genome sequences, will be used for studying a myriad of biological systems. As agricultural researchers adopt these new techniques, the scope of functional genomics studies will increase not only in number, but also in the range of agricultural systems in terms of applicability. There are many different techniques for utilizing functional genomics approach and in addition to that innovative high through-put technologies are accelerating the amount and complexity of data being collected.

Functional genomics is context dependent and is typically used to measure the degree of changes occurring in a biological system when subjected to perturbation (e.g., in time series such as growth or disease progression, or in comparison such as affected versus non-affected) as phenotype is influenced by both genotype and environment. Although based at a genome-wide level, functional genomics predicates on molecular biology to provide individual molecular interaction data (including pathways analysis) for their functional modeling [8].

Plant genomics forges to improve our ability to pinpoint the genotypes with optimal agronomic traits in order to improve yield, issue of great importance to combat increasing world hunger. Advances in our understanding of gene function and the availability of genomic maps along with a better understanding of genetic variation will alter the way plant breeders identify genes underlying traits and manipulate the same.

Different approaches of functional genomics include:

- 1. Transcriptomics:** studies of gene expression at the transcript or RNA level, including both mRNA and ncRNA gene expression in a cell
- 2. Proteomics:** approaches which focus on proteins being expressed in a biological system but also include study of protein structures.
- 3. Metabolomics:** studies the metabolome, i.e. all metabolites in a biological system at a given time under a defined genetic background
- 4. Interactomics:** studies the molecular interactions between host and pathogen and encompasses such interactions. This branch has specific relevance to agriculture systems, under crop protection category, per se.

- 5. Nutrigenomics:** studies effect of food and food constituents on gene expression. It focuses on identifying molecular level interaction between nutrients and other dietary bio-actives with the genome.

The "Omic" era has entered into a very crucial phase where functional genomics has taken up the focal role of addressing issues regarding function of genes at different levels pertaining to crop improvement regime. This demands a brief mention of some reverse genetic tools which might come in handy for better understanding of genes and their functions.

1. RNA interference (RNAi):

The use of RNAi to eliminate messenger RNA is a novel approach to understand gene function. Owing to its exquisite specificity and controllability, the technique is chosen over conventional methods to locate gene function at particular developmental and physiological stages [9].

2. Mutagenesis:

Recently, newer approaches combine mutagenesis with sensitive methods to instigate diversity in model crop species, as was done in maize by introducing its Ac-Ds transposable element into heterologous species [10]. Another pioneering way is TILLING (Targeted Induced Local Lesions in Genomes) [11] which was recently used to develop two Ug-99 stem rust resistant wheat varieties [12].

3. Examining non-coding regions:

Once termed "junk" DNA, it is becoming clearer that the presumed non-coding regions can carry regulatory and protein-coding information. Thus, researchers need to be aware that strategies for sequencing large genomes that focus on single copy sequence (assumed a gene) against repetitive DNA sequences, may miss regions of the genome that are important for explaining phenotypic variation [13].

Genomics and Functional Genomics in Agriculture: Current Status

Release of genome sequences of model crop plants in past two decades has significantly aided in acceleration of the crop improvement regime in agriculture. It initiated with sequencing of the small genome of *Arabidopsis thaliana* in 2000 that grabbed considerable attention by researchers worldwide and soon became cornerstone of modern plant molecular biology (The Arabidopsis Genome Initiative 2000). Nowadays, *Physcomitrella patens*, a bryophyte is gaining popularity among scientists for functional analysis experiments. Owing to multitude of properties it possesses like small genome size (just thrice the size of *Arabidopsis* genome), dominant haploid gametophytic stage and its ability to integrate transforming DNA at high frequency by way of homologous recombination, *Physcomitrella* is gaining popularity as the new model plant for functional analysis [8]. *Oryza sativa*, two strains of rice (*indica* and *japonica*) became the first crop plant whose genome was sequenced and released in 2002 [14, 15].

Since then innovative biotechnological tools have expedited the genome sequencing of many crucial crop plants namely, potato, mustard, tomato, wheat and chickpea [4]. Recently, the genome of diploid ancestors (*Arachis duranensis* and *Arachis ipaensis*) of cultivated peanut has been sequenced and released [6]. These reference genome sequences act as powerful tools in genetic improvement of valuable crops.

One of the practical applications of usage of reference genomes of crops is for exploration of molecular markers. In an experiment conducted on foxtail millet, 28,342 microsatellite repeat-motifs were found spanning 405.3 mb genome. It would accelerate the construction of high-density genetic link-age map and fine mapping of Quantitative Trait Loci (QTL) for important agronomic traits in foxtail millet [16]. Likewise, these genome sequences are also used for crop improvement as was done by Hanafy *et al.* [17] in *Vicia faba*, where transformation with potato PR10a gene led to the development of drought and salinity tolerance in the former. The employment of modern and hi-tech techniques in genomics has led to burst of information which has been skilfully curbed into various databases for their easy usage by researchers. To name a few are, CMD, Cotton Marker Database; VegMarks, a marker database for vegetables and Pea-nut Marker Database, Foxtail millet Marker Database (FmMDb). For addressing the importance of transcription factors (TF) many databases have been developed like Plant Transcription Factor Database (PlantTFDB), Database of *Arabidopsis* Transcription Factors (DATF), Database of Rice Transcription Factors (DRTF), Database of Poplar Transcription Factors (DPTF) [4]. Recently, the National Agricultural Biotechnology Information Center developed an access portal to search, visualize, and share agricultural genomics data focusing South Korean information and resources. The portal features an agricultural biotechnology database containing a wide range of omics data from public and proprietary sources [18].

Major Concerns

Public concerns about bioengineering fall within five categories: (i) safety issues related to human health, food safety and antibiotic markers (ii) concerns about detrimental environmental impacts such as loss of biodiversity, gene transfer to wild relatives, non-target effects arising from insect resistant crops and escape of bioengineered crops (iii) regulatory concerns, such as unsatisfactory regulation, labelling policy and the right to choose (iv) economic concerns, such as control of biotechnologies by big multinational companies and rich nations resulting in limited impact on developing countries (v) ethical concerns [20].

Some of these concerns are legitimate others merely result from lack of information or misinterpretation of the technology, whereas many others are illogical. But however the case may be, these concerns influence the acceptance or denial of biotechnology by the consumer at the receiving end. It must be noted that every technology has pros and cons hence, the addressal of the highlighted concerns should be with sound scientific logic and not emotional and unfounded speculation. So far, scientists followed rational approach to the issue and thereby failed to understand that public opinion which is not just moved by scientific facts but also other “non-scientific” considerations. It is therefore imperative to educate and make the public aware of the importance of science in decision making, hence, shifting from “educating the public” to “engaging with the public” approach, through discussions with stakeholders such as farmer, consumer and regulatory organisations and throughout the consequences of not applying modern biotechnology tools in agriculture must be explained and asserted.

Conclusion

Plant genomic era has entered into the phase of rapid functional characterization of all plant genes. Functional

genomics has the central role in strategizing provision of molecular solutions for addressing the prospective changes in the environment in addition to crop improvement and eventually food security. A plethora of high through-put and next generation technologies has been developed for putting the task of crop improvement at fast pace. Explosion of information resulting from the usage of all these technologies is difficult to handle but still is being skillfully managed into efficient databases. But, every technique is not sufficient in its own and carries certain limitations. Therefore, for achieving food security via crop improvement, intelligent integration of the efficient technologies is of prime importance. System integration of all the data from different levels of functional analysis will lead to complete blueprint of the complex network of gene activities of a plant. One such attempt is Rice 2020, a project launched by International Rice Functional Genomics Steering Committee (IRFGSC) which aims at coordinating the functional genomic research in the field of rice [21]. But, while laying out strategies for scientific research for crop improvement, the end user has to be considered too, for whom scientific facet of the product comes secondary to the emotional evaluation of it. Hence, there is a need of shift from “educating the public” to “engaging the public” approach and thus awaring the non-scientific sector, about the importance of biotechnology and convincing them for adoption of the same.

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