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Augmentation of crop productivity through interventions of omics technologies in India: challenges and opportunities

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Abstract

With the continuous increase in the population of developing countries and decline of natural resources, there is an urgent need to qualitatively and quantitatively augment crop productivity by using new tools and technologies for improvement of agriculturally important traits. The new scientific and technological omics-based approaches have enabled us to deal with several issues and challenges faced by modern agricultural system and provided us novel opportunities for ensuring food and nutritional security. Recent developments in sequencing techniques have made available huge amount of genomic and transcriptomic data on model and cultivated crop plants including *Arabidopsis thaliana, Oryza sativa, Triticum aestivum* etc. The sequencing data along with other data generated through several omics platforms have significantly influenced the disciplines of crop sciences. Gene discovery and expression profiling-based technologies are offering enormous opportunities to the scientific community which can now apply marker-assisted selection technology to assess and enhance diversity in their collected germplasm, introgress essential traits from new sources and investigate genes that control key traits of crop plants. Utilization of omics science and technologies for crop productivity, protection and management has recently been receiving a lot of attention; the majority of the efforts have been put into signifying the possible applications of various omics technologies in crop plant sciences. This article highlights the background of challenges and opportunities for augmentation of crop productivity through interventions of omics technologies in India.

Introduction

Agriculture is the pride of India. Indian agriculture has witnessed various revolutions (green revolution, white revolution, blue revolution and now brown revolution), which have made significant strides in terms of production and productivity, availability of food grains, horticultural produce, milk, meat and fish products in India. A critical role was played by government bodies such as the Indian Council of Agricultural Research (ICAR), Department of Biotechnology (DBT), Council of Scientific and Industrial Research (CSIR) and other government-funded as well as private organizations in ushering these revolutions. Although the total area under cultivation has remained the same, 40 ± 2 million hectares for the last 40 years, production has increased apparently. Production of food crops, horticultural crops, fisheries and eggs has increased by 4.5, 8, 9 and 27 times since 1950–1951, respectively. India has become a leading producer of many crops, which were previously unknown and unrecognized, but have now emerged as economically important. Although Indian agriculture has faced numerous challenges and shortcomings, yet it has exhibited impressive growth (Singh et al. 2013a; Ma et al. 2013). If Indian agriculture has to achieve the broad goal of sustainable growth, it is important that the omics-based approaches are extended to the total agricultural production consumption system, that is, across the complete agricultural value chain. This would need the use of omics technologies for further increase in

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agricultural productivity, product quality and resource use efficiencies that reduce farm costs, increase the rate of production and raise incomes besides conserving and enhancing the quality of natural resources (Narsaiah et al. 2012; Ma et al. 2013; Hollister 2014; Jung and Main 2014).

As per recent FAO report, India is the leading producer of eight commodities with higher production and productivity than the rest of the world. For example, two to three times increase in banana production has been possible due to adoption of in vitro quality planting material, fertigation, efficient mat and bunch management. Some vegetables such as tomato, cauliflower and potato, which were earlier temperate, can now be grown under tropical environmental conditions (Singh et al. 2013a; Mohanty et al. 2017). At the global level, fulfilling the food requirements of a population which is expected to be about 9.0 billion in 2050 is a cause of concern which has been discussed across the world. This situation is further complicated by climate change that results in an increase in abiotic and biotic stresses in crop plants, which further impose constraints on food production. The increasing temperature along with shifting pattern of rainfall and rising incidence of extreme weather events such as floods, droughts and frost further add to the complexity of the problem (Narsaiah et al. 2012; Ma et al. 2013; Singh et al. 2013a; Hollister 2014; Jung and Main 2014). Consequently, the challenge before the agriculture sector is to produce more food with declining arable land and water. Addressing the growing needs of the people and reducing unequal social satisfaction, research focus, therefore, has to be reoriented to utilize the emerging knowledge (Shekoofa et al. 2014). Omics-based approaches are now being utilized by agriculturists for improving crop productivity (Weckwerth 2011; Grover et al. 2013; Gupta et al. 2017). For example, a hybrid pigeonpea variety (GTH-1) has been developed by the International Crops Research Institute for the Semi-arid Tropics (ICRISAT) and Indian Council of Agriculture Research (ICAR) using genomics-assisted breeding technology. This variety has produced 32% more yield as compared to the best local variety (Saxena and Nadarajan 2010). Several high-yielding Basmati rice varieties including Pusa-1509 have also been developed by the Indian Agricultural Research Institute (IARI), New Delhi, through marker-assisted selection (MAS) and molecular breeding approaches. These varieties offer several benefits over other Basmati varieties in terms of less number of days required for maturity, better cooking quality and higher productivity (Singh et al. 2014). Previous research has demonstrated the impacts of Bt cotton in India; its cultivation reduced application of pesticides by 40% and provided yield advantages of 30–40% over conventional varieties (Sadashivappa and Qaim 2009). Furthermore, DuPont Pioneer (https://www.pioneer.com) and Monsanto (https://monsanto.com/) have, respectively, developed T series soybean

cultivars and sunflower, soybean and maize cultivars, respectively, for commercial production using genomics-assisted breeding approach (Sam et al. 2007; Scheben et al. 2016). Besides, some mustard varieties, i.e., Coral-432, NRCHB 5-6, NRCDR 601, NPJ 112 (Pusa Mustard 25), RYSKS-2 and DMH-I, recently released by the Indian Council of Agriculture Research (ICAR), have at least 10% higher yield than other local varieties along with better tolerance to several abiotic and biotic stresses (https://timesofindia.indiatimes.com/city/nagpur/5-varieties-of-rapeseed-mustard-released-for-entire-country/articleshow/4872591.cm).

During the past few decades, there have been tremendous progresses in genetic and genomic technologies, assisting us to understand the complex biological systems in an integrative and predictive manner (Filipp 2013; Mewalal et al. 2014). Since the sequencing of the human and several plant genomes, efforts were made to elucidate the data to discover a number of agriculturally important traits/genes and their roles (Kumar et al. 2015a). Several tools for disclosing the functionality of the genes/traits have recently emerged. Initially, functional genomics tools evolved based on comparative studies in relation to model organisms. Accumulation of massive uncharacterized data demanded the requirements to develop novel approaches and technologies that may be useful in assigning functions of the sequenced genes. Advances in computational biology and software packages have opened the gates for further evolution of novel technologies to be capable of taking an applied approach by studying the components of biological systems that are required for proper functioning of the cell and acquire a holistic systems biology-based approach in agricultural research. Besides genomics, certain other tools and technologies have been developed in the last few decades which take an 'omics' approach, i.e., an integrated systems-based approach for the study of cellular structure, function and its dynamics. It is expected that the applied integrative omics-based approaches are helpful in understanding the cause and effect relations between genotype and phenotype (Cowie et al. 2013; Kumar et al. 2015a). These 'omics'-based approaches include the incorporation of genomics, transcriptomics, proteomics, metabolomics and other omics science and technologies to perform the non-targeted studies of biological molecules involved in the appropriate working of the cells and their responses with respect to environmental changes (Fig. 1) (Jung and Main 2014).

Agricultural constraints and their mitigation through omics technologies

The world's population may exceed 10 billion by the end of the century. Besides, the increased energy demand, water scarcity, climate change and environmental destruction,

Fig. 1 The omics workflow for revealing the complexity of the crop plant systems and its key components linked to productivity via integration and analysis of big molecular data obtained through omics-based experimentation technology
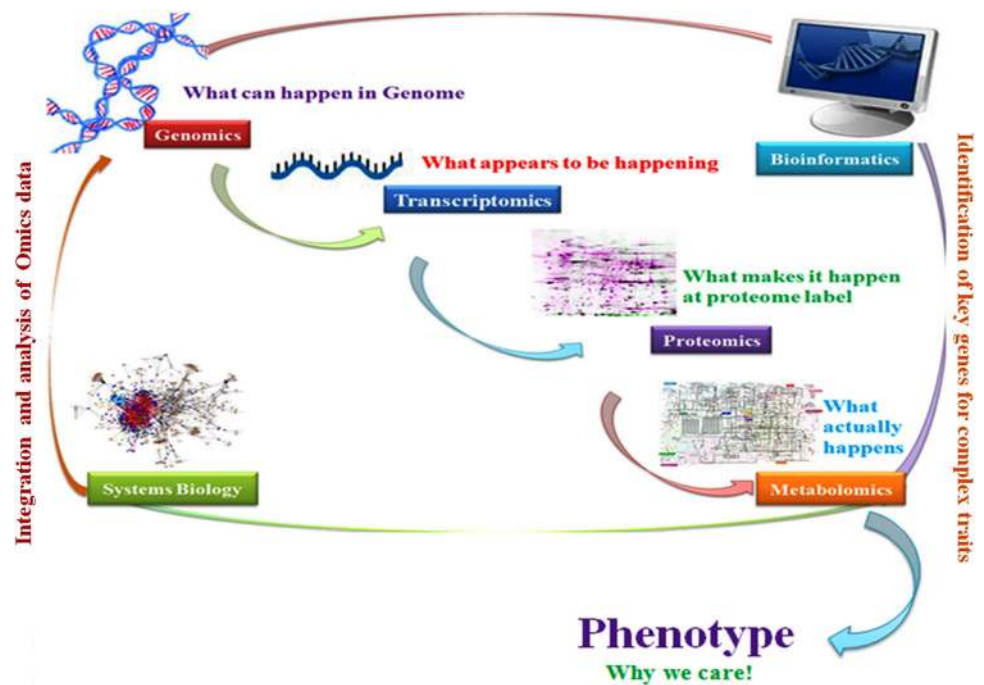
which have been brought about by the increasing population, would all pose a tremendous challenge to future agricultural production (Lamberth et al. 2013; Agrawal et al. 2013; Wortman and Lovell 2013; Nelson et al. 2014; Haddeland et al. 2014). The available statistical data with respect to climate change, groundwater depletion and its effect on crop productivity and malnutrition along with their mitigation through omics technologies are discussed in following sections.

Food security

Food availability is a prerequisite for food security, which is an important element to alleviate poverty. India is more or less self-sufficient in cereals; however, the productivity of pulses and oilseeds is limited. Due to modifications in consumption patterns, the demand for fruits, vegetables and dairy products has been increasing. Recently, a QTL that influenced grain yield in wheat was identified in double haploid lines which were obtained from a cross between two Chinese varieties, Hanxuan 10 and Lumai 14 (Wu et al. 2012). Though Li et al (2012) observed QTL controlling grain weight on chromosomes 1B, 2A, 2D, 4A, 4B and 7B, yet no single QTL was seen to be effective at all phases of grain development. Utilization of omics to identify QTLs and other key genes controlling grain yield and their development in different crop plants is necessary to increase crop productivity for meeting the growing demands for food via adoption of omics-based technology in future (Curtis and Halford 2014; Kumar et al. 2015a; Nadolska-Orczyk et al.

2017; Varshney et al. 2018; Wambugu et al. 2018; Xie and Wang 2018).

Nutritional security

Generally, nutritional security is referred to as the measurement and availability of nutrient in food for development of society. Nutritional security is very important for the individual, home and community as well as for nation. In developing countries like India, large sections of the population are under-nourished. Due to malnutrition, 46% of the rural and 33% of the urban population with a total of 43% of children are underweight; 51% of the rural and 40% of the urban population with a total of 48% of children are stunted, whereas 21% of the rural and 17% of the urban population with a total of 20% children are wasted throughout the India (Fig. 2) (Gupta 2015). Since it is a major barrier to economic and social upliftment, there is a need of developing functional food with improved nutritional quality and quantity affordable to the masses (Nelson et al. 2014). Advanced efforts have been attempted by scientists to improve nitrogen use efficiency in plants such as *Arabidopsis*, rice, wheat and maize through omics approaches for improving nutritional security, because N is a key source for the growth and development of crop plants that ultimately leads to accumulation of nutrients, but excessive external use of N can result in environmental damage and high production costs (Tiwari et al. 2018). Omics-based sciences have the ability to overcome malnutrition and hunger through development of superior environmentally friendly crops for society through
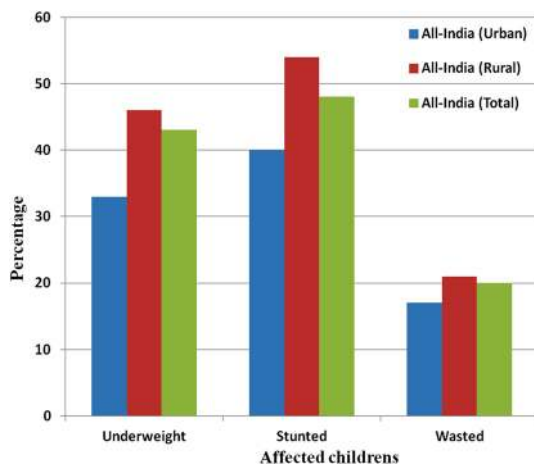
Fig. 2 The number of stunted, wasted and underweight children due to malnutrition, unavailability of food and insufficient amount of nutrients in both rural and urban areas of India in terms of percentage

genomics-assisted crop breeding approaches and genome engineering (Kumar et al. 2015a).

Food safety

Crop productivity is far from satisfying the requirement of the people for food under current conditions and there is a question confronting agri-food researcher whether the emphasis should be on quantity or quality (Kumar et al. 2015a). Food safety is receiving heightened attention worldwide, as the key links between food and health are increasingly recognized. Improving food safety is a vital constituent of providing food security, which is possible when people have access to enough healthy food. In this age of globalization, as trade in crop produce expands all over the world, food safety is a common concern among both developed and developing countries (Kulasekaran 2012). Efforts have been made by researchers to reduce allergenicity in soybean via construction of a gene silencing vector to suppress the expression of P34 protein responsible for allergenic effects, in transgenic soybean lines (Herman et al. 2003). Besides, most food safety-related traits have been also discovered which can be utilized to develop soybean varieties with hypoallergenic properties (Joseph et al. 2006; Watanabe et al. 2018). Recent transcriptomics study has uncovered an indispensable and profitable knowledge into pathogenicity, survival and adjustment of pathogens in food (Joseph et al. 2006). It has been utilized to examine intracellular expression of genes in *Listeria monocytogenes* amid contamination and host adaptation, and those genes initiated by the transcriptional regulars PrfA, sigma B regulon and VirR (Hain et al. 2008) The omics-based innovation specifically for RNA profiling will prompt revelation of more novel tags

that are differentially expressed. While pragmatic uses and utilization of metagenomics, transcriptomics and proteomics information and related apparatuses are less conspicuous, these instruments have likewise begun to yield practice food safety solution (Chawla et al. 2018; Ojiewo et al. 2018). Therefore, the problem related to food safety can be resolved by the use of omics for obtaining higher productivity.

Energy security

With the decrease in fossil fuel deposits, there is increase in energy prices, because of which progressively developed countries are vigorously researching to develop viable bio-energy sources, the generation of which would require large amounts of crop plants products (biomass). Energy demand is still on the rise now, which means that huge quantity of crop products will be used to produce more fuel (Nelson et al. 2014; Haddeland et al. 2014). Recently, novel GM loblolly pine plants with altered cell wall and lignin composition are being optimized, in a xylem particular way, by means of control of glucommann (LpGluM) genes and three genes encoding NAC (NAM, ATAF1/2 and CUC2) transcription factor and domain proteins, i.e., LpNAC1, LpNAC2, and LpNAC3 that are involved in the plant polysaccharides regulation. A definitive objective is to enhance the physical and chemical properties of wood for proficient deconstruction and sugar discharge for large-scale production of cellulosic ethanol. Besides, Populus and Eucalyptus plants are also utilized for the nproduction of bioenergy through biotechnological approaches (Al-Ahmad 2018). Therefore, collaborative approaches of genetics, advanced breeding and omics technologies, such as those carried out on *Pinus* and other plants for characterization of novel genes and transcription factors, are expected to open up new avenues for increasing biomass which can be harvested for generation of fuels (Al-Ahmad 2018; Jouzani and Sharafi 2018; Wambugu et al. 2018).

Climate change

Climate is one of the most important factors influencing agricultural practices and crop productivity. Climate change exerts harmful influence on productivity of the crop plants, which decreases the per unit yield of main crops such as wheat, pulses and oilseeds. Influence of this kind is more conspicuous in low-latitude area of India. There has been increasing concern regarding the changes associated with climate becoming warmer, occurrence of new crop diseases and pests, expanded area, increased hazard and difficulty in control (Wortman and Lovell 2013; Nelson et al. 2014; Haddeland et al. 2014). In this way, agricultural production

management would become extremely challenging. Wheat was a highly affected crop, followed by pulses and oilseeds. 67.22% of the cultivated area of wheat, 1.32% of cereals, 11.09% of pulses, 6.24% of oilseeds, 3.82% of vegetable, 1.13% of cumin, 1.02% of coriander, 0.98% of isabgol and 7.18% area of other crops are affected due to climate change and unusual rainfall in the country (Fig. 3) (http://businessec onomics.in/?p=2439). Transcriptomic and proteomics studies conducted in different plants have determined several putative genes. i.e.. *Apx1, Mbf1c*, At1g26580 associated with multiple abiotic stress regulation in plants, which could be potential targets for the development of stress tolerance. Besides, some achievement has just been accomplished in the development of crops tolerant to a specific abiotic stress condition by genetic manipulation of key genes (Zandalinas et al. 2018). Therefore, omics-based approaches have potential to produce climate-resilient crops through genetic improvement.

Shortage of water

Freshwater for irrigation is a backbone of agriculture and directly linked to crop productivity. At present, demands for agriculture water accounts for 69% of the world total water consumption and surpasses more than 89% in some arid countries. As population growth and urbanization continues, the proportion of domestic water consumption has also increased. The Tamil Nadu state is dealing with the maximum groundwater depletion at 76%, whereas Delhi has its share of 62%. The top Indian states in terms of percentage of groundwater depletion of are shown in Fig. 4 (http://scroll.in/article/676038/imagine-the-qutub-minar-under ground-thats-how-low-delhis-water-table-has-fallen). The
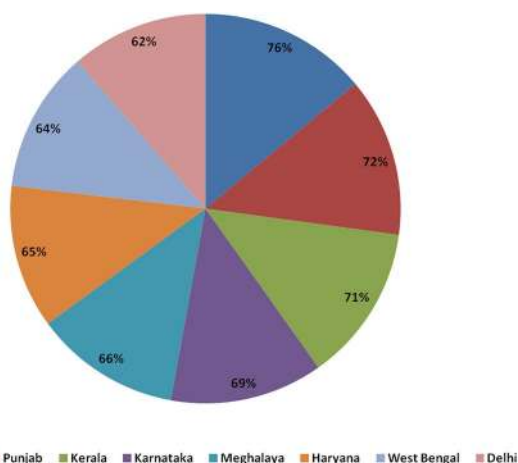

Fig. 4 Pie chart depicting the percentage of groundwater depletion in different Indian states

alternation of physiological activities in response to drought and heat stress and their combination have been determined in several plant species. It was investigated that the photosynthetic machinery is repressed in responses to several abiotic stresses. However, the impact of drought, heat and their mix on photosynthetic activity could be distinctive depending upon plant species. Transcriptomic studies conducted on *Arabidopsis thaliana* in response to drought, heat and their combination clearly demonstrated the expression of many genes including different heat shock proteins (HSPs), MYB transcription factor and several protein kinases (Zandalinas et al. 2018). Besides, *Apx1* gene was investigated in *A. thaliana* that is specifically required for the tolerance to the combination of drought and heat stress (Koussevitzky et al. 2008) Therefore, omics-based approaches have potential to decode the molecular mechanism of drought for

Fig. 3 The affected cropping area in India due to climate change in terms of percentage. Wheat is an extremely affected crop followed by pulses and oilseeds
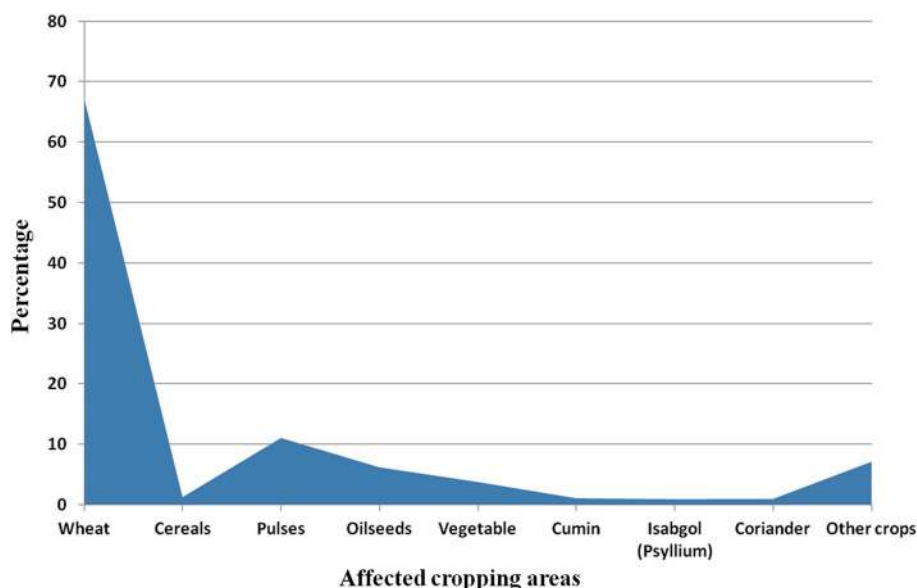
identification of key genes which can further be exploited for developing drought-resistant crop plants through genomics-assisted plant breeding and genetic engineering to combat the problem of water shortage.

Loss of soil fertility and degradation

The severity of soil degradation and loss of soil fertility have been growing in many places of the world. Land degradation and desertification, which are caused by unauthorized cultivation of marginal land, deforestation for farmland expansion with bad farming practices and soil degradation, have all degraded soil to a certain extent. The harmful effects of land degradation include decreased crop productivity, population migration, food insecurity, destruction of basic resources and ecological system, and loss of biological diversity due to habitat changes (Montgomery 2007). It was already determined that the legumes plants fix soil nitrogen and enhance soil health (Ojiewo et al. 2018). Besides, the establishment of artificial symbioses among nitrogen-fixing microbes and non-legume plants is the major breakthrough in the field of agricultural sciences. Ongoing advances in understanding endosymbiotic and endophytic N fixation with non-legume crop plants have demonstrated a unique opportunity for designing non-legume N-fixing crops. This has become possible with the availability of several genomes of N-fixing microbes, i.e., *Azoarcus* sp. BH72, *Herbaspirillum seropedicae* SmR1, *Gluconacetobacter diazotrophicus* Pal5, *Pseudomonas stutzeri* A1501, *Azospirillum* sp. B510 and *Klebsiella pneumoniae* 342 along with genomes of crop plants decoded by omics technologies (Santi et al. 2013). Therefore, artificial symbiosis in many crop plants with N-fixing microbes will ultimately increase soil fertility and decrease the risk of their degradation, population migration and food insecurity as well as increase crop productivity.

Human activities influencing ecosystems

To protect our ecosystem from extensive use of fertilizers by growers is the major challenge. To improve agricultural sustainability together with long-term income, special attention has to be given for newer strategies for crop protection such as integrated practices, to eradicate or control pests (Wortman and Lovel 2013; Haddeland et al. 2014; Diepens et al. 2014). Some newly designed crop plant varieties of rice and wheat have potential to protect themselves from several abiotic and biotic stresses and providing higher yield with less use of fertilizer (Lesser and Kolady 2011; Singh et al. 2011; Huang et al. 2017). Therefore, advances in omics are very useful in designing of smart crops for sustainable agriculture to protect the ecosystem (Kumar et al. 2015a).

Roles of omics technologies in agricultural production

In India, agriculture has always been regarded as the backbone of economy. Therefore, it is important that scientists, extension workers and farmers are aware of the current agriculture practices, technologies and research for better and sustainable development (Grover et al. 2014; Kumar et al. 2015a; Kumar 2015). Large-scale genome sequencing projects are giving biological and agricultural scientists access to an exponentially growing lists of genomes, from organisms covering all three forms of life. This has brought about a paradigm shift in the way scientists address the problem of food and nutritional security. Exciting molecular technologies to elucidate genomic data have taken the investigation of gene structure and function to an unprecedented level and more comprehensive understanding of cellular processes. Conventional biological research has changed fundamentally with the advent of the science of 'omics'. Although a majority of the omics approaches are still in the developmental phase, tremendous effects have been shown on world agriculture in the form of "GENE REVOLUTION" (Kumar 2015). Omics technologies have substantially changed both the approach and the design of research experiments. These technologies allow the generation of large-scale data at each level of information from gene sequence, expression to protein as well as metabolite patterns determining variability in cellular networks and function at a systems level. This has already signaled a new era of approaching scientific queries, that is, the advent of 'big biology' and a system based approach to scientific practice with global measurements of metabolic pathways in agricultural sciences (Koyuturk 2010; Kumar et al. 2015a).

In view of the amplified throughput data availability, the process of research has fundamentally been altered in 'omics science'. Consequently, a scientist addresses a scientific problem by postulating a hypothesis and working through the experimentation to prove or disprove the hypothesis. With the omics-based approach, inquiring an initial research question is not always compulsory or a prerequisite (Weisenburger 1993; Sachs et al. 2005; Ozdemir et al. 2009; Koyuturk 2010; An and Lin 2011; Martinez-Gomez et al. 2012). Genomics or proteomics data can be collected in an omics-based experimentation without an existing hypothesis. The data in turn can be analyzed for deriving useful information that can lead to inventions and testing of novel hypotheses. 'First hypothesize-then-experiment' tradition has changed to 'first experiment-then-hypothesize' approach which offers the promise of discovering unprecedented patho-physiological mechanisms of stress tolerance and other complex traits in the

case of crop plants (Nadella et al. 2012; Martinez-Gomez et al. 2012; Kujur et al. 2013; Henry et al. 2014; Mano et al. 2014; Rahman et al. 2014; Tohge et al. 2014).

Unraveling the genome sequences is only the beginning of the era of genome biology and genomics. This is followed by the study of the function of numerous genes, comparison of genes in one crop with another and to generate the holistic structures of proteins from several protein families. Thus, such approaches can help in deriving clues for their functional analysis (Henry et al. 2014; Rahman et al. 2014). In agriculture, the major applications of genomics is to gain a bigger understanding of plants so that agronomically important genes can be discovered and targeted to develop better, healthy and safe food. The attention is also on the protection of the environment by not adopting a sustainable agricultural practice (Martinez-Gomez et al. 2012).

Unlike the genome, the proteome is highly dynamic and changes in response to different environmental stimuli from time to time. The goal of proteomics research is to understand how the structure and functional dynamics of proteins allow them to function, work together and determine individual roles that can contribute to crop productivity (Mano et al. 2014; Tohge et al. 2014). Similarly, metabolomics can be used to identify and characterize differences among the quantity of thousands of biological molecules between a healthy and unhealthy or diseased plant to decipher plant defense metabolites. The technology can also be used to investigate the nutritional difference between traditional, commercial and GM crops. Contiguous to this interpretation and integration of the experimental data within the context of the whole cell as well as cell physiology, development of bioinformatics tools and databases to store and integrate different types of data sets is still a major task ahead (Kumar et al. 2015a; Martinez-Gomez et al. 2012).

Opportunities in omics technologies

To make modern agriculture sustainable, it is necessary that scientists adopt innovative technologies for crop improvement. Molecular approaches including genomics and genetic engineering have emerged as powerful tools to assure rapid and precise selection and implementation of the trait(s) of interest for crop improvements (Kumar et al. 2015a).

Next generation sequencing and high-throughput genotyping have helped immensely in understanding the functions and regulation of genes in crop plants. Plant genomics and bioinformatics are rapidly developing and deeply improving understanding of plant biology through development of novel tools and techniques to understand plant systems which will ultimately lead to enhanced and sustained agriculture production (Wei et al. 2013).

The ever-increasing availability of genome sequences in crop plants has facilitated the development of genetic and genomic resources that will allow us to address biological functions and a number of basic processes relevant to crop production (Tohge et al. 2014). The major key areas of omics sciences are genomics, transcriptomics, proteomics, metabolomics, bioinformatics and systems biology, and its associated techniques as well as technologies such as nutrigenomics for designing of functional foods and nutraceuticals, other omics for microalgal-based biofuel production, transgenic plant analysis, computational regulomics and network biology, and analysis of RNA splicing, with new fields, including glycomics, miRNA and metagenomics (Fig. 1) having incredible prospects for robust crop productivity and sustainability (Martinez-Gomez et al. 2012; Tohge et al. 2014; Kumar et al. 2015a).

This article provides a comprehensive overview of 'omics' technologies and application in the area of agriculture to improve crop productivity. The approximate experimental cost of sequencing technologies in India as per NxGenBio Life Sciences, New Delhi, for sequencing of one sample with single library is provided in Table 1. Some of the opportunities of these technologies given in Fig. 5 are summarized.

Genomics and bio-resource

Bio-resource refers to the total biological variation manifested as microbes, plants, animals from which certain product could be derived and utilized as drugs, food and feed. They could also be a source for the development of improved crops and animals for higher yield and tolerance to biotic and abiotic stresses. There is dependence on these bio-resources for the continued existence of mankind. Therefore, human beings have to bear the responsibility of using and preserving them for future generations (Sayers et al. 2009). India harbors two hot spots of biodiversity in the world. The Eastern Himalayan region and the Western Ghats are the abode of numerous plants, animals and microbial species. Since utilization of the available bio-resources is an inevitable part of human existence, it is to be ensured that a balance exists between the use of resources and their conservation for their sustainable exploitation (Sayers et al. 2009; Jung and Main 2014; Haddeland et al. 2014).

At the level of DNA, genomic data reveal the information that is stored in the genomes of organisms and passed along generations (Liu et al. 2014). These include sequences of genes coding for functional proteins, regulatory motifs that serve as markers for the regulation of the expression of specific genes, as well as individual differences in the genetic composition of populations, such as single nucleotide polymorphisms (SNPs) and copy number variants

Table 1 Intervention of sequencing technology and its approximate experimental cost in India; the mentioned prices are for sequencing of one sample with a single library

S. No.	Technology/methods	Read length	Output per lane	Output per run	Per lane cost (INR)	Per run cost (INR)
Second-generation sequencing technology						
1.	454 Sequencing	Up to 1 kb	500 MB	–	–	500,000 Outdated/discontinued
2.	Illumina HiSeq1000	100 bp	15 GB	–	300,000	2,100,000 Outdated/discontinued
3.	ABI SOLiD system	50–100 bp	–	–	–	Outdated/discontinued
4.	Polonator G.007	26 bases per amplicon	–	–	–	Outdated/discontinued
5.	Ion Torrent Sequencing	Up to 200 bp	1 GB	1 GB		100,000
Third-generation sequencing technology						
6.	PacBio	800–1000 bp	–	–	–	100,000
7.	HeliscopeTM Sequencer	33-nt read length	–	–	–	Outdated/discontinued
Fourth-generation sequencing technology						
8.	Oxford Nanopore	62–70 bases sequences per DNA nanoball (DNB)	–	–	–	110,000
9.	Illumina HiSeq3000	150 bp	50 GB	400 GB	275,000	2,000,000
10.	ABI SOLID 550XL system	75 bp	120 GB	120 GB	–	200,000 Outdated/discontinued
11.	Ion Proton	200 bp	6 GB	6 GB	–	150,000
12.	Pac-Bio RSII	1–30 kb	750 MB	750 MB	–	125,000

Fig. 5 Science of omics to increasing crop productivity: an overview
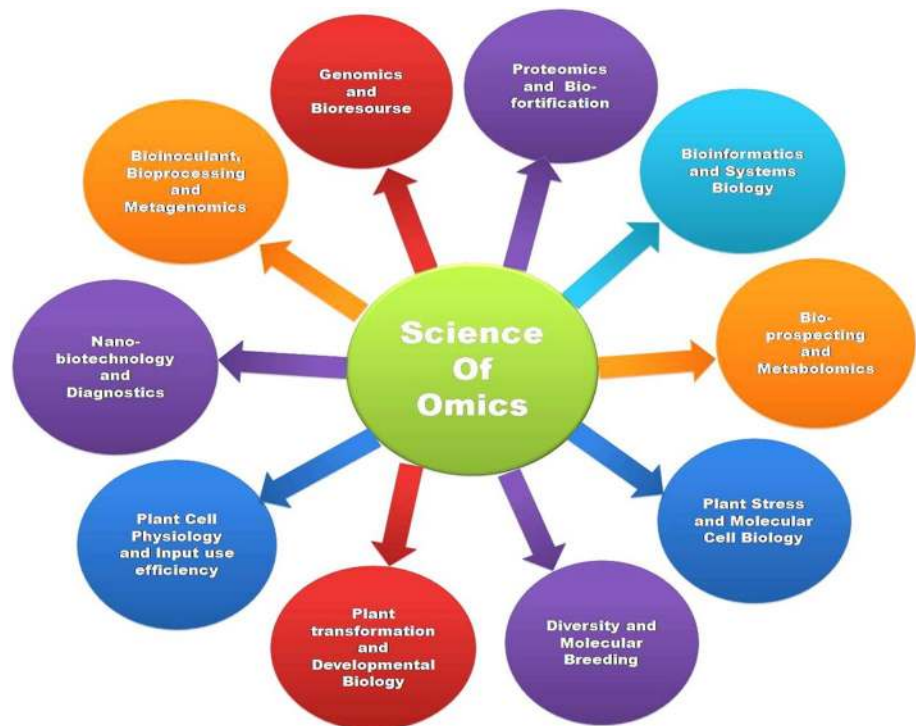
(CNVs—multiplicity or lack of certain DNA segments in genomic sequences), inversions or transpositions. Sequence data drives translational research through genome-wide association studies (GWAS), discovery of driver mutations and structural variants in progressive diseases of plants, and transfer of biological knowledge across model organisms via comparative genomics (Ning and Lo 2010; Mochida and Shinozaki 2011; Ma et al. 2013; Martinez 2013).Genome

sequencing is traditionally achieved by exploiting the natural process of DNA replication. On the other hand, identification of SNPs and CNVs has been usually carried out using DNA microarrays, which exploit the natural process of hybridization. Besides, sequencing technology and associated computational techniques are now being transformed by the appearance of short read sequence data, also known as next-generation sequencing (NGS) (Martinez 2013; Kumar et al. 2015a). NGS has broadly been used for the de novo sequencing, whole genome sequencing (WGS), whole genome resequencing (WGRS) and genotyping by sequencing (GBS). It would serve as a powerful tool for decoding the genetic basis of agriculturally important traits in crop plants (Muthamilarasan et al. 2016) (Fig. 6).

The whole sequencing of the *Arabidopsis thaliana* genome has been regarded as a landmark in plant biology. After that, more than 60 plant genomes have been sequenced so far and sequencing of several other genomes is underway. In India, more than seven genomes including rice, tomato, pigeonpea, wheat, *Puccinia triticina, Tilletia indica* and tulsi have been successfully completed with the effort of national and international group of scientists (Sasaki 2005; Consortium 2012, 2014; Singh et al. 2012, 2014a, b; Upadhyay et al. 2015a; Kiran et al. 2016; Sharma et al. 2016). The sequencing of mango genome and its analysis is ongoing (Singh et al. 2014a, b). Over the last two decades,

comparative genomics has revealed that the organization of genes within crop plant genomes has remained conserved over the evolutionary periods. Advances in the field of structural and functional genomics and equitational bio-resource utilization will encompass a wider range of technologies and disciplines such as biocomputational engineering, bioenergies and genome systems analysis so as to help achieve the goal of world food and nutritional security (Vij and Tyagi 2007; Hamblin et al. 2011; Anderson et al. 2014; Kumar et al. 2015a; Thao and Tran 2016). The scientists of GBP-UAT Pantnagar, India, are currently working on deciphering the complete genome sequence of an economically important fungal pathogen Karnal bunt (*Tillitia indica*) of wheat, for identification of genes/proteins involved in pathogenesis (Kumar et al. 2017). This study will enable to boost scientific efforts in molecular breeding and disease management (Kumar et al. 2015a).

Transcriptome

NGS has revolutionized transcriptome sequencing as compared to genome sequencing. Due to the profit of cost-effectiveness and high coverage, transcriptome sequencing of the majority of the crop plants has been performed to find out genes and gene families involved in various biological processes. In addition, RNA-sequencing (RNA-seq) reveals the relative abundance of transcripts in a given sample (tissue and/or condition specific) and also allows high-throughput development of molecular markers (Muthamilarasan et al. 2016). In the past years, transcriptomics has been executed by a comparative approach using cDNA-AFLP, suppression subtraction hybridization (SSH) and microarray analysis. Whole transcriptome sequencing in millets was first decoded in foxtail millet, in which RNA-seq was performed in root, stem, leaf and spica samples using the Illumina GA II platform. The average size of transcripts was predicted to be 2522 bp with an intron length of 442 bp, average exon length 256 bp and average exons per gene 4.3. This analysis showed that ~ 81.7% of genes were expressed, whereas 1367 were pseudogenes (Muthamilarasan et al. 2016). For the first time, the transcriptome of developing spikes of finger millet (*Eleusine coracana*) was sequenced in India for understanding the molecular basis of three complex agriculturally important traits, viz., nutritional quality (micronutrient Ca^{2+}, Fe^{2+}, Zn^{2+} and protein quality), nitrogen use efficiency and stress responsiveness (Kumar et al. 2015b). In addition, several other efforts in transcriptome sequencing were made by Indian scientists in different crop plants and many more are underway to decode the complexity of important agricultural traits for improving crop productivity (Dutta et al. 2011; Thakur et al. 2013; Prasath et al. 2014; Paritosh et al. 2014;
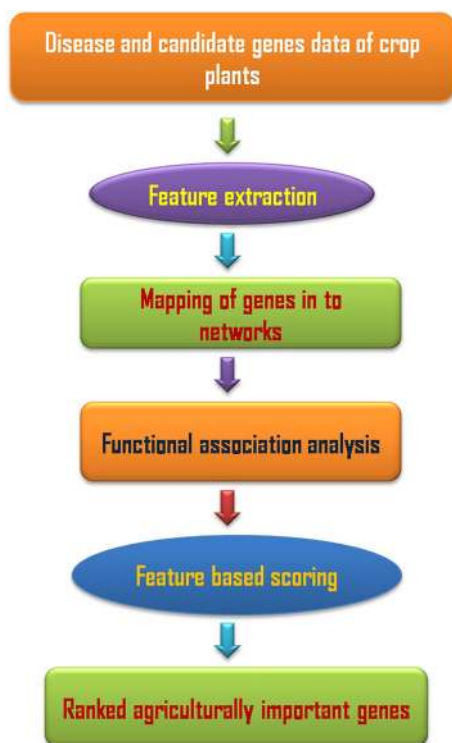
Fig. 6 Schematic diagram of the network-based disease gene prioritization at the crop improvement level

Garg et al. 2015, 2016; Shukla et al. 2015; Reddy et al. 2015; Mahato et al. 2016; Meena et al. 2016; Devi et al. 2016).

Functional genomics aims at developing and synthesizing genomic and proteomic knowledge into recognizable, sensible information, which would unravel the dynamic properties of plant systems at the molecular and cellular level (Vij and Tyagi 2007; Hamblin et al. 2011; Kumar et al. 2015a, b, 2017). This could offer a complete picture of biological functioning that is taking place in the plant cell. Further, it will also provide an opportunity to explore genomics for identification of novel genes from bio-resources having hidden value for engineering superior traits. This could also help in superior trait identification and their introgression into plants (Sayers et al. 2009; Rahman et al. 2014). In the twenty-first century, optimal utilization of available bio-resources in sync with the genomics approaches is poised to become a major platform for driving significant progress over the next 20–50 years. The knowledge and understanding of genome sequences and their relation with metabolic control mechanisms will allow a sound scientific basis for a healthier and more reliable food supply (Kumar et al. 2015b). The partial list of genomes and transcriptomes sequencing done by Indian scientists are given in Table 2 (Sasaki 2005; Dutta et al. 2011; Consortium 2012, 2014; Singh et al. 2012, 2014; Thakur et al. 2013; Prasath et al. 2014; Paritosh et al. 2014; Kumar et al. 2015b, 2017; Upadhyay et al. 2015a; Garg et al. 2015, 2016; Shukla et al. 2015; Reddy et al. 2015; Kiran et al. 2016; Sharma et al. 2016; Mahato et al. 2016; Meena et al. 2016; Devi et al. 2016; Shankar et al. 2016; Hittalmani et al. 2017; Varshney et al. 2017).

Big data in genomics: challenges and solutions

These revolutionary modifications in big data generation and gaining are profound challenges for storage, transfer and security (Sayers et al. 2009). Indeed, it may now be less costly to generate the data than to store it. One model of this issue is the National Centre for Biotechnology Information (NCBI). The NCBI has been leading big data efforts in plants and other organisms since 1988, but neither the NCBI nor anyone in the private sector has a complete, low-cost, and secure solution to the problem related to data storage and security (Sayers et al. 2009; Lal et al. 2013; Gour et al. 2013). Since these potentials are beyond the reach of small laboratories and small institutions, therefore it imposes various challenges for future agricultural research. Another challenge is to transfer data from one site to another; it is mainly done by shipping external hard disks through mail (Marx 2013).

Proteomics and biofortification

One of the greatest problems for low income developing country including India is undernourishment and malnutrition among the children and women. According to the estimates of World Bank, India holds second rank in the world, after Bangladesh, in terms of the number of children suffering from malnutrition (Kulasekaran 2012; Gupta 2015). In India, 47% of the children exhibit a degree of malnutrition. 50% of poor women of reproductive age are anemic in India. Protein energy malnutrition and micronutrient deficiencies of vitamin A, iron and zinc contribute to high mortality rate in children and women due to onset of various illnesses and diseases. Biofortification is seen as an effective strategy for coping with the problems of protein energy malnutrition and micronutrient deficiencies, prevalent among children and women in the developing world including India (Kulasekaran 2012; Lee et al. 2012; Kumar et al. 2015a).

The objective of biofortification is to enrich plant foods in essential micronutrients and proteins as plants grow naturally (Lee et al. 2012; Kumar et al. 2015b). It has been realized that biofortification of staple food crops such as rice and wheat would solve the malnutrition problem associated with the rural poor, as these staple foods predominate the diet of poor people (Blancquaert et al. 2014). In this regard, genetic engineering methods hold a great promise for development of biofortified foods. The genetic engineering-based strategies include insertion of novel genes from heterologous system, overexpression of already existing genes, disruption of pathways involved in synthesis of inhibitors of trace elements absorption and synthesis of the enhancers of trace element absorption to increase the nutrient contents in staple food crops. Its application has already been seen in the form of golden rice developed to solve the problem of vitamin A deficiency (Lee et al. 2012; Blancquaert et al. 2014; Kumar et al. 2015b). However, implementation of such methods requires identification of nutritionally important genes and promoters which are associated with accumulation of high quality of proteins and micronutrients in seeds of staple crops (Lee et al. 2012; Kadiyala et al. 2012; Ramachandran 2013; Blancquaert et al. 2014).

Proteomics technologies aim at studying the global patterns of protein content, protein activities, modifications and localization, and interactions of proteins with other proteins or molecules of the cell (Deracinois et al. 2013). The proteomics techniques such as 2D gel electrophoresis and MALDI-TOF have potential for the detection and identification of proteins expressed in a particular tissue, organ or organelle which in turn facilitates identification of relevant genes through reverse genetics approach.

Table 2 Partial list of sequencing of the genome(s) and transcriptome(s) by Indian scientists

S. no.	Name of crops	Genomes/or transcriptomes	Research institutes/university	References
1.	Rice	Genome	Indian Initiative for Rice Genome Sequencing (IIRGS), University of Delhi and Indian Agriculture Research Institute	Project IRGS (2005)
2.	Tomato	Genome	Indian Initiative on Tomato Genome Sequencing, University of Delhi, National Research Centre on Plant Biotechnology and National Plant Genome Research Institute	Tomato Genome Consortium (2012)
3.	Pigeonpea	Genome	National Research Centre on Plant Biotechnology	Singh et al. (2012)
4.	Wheat	Genome	Punjab Agricultural University, National Research Centre on Plant Biotechnology and University of Delhi	International Wheat Genome Sequencing Consortium (2014)
5.	Mango	Genome	National Research Centre on Plant Biotechnology	Singh et al. (2014)
6.	*Puccinia triticina* Wheat rust pathogen	Genome	National Research Centre on Plant Biotechnology	Kiran et al. (2016)
7.	*Tilletia indica;* Karnal bunt Wheat pathogen	Genome	G. B. Pant University of Agriculture & Technology; Indian Institute of Wheat and Barley Research and Indian Agricultural Statistics Research Institute	Sharma et al. (2016), Kumar et al. (2017)
8.	Tulsi	Genome	National Centre for Biological Sciences (TIFR); Manipal University; Centre for Cellular and Molecular Platforms and SASTRA University	Upadhyay et al. (2015a, b)
9.	Finger millet	Genome	University of Agricultural Sciences, Bengaluru	Hittalmani et al. (2017)
10.	Pearl millet	Genome	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad with International collaboration of the several other institutions	Varshney et al. (2017)
11.	Pigeonpea	Transcriptome	National Research Centre on Plant Biotechnology	Dutta et al. (2011)
12.	*Venturia inaequalis* Apple scab pathogen	Transcriptome	Institute of Himalayan Bioresource Technology	Thakur et al. (2013)
13.	Ginger	Transcriptome	Indian Institute of Spice Research	Prasath et al. (2014)
14.	Mustard	Transcriptome	University of Delhi	Paritosh et al. (2014)
15.	Finger millet	Developing spikes transcriptome	G. B. Pant University of Agriculture & Technology	Kumar et al. (2015b)
16.	Kalmegh	Transcriptome	Central Institute of Medicinal and Aromatic Plants, National Botanical Research Institute	Garg et al. (2015)
17.	Bitter gourd	Transcriptome	Indian Institute of Vegetable Research, Banaras Hindu University and Genotypic Technology (P) Ltd	Shukla et al. (2015)
18.	Senna	Transcriptome	Directorate of Medicinal and Aromatic Plants Research	Reddy et al. (2015)

Table 2 (continued)

S. no.	Name of crops	Genomes/or transcriptomes	Research institutes/university	References
19.	Chickpea	Transcriptome	National Institute of Plant Genome Research, International Crops Research Institute for the Semi-Arid Tropics , RMIT University, Jawaharlal Nehru University	Garg et al. (2016)
20.	Mango	Leaf transcriptome	National Research Centre on Plant Biotechnology	Mahato et al. (2016)
21.	Lemongrass	Transcriptome	Central Institute of Medicinal and Aromatic Plants	Meena et al. (2016)
22.	*Cymbopogon winterianus*	Transcriptome	Assam Agricultural University	Devi et al. (2016)
23.	Rice	Transcriptome	National Institute of Plant Genome Research and Jawaharlal Nehru University	Shankar et al. (2016)

Such approaches, therefore, can be utilized to identify key candidate genes involved in uptake, transport, accumulation and availability of a potentially useful protein or micronutrient in the seeds (Deracinois et al. 2013; Vanderschuren et al. 2013; Kumar et al. 2015a). These studies also facilitate the understanding of the molecular mechanism of remobilization of nutrient from leaves to grain seeds and its subsequent compartmentalization within the seed. The unraveling of such molecular mechanism involved in synthesis and accumulation of seed storage proteins and other nutritionally important nutrients would help in the identification of key genes/transcription factors/promoters which could subsequently be transferred into staple food crops for biofortification (Lee et al. 2012; Kadiyala et al. 2012; Ramachandran 2013; Deracinois et al. 2013; Vanderschuren et al. 2013; Blancquaert et al. 2014). Some examples of such biofortification strategies may include the manipulation of enzyme levels in biosynthetic pathways to increase the levels of accumulated vitamins, higher expression of the molecular "pumps" that allow plants to take up more minerals from the soil or deposit a specific nutrient in seed grain and elevation of protein content by integration of genes from protein-rich crops into staple food crops (Goel et al. 2012; Blancquaert et al. 2014). A recent example of the latter is the development of genetically engineered potato expressing the gene of an *Amaranthus* protein so as to enhance the protein content of potato (Chakraborty et al. 2010). Another approach is to transfer the genes for good-quality proteins rich in essential amino acids into staple crops. Ethnic cereal crops, which unfortunately are neglected crops, are bestowed with good-quality proteins such as prolamins and mineral sequestering proteins (calcium-binding protein) and micronutrients such as calcium, iron and zinc (Kumar et al. 2015b; Chinchole et al. 2017). In these crops, the seed storage protein genes are regulated by the concerted or combinatorial action of seed-specific transcription factors which bind to their respective DNA binding sites on the promoter region. Advances in proteomics can be utilized to investigate the role of these components in the accumulation of seed storage proteins in seeds by performing proteomics-based co-expression analysis. Besides, isolation, identification and expression analysis of plant-specific Dof transcription factors genes were done to understand their role in the plant developmental process (Kadiyala et al. 2012; Ramachandran 2013; Deracinois et al. 2013; Vanderschuren et al. 2013; Gupta et al. 2014a, b, 2018; Gujjar et al. 2018). The transporter proteins involved in the accumulation of micronutrient in the seeds can be identified and their genes can subsequently be overexpressed in staple crops so as to increase their bioavailability in the seeds. It will certainly help in opening new vistas for biofortification research programs (Lee et al. 2012; Blancquaert et al. 2014; Kokane et al. 2018).

Proteome

Although the transcriptomics-based analysis of gene expression gives an approximate idea about the relative abundance of the related protein in a sample, it cannot necessarily be related to proteome and its function. The latter is because the expression of gene, after transcription, is regulated through different mechanisms including mRNA degradation, alternative splicing and post-translational modification (Ma et al. 2013; Filipp 2013; Kumar et al. 2015a, b). Proteomic screening identifies molecular abundance and activity at the functional stage. A universal method, 2-D polyacrylamide gel electrophoresis, facilitates the partition or separation of proteins in a sample of interest based on their isoelectric point and other electrochemical properties. Separated proteins can then be determined using mass spectrometry (MS) (Tsugita and Kamo 1999; Weiss and Gorg

2007). Although proteomic screening methods are helpful in quantifying the expression and variation or modification of proteins at the functional stage, setup of proteomic screening techniques can only control and manage the expression of a partial or limited subset of proteins in the particular cell at a time. Furthermore, advanced techniques such as flow cytometry facilitate the activity of screening of the protein at the resolution of thousands of cells; but this comes at the price of a limited coverage of the proteome (Galbraith 2014). Proteomic data enable detection of functional proteins and their modifications that have a role in the development and progression of disease and development of causal models for cellular signaling, driving translational science at the functional level in crop plants (Quirino et al. 2010; Lodha et al. 2013; Gong et al. 2015).

Interactome

High-throughput screening techniques have made it possible to identify the physical interactions among proteins. A commonly used technique, yeast two-hybrid (Y2H) identifies interactions involving a couple of proteins by using the modularity of the activating and binding domains of eukaryotic transcription factors. In yeast two-hybrid, the activating and binding domains of a particular transcription factor are separated, and each domain is merged to one of the two (prey and bait) proteins (Damon et al. 2012). Then, the interaction between the two proteins is identified by reporter gene expression that is the target of the transcription factor (Cao and Yan 2013). On the other hand, tandem affinity purification (TAP) identifies interactions between an individual bait protein and several other proteins (Van Leene et al. 2015). This is achieved by tagging the target protein of interest and inserting it into the host. When the bait protein is retrieved with other proteins associated with it, these interacting proteins are investigated using MS (Weiss and Gorg 2007).

The identified protein–protein interactions (PPIs) using wet laboratory experimentation are known as protein–protein interaction networks, which provide a high-level as well as static understanding of cellular organization, commonly called as the interactome (Boruc et al. 2010; Zhang et al. 2010). Recently, established protein–protein interaction network models imagine binary interactions between pairs of proteins, which describe the outcome of Y2H experiments (Cao and Yan 2013). On the other hand, multiple protein–protein interactions identified by TAP are shown by either a star network at around the bait protein (spoke model) or a cluster of all proteins obtained by the bait protein, within itself (matrix model) (Zhang et al. 2010; Cao and Yan 2013). A key limitation of high-throughput protein–protein interactions, however, is their unfinished and noisy nature. In addition, these interactions just signify a picture of the complex and dynamical organization of the proteins in the cell (Zhang et al. 2010; Pathak et al. 2013a; Cao and Yan 2013; Kumar et al. 2015a). In recent years, PPI networks have been extremely useful in understanding the systems biology of complex diseases, through identification of protein complexes, functional modules and signaling pathways network-based functional annotation, network-based disease gene prioritization, and identification of dysregulated pathways in plant systems (Pathak et al. 2013a, b; Kumar et al. 2015a).

Bioinformatics and systems biology

The life sciences are now in the midst of a truthful biological revolution similar to what biophysics experienced after the turn of the last century (Mount 2001). Nowadays, researchers are making constant effort to gain insight into biological systems through their molecular function. Subsequent coordinated activities are just in a stage of unparalleled growth and development that is reflected by the quantity of data generated from every experiment (Kumar et al. 2015a). This huge information from seemingly disparate data sets is converted into useful knowledge through bioinformatics (Mount 2001; Wang et al. 2005). Bioinformatics is the application of information technology to facilitate gathering, linking and manipulating diverse types of biological data to understand new biological insights.

In other words, bioinformatics is an information management and manipulation system for molecular biology, biochemistry, health sector, environmental biology and agriculture by addressing biological data collection, data mining, data analyses, interpretation and finding of genes and protein, modeling and product design especially drug/agrochemicals discovery (Jayaram and Priyanka 2010; Verma et al. 2017). It is used to predict the structure as well as function of newly investigated proteins and protein sequences for making a cluster of associated sequences into families and constructing phylogenetic trees for evolutionary relationships analysis (Mount 2001; Wang et al. 2005; Jayaram and Priyanka 2010).

In an agriculture-dependent country like India, bioinformatics has a very important role to play where it can be used for improving the nutritional content, increasing the yield of the agricultural produce and implanting resistance to several biotic and abiotic stresses (Jayaram and Priyanka 2010). Recently, the defense inducer(s) and antifungal molecule(s) against *Alternaria* blight disease of oilseed *Brassica* were investigated through bioinformatics approaches (Upadhyay et al. 2015a, b, 2016; Pathak et al. 2016, 2017a, b). In India, the national level high performance computing for agricultural research "Advanced Supercomputing Hub for Omics Knowledge in Agriculture (ASHOKA)" has been established

at the Indian Agricultural Statistics Research Institute as a program "Centre for Agricultural Bioinformatics" (Rai 2014) for providing computational support to ICAR as well as other scientific and educational institutions in India, working in the area of computational biology and bioinformatics with respect to agriculture and crop productivity (http://cabgrid.res.in/cabin/). Department of Information Technology, Government of India, is starting an "Agri Bioinformatics Promotion Research Program" for crop improvement, disease detection and pest control (http://meity.gov.in/content/bio-informatics). The BTISNet program of DBT for bioinformatics research and education has also been adopted by various institutions across the country (http://btisnet.gov.in/).

Plants and animal genome sequencing projects hold enormous contribution for agricultural scientific community. Bioinformatics plays a vital role in the integration as well as analysis of genomics, transcriptomics and other high-throughput sequencing data, which hold great potential to redesign crops for improved productivity (Consortium 2012, 2014; Singh et al. 2012, 2014a, b; Kiran et al. 2016).

There has been a paradigm shift from single gene approach (i.e., gene by gene approach) in understanding the mechanism of biological phenomenon to working with several genes at a time (Kumar et al. 2015a). This shift has resulted from the observation that any biological response results from cross talk of many biomolecules which act in an inter-dependent manner. As a result, many high-throughput technologies have been evolved which provide a glimpse of all the molecules involved in the process (Kumar et al. 2015a; Gupta et al. 2015). The process has been accelerated by research in the field of genomics. However, there exists a wide gap between genotype and phenotype in manifestation of a trait (Kumar et al. 2015a). To fill this gap, research is conducted at different levels—whole plant, cellular, biochemical, gene and protein levels. All these areas of unparalleled scientific efforts have led to the accumulation of large quantities of biological information. Bioinformatics which is culmination of biology and computational technology attempts to use these data to design novel strategies to get a holistic view of biological system and to design novel strategies to address the problems of agricultural, medicinal and industrial importance (Gupta et al. 2015; Kumar et al. 2016). Systems biology aims to develop and use well-organized and efficient algorithms, data structure, visualization and communication tools for the integration of these biological data with the goal of computational modeling and simulation. 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 described 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 the molecular mechanism of agriculturally important complex traits linked to crop productivity (Kitano 2002; Kumar et al. 2015a; Pathak et al. 2017b).

Bioinformatics and systems biology tools including simulation, docking and protein–protein interaction can be employed to search the important genes for specific function or manipulate the sequence for better fit and study the function of these genes or protein at the system level (Mount 2001; Kitano 2002; Wang et al. 2005; Jayaram and Priyanka 2010; Rai 2014; Avashthi et al. 2014; Gupta et al. 2015; Pathak et al. 2016, 2017a). This specified genetic and genomic knowledge could then be utilized to produce resistant, nutritionally improved and productive crops (Kumar et al. 2015a). Several bioinformatics tools and databases, viz., RetroPred (Naik et al. 2008), pTAREF (Jha and Shankar 2011), QlicRice (Smita et al. 2011), Mirtron-Pred (Joshi et al. 2012), STIFDB2 (Naika et al. 2013) and RiceSRTFDB (Priya and Jain 2013). Rice blast infection prediction (Kaundal et al. 2006), MCDRP (Gaur et al. 2014), Bhageerath (Jayaram et al. 2006), etc., have been developed by Indian scientists and many more are underway for conducting research in area of agricultural sciences with respect to plant molecular biology and biotechnology.

Expression data analysis for diagnosis and prediction

Systems-based approaches have proven of big utility for the management of plant diseases, with growing power expected to continue to appear in the future (Dodds and Rathjen 2010; Kumar et al. 2015a). Although notable and major challenges remain, one of the areas that has revealed significant promise is the mining of data sets related to gene expression for investigation of molecular signatures that can be utilized for disease management. These types of studies normally involve the collection of data samples from two or more sources with respect to infected and normal plant, by using these data sets to train a molecular classifier and another set on which to test (Furey et al. 2000). In the absence of the true test set data, resampling techniques or methods such as cross validation are commonly used to determine the probable performance of the classifier on analysis of future data (Furey et al. 2000; Yue et al. 2003). Challenges often occur in these studies when several measurement platforms are utilized in training and test data sets (Wing 2006). The capability of creating a precise classifier is a function of factors, e.g., (i) the mass of the training set relative to the number of characteristic features, (ii) the computational method used, and (iii) the natural distinctness of the chosen phenotypes. Usually, the number of samples is far fewer than the number of transcripts, leading to overfitting being a major problem.

This leads to the requirement for bioinformatics methods that aid in evading overfitting after selecting a classifier (Mount 2001; Wing 2006).

Bio-prospecting and metabolomics

Bioprospecting is the science of investigation, screening and extraction of biological diversity for genetic, genomic and biochemical resources. The indigenous knowledge is also applied to develop a commercially valuable product (Purkayastha 2016). In other words, it can be said that it is a scientific research that looks for a useful application, process or product in nature. A common perception is that bioprospecting is a new science linked to modern biotechnology (Purkayastha 2016; Talukdar et al. 2012; Zotchev et al. 2012). However, the fact is that humankind has been studying, manipulating and exploiting natural diversity ever since the emergence of *Homo sapiens* over 150,000 years ago. Early ancestors explored biodiversity and learned how to derive benefits from nature. Early bioprospecting led to the improvement of methods for growing food, building shelters and maintaining health. In the genomics era, scientists continue to find useful applications for compounds from nature. Bioprospecting is simply an extension of a long history of exploring nature to improve the quality of life. Bioprospecting should bolster economic and conservation goals underpinning bio-medical, agricultural and veterinary advances required to combat disease and sustain growing populations (Wing 2006; Beattie et al. 2011; Talukdar et al. 2012; Zotchev et al. 2012; Saslis-Lagoudakis et al. 2012; Silva et al. 2012; Sprocati et al. 2014; Purkayastha 2016).

The term metabolomics is the newly emerging field of the omics research and an integral part of bioprospecting (Joshi et al. 2002). It is a broad and simultaneous methodical investigation of metabolite levels in the metabolome and their changes over time as a consequence of stimuli. Metabolome is the qualitative and quantitative assessment of all low molecular weight compounds present in cells and is required for maintenance, growth and cellular normal function. Metabolomics facilitate the identification and quantification of economical valuable products from natural resources (Joshi et al. 2002; Seifert et al. 2013). Several techniques have been applied for metabolome analysis according to the type of sample to be analyzed such as NMR, HPLC, GC-MS and CE-MS (Seifert et al. 2013; Gong et al. 2013; Wen et al. 2014; Caspi et al. 2013). Bioprospecting has frequently been cited as a sustainable use of biodiversity. But there is a growing concern that many pharmaceutical firms and biotechnology companies explore natural resources to develop profitable and patented product without giving any recognition and money to the people who maintained and improved the traditional plant varieties for medicines. It is

termed as biopiracy and there are no effective guidelines and conditions to stop it. To overcome the problem of biopiracy, it is necessary that the terms and conditions applying for exploring biodiversity to investigate useful and novel information should be equally shared with pharmaceutical companies and local people (Joshi et al. 2002; Silva et al. 2012; Seifert et al. 2013; Gong et al. 2013; Wen et al. 2014; Caspi et al. 2013). Besides, it will provide an opportunity to learn how to convert bio-resource into wealth and also rejuvenate old principles of Ayurvedic biology into newer scientific perspectives for exploring optimum use of huge bio-resources for biomedical and agricultural applications (An and Lin 2011). The scientists of GBPUAT, Pantnagar, are currently working on genetic enhancement of aromatic rice landraces for blast resistance and quality traits through molecular breeding to develop high-yielding ideal plant type, blast-resistant and good-quality aromatic rice diversity for wider adaptability by farmers.

Metabolism, i.e., chains of chemical reactions that change various forms of matter and energy into one another, is one of the fundamental processes in living systems (Kumar et al. 2015a). The organization of metabolic reactions is generally abstracted using metabolic network models, which represent the complex web of relationships between metabolites (compounds consumed and/or produced by reactions) and enzymes (gene products that catalyze reactions) (Filipp 2013; Babu et al. 2012). Today, several well-characterized metabolic pathways for diverse species, including humans and other model organisms, are available in public databases (Caspi et al. 2013). However, large-scale analyses of the kinetics of metabolic networks are bound by data availability and computational complexity. Nevertheless, flux balance analyses that rely on steady-state assumption provide significant insights into the dynamics of metabolism (Filipp 2013; Kumar et al. 2015a). These analyses are enabled by monitoring of the abundance of metabolites via NMR and MS, as well as monitoring of the abundance and functional activity of enzymes through transcriptomic and proteomic screening for decoding of complex agricultural traits (Joshi et al. 2002; Filipp 2013; Babu et al. 2012; Gong et al. 2013; Agrawal et al. 2013; Seifert et al. 2013; Wen et al. 2014; Caspi et al. 2013; Schweiger et al. 2014; Bueno 2015).

Advances in metabolic engineering have enabled to overcome the challenges of heterologous production of the plant-based natural products in microorganisms. Omics-based approaches are being used to identify all the genes responsible for biosynthesis of the desired product, followed by their expression in microbes to synthesize the desired product (Pickens et al. 2011). In *E. coli* and yeast, several metabolites such as terpenoids, paclitaxel (Huang et al. 2001; Engels et al. 2008), artemisinin (Martin et al. 2003; Ro et al. 2006) and alkaloid intermediate reticuline have been successfully produced by following the above approach

(Minami et al. 2008; Hawkins and Smolke 2008). Besides, metabolic pathway was also engineered to successfully produce flavonoids and stilbenes: a plant aromatic polyketide in *E. coli* (Horinouchi 2009). Moreover, some progress has been made to disclose the expression problem of the plant-derived cytochrome P450 (Gillam 2007). Recent progress in omics science and technology is therefore being used to produce the desired product with high yield through metabolic engineering approaches (Pickens et al. 2011).

Plant stress and molecular cell biology

The world today faces societal challenges in the areas of agri-food nutrition, energy, environment and health sector. Although, the "green revolution" had an immense impact on agriculture in India since the 1960s, its profits were limited (Kesavan and Swaminathan 2008). For the farmers in stress-prone agriculture, the "green revolution" had made only a moderate impact. A major challenge in modern agriculture is to cope with biotic and abiotic stresses in an economical and environmentally sustainable way. Additionally, the global population is likely to cross 7 billion by 2025 and 10 billion by 2050, which will put extra burden on the already saturated crop yields (Singh et al. 2013a; Kumar et al. 2015a).

The role of mitogen activated protein kinases (MAPKs) cascades in plants has been well documented during various biotic and abiotic stresses (Pathak et al. 2013a, b). A recent study suggested the role of a least studied C group of rice MAPK during biotic stress response. The study revealed the role of OsMPK7 in imparting disease resistance against *Xanthomonas oryzae* the major pathogen of disease (Jalmi and Sinha 2016). Comparative microarray studies have indicated that the genes, i.e., serine carboxypeptidase S28, SCPL20, RD20, LCAT3 and NHX2 are up-regulated in response to *B. cinerea* and abiotic stresses such as heat, salinity and osmotic stress in *Arabidopsis thaliana* (Gujjar et al. 2014; Sham et al. 2015). Previous studies have also demonstrated that various transcription factor genes, i.e., WRKY17, WRKY22, WRKY44, WRKY51, WRKY57, WRKY58, WRKY65, WRKY70, WRKY72, WRKY98, WRKY104, CBF/DREB1 and NAC are differentially expressed in response to many abiotic stresses (Kayum et al. 2016; Gujjar et al. 2018; Karkute et al. 2018).

Tackling recalcitrant diseases like Karnal bunt caused by *Tilletia indica* in wheat and *Alternaria* blight incited by *Alternaria brassicae* in *Brassica* is a major problem and several approaches have been followed by Indian scientists to address the complexity of these agriculturally and economically important diseases. These approaches include molecular and immune diagnostics for plant disease surveillance (Singh et al. 2013a, b; Pathak et al. 2016), molecular pathotyping for pathogen indexing program and molecular

signaling for characterization of resistance (Kumar et al. 2015a).

Environmental stresses, including biotic as well as abiotic stresses, present some of the most enduring factors which limit crop productivity (Weckwerth 2011; Filipp 2013; Mewalal et al. 2014; Kumar et al. 2015a). Apart from various biotic stresses caused by a diversity of plant pathogens and several abiotic stresses such as extreme temperatures, drought, salinity and radiation have detrimental effects on plant growth and productivity, especially when several of them occur simultaneously. In the world, only 9% of the area is conducive for crop production, while 91% is under one or the other kind of environmental stress. Ironically, the area under stress is likely to increase further due to land degradation and urbanization (Nelson et al. 2014; Haddeland et al. 2014; Gupta 2015). There is also impending concern about the impacts of climate change and its variability on agricultural production. Research proves that while plants would react positively to elevated CO_2 in the absence of environment change, the impacts of high temperatures, changed patterns of precipitation and likely increased frequency of disastrous events, such as flood and droughts, will possibly combine to decrease yields and increase production risks worldwide (Soon et al. 1999).

In a few years, the effect of 'global warming' on the production of crop will become an extremely 'contentious' problem (Sultan 2012). Resolving this issue at the plant systems level is approximate exclusively to a question of coping with stress on plant. It is to be noted that global environmental concerns are born out of the recognition that ecological processes do not always respect national boundaries and that environmental problems often have impacts beyond borders; sometimes globally (Sultan 2012; Nelson et al. 2014; Haddeland et al. 2014). Viruses, bacteria, weeds, fungi, insects and other pests and pathogens are a key constraint to crop productivity from fields to markets, in the developing world (Thakur et al. 2013; Kumar et al. 2015a; Sharma et al. 2016). With little resources to fight or stop infection and infestation, humans farming small tracts of land are most susceptible to these stresses and can have devastating crop losses. Presently, most crop plant protection strategies and management involve genetic improvement to develop resistance against pests and pathogens as well as develop agrochemicals with desired affinity, efficacy and potency (Lamberth et al. 2013; Rai 2014; Gupta et al. 2015; Kumar et al. 2015a; Pathak et al. 2016, 2017a, b; Mamgain et al. 2018).

International agricultural and environmental research institutions are now re-discovering plant stress as a key constituent of global warming effect on local as well as global food production. Advances in plant molecular cell biology have offered new information and technologies required to address these issues and challenges (Filipp 2013; Kumar et al. 2015a). A promising source of excitement are the

powerful tools of modern plant molecular cell biology in functional genomics and gene expression profiling in stress response that seems to provide a ray of new hope (Toenniessen et al. 2003). These include the use of microarrays and genome mapping to detect and precisely manipulate stress-response genes in breeding programs, and in the growing ability to engineer new or 'foreign' genes into plant genomes (Datta 2013). Great advances have been made in recent years in understanding the molecular basis of plant response and plant tolerance to various biotic and abiotic stresses (Pathak et al. 2013b). Despite this, it will be prudent to admit that a huge gap persists between the findings at the molecular level and the application of this knowledge at the whole plant level for improved yield on-farm. Nevertheless, plant genomics remains a major component of food security, at the international level, and prosperity for the foreseeable future (Filipp 2013; Kumar et al. 2015a).

Network-based disease gene prioritization

Characterization of disease-associated difference in plant genome is an important step toward enhancing understanding of the cellular mechanisms that drive complex diseases, with profound applications in modeling, diagnosis and management intervention (Kumar et al. 2015a; Pathak et al. 2016). Genome-wide linkage and association studies in healthy and affected plants provide chromosomal regions containing hundreds of polymorphisms that are potentially associated with certain diseases (Gupta et al. 2014a, b; Li et al. 2016). These polymorphisms often span up to the 300 genes, only a few of which probably have a role in the manifestation of disease (Koyuturk et al. 2011; Sheikh et al. 2013). Investigation of that many candidates via sequencing is clearly an expensive task, thus not always a feasible option. Consequently, computational methods are primarily used to integrate omics data sets to prioritize and identify the most likely disease-associated gene and proteins (Kumar et al. 2015a). Protein–protein interactions provide an invaluable resource in this regard, since they provide functional information in a network context and can be obtained at a large scale via high-throughput screening (Sheikh et al. 2013). Network-based analyses of diverse phenotypes demonstrate that products of genes that are implicated in similar diseases are clustered together into "hot spots" in PPI networks (Ma'ayan 2011; Kanaya et al. 2014).

Diversity and molecular breeding

Diversity is one of today's buzzwords and concept of diversity can be examined as a positive aspect of globalized society. Diversity is in several ways reflective of current world

order, but there are methods of taking this further without compulsorily endangering its alternatives (Arif et al. 2010). There is a lot of scope to discover the series of what diversity means and investigate modes of diversity in real-life conditions. Genetic and genomic diversity offers opportunities to utilize various genomic resources and technologies such as molecular marker technology and molecular breeding in an effort to breed new varieties of desirable traits. Improved varieties, landraces and wild species can be explored for their desirable traits and this knowledge can be further utilized to develop new varieties through marker-assisted selection (Arif et al. 2010; Singh et al. 2011; Govindaraj et al. 2015).

Molecular markers are DNA-based markers which are either coding or noncoding sequence in nature and that assist in crop breeding programs (Singh and Singh 2015). The restriction fragment length polymorphism (RFLP) was the first DNA-based marker to be used successfully in crop improvement, followed by others such as AFLP, SSR, DarT and SNPs, for significant use in plant breeding programs, and molecular markers essentially need to be present in abundance in the genome and be polymorphic in nature, among the various other salient features required. Continuous progress in development of such new and specific types of markers play crucial role in identifying the genomic variability and diversity present within the same and across the species of the crop plants (Gupta et al. 2014c; Kumar et al. 2016). These markers help in effective utilization of germplasm and improve the genetic gains more precisely and efficiently by using marker-assisted selection (Arif et al. 2010; Singh et al. 2011; Fahad et al. 2014; Broughton et al. 2014; Govindaraj et al. 2015; Singh and Singh 2015).

In a study, 113 finger millet genotypes were collected from different parts of Uttarakhand and analyzed by genotype by sequencing (GBS) method using the Illumina platform. The GBS data were used for the analysis, identification, association mapping and functional validation of important agricultural traits of finger millet through experimental and computational approaches (Kumar et al. 2016).

Plant transformation and developmental biology

In the last 25 years, various key components associated with the development of plants and their physiological and biochemical mechanisms were identified (Schmid et al. 2005). *Arabidopsis thaliana* was considered as model organisms for developmental biology that facilitated researchers in the improvement of other economic and agriculturally important crops plants through omics sciences and technology (Schmid et al. 2005; Van Norman and Benfey 2009). The practice of plant tissue culture has changed the approach of

some nurserymen for performing plant propagation. Plant tissue culture consists of a set of in vitro techniques, methodology and strategies that are a branch of plant biology and biotechnology (De Filippis 2014). Advances in omics dramatically changed the outcome of tissue culture through genetic transformation technology by using key genes investigated via omics-based experimentation for development of the desired product. It has been playing a significant role in basic and applied research, including crop improvement (De Filippis 2014). In modern agriculture systems, only about 150 species of plants are extensively cultivated. a large number of these have reached the limit of their improvement by traditional methods (Johnson 2008). The utilization of tissue culture technology, as a key tool or attached to other methods, including rDNA technology, is at the vanguard in the modification and improvement of crop plants for agriculture and related discipline such as horticulture and forestry (Schmid et al. 2005; Johnson 2008; Van Norman and Benfey 2009; Singh et al. 2011; Naik and Chand 2011; Rathore et al. 2011; Wang et al. 2012; Brookes and Barfoot 2013; Fahad et al. 2014; Broughton et al. 2014; De Filippis 2014; Valkov et al. 2014; Okay et al. 2014; Pant 2014; Motte et al. 2014; Singh and Singh 2015; Kumar et al. 2016). Tissue culture techniques, in association with molecular biology techniques, have been successfully applied to incorporate specific traits by gene transfer technology. Commercially glyphosate-tolerant soybeans, lepidoptera-tolerant corn, glyphosate-tolerant cotton, Bt cotton and Bt maize are commercially released varieties. Since their availabilities, these technologies have been adopted at an effective rate (Naik and Chand 2011; Wang et al. 2012; Brookes and Barfoot 2013; Okay et al. 2014). The major reason for the quick acceptance is that the new technologies provide an excellent deal for farmers. Recent estimates place cost or price reductions in the case of soybeans in the USA at about US$20 per hectare, mainly because of decrease in energy costs (weed management cost) (McFarlane et al. 2010).

In vitro techniques for the protoplast, anther, microspore, ovule and embryo culture have been utilized to create novel genetic variant in the breeding lines (Chawla 2002). Cell culture technology has also made somaclonal and gametoclonal variants with the potential of crop improvement. The single cell and meristem culture can be successfully used to eradicate plant pathogens from planting material and improve the growth as well as yield of established cultivars (Chawla 2002; De Filippis 2014). Large-scale micropropagation and tissue culture laboratories are offering millions of plants for commercial purposes (Giles and Morgan 1987). With respect to medicinal plants, useful metabolite production by plant cell and tissues culture has been performed on a growing scale since the end of the 1950s (Filova 2014). Their outcomes stimulated recent studies on the commercial application of this technology in various countries including India. However, there are still small barriers that must be defeated before commercialization of several other products (Giles and Morgan 1987; Chawla 2002; Filova 2014). To overcome the barriers hindering commercial and industrial applications of plant tissue cultures, however, it is essential to conduct more basic and fundamental research, including deciphering of the biosynthetic pathways of many useful bioactive compounds and secondary metabolites in plants and the mechanisms for their biosynthesis. Association with a number of researchers working in other scientific fields is also very useful.

Similarly, foreign proteins can be synthesized using plant tissue culture and transgenic plants. For choosing the technique for commercial production, a case-by-case analysis is needed. A broad range of issues must be considered, including production cost, market volume, efficacy, safety as well as product stability, and whether the foreign protein has various biochemical or pharmacological features compared with material from available sources (Ferrante and Simpson 2001). Plant cell and root cultures have been verified for recombinant protein production. The role of plant cell culture as a way for commercial production of protein is not clear at the time, but is likely to depend on the capability to express proteins of high levels in vitro by changing the culture conditions (Gharelo et al. 2016). The stability and extracellular localization of secreted proteins in the medium of the plant cell cultures may be significant keys to the economic feasibility, permitting easier product recovery without destroying the biomass, for the reason that the controlled environmental condition in plant cell cultures facilitates advantages for regulatory compliance and GMP. A potential niche for reactor-scale plant cell and tissue culture is the fast production of low-to-medium volume of therapeutic proteins (Ferrante and Simpson 2001; Gharelo et al. 2016). Technologies for changing the glycans of plant glycoproteins may be needed before plant systems can be completely exploited for the production of vaccines and injectable drugs (Doran 2000). Considering the recent trends in plant tissue culture and transformation, there is need to explore "what is being completed" and "what can be completed" in case of tissue culture of commercially valuable plants.

Plant cell physiology and input use efficiency

Molecular biology and cell physiology mostly concern themselves with recognizing the interactions between the various cell systems, including the interactions between nucleic acid (DNA, RNA) and protein biosynthesis and studying how these interactions are regulated (Alberts et al. 1995). This discipline of science overlaps with biochemistry which is the learning of the chemical substances and fundamental

processes happening in living organisms. Biochemists focus heavily on the role, structure and function of biomolecules. Rapid advances in the field of plant cell physiology and input use efficiency have enabled identification of molecular principles which underlie plant behavior (Buchanan et al. 2015). The identification of various factors and their cognate target sites involved in the regulation of plant development and adaption processes has led to distinct molecular models which explain how plants cope with different environmental stresses of light, water, nutrient conditions and various biotic stresses. It can be used to model and analyze important and complex traits linked with crop productivity such as water use efficiency, nitrogen use efficiency, photosynthetic efficiency and other essential traits associated with plant architecture and plant cell physiology for future Omics-based applications in crop plants (Kumar et al. 2015a).

This in turn has facilitated formulation of effective strategies to develop stress-tolerant crop varieties through molecular manipulation of key genes or proteins (Bita and Gerats 2013). The recently developed skill to recognize entire genomic sequences has provided the data required to accomplish massive assessments and comparisons of derived protein sequences, the outcome of which may be utilized to formulate and test hypotheses regarding biochemical function of a specific plant protein (Collins et al. 2003). With the advent of omics technologies it has become possible to understand the behavior of whole genome and gene networks involved in regulation of complex agronomic traits. This has been possible due to availability of molecular maps, quantitative trait loci (QTLs), genomic and expressed tag sequences from model plant *Arabidopsis thaliana* and various crop plants such as rice and sorghum (Li et al. 2014). Comparative and functional genomics approaches are being utilized for understanding gene functions and for studying simultaneous interaction of various genes governing a complex agronomic trait (Kumar et al. 2015a). With the inception of genomic research, coordination of regulation of a set of genes is possible by transfer of key regulatory master switch gene.

Nanobiotechnology and diagnostics

Molecular diagnostics technologies will also play an important role in practice of agriculture, food and biological warfare in the twenty-first century (Dawidziuk et al. 2014). Nanobiotechnology broadens the limitation of molecular diagnostics to the nanoscale level. Recent advances in genomics and proteomics have provided us a number of different molecular markers, which are specific for various crop plant diseases. Nanotechnology can utilize high-throughput data obtained through omics-based experimentations, which are able to allow us for more specific and efficient diagnosis

of diseases linked to crop productivity (Hood et al. 2012; Lee 2014).

In general, it has been most significant innovations of recent years and has quickly become the basis of various products that are currently in use, especially in crop plants (Rai and Ingle 2012; Grobe and Rissanen 2012). The success of this advanced technology has been in its power to present smarter solutions that have broad applications in agriculture (Grobe and Rissanen 2012). The potential of nanodiagnostics arises from the fact that most biological molecules and cell organelles fall within the nanometer scale. Conventional methods of pathogen detection have often depended on recognition of disease symptoms, isolation, culturing and identification of organisms by morphology as well as biochemical tests. The major limitations of these culture-based morphological approaches, however, are the dependence on the ability of organism to be cultured, time-consuming nature and the need of a wide taxonomic expertise (Perez-Fernandez 2012; Kole et al. 2013; Husen and Siddiqi 2014; Kumari and Yadav 2014). Laboratory diagnostics for plant pathogens have traditionally relied on methods of detecting the pathogen by antibodies or culture using a variety of techniques such as neutralization, enzyme-linked immunosorbent assay, complement fixation and agar gel immunodiffusion. The field of nanobiotechnology and molecular diagnostics has mainly increased sensitivity and faster detection (Singh et al. 2013a, b).

Nanobiotechnology can be exploited to develop biosensors and other efficient diagnostic tools for crop diagnostics (Moreau et al. 2012). Nanobarcodes and submicrometer metallic barcodes along with striping patterns made by sequential electrochemical depositon of the metal demonstrate differential reflectivity of the adjacent stripes facilitating investigation of the striping patterns by using conventional light microscopy (Kawadkar et al. 2011). The processes and products that are precise and impossible to achieve through conventional systems can be achieved by atom by atom manipulation using nanobiotechnology (Singh et al. 2013a). Nanoparticles are able to control crop diseases. Nutrient deficiency and food contaminants can also be detected using nanosensors (Manjunatha et al. 2016). "Smart delivery systems" for agriculture can have timely controlled, spatially targeted, self-regulated and remotely regulated, pre-programmed as well as multi-functional features to avoid biological difficulties to successful targeting. It can examine and monitor the effects of delivery of bioactive molecules or nutrients or any important molecules such as pesticide. A small sealed package brings the drug which opens up only when the required location or site of the infection of the human and animal system is reached in the case of smart delivery system. The nano food packaging sector has experienced some of the most significant developments in terms of commercialization (Scrinis and Lyons 2007).

Manufacturers are using nano techniques with the aim of improving the quality, durability and shelf life of packaged foods. Nanobiotechnology can be employed to synthesize smart nano-devices that release active herbicide and insecticide molecules only when moisture is available in rain-fed system besides targeting both leaves and tubers (Grobe and Rissanen 2012; Singh et al. 2013a). Nanoinsecticides are better than the conventional insecticides due to their small size, reduced run off, higher water suspension/solubility, less damage to the environment. Nanofertilizers may be applied as a strategy to regulate and control smart release of the nutrients that commensurate with crop requirement (Kah 2015).

In a study conducted at GBPUAT, Pantnagar, antisera were successfully produced in albino white New Zealand rabbits against teliospores, soluble cytoplasmic and the insoluble cell wall antigens of vegetative mycelium of fungal pathogen. The various immunological laboratory-scale formats such as dot immunoblot binding assay (DIBA), seed immunoblot binding assay (SIBA), indirect immunofluorescence test (IIFT) and indirect microtiter ELISA have been developed for quick detection of infection and infestations of KB teliospores in wheat samples for declaring it pathogen free and will strengthen the quality and regulatory aspects of seed certification and quarantine regulation. The ELISA-based immuno-dipstick assay and gold nanoparticles-based lateral flow immunodiffusion tests have been also developed and are quite sensitive to detect only few teliospores (as low as five) and apply for on-site diagnostics at field level. The ultimate goals of nanodiagnostics, nano delivery and nano safety are revolutionizing crop plant biology (Gupta et al. 2001; Kumar et al. 2004).

Bio-Inoculant, bioprocessing and metagenomics

Bioprocessing is associated with the utilization of biological resources such as microorganisms, plant, animal cells and enzymes in converting raw materials into different new value-added food as well as non-food products (Beattie et al. 2011; Saslis-Lagoudakis et al. 2012; Talukdar et al. 2012; Zotchev et al. 2012; Sprocati et al. 2014; Purkayastha 2016). Research on bioprocessing focuses on three key thrust areas, namely enzyme technology, fermentation and microbial technology, plant metabolites and cell culture technology (Costa et al. 2013). There is need for extensive research which has the potential for facilitate the agri-food industry to enhance process efficiency, improve product quality and extend shelf life of processed as well as fresh agri-food products. In the genomic era, vast genome sequence information can be utilized to manipulate the metabolism of the organism resulting in more efficient strains for bioprocessing

purposes. The science of omics can be used to produce more efficient enzymes, optimize fermentation conditions and identify new gene targets for enhancing the bioprocessing of crop produce (Beattie et al. 2011; Talukdar et al. 2012; Zotchev et al. 2012; Sprocati et al. 2014). Functional genomics approaches provide insight into cell's metabolism which can be exploited for metabolic engineering to develop value-added products (Georgiev et al. 2009).

Bioinoculants have revealed big potential as a renewable, supplementary and environmental-friendly resource of plant nutrients, and are a key element of integrated nutrient management (INM) (Jat et al. 2015). Bioinoculants are the live microbial cells of single species or consortium of different microbial isolates that are applied to the soil or treated with plant/seed material to improve plant health. Broadly, bioinoculants include biofertilizers and biopesticides. Omics technologies can be utilized to authenticate different strains of bioinoculants to maintain quality standards and to identify different genes which could be used to develop improved strains of bioinoculants (Balachandar 2012; Malusá et al. 2012).

Metagenomics is the study of metagenomes, genetic material recovered directly from environmental samples. It holds immense potential to study useful microbial diversity present in the environment, which is non-culturable and cannot be studied by traditional microbiological methods (Singh et al. 2009). Science of "Omics" has revolutionized the study of microbes present in the environment and enhanced understanding of the composition, physiology and phylogeny of microorganism communities. At present, there is a major emphasis on the use of "omics"-based approaches such as genomics, proteomics and transcriptomics to determine the uniqueness and functional features of microbes inhabiting various environments (Singh et al. 2009, 2010; Suyal et al. 2014). Needless to say, such recent developments will be of significant value in discovering new microbes and microbial genes and to exploit them in solving the urgent challenges facing the environment, agriculture and human health.

Challenges in omics

We have entered into the era of omics from the past decades that may lead to holistic approach for interpreting the complex nature of biological systems at the molecular to cellular level. The completion of several genome projects will allow us to define the functional relationship among one or more particular genes involved in the productivity, disease resistance and physiological processes of crop plants. Additionally, the expression of these gene, mRNA stability and final protein product can be altered by a wide range of physiological processes, alternative splicing, post-translational modification, epigenetic modifications and single

nucleotide polymorphisms, etc., but they present a complex challenge to the scientific community. With the beginning of newer techniques and technologies, the omics science and its applications in diverse areas are quickly increasing. Such types of emerging fields including next generation sequencing, regulomics, spliceomics, metagenomics, environomics and bioinformatics present great solutions to fight global challenges to crop productivity and the environment (Ning and Lo 2010). Currently, the potential challenges of omics are availability of computational resources. Big amount of data have been and are being generated. This has imposed certain challenges including storage and analysis of the data: lack of reference database, and the reference phytochemicals for metabolomics, where some metabolites with unknown structure might be produced; reproducibility: inability of one group's findings to be replicated by another group or person; noise: omics-based science can generate huge data that noise overwhelms indication. Why is it that researchers get fewer genes as apparatus and methodologies advance?; fishing: the look for novel genes in complex samples, i.e., discovery-mode "omics", has been frequently criticized as a "fishing expedition" in which one blindly expects to find something attractive and often falls short (Ning and Lo 2010; Costa 2012; Gomez-Cabrero et al. 2014; Cambiaghi et al. 2017).

Future perspectives

The growing demand for improved crop varieties, effectiveness and quality of crop product and major challenges faced by modern agriculture are the key factors that force the scientific community to adopt innovative omics-based technology for enhancing crop productivity in India. Omics science and technology, viz., genomics, transcriptomics, proteomics, metabolomics, bioinformatics, systems biology and other omics-based approaches having tremendous potential to decipher the complexity of important and complex traits linked to productivity of the crops such as nitrogen use efficiency, photosynthetic efficiency, water use efficiency, plant architecture, biotic and abiotic stress tolerance and nutritional quality. Currently, the cost of omics-based applications for crop plants is still extremely high, but it is expected to decrease with technological advancements in the future. Advances in these approaches can lead to bridging the gap between genotype to phenotype by utilizing quantitative and automated screening and selection methods that target whole crop plants system and quality traits, which enhance the release of new high yielding varieties with rich amount of nutrients to the farmers, and reduces large-scale field studies and developmental process. Besides, the omics-based technology will also enable bridging the gap between gene–environment interactions, because many key traits depend upon the interaction with environment for a particular biological

function. It will help in the creation of 'smart crops' for higher yield and sustainability that are capable of fulfilling the need of rapidly growing population for securing food and nutritional security in future.

Conclusion

This article highlighted the importance of new omics-based tools and technologies in the improvement of crop productivity. A thorough understanding of genomics, transcriptomics, metagenomics, proteomics, metabolomics, bioinformatics and other related areas of omics have opened up new perspectives for investigating functions and interactions of plants with abiotic and biotic stress agents. The omics-based researches have become very helpful for solving various agricultural challenges. Therefore, additional resources should be allocated for improvement of omics-based technologies to effectively target plant systems for crop improvement programs. A public conversation is necessary in addition to research and development for promoting the application of omics science and technology in India for upliftment of the agri-food nutrition sector in the future.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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