



EXPANDING THE FRONTIERS OF RICE RESEARCH THROUGH OMICS

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ABSTRACT

Rice is an important food grain and a staple food for nearly 60% of the world's population. In post-genomic era, comprehensive data from “omics” technologies have been extensively applied to rice to elucidate its cellular intricacies and regulatory mechanisms. The present review deals with current scenario of “omics” applications in understanding this important food crop and highlights the essentiality of genomics and transcriptomics in rice research. It includes a brief coverage of improvement in genetic mapping, rice trait analysis, developmental understanding of the rice embryogenesis etc. aided by high-throughput sequencing technologies. The review also discusses application of basic and applied proteomics and metabolomics research in providing new directions to improvement of qualitative and quantitative traits. These include another proteome and seed development, tackling of biotic and abiotic stress, pathogen infections etc. Towards the end, the review addresses the application of data science into this field, shortlisting relevant database (for the omics) discussed above.

Key words : Rice, *Oryza sativa*, Genomics, Transcriptomics, Proteomics, Metabolomics, Database

INTRODUCTION

Cultivated rice (*Oryza sativa* L.) is known as a staple food of human and widely consumed by more than 3 billion people worldwide accounting for around 50-80% of daily calorie intake. According to FAOSTAT data (2012), rice is the third highest globally harvested crop among all agricultural crops (<http://faostat3.fao.org/browse/rankings/>, 2015). Over 150 million hectares of agricultural land is planted with rice annually and the world production is around 600 million tons. Asian countries are the key producers of rice contributing around 75% of the total rice production, with China and India contributing to nearly half of the world output (Delseny et al., 2001). Based on a recent survey (1st July 2015) by United Nations Department of Economic and Social Affairs, Population Division, the world's population was 7.349 billion which is soon expected to reach up to 10 billion in 2056 and India's population will surpass China by 2022 (<http://www.worldometers.info/world-population/>, 2015). In order to meet the growing need of food for human consumption, rice production must increase proportionately at a sustainable rate without additional land for growing this crop.

Besides economic significance, rice has also evolved as a model crop among monocotyledons due to availability of complete genome sequence (Yu et al. 2002; Huang et al. 2013). This provides a means for several omics studies like genome-wide transcriptome, proteome and metabolome analyses (Agrawal & Rakwal 2011; Kyndt et al. 2012; Chen et al. 2014). In 2002, the first draft genomic sequences of two rice subspecies, *O. sativa* ssp. *japonica* (Nipponbare) and *O. sativa* ssp. *indica*, were released (Goff et al. 2002; Yu et al. 2002). This was followed by assembly of reference genome by re-sequencing of rice genomes through high throughput technologies (HTT) (Gao et al. 2013; Sabot et al. 2011). Till 2012, about 756 rice genes accounting for only 2% non-transposable element have been functionally elucidated by genetic analysis (Chandran & Jung 2014).

In order to further explore the functional aspect of rice genome, transcriptomics and proteomics of rice have also been studied extensively. A tremendous progress has been observed in the techniques relevant to almost all tissues, organs and organelles of rice. Identification and analysis of differential expression of genes under varied conditions has been made possible by transcriptomics analyses. The achievements in global mapping of phosphorylation sites and identification of numerous novel secreted proteins (secretome) are noteworthy (Que et al. 2012; Agrawal et al. 2010). Established proteomes have also assisted in re-annotating the rice genome and unraveling the proteins of unknown functions. Such findings are likely to be translated for genetic improvement

with respect to different agronomic traits, nutritional quality and tolerance to different biotic and abiotic stresses. Besides genomics, transcriptomics and proteomics, metabolomics also forms a necessary component of omics technologies. One of the fundamental aspects is the presence of secondary metabolites which are responsible for several characteristics of food grains such as rice quality, defense mechanism and nutritional aspect (Chandran & Jung 2014; De & Nag 2014). Till now, there are around 243 publications comprising various rice omics related data (Data search from Scopus database on 15-06-2016). Thus, a tremendous progress has been made in the diverse omics fields of rice research i.e. proteomics followed by genomics, metabolomics and transcriptomics shown in **Figure 1**.

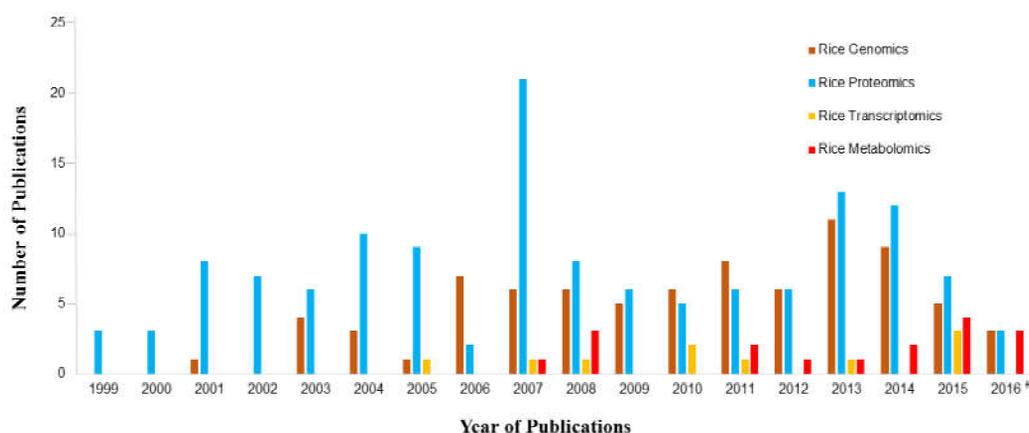


Fig. 1. Number of publications on rice omics research from the year 1999 to 2016#, where (#) represents 2016 as continued year.

The present review portrays the omics technologies like genomics, proteomics, transcriptomics and metabolomics to highlight the advances made in rice omics research. This review is expected to aid in comprehending the current rice-omics scenario and how application of data science is increasing its potential across the scientific community.

RICE GENOMICS STUDY

The publication of both *O. indica* and *O. japonica* rice reference genome sequences facilitate a search for the identification of highly dense polymorphic markers (Shen et al. 2004; Feltus 2004). Individual rice chromosome centromeres have also been fully sequenced and

assembled which offers an essential foundation for future functional analyses and construction of plant artificial chromosomes (Wu et al. 2004; Nagaki et al. 2004). Such information directly relates to the phenotypic traits. Currently, the cloning of genes and functional analysis of important cultivars related to the plant architecture and yield have been remarkably improved by pursuing several meticulous approaches. These include generation of cross populations, mutant screening, identification of wild variants related to the traits, and comparative genome analysis (Shomura 2008; Jiang et al. 2012). For example, recently defined quantitative trait loci (QTL) and dense and erect panicle 1 (DEP1) are significantly responsible for controlling rice grain number, weight and size (Ashikari 2005; Huang, et al. 2009). Furthermore, cloning and characterization of quantitative trait locus demonstrates that Ideal Plant Architecture (IPA) and Wealthy Farmer's Panicle (WFP) are the reasons behind higher number of panicle branching and higher grain yield in rice (Jiao et al. 2010; Miura et al. 2010). Research has also revealed that microRNAs play a key role in regulating vast range of biological activity (Xie et al. 2006). The different facets of rice genomics are described below-

Next Generation Sequencing (NGS) in rice genomics

Rice genomics study has greatly accelerated by arrival of next generation sequencing (NGS) technology. It has been previously reported that rice genome is relatively small (430 Mb) and it has modest level of repetitive sequences (**Table 1**). Availability of both wild and cultivated rice genome and combination with new genomic approach has ushered rice genomics studies. Re-sequencing using microarray has identified genome-wide SNP variation in cultivated rice and revealed the relation with other landraces (McNally et al. 2009). Re-sequencing of 50 accessions from 40 cultivated and 10 wild rice varieties reveal thousands of genes with notably lower diversity in cultivated rice but not in wild rice, which signifies that candidate regions might be selected during domestication. Some of these variants are also associated with important biological features which can make a significant impact on the yield of cultivated rice (Xu et al. 2012). The new approaches in genomic study have opened new vistas in research and applications like evolutionary trend and relationship, gene mapping, mutant analysis for agronomic traits etc. A study involving NGS by He et al. (2011) with 66 accessions from three taxa provides insights into the diversity and domestication of rice traits. Recently, it was found that *Oryza sativa* ssp., *japonica* rice was first domesticated in the middle area of the Pearl River in southern China from a specific population of

O. rufipogon. The same study also unveiled that subsequent cross between *japonica* rice and local wild rice lead to generation of *Oryza sativa* ssp. *indica* in South East and South Asia (Huang et al. 2012). NGS has also provided fresh perspectives on the impact of transposable elements (TE) in the genome dynamics of the species and molecular spectrum of somaclonal variation in regenerated rice and identification of rare and spontaneous mutations with high confidence within the genomes (Miyao et al. 2012).

Table 1: Basic characteristic features of *Oryza sativa* genome

Features	<i>Oryza sativa japonica</i>	<i>Oryza sativa Indica</i>	Reference
Number of chromosome	24(2n)	24(2n)	Kurata et al., 2002;
Genome size (Mb)	430	466	Goff et al., 2002; Yu et al., 2002
Gene Count (coding genes)	35,679	40,745	http://ensemblgenomes.org/
Gene Count (non-coding genes)	55,401	45,577	http://ensemblgenomes.org/
Gene transcript [#]	97,751	88,438	http://ensemblgenomes.org/
TE-related Gene	17,272	NA	http://ensemblgenomes.org/

[#]Nucleotide sequence resulting from the transcription of the genomic DNA to RNA. One gene can have different transcripts or splice variants resulting from the alternative splicing of different exons in genes.

Genetic mapping of rice

NGS provides an opportunity to expedite the genotyping operation for effective genetic mapping and genome analysis over tedious traditional breeding approach which requires several years for successful development of new cultivar. These facilitate the process of selection of offspring with desirable trait, which lead to development of new cultivar with better efficiency and high accuracy. Genotyping by resequencing of 150 rice recombinant inbred lines (RILs) (*indica* rice cultivar 93-11 and the *japonica* rice cultivar Nipponbare) was developed to construct SNP-based ultra-high-density linkage maps (Huang et al. 2009). Another study carried out for linkage analysis explored the quality of developed bin map for QTL mapping

which can significantly speed up the map-based gene cloning process (Wang et al. 2011).

Genomics in rice traits analysis

Mutant identification and analysis is vital for genetic improvement of rice and genomic study can greatly enhance the process. MutMap, CloudMap are the methods for rapid gene isolation using a cross of the wild type parental line with mutant type (Abe et al. 2012, Minevich et al. 2012). It involve whole-genome re-sequencing of pooled DNA from an isolated population of plants that shows a useful phenotype. Tian et al. (2009) showed via candidate gene association analysis approach, that 18 Starch Synthesis-Related Genes (SSRGs) are responsible for taste and other dietary properties of rice (Tian et al. 2009). Sequencing-based genome-wide association studies (GWAS) has also recently appeared as a method for dissecting agronomic traits in different rice landraces (Huang et al. 2010).

Genotyping-by-sequencing

Genotyping-by-sequencing (GBS) is the latest application of next-generation sequencing protocols and is appreciated for being rapid, simple and reproducible. GBS has been found to be useful in generating high density SNP markers essential for mapping in breeding population (Spindel et al. 2013) More recently in 2015, a tool named as WIPPER was developed which adorns the efficient field phenotyping platform for large-scale applications (Utsushi et al. 2015). Apart from this, GBS technique has also been involved in generating Multi-parent Advanced Generation Inter-Cross Populations (MAGIC) in rice and it can have probable utilizations in quantitative trait loci (QTLs) mapping and rice varietal improvement (Bandillo et al. 2013).

RICE TRANSCRIPTOMICS STUDY

Study of RNA transcript profile, known as transcriptomics has opened a new aspect of genome functions. Because the information contained in a structural gene is transmitted via the transcript for eventual protein synthesis. While genomics give information about genome size, gene complement and their structure, it is transcriptomics which reveals how the genome functions at different stages of life cycle under different physiological conditions and in response to environmental stresses. Gene expression is basically differential and earlier it was studied by microarray analysis. However, microarray analysis suffered from some limitations and drawbacks like it was dependent on available probe sets. Moreover, microarray hybridization signals cannot distinguish alternative transcripts. Transcriptomics take

care of these drawbacks and hence going to stay as a reliable tool to study gene expression profiles.

Developmental biology of rice embryo

Rice (*Oryza sativa*) is a model monocot with a known genome sequence and is used for studying embryogenesis in plants. The transcriptome profile of rice developing embryos was analyzed using RNA-Seq to gain understanding of the molecular and cellular events related to rice embryogenesis (Xu et al. 2012). RNA-Seq analysis showed that around 27,190 genes were expressed during three developmental stages of rice embryo, namely, 3-5, 7, and 14 DAP. Out of these genes, 1,011 were differentially expressed genes. Genes related to metabolism, transcriptional regulation, nucleic acid replication/processing, and signal transduction were expressed during early and middle stages while protein biosynthesis-related gene expression spiked during middle stage. The genes highly expressed during late stages were related to starch/sucrose metabolism as well as protein modification.

Different developmental stages of rice anther

Understanding anther biology is a key to understand rice reproduction and fertility which in turn is related to rice productivity. Transcriptome analysis has already contributed significantly in this direction. The development process of male gametophyte and pollen contains stages like pre-meiotic anther (PMA), meiosis (MEI), tetrad (TET), uninuclear (UN) microspore, bicellular (BC) pollen, tricellular (TC) pollen, MEI, TET and UN tapetum. With the help of 44K rice microarray chip, the LM-separated microspore/pollen and tapetum cell RNA was isolated and studied. Additionally, promoter motifs and their enriched functions were identified which provides biological insights into developmental procedure of male gametophyte and pollen. All these contribute to understand molecular basis of cytoplasmic male sterility, self-incompatibility etc. which are the basis for hybrid rice production (Zhang et al. 2009).

Effects of biotic and abiotic stress in rice

With climatic changes and environmental degradation, biotic and abiotic stresses are on the rise and a growing challenge to researchers and food security. Transcriptomics have been applied to understand the effects of biocontrol agents and abiotic stresses like drought on the crop and molecular mechanisms employed by rice plant to tackle it. Recently, Affymatrix-based whole genome arrays were used to identify the molecular response related elements in rice to the commonly used herbicide, Quinclorac which showed over expression of several detoxifications

related pathways, for e.g.- Cytochrome P450, ABC drug transporter etc. (Xu et al. 2015). This work provided potential markers for environmental monitoring and detoxification of Quinclorac and also paved way for future studies related to similar chemicals employed in biocontrol.

Understanding drought as well as heavy metal resistance has also been aided by application of RNA-Seq and microarray in rice. Identification and characterization of novel genes related to metal homeostasis were carried out via microarray studies, especially targeting the transporters and heavy metal detoxification proteins (Ogo et al. 2014). Also, RNASeq of drought-resistant rice transcriptomes showed that stress-related pathways developed in a rice plant might aid in tolerating other unrelated stresses. It was shown by Oono et al. (2014) that plants acclimatized to drought resistance could aid in Cadmium (Cd) tolerance (Oono et al. 2014).

In the field of biotic stress study, transcriptome sequencing of common rice pests like *Chilo suppressalis* and *Nilaparvatalugens* were performed to understand their internal mechanisms and response to different biocontrol measures (Xu et al. 2015, Lao et al. 2015). These studies will help in development of novel pest control strategies with better efficacy.

RICE PROTEOMICS STUDY

The study of protein complement of an organism, referred to as proteomics is growing in importance and application. Since proteins are the workhorses of a biological system, study of proteomics can unveil many critical biological processes hitherto unknown. Since 1990s when the first proteome study on rice had been initiated, a significant progress has been made for the isolation and characterization of proteins. Rice proteomics studies are performed mostly by gel-based tools like one-dimensional polyacrylamide gel electrophoresis (1DE), two-dimensional polyacrylamide gel electrophoresis (2DE), SDS-PAGE or gel free tools like mass spectrometry (LC-MS/MS), multidimensional protein identification technology (MudPIT) and combination of these two approaches (Agrawal et al. 2010, 2013). With the recent development in quantitative high-throughput protein identification approaches (ICAT and SILAC), identification of rice proteins have been dramatically enhanced (Vala et al. 2014). The case examples of proteomics-based discoveries in enhancing the rice productivity and their tolerance towards ever-changing environmental factors are mentioned below.

Anther proteome and seed development

Cytoplasmic male sterility (CMS) is widely observed in flowering plants and its importance has been well-documented. Existing studies revealed that among 97 non-redundant proteins, 8 were differentially expressed during CMS in rice. The identified proteins are basically related to enzymes of catalytic activity, structural molecular activity, binding, transport, antioxidant activity etc. (Sun et al. 2009). Another study by other group also identified such CMS associated proteins which are related to protein biosynthesis, energy metabolism, cell wall formation, stress response and pollen development (Xiao et al. 2009).

RNA binding proteins (RBP) were found to play significant role in nucleus and cytoplasm during mature and developing stages of seeds. Crofts and coworker identified 18 RBPs by using 1D approach; which are cytoskeleton associated and responsible for controlling expression of seed storage proteins like globuline and glutelin (Crofts et al. 2010). Importance of rice bran for pharmaceutical and nutritional purpose was observed when about 43 unique proteins involved in several signaling and metabolism processes were identified by using a combination of 1DE, 2DE and shotgun techniques. It appears that modern trends in rice proteome research reveal the inside story of gene expression but need further in-depth analysis to validate these observations and proceed towards their implementation in translational research.

Understanding response to abiotic and biotic stress

Abiotic stress

Abiotic stresses like drought, temperature variation, unseasonal rainfall, toxic heavy metals, salt stress, nutrient deficiency, oxidative stress have attracted the interest of rice proteome researchers (Agrawal et al. 2011). One major observation in rice proteome was the degradation of RuBisCO by different stress factors like heavy metal stress or temperature stress which severely impair the photosynthesis. However, proteomic study demonstrates that certain proteins expressed under such stress conditions help to recover photosynthesis and revival of the plant. Till date, differentially expressed metabolic proteins are enolase, triosephosphate isomerase, cytoplasmic aconitate hydratase, putative transketolase, fructose-bisphosphate aldolase, cytosolic 6-phosphogluconate dehydrogenase, glutamine synthetase and UDP-glucose pyrophosphorylase. These identified proteins are supposed to play a key role in regulating starch and sucrose production, Calvin cycle, Pentose Phosphate

pathway, TCA cycle etc. under different abiotic stresses (Kosová et al. 2011, Kim et al. 2014).

Biotic stress

Several biotic factors impacting rice like virus, bacteria, fungi, and insects are responsible for huge economic loss in Indian subcontinent (Rampitsch et al. 2012). Pathogens like *Magnaporthe oryzae* have been screened for understanding their secreted proteome or secretome. In *M. oryzae*, 85 differentially modulated proteins involved in cell wall formation lipid hydrolysis and ROS detoxification were found (Wang et al. 2011). In 2012 another study by Jung et al. conveyed valuable information about pathogen-secreted proteins which could be helpful in understanding the early interactions between germinating *M. oryzae* and rice leaves. A large-scale gel based and gel-free proteomics investigations of *in vivo* secreted proteins of infected rice leaves was conducted which identified 291 rice secreted proteins related to cell signaling, defense mechanism and cell wall hydrolysis. These results explain that spontaneous cell death progress of closely involved in host defense-related protein expression and secretion via auto-activation of the host defense mechanism (Kim et al. 2013).

Advancement in rice proteomics has resulted in an increased perception of the proteomes of tissues, organs, and organelles under both normal and noxious environmental conditions. Well accepted proteomes have aided re-annotation of rice genome thus revealing new functions for previously known proteins. Moreover, rice proteomics has become a paradigm for studies related to cereal crops, such that proteomics-based findings in rice are likely to be translated to improving other crop plants against ever-changing environmental factors. Rice proteomics might play a major role in addressing global problems of food security, the solution of which will be essential in meeting the demand of growing human population, projected to add 2-3 billions more within next 30 years.

RICE METABOLOMICS STUDY

Biological processes, developmental activity and many quality traits are immensely influenced and regulated by a number of metabolic compounds apart from DNA, RNA and protein. Study of metabolomics encompasses all these diverse compounds other than DNA, RNA and protein. These compounds are mostly secondary metabolites and are associated with diverse traits like yields, nutritional, nutraceutical value, taste, color, fragrances, defense against biotic and abiotic stress etc. (De and Nag 2014). Unlike DNA, RNA and protein which are fairly homogenous

in basic structure and function, secondary metabolites are highly diverse in chemical structure, property and function. One such group of compound flavonoids is well over 9000 in number. Thus metabolomics is far diverse in dimension and scope. But synthesis of metabolites is under the control of genes and hence metabolomics is interrelated with other omics.

Metabolomics studies involve various analytical chemistry methods along with bioinformatics techniques to measure metabolites quantitatively and qualitatively and to derive relationship among the metabolites and genetic loci traits (Oikawa et al. 2008). Molecular detection techniques like gas chromatography–mass spectrometry (GC–MS), liquid chromatography–mass spectrometry (LC–MS), capillary electrophoresis–mass spectrometry (CE–MS) and nuclear magnetic resonance (NMR) are commonly used methods in metabolic profiling (Kusano et al. 2007). Metabolic compounds are highly diverse like phenolics, flavonoids, alkaloids, amines, amides, fatty acids, organic acids, pigments, phytosterols etc. many of them are structurally and functionally unrelated. Hierarchical clustering provides an insight view of diversity of metabolite profile of a sample by calculating similarities and differences among the metabolites (De and Nag 2014). Routinely used technique like LC-MS, GC-MS/MS has limitation in clearly identifying large number of unknown metabolites due to lack of reference chemicals in untargeted metabolic profiling. As against this an approach of combining accurate mass of precursor ion and fragmentation of collision-induced dissociation (CID) MS/MS with NMR spectra results in better resolution of metabolic profile (Yang et al. 2014).

High-throughput analysis without derivatization is also used in rice metabolomics study. Capillary electrophoresis – mass spectrometry (CE-MS) and Capillary electrophoresis-diode array detection (CEDAD) can very efficiently detect low charge and small size molecular metabolites (Sato et al. 2008, Soga et al. 2000). As a result of these two combined methods, more than eighty major metabolites like amino acids, sugars, organic acids and nucleotides have been identified in rice foliage. Kohnen's self-organizing map (SOM) and Sammon's 20-network layout allowed visualization of dynamic activities of metabolites subset that exhibit synchronous time dependent fluctuation. It also assisted in classification of the biochemical pathways activated by the light and dark cycle by unsupervised clustering of comprehensive metabolic profiles (Sato et al. 2008). From another experiment, 91 abundantly found flavonoids involved in various physiological functions were detected in various tissues during different developmental stages in two varieties of japonica and indica rice (Dong et al. 2014). Kusano et al. (2015)

demonstrated the phytochemical diversity by identifying around 136 secondary metabolites using different techniques.

Stress tolerance of rice

Metabolomics is generating research interest among researchers trying to develop various stress tolerant rice varieties. Tolerance and susceptibility to abiotic stress is due to accumulation or non-accumulation of specific metabolite. For instance proline accumulation in response to drought in rice and its positive co-relation with drought tolerance is well documented. Specific adaptive response of rice to salt stress was studied by metabolic profile analysis of leaves and roots of two rice varieties, FL478, salt-tolerant recombinant inbred line and IR64, a salt-sensitive variety. A hierarchical clustering was performed to get an overall view of metabolite changes in response to salt stress. As an adaptive strategy to tackle stress increase in sugars and amino acids and a significant decrease in organic acid were seen in both the tissues of FL478 in contrast to IR64 (Zhao et al. 2014). Phytohormones like ethylene play a role by acting as volatile signal molecule under high stress condition (Misyura et al. 2014).

Pathogen infection in rice

Metabolomics along with other omics were applied for better understanding of plant's complex response to pathogen infections. Using metabolomics and proteomics in tandem, Sana et al. (2010) showed that in response to pathogenic attack, there is activation of certain genes and a concomitant increase in precursor of some alkaloid which ultimately confer resistance to pathogen in rice (Sana et al. 2010).

DATABASES IN THE FIELD OF RICE-OMICS

The current literature on rice research is interspersed with databases on genome, transcriptome, proteome and metabolome. Data sources include whole genome sequencing data, protein-protein interaction data, RNA-Seq data or Metabolome analysis data. Systematic storage of data; their easy accessibility and retrieval is a basic necessity in rice research. Since these databases constitute an integral part of rice research, a few relevant databases are discussed below-

Rice genome databases

Major initiative for rice genome database came from International Rice Genome Sequencing Project (IRGSP). The important rice genome data bases with relevant data are given in Table 2.

Table 2 : Major databases on rice genome

Sl. No.	Database Name	Description	Developed by	URL
1	MSU-RGAP	It provides genome sequence from the Nipponbare subspecies of rice and annotation of the 12 rice chromosomes (Kawahara et al. 2013).	Michigan State University	http://rice.plantbiology.msu.edu/
2	RAP-DB	Facilitate annotation of the rice genome sequence and aid in comprehensive analysis of the genome structure and function (Ohyanagi et al. 2006).	National Institute of Agrobiological Sciences, Japan	http://rapdb.dna.affrc.go.jp/
3	RiceGE	It is Rice Functional Genomic Express Database	Salk Institute Genomic Analysis Laboratory	http://signal.salk.edu/cgi-bin/RiceGE
4	Gramene	It is a curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species (Jaiswal et al. 2006).	Cold Spring Harbor Laboratory, Oregon State University, and EMBL-EBI	http://www.gramene.org/
5	Oryza sativa Genome DB	It provides a convenient sequence-centered genome view for <i>Oryza sativa</i> (ssp. japonica), with a narrow focus on gene structure annotation.	Iowa State University	http://www.plantgdb.org/OsGDB/
6	Rice DB: an <i>Oryza</i> Information Portal	It is a database on gene identifiers, functional & proteomic annotations, subcellular localization, phenotypes and upstream transcription motifs (Narsai et al. 2013).	The University of Western Australia	http://ricedb.plantenergy.uwa.edu.au/index
7	Oryzabase	The Oryzabase consists of Strain stock information, Mutant information, Chromosome maps, Gene dictionary (Kurata and Yamazaki 2006).	National Bio-resource Project, Japan	http://www.shigen.nig.ac.jp/rice/oryzabase/

8	TIGR Rice Genome Annotation DB	Rice Genome Annotation Database (Ouyang et al. 2013).	J. Craig Venter Institute	http://blast.icvi.org/euk-blast/index.cgi?project=osa1
9	MOsDB	It is database on gene sequences and gene annotation information of two <i>Oryza sativa</i> subspecies: japonica and indica (Karlowski et al. 2003).	Helmholtz Zentrum München	http://pgsb.helmholtz-muenchen.de/plant/rice/
10	RiTE	It consists of repeated sequences and transposable elements (TEs) of several species of the <i>Oryza</i> (rice) genus, and the closely-related <i>Leersia perrieri</i> (Copetti et al. 2015).	University of Arizona	http://www.genome.arizona.edu/cgi-bin/rite/index.cgi
11	Rice phylogenomics database	Phylogenetic approach used in comparative genomics to predict the biological functions of members of a large gene family by assessing the similarity among gene products (Jung et al. 2015).	UC Davis, University of California	http://ricephylogenomics.ucdavis.edu/
12	Rice GT Database	Database contains information on 793 putative rice GTs (gene models). It includes an interactive chromosomal map showing the positions of all rice GTs (Jung et al. 2015).	UC Davis, University of California	http://ricephylogenomics.ucdavis.edu/cellwalls/gt/genInfo.shtml
13	Rice GH Database	Database contains information on 614 putative rice GHs (gene models) (Jung et al. 2015).	UC Davis, University of California	http://ricephylogenomics.ucdavis.edu/cellwalls/gh/genInfo.shtml
14	Rice TF Database	Host functional genomic information for all putative rice transcription factors (TFs) and other transcriptional regulators (Jung et al. 2015).	UC Davis, University of California	http://ricephylogenomics.ucdavis.edu/tf/genInfo.shtml
15	Rice Transporter Database	Host functional genomic information for all putative rice transporters (Jung et al. 2015).	UC Davis, University of California	http://ricephylogenomics.ucdavis.edu/transporter/genInfo.shtml

Rice transcriptome databases

Several web-based tools are available for analyzing rice transcriptome making it convenient for any person to understand complex genomic data in an easy platform (Jung et al. 2015). These databases have expanded our understanding of the complex molecular and cellular events in rice and laid the foundation for future studies in rice and other cereal crops. The tools are listed below-

Table 3 : Available databases on rice transcriptome

Sl. No.	Database Name	Description	Developed by	URL
1	Rice Genome annotation	Provides high quality annotation for genes found in rice (Ohyanagi et al. 2006).	MSU Rice Genome Annotation Project Team	http://rice.plantbiology.msu.edu/expression.shtml
2	Genvestigator	Expression visualization tool which assists in prediction and analysis of genes (Hruz et al. 2008).	NEBION and ETH Zurich	https://www.genestigator.com/gv/index.jsp
3	RiceeFP Browsers	Deals with functional genomics and other omics data (Winter et al. 2007).	Arabidopsis Research Group, University of Toronto	http://www.bar.utoronto.ca/
4	Gene Expression Atlas in RiceGE	Provides normalized expression levels of nine Affymetrix dataset (GPL2025) microarray and fold change for an Agilent Rice 22K dataset (GSE661 for ABA)	Salk Institute of Genomic Analysis Laboratory	http://signal.salk.edu/cgi-bin/RiceGE5
5	Rice Expression Profile Database (RiceXPro)	It is a repository of gene expression profiles derived from microarray analysis of tissues/organs encompassing the entire growth of the rice plant under different conditions (Sato et al. 2010).	National Institute of Agrobiological Sciences	http://ricexpro.dna.affrc.go.jp/
6	FiT-DB Field	Provides statistical modeling of transcriptional dynamics in field	National Institute of	http://fitdb.dna.affrc.go.jp/

	Transcriptome Database)	study conditions (Nagano et al. 2012).	Agrobiological Sciences	
7	Oryza sativa Transcriptome	Provides information mRNA, ESTs, etc of Oryza sativa	NA	http://www.bioinformatics.org/zEST/Oryza_sativa/index.html
8	RGKbase	It is an annotation database for rice comparative genomics and evolutionary biology (Wang et al. 2013).	Chinese Academy of Sciences	http://rgkbase.big.ac.cn/RGKbase/index.php
9	ROAD	Rice Oligonucleotide Array Database (Cao et al. 2012).	University of California, Davis	http://www.ricearray.org/index.shtml

Rice proteome databases

There are a number of rice proteome databases to assist functional genomics study of rice. These databases are diversified as the area of rice proteomics study is vast. A few relevant databases, which are generally devoted to mapping of phosphorylation sites, interaction sites, functional & proteomic annotations, subcellular localization are listed in Table-4.

Table 4 : Available databases on rice proteome

Sl. No.	Databases	Description	Developed by	URL
1	Phospho Rice	Meta-predictor of rice-specific phosphorylation sites (Que et al. 2012).	Fujian Agriculture and Forestry University, China	http://bioinformatics.fafu.edu.cn/PhosphoRice
2	Oryza PG-DB	Rice proteome database based on shotgun proteogenomic (Helmy et al. 2011).	Institute for Advanced Biosciences (IAB), Keio University, Japan	http://oryzapg.iab.keio.ac.jp/

3	PRIN	Predicted rice interactome Network (Gu et al. 2011).	Zhejiang University, China	http://bis.zju.edu.cn/prin/
4	Rice proteome database	First detailed database to describe the proteome of rice (Komatsu et al. 2004).	National Institute of Agrobiological Sciences, Japan	gene64.dna.affrc.go.jp/RPD/
5	RiceRBP	Facilitate the study of plant RNA-binding proteins (Morris et al. 2011).	Washington State University	cgi-bin/RiceRBP/home.plwww.bioinformatics2.wsu.edu/
6	DIPOS	Complete rice protein interaction database (Sapkota et al. 2011).	Sapkota et al. 2011	http://www.comp-sysbio.org/dipos/?id=5
7	Plant-PrAS	Database of Physicochemical and Structural Properties and Novel Functional Regions in Plant Proteomes (Kurotani et al. 2014)	Integrated Genome Informatics Research Unit, RIKEN CSRS	http://plant-pras.riken.jp/
8	Rice DB:	It is a database on gene identifiers, functional & proteomic annotations, subcellular localisation, phenotypes and upstream transcription motifs (Narsai et al. 2013).	The University of Western Australia	http://ricedb.plantenergy.uwa.edu.au/index

Rice metabolome databases

Rice metabolites datasets are submitted in different plant metabolites databases and therefore it is scattered all over the world web space. The number of specialized databases solely dedicated to rice metabolomics is limited, but rice datasets are abundantly stored in general plant metabolic databases. Databases are generally dedicated to full annotation of metabolites, structure elucidation, metabolic profiling information and metabolic pathways information. The MS/MS spectral data, NMR data for compound structure elucidation are stored in available databases (Table 5). The datasets in many databases are in raw format, but few databases also provide data analysis tools.

Table 5 : Available databases on rice metabolome

Sl. No.	Database Name	Description	Developed by	URL
1	MassBank	metabolite annotation, MS/MSdatabases (Horai et al. 2010).	Nara Institute Of Science And Technology, Japan	http://www.massbank.jp/index.html?lang=en
2	METLIN	Repository of metabolite information and tandem mass spectrometry data designed to facilitate metabolite identification in metabolomics (Tautenhahn et al. 2012).	Scripps Center for Metabolomics and Mass Spectrometry	http://metlin.scripps.edu/index.php
3	LipidBlast	Tandem mass spectral (MS/MS) database dedicated to annotate and identify hundreds of lipids (Kind et al. 2013).	UC Davis, University of California	http://fiehnlab.ucdavis.edu/projects/LipidBlast/
4	ReSpect	Collection of literature and in-house MSn spectra data (Sawada et al. 2012).	RIKEN Center for Sustainable Resource Science	http://spectra.psc.riken.jp
5	KNAPSAcK	Comprehensive Species Metabolite Relationship Database (Afendi et al. 2012).	Csb lab, Nara Institute of Science and Technology (NAIST), Japan	http://kanaya.naist.jp/KNAPSAcK/
6	MetaCyc	Curated database of experimentally elucidated metabolic pathways from all domains of life (Zhang et al. 2005).	SRI International, USA	http://metacyc.org
7	KEGG	Facilitate understanding of high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information (Kanehisa et al. 2000).	Kanehisa Laboratories, Kyoto University	http://www.genome.jp/kegg

8	PRIME	Metabolite annotation, plant metabolomics (Sakurai et al. 2013).	RIKEN Plant Science Center	http://prime.psc.riken.jp/
9	Golm Metabolite Database	Metabolite annotation, plant metabolomics (Kopka et al. 2005).	Max Planck Institute of Molecular Plant Physiology	http://csbdb.mpimp-golm.mpg.de/csbdb/gmd/gmd.html
10	RiceCyc DB	Rice metabolic pathways (Jaiswal et al. 2006).	Gramene Database	http://pathway.iplantcollaborative.org/RICE/class-tree?object=Pathways http://pathway.gramene.org/ricecyc.html

CONCLUSION

The challenge in rice research is multifaceted. Rice is the staple food for more than half of the world population. So rice production is directly related to global food security. On one hand, there is need for increased production to feed the ever-growing population, on the other hand, global warming, pollution and climate change is exerting abiotic stresses which together with biotic stress and other adverse factors are exerting negative impact on rice productivity. This raises a question- "what will happen when global population will be around 10 billion in 2056?" The situation is already grim, because rice production has been, by and large, stagnant in the recent years and not adequate to feed about 800 million more people who go to bed hungry every night (Zhang 2013). Conventional research on rice has its limitation but omics study has opened a new vista to explore the hitherto little known biological processes at molecular level. This is likely to pave ways for solving the prevailing problems to enhanced qualitative and quantitative improvements in rice.

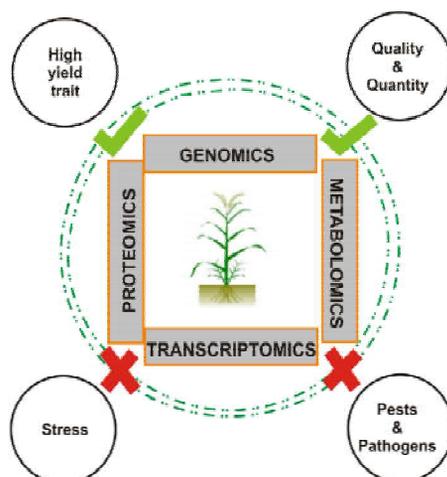


Fig. 2 : Inter-relationship between fundamental omics and area of applications

It is now clear that omics study are inter-related and individual omics cannot deliver good in isolation, only when they are used in tandem they become more productive (**Figure 2**). For instance metabolome studies provide better understanding of host pathogen interaction. But metabolome itself is dependent on genomics and transcriptomics. Guo et al. (2014) studied cell wall biosynthesis in rice by metabolic profiling using 29 different tissues of rice and used canonical correlation analysis (CCA) to explore gene expression network. They found a positive co-relation between gene modules, expression pattern and cell wall characteristics (Guo et al. 2014). Omics studies are witnessing rapid changes in genetic mapping and trait analysis, SNP based detection and GWAS methods become main choice of researchers for genetic map construction and high yield trait detection. For gene expression analysis transcriptomics study has changed from micro array to next generation sequencing for more precise elaboration of every expressed gene. Proteomics research has also seen a shift change for gel based and gel free methods to quantitative approach like SILAC. This review deals with rice research from four different dimensions and also, portrayed the results of amalgamation of other field of research into this field, i.e., the biological databases. Application of cutting-edge technologies can aid this important crop becoming better in terms productivity and stress-resistance.

Every research area is important since it generates new knowledge and explore avenue for the betterment of mankind. But food security is related to social security and stability of human society. Rice research is the spearhead of tool to

ensure food security and rice omics study is the new avenue which offers great promises.

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