

Omics Technology for Abiotic Stress Response in plants

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ABSTRACT- *Abiotic stress is one of the major factors which affect the growth and yield of crops. This is due to several imbalances which occur at the plants molecular, cellular and developmental levels during stress conditions. Due to these disturbances in plants, the defence mechanism gets activated in response of stress and the detection of these changes is possible because of computational biology that facilitate the multi-target approach. However, with the advancement of omics technology plants are seen to acclimatize themselves by modulating at the genomics, transcriptomics, proteomics. In this review, all the molecular changes of plants under stress is discussed and the new insights which are obtained from the integration of omics are highlighted.*

Keywords: *Omics, Genomics, Proteomics, transcriptomics, abiotic stress*

INTRODUCTION- Plants are sessile organisms that have ability to survive and respond to different climatic conditions under certain level and these variable environmental conditions control different physiological factors like duration of their vegetative phase, beginning of a reproductive stage, the ability of flowering. There are various factors which affect the growth and productivity of plant i.e. biotic and abiotic factors. Abiotic factors are the major threat toward the plant which severely affect the productivity of the plant and become the major cause of crop yield loss (Canter, 2018; Zorb et al. 2019). Abiotic stress like drought and salinity leads to loss of water and osmotic disorder in the cell which causes disturbance in ions, hyper osmotic stress and accumulation of reactive oxygen species (ROS). Excess of ROS leads to damage in DNA, proteins and lipids which can cause cell death. In defence of these abiotic stresses, plants develop various strategies like biochemical, physiological and metabolic but the prediction of a signalling pathway that is used under biotic and abiotic stress is difficult to predict.

To understand the effect of stress on crops the understanding of genes, signalling in cells, and all other processes in plants under stress are important to classify by omic technology which provides insight to the plant and helps us to identify all the aspects of the plant. For better analysis of the biological network and function of plants, omics become an essential tool (Parida et al. 2018).

Omics technology is targeting the characterization of plant genes and biomolecules as for maintaining homeostasis and signalling of cells under different stress. Transcriptional, proteomics and genomics are the different levels of omic technology and their study is important to understand the reaction in plants under stress (Shen et al. 2018). Due to omic technology and recent progress in experimental procedures, analysis of data and visualization helps to study the function or changes in gene at all times (Sussman et al., 2009). In this computational technology, all the approaches have classification of genes, their regulators

and interactors at different stages of stress. Studies show that for understanding plant response and to understand plant genomics properly a cheaper and assessable method is approached called “Next generation sequencing” (Aranzana, M.J et al. 2019). The transcriptome analysis is the primary level of gene expression done by EST’s (expressed sequence tags) and techniques based on microarray (Ambrosone et al. 2017, Redman et al. 2017). RNA sequencing is also most widely using technologies for genome expression. (Bokszczanin et al.2015: Aranzana et al. 2019). The Omics method provides an insight of interaction, development and functioning of cells in plants by an advanced technology. Omics technology provides the novel insights for understanding the response of plants under stress condition (Mosa et al., 2017; Parida et al. 2018).

EFFECT OF ABIOTIC STRESS- Abiotic stress can initiate wide number of responses in plant ranging from disturbances in transport and metabolic pathways leading towards decline in development. The initial impact of the stress is on ion imbalance and hyperosmotic stress that outcomes in accumulation of reactive oxygen species, which is toxic to the plant cell at higher concentration causing damage to lipids, DNA, proteins that brings about cell death (Apoptosis) (Debnath et al. 2011). For understanding of all these complex administrative pathways and quality related stress a few multidimensional methodologies are concentrated as multi omics approach such as genomics, proteomics, transcriptomics and metabolomics (Fig1).
(Wang et al. 2016).

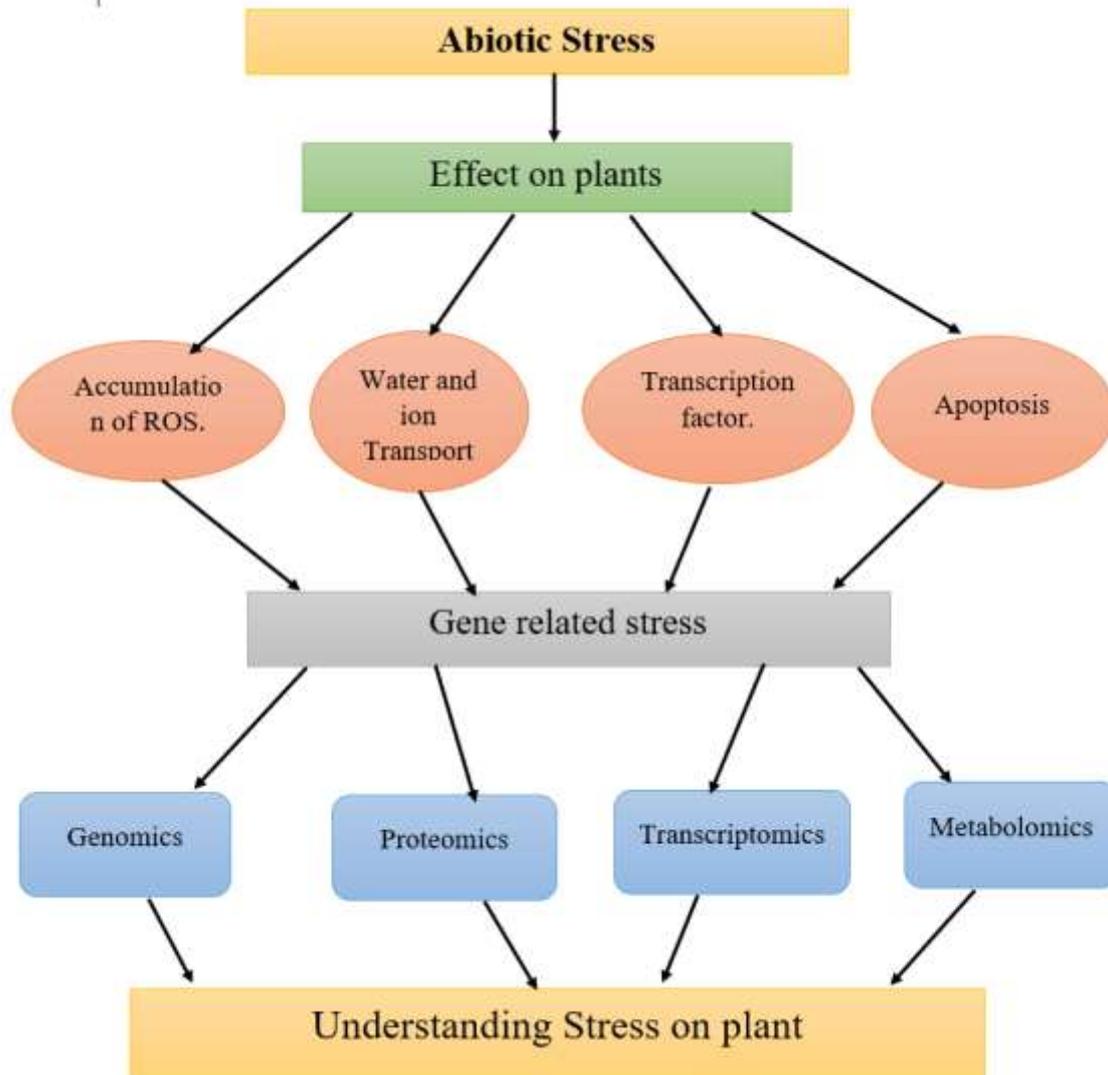


Figure-1 Effect of abiotic stresses and gene related stress detected by omics technology. (Debnath et al. 2011; Mehta et al. 2019)

Drought and salinity are two major factor which limiting the productivity of crops globally (Chawla k, et al. 2011).

SALINITY STRESS- All the plants are having their certain threshold up to which they can tolerate salinity without any loss in yield but when there is high salt in soil then plants show negative response on growth and development of the plant. Most common response shown by plant cells under high salt conditions is growth inhibition proved. In the world 20% of irrigated crops face high salinity stress which results in ion disturbance and osmotic imbalance in the cell (Negi et al., 2016; Isayenkov and Maathuis, 2019). Under high salt stress, the plants start decreasing its leaf surface expansion, reduction in osmotic rate of growing medium and ion misbalance. This leads to growth inhibition as there is disturbance in transport and metabolic rate (Sairam and Tyagi, 2004). In the coastal area, high Na^+ levels disturb the nutrition of potassium and high salt also inhibit many enzymes when accumulated in cytoplasm. This salinity adverse effect causes disturbance in nutrients and metabolism of plants and leads to accumulation of reactive oxygen species (Jaleel and Panneerselvam,

2007). High salt leads to alkaline soil and also causes disturbance in chlorophyll a and b ratio and there is significant enhancement of peroxidase, superoxide dismutase, catalase that is studied under plant stress.

DROUGHT STRESS- Plant productivity and yield are adversely affected by drought stress (Shao et al. 2009). There are various changes in plant morphology, physiology, metabolism under drought conditions. It causes various effects on leaf and root development which cause influx of carbon dioxide and have a bad effect on uptake of mineral, membrane structure, metabolic pathways photosynthetic activity, pigment content (Benjamin and Nielsen, 2006; Prabha et al. 2009). Water stress leads to loss of transpiration and photosynthesis in plants as there is closure of stomata occur by stress signal of abscisic acid and also accumulates proline, mannitol, sorbitol. (Demirevska et al. 2009).

Various efforts have been made to provide solution to single trait stress, however this is not the practical approach because the response of plant in the field is different as it is imposed by many factors and stresses concurrently. Last few decades, improvement in stress tolerance has been observed in conventional breeding but in many places traditional varieties are affected by stresses. Hence, considering the environmental potential, using multidisciplinary in primitive crops provides a better strategy to improve stress (Chaudhary et al., 2015; Chopperla et al. 2018)

ROLE OF OMICS TECHNOLOGY IN CROP DEVELOPMENT – Omic is a rapidly growing approach and this technology provides the methods, technological ability, and interdisciplinary advancement to enhance the knowledge and detection of all the genetic and transcriptomic activities of the plant (Fig 2). As this genomic, metabolomic, transcriptomic are very advanced technologies as these tools detect simultaneously and provide gene, protein expression profiles. Omics technology not only enhances the level of understanding but also provides the novel insights for understanding the plant response under stress. The studies used to focus on regulators and signalling pathways and detect even the minute changes in the plants, hence for crop improvement the omic technology is acceptable.

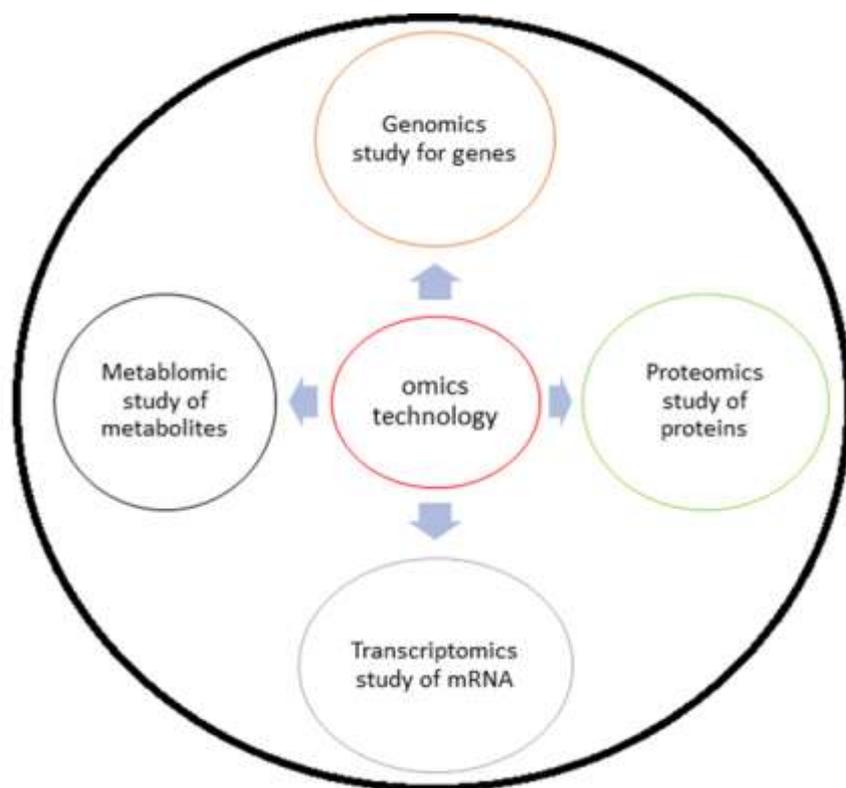


Figure 2 - Levels of omic technology that is used to detect different stress responses in plants.

GENOMICS STUDY- Genomics deals with the study of genome and biology of organism which identify the whole genetic information of organism that is coded with genes and sequence of DNA (Gilliham et al. 2017). The beginning of first-generation genome sequencing techniques was started in 1970, later on, in 1990 the next generation sequencing technique started to begin and currently using 3rd generation (Sequencing technique) (El-Metwally et al. 2013,2014). Genomic study includes extraction of DNA, sequencing, assembling and annotation of all the genomes.

Genomics research for crop improvement is improving at a fast rate as functional genomic techniques have been adopted to reveal the gene characteristics and the interaction between genes, all these characteristics and interactions help us to improve the quality of plants. Functional genomics techniques are used for hybridization and in sequence methodologies for the plants under stress (Zhang et al., 2017; Wang et al., 2018). Next generation sequencing methods like shotgun have been used for producing molecular markers which is used to detect the DNA polymorphism. The next generation techniques allow us to understand millions of molecules simultaneously, the whole genome project also used as conventional method of sequencing. High throughput results of these methods for several plants used for transcriptomic and genomic understanding also helps to improve the quality of plant. Various tools are developed to analyse plant genes and monitor the ability of plant response. Genomics technique has been used for identifying the genes for the development of stress tolerant plants (Le et al. 2012; Goodwin et al. 2015; Gilliham et al. 2017) For monitoring the level of stress in plants like *Arabidopsis* (Swindell, 2006) microarray technique is developed for analysing transcription in drought stress. Most of the genes are still unknown and yet to be explored.

Exposure of salt brings various changes in plants as salt responsive genes have been identified and studied. *Beta vulgaris* (high salt tolerant plants) can be easily distinguishable from Citrus species (salt sensitive plants) as these stress tolerant plants are able to activate those genes that help them to survive in stress conditions. Identification of these stress tolerance genes several experimental procedures are involve like cDNA screening libraries that are formed from the mRNA isolated from the saline stress tolerant plants. For this one most widely used method is salt responsive CDNA clones that have screening with probes that are isolated from the genes of saline stress tolerant plant and saline stress sensitive plant. mRNA of saline stress tolerant plants is isolated and identified. Studies reported that c-DNA clones that have SAMS (S-adenosyl-l-methionine synthetase) gene, called PgSAM and this gene defend the plant against salt stress or any other abiotic stress (Pulla and coworkers (2009). *Panax ginseng* plant which is a medicinal plant is having the gene PgSAM that encodes for 307 amino acid residue and have the sequence similarity with plants (SAMS). The enhancement in the expression of Cit-SAP gene which is treated with salt cultured citrus cell and citrus plant is irrigated with Nacl water that enhance the level of free- radicals. In *Oryza sativa* (rice) various effects of genes have been identified (salt stress, cold stress, Drought stress). For identifying the effect on genes, microarray technique is used. There are 1,700 c-DNA libraries that have been recorded for drought, salt, cold stress. The gene induces stress response adopted by microarray analysis using RNA gel-blotting technique. Total 73 genes have been identified in stress inducible genes in rice. Various genes like 36,62,57 and 43 were express water stress, salt stress, cold stress. Gene 51 is reported in *Arabidopsis* plants having the same function of gene. Stress expressible genes in transcriptome analysis show some variations in *Arabidopsis* and *Oryza sativa* in stress response (Rabbani et al.,2003).

PROTEOMICS STUDY- Proteomics is the study of proteins which are expressed in cell compartments of organism (Tyres and Mann 2003; Luan et al., 2018). Identification of sequence of peptides and alteration in proteins is studied by MS- spectra (Nakagami et al., 2012), 2-dimensional gel electrophoresis (Luan et al. 2018). Proteomics study is a key tool for exploring molecular mechanisms which are associated with carcinogenic metals and species of plant (Ahsan et al.,2009). In response to stress, plants induce the several genes that are protects themselves and also synthesis different osmoprotectants and proteins like late embryogenesis abundant proteins (LEA), antifreeze proteins, chaperons and other detoxification enzymes. The different function of the genes or proteins are explained in table 1.

Protein/Genes/Ions	Role	Description	Reference
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<p>Late embryogenesis abundant protein</p>	<p>Cellular protection</p>	<p>Late embryogenesis abundant proteins are mainly involved with higher plants and protect the plant from stressful environment, mostly from drought stress. So, identifying and characterization of Late embryogenesis protein is done when plant suffering from water scarcity. According to the mRNA homology and amino acid sequences all the late embryogenesis proteins are characterized in to six categories. These protein helps to maintain the cellular structure and structural components of the plants.</p>	<p>(Shao et al. 2005).</p>
<p>P5CS</p>	<p>Osmotic adaptation</p>	<p>P5CS is a gene encoded enzyme that is associated with the production of sugar alcohol, proline and glycine. Plants like sugar beet, spinach, barley in response to salt stress leads to conversion of choline to glycine and production of P5CS gene this down regulate the salt stress in plant mannitol dehydrogenase gene, allow its entry in central carbon metabolism. That's why there is an increase in the amount of mannitol during salt stress as mannitol acts as osmo-regulator and manage the salt stress.</p>	<p>(McCue and Hanson, 2004)</p>

Na ⁺ ion	Ionic balance	During salt stress plants are involved in membrane transport in which there is division of sodium ions as this mechanism is involved in maintaining transport of ions and maintaining ion balance in plants. Sodium ion disbalance causes ionic toxicity in cells and osmotic imbalance due to accumulation of sodium, So Na ⁺ is eliminated from the cytosol and concealed in vacuole this process is done by sodium hydrogen antiporter.	(Dai et al. 2018)
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Table-1- List of Proteins, Genes and their role in abiotic stress.

Proteomics approach generates huge amounts of data as described in Table 1, different proteins, genes, ions, affected under stress condition and all these changes are studied by genome wide or by proteome profiles (Hopf et al. 2013; Liu et al. 2015; Kosova et al. 2018). For different stresses, plants respond differently proteome approach has been utilized for analysis of abiotic stress occur in plants are listed in Table-2

Plant	Stress	Response	Proteome technique	Reference
<i>Oryza sativa</i>	Drought	Alteration of protein, Accumulation of reactive oxygen species.	Post transcriptional modification for enhancing tolerance	Wu et al. (2016). Pandey et al. (2010).
<i>Brassica juncea</i>	Cadmium stress	Alteration of metabolism and accumulation of ROS	Post translational modification	Alvarez et al. (2009).
<i>Arabidopsis. Thaliana</i>	Temperature stress	Alteration in protein signalling.	mRNA translation	Yanguuez et al. (2013).
<i>Glycine max</i>	Multiple stress	Change in nuclear proteome and chromatin remodelling	Detected by qualitative proteomic approach.	Zhang et al. (2014), (Yin and Komatsu 2016).
<i>Cicer arietinum</i>	Heat stress	Changes in 248, 590,797 proteins are differently regulated in leaf	Detected by leaf proteome	Santisree et al. (2017).

<i>Triticum aestivum</i>	Drought stress	Upregulation of phosphorylated proteins, chaperons, transcriptional factors.	Studied by phosphoproteome technology.	Zhang et al. (2014).
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Table-2 List of different proteome technique used to detect multiple stress in different plants.

TRANSCRIPTOMICS STUDY- Transcription study is about expression profiles of RNA in temporal and superficial bases (Duque et al. 2013; El-Metwally et al. 2014; Shen et al. 2018). It includes all the coding and non-coding of RNA transcript sequence in the cell. In transcriptomics the RNA profiling is done by sequencing of RNA, Micro-array technology, Digital gene expression profiling (DGE) and continuous analysis of expression of genes (SAGE) (Leisner et al. 2017; Kreszies et al. 2018) (Fig-2). These tools help in characterization of genes which alter during stress and all these genes can be compared with stress tolerance genes or genes of plant which is under stress control conditions (Le et al. 2012; Zhang et al. 2014; Jogaiah et al. 2013; Agarwal et al. 2014). Transcriptomics has the capacity to postulate the representation of transcript abundance.

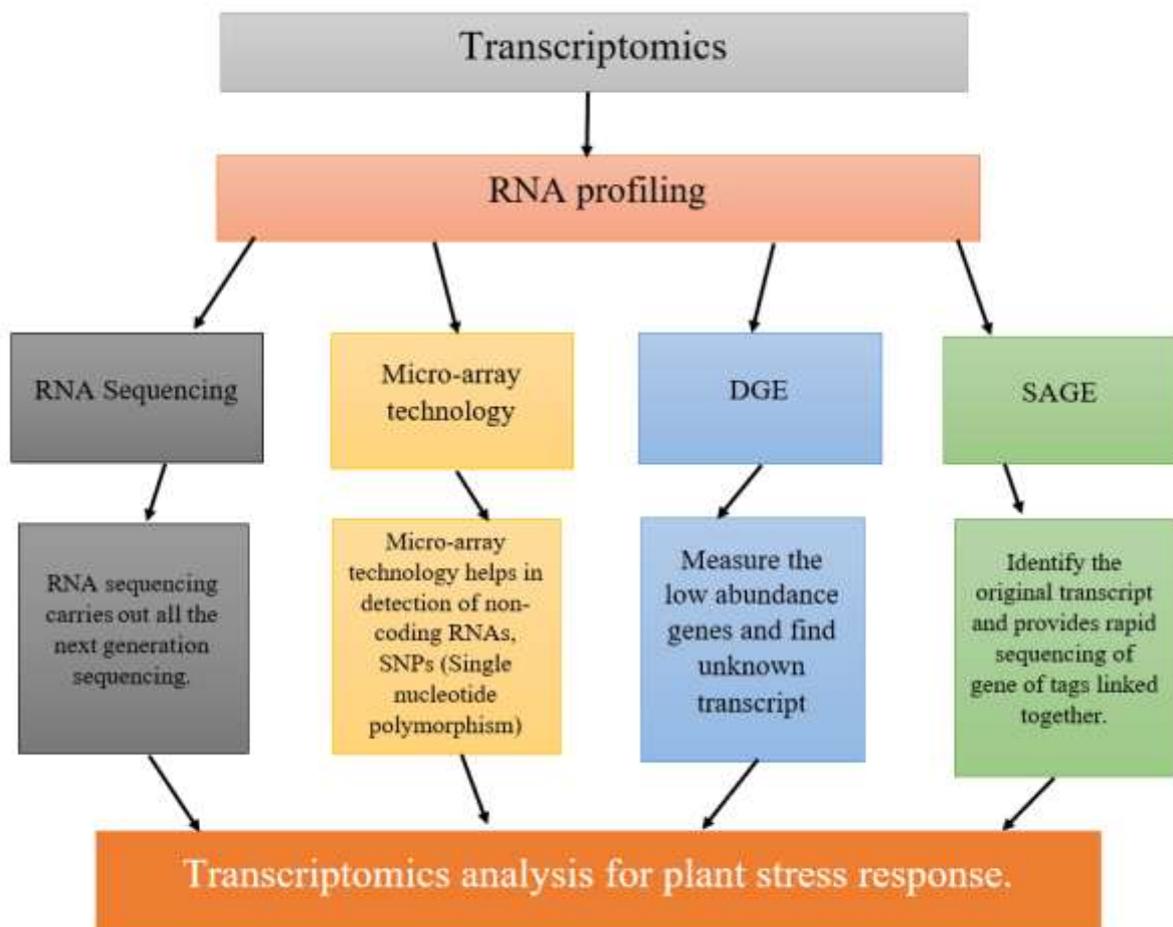


Figure-2 This figure is showing transcriptomic study and various levels of transcriptome to detect the plant stress (Sahil Mehta et al. 2019).

Transcriptomics provide analysis of different plant response under the stress and different plants are showing various effects in stress as in *Arabidopsis* plant under drought and heat stress show variations in 53 unique proteins of plant (Rizhsky et al. 2004) and similar responses were observed in sunflower plant these cases to detect the variation in genes different transcriptome tools used to detect the variation. Li et al. 2013 identified 5350 transcripts differentially expressed using the gene of *Affymetrix* in the *panicum virgatum* under light, salt, heat and cold stress. Leisner et al. 2017 reported a notable reduction in photosynthesis and in conductance of stomata when he subjected soya bean (*Glycine max*) plants under multiple stress such as low rainfall, ozone stress, Temperature stress. By RNA sequencing they analyse the effect of stress on seed coat transcriptome and reported approximately 1576,148 and 48 genes were showing different responses under heat stress, ozone stress and several other stress. Furthermore, Kreszies et al. (2018) took the roots of barley (*Hordeum vulgare*) plant to study the response of osmotic stress on transcriptomic level by adopting the method of RNA sequencing. During stress conditions, also analyse the over expression of gene which cause disturbances in biosynthetic pathway. Transcriptomics approach has been widely used in various crops such *Arabidopsis thaliana*, *Chrysanthemum*, *Cassava* to detect the effect of stress under various environmental conditions such as salinity, low and high temperature, water, heavy metal stress (Table 3)

Plant	Stress	Effect	Transcriptome tool	References
<i>Cicer arietinum</i>	Salt and drought stress	Cytosolic ascorbate upregulated	NGS and SAGE	Molina et al. (2008, 2011)
<i>Arabidopsis thaliana</i>	High light, salt, heat, cold	Changes in transcripts	Microarray analysis	Rasmussen et al. (2013)
<i>Panicum virgatum</i>	Heat stress	5350 Differentially expressed transcript using the <i>Affymetrix</i> gene	Chip bases transcriptome result	Li et al. (2013)
<i>Chrysanthemum</i>	Drought stress	Alteration in genes	RNA sequencing	Xu et al. (2013).
<i>Chenopodium</i>	Drought stress	Changes in transcriptome profile	RNA sequencing	Raney et al. (2014).
<i>Glycine max</i>	Ozone stress, low rainfall high temperature stress	Reduction in stomatal conductance and photosynthesis and effect on seed coat.	RNA sequencing analysis	Leisner et al. (2017)

<i>Oryza sativa</i>	Salt, drought and heavy metal stress	Changes in transcriptome	Meta-analysis	Muthuramalingam et al. (2017)
<i>Hordeum vulgare</i>	Osmotic stress	Changes in transcriptome	RNA sequencing approach	Kreszies et al. (2018)
<i>Triticum aestivum</i>	Drought, salt, heat stress	Variance in expression of heat shock protein 20	RNA sequencing	Muthusamy et al. (2017)
<i>Cassava</i>	Cold and drought stress	MeMYB2 gene acts as a negative regulator.	RNAi technology	Ruan et al. (2017)
<i>Camellia sinensis</i>	Multiple stress	Changes in HD-Zip genes	Genomic technology	Shen et al. (2018)

Table-3 List of Different Transcriptomics Technique used to detect Different Stress in several Plants.

METABLOMICS STUDY- Metabolomics is for used for characterization, identification and detection of all the metabolic changes in plants during the stress (Collino et al. 2013: Dubery et al. 2013: Freund and Hegeman 2017: Parida et al. 2018). The metabolomics technology produces the data by comparing the data with proteomics and transcriptomics (Dos Santos et al. 2017). The recent progress in mass spectroscopy with chromatography (gas or liquid), High performance liquid chromatography, Nuclear magnetic resonance (NMR), DIMS (Direct injection mass spectroscopy) all these techniques are used to detect stress and do profiling of metabolites in plants (Wolfender et al. 2013: Parida et al. 2018). This proves that different levels of metabolomics used to understand the plants and their interaction as this technology provides accurate, precise results as well as help us to understand the signalling and regulatory cycles (Carreno-Quintero et al. 2013: Cusido et al. 2014: Shen et al. 2016: Dos santos et al. 2017: Parida et al. 2018). Metabolomic tool become one of the best methods to study about molecular mechanism in stress response as in several plants under stress produce different metabolites like in *Arabidopsis thaliana* under water scarcity condition lead to production of metabolites like proline, GABA (gamma- aminobutyrate), Tricarboxylic acid metabolites (Urano et al. 2009). For triggering the metabolites under stress conditions there is involvement of ABA dependent transcriptional regulation. For understanding metabolites response in plant metabolome profiling technique is used and in *Arabidopsis* plant this metabolome profiling shows production of photorespiratory intermediates like glycolate and glycine. In chilling stress, they observed the accumulation and increase of fructose and phenylaniline levels and decrease in the production, although the mechanism of this process is still unknown. (Caldana et al. 2011). The OPTIMAS-DW a data resource platform which is used to contain various data domains along with integration of metabolomic, transcriptomics, proteomics data. This data base helps to understand the modulating steps in plants like nitrogen metabolism control (Amiour et al. 2012). For *zea mays* plant this OPTIMAS-DW database is used to understand different effects (Colmsee et al. 2012). There are some reports of enhancements of tocopherol in shoot of maize and decrease in abscisic acid under salt stress. Under different stress there is induction of different

metabolites and these changes are detected by metabolomic technology which help us to understand the different effects and changes during stress condition. Various changes occur in metabolite profiling of *Zea mize* and *Triticum aestivum* due to the disturbances in different level of metabolites and in branched chains off amino acids when they are exposed to water stress (Witt et al. 2012; Bowne et al. 2012). Verslues and Juenger et al. (2011) studied *Arabidopsis thaliana* plant under drought stress response and revealed a significant role of the regulation of metabolism which include accumulation of osmolytes and regulation of photosynthesis.

BIOINFORMATICS: A TOOL FOR INTERPRETATION - In Omics technology, there are various processes such as mass spectrometers, sequencing techniques. These tools produce sufficient amount of data to analyse, study and store for future (El-Metwally et al. 2014). All techniques of omics technology bind with tools of bioinformatics algorithms technologies that help in providing information to the researcher about the genes, proteins and other processes in a quick, accurate and efficient (Mc Dowdall et al. 2009; Falda et al. 2012; Franceschini et al. 2013; Orozco ett al. 2013; Franz et al. 2016). These data of genes, proteins, sequences are interpreted by various tools of bioinformatics and many databases are available online that storing information regarding plant stress biology (Table 4).

Sr. no.	Database	Function	Reference
1	QlicRice	This database is for abiotic stress response in rice	Smita et al. (2011).
2	STIFDB2	This database is a new version of the stress response database.	Naika et al. (2013).
3	PSPDB	This database if for <i>Oryza sativa</i> transcription factor	Kumar et al. (2014).
4	miRbase	In this there is collection of microRNA sequence with detailed data	Kozomara and Griffiths-Jones (2014).
5	PNRD	This database contains non-coding RNA detail	Yi et al. (2015).

Table-4 List of Important Bioinformatics Database used in the study of Plant Sciences.

CONCLUSION AND FUTURE PROCEPECTS – Omics technology have been used to understand how plants react towards various stresses. For understanding of the complex interaction in plants and knowledge of omics is required to improve the productivity of plants. This computational biology in the post genomic area is uplifting the knowledge and provides us better insight to understand the different biological complexities, effects and interactions during stress conditions. This multi omic studies offers new approach to increase the stress tolerant crops which is way better and able to resist stress and give better productivity.

Recent development in instrumentation, computational biology, statistical tools have reduced the expenses of omics however combined investigation needs technical experts and tools. In future researchers should adopt multi omic studies which provides completely new way. The use of best methods for combining genetic, molecular, physical study methods should provide better results in future. Future progress in vitro procedures and the biology system will help us to understand how plants efficiently defeat stress and provide the best productivity. Although many models always have the threat of multiplying some errors so it is necessary to understand all aspects and learn about causes of error. A globally applied computational

biology technology is the best method to predict the future insight and provide high throughput data.

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Front Plant Sci 9:64

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