Chapter 8
Omics Technology: Revolution in Plant Biology

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8.1 Introduction

In the age of rapid developments in the field of science and technology, there is a great shift from macro- to micro- or even nanolevel developments. Twenty-first century is considered the century of nanodevelopments, where millions of nanotechnologies, such as omics, have emerged and replaced the old ones. Omics are among those revolutionary technologies that are helpful in understanding, altering,

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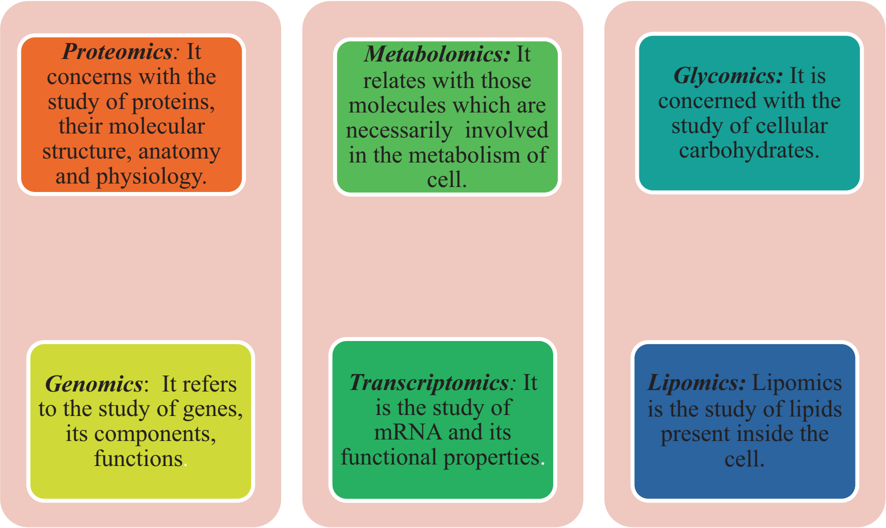
mapping, and shaping the genetic constitution of an individual, including individual plants. Of the approximately 391,000 plant species available on earth, 94% are flowering plants and have significant importance for human needs, such as food, shelter, health, etc., as well as for the whole ecological system. To understand plant genetics with respect to its adaptation to environmental adversaries, a prominent area of research for crop improvement is plant genomics. For a better exploitation of plants, it is imperative to better characterize plants genotypically and phenotypically; that is, we need new advanced tools. Advancements in RNA or DNA sequencing techniques revolutionized transcriptomics and genomics. Similarly, analytical techniques such as HPLC, LC-MS, GC-MS, and MALDI-TOFF helped in the development of metabolomics, proteomics, and lipidomics. Various researchers are of the view that if all the techniques for prebreeding are combined, we will have extensive and elaborated information to explain phenotypic unique variations in genetics (Scossa et al. 2021).

There is constant pressure to increase the production of major crops, like maize, rice, wheat, and cotton. Moreover, climate change causes a further decrease in productivity (Voss-Fels et al. 2019). There is an urgent need to develop high-yielding and resistant cultivars for greater production with lesser inputs using new techniques such as omics, which may help in feeding nine billion people in 2050 (Godfray et al. 2010a, b). Technologies like proteomics, genomics, and transcriptomics are helpful in the identification of relevant genes, proteins, and molecules, which play important roles in plant stress tolerance (Soni et al. 2015). The different disciplines of omics are listed in Fig. 8.1.



Proteomics: It concerns with the study of proteins, their molecular structure, anatomy and physiology.

Genomics: It refers to the study of genes, its components, functions.

Metabolomics: It relates with those molecules which are necessarily involved in the metabolism of cell.

Transcriptomics: It is the study of mRNA and its functional properties.

Glycomics: It is concerned with the study of cellular carbohydrates.

Lipomics: Lipomics is the study of lipids present inside the cell.

Fig. 8.1 The different omics disciplines

Table 8.1 Advance operations of omics in plant sciences

Transcriptomics	miRNomics	Epigenomics	Genomics
Gene expression analysis	Expression analysis	Targeted bisulfite sequencing	Targeted sequencing
Noncoding RNA analysis	miRNA identification	CHIP-seq	Whole-exome sequencing
Gene fusion detection	miRNA editing	MeDIP-seq methylCap-seq	Whole-genome sequencing
mRNA splice analysis		Whole-genome bisulfite sequence	
RNA editing			

Metabolomics techniques enlighten us about the depth of complex metabolic mechanisms, the diverseness of biological processes involved in plant growth and development, and stress resistance against biotic or abiotic stresses. A few metabolites were routinely analyzed in plants using spectrophotometric techniques. However, GC-MS and LC-MS helped in analyzing small to large metabolites present in low or high quantities. Furthermore, associated bioinformatics tools helped in the exploration of complex metabolic networks and complicated biosynthetic pathways. Large data sets or reference databases have already been developed for different plant species for bioinformatics analysis. Recent research has shown significant advancements in the field of metabolomics, which have opened the doors for more improvements in plants for commercial cultivation (Shalini et al. 2018). The advance applications of omics in plant sciences are listed in Table 8.1.

The cryopreservation of plants is a complex process for the preservation of quality donor parent materials, which usually involves preculture, preconditioning, cryopreservation, cryoprotection, rewarming, and regrowth (Kaczmarczyk et al. 2012; Reed 2008). Cryobionomics gives us information about cryoinjuries on stored germplasm, cell signaling during this process, the mechanism of regrowth, as well as the implications of genetic constancy in stored material. Research on omics will dig into the whole cryopreservation mechanism and help in tackling the issue of the recalcitrance of germplasm. Omics, in general, have unlimited application not only in plant divisions but also in all divisions of living beings (Carpentier et al. 2005; Vertommen et al. 2007). The different kinds of omics are listed in Fig. 8.2.

This chapter significantly reveals how important omics disciplines are due to their revolutionary contribution in the genome of plant sciences and their helpful application in food safety, security, sustainability, and the welfare of mankind.

8.2 Genomics as a Revolutionary Discipline

Genome is the complete set of genetic information of an individual's DNA. Genomics is a discipline concerned with the internal structure of genomes, the functional properties and mapping of genomes, and the editing of genomes. Genomics works on the

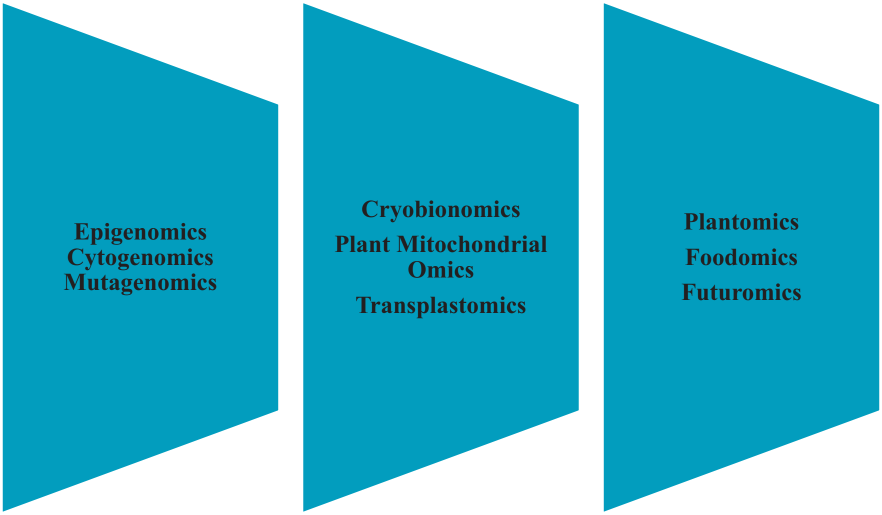


Fig. 8.2 A list of the different omics disciplines

phenomena of quantification and combined characterization of an individual's genes, their interaction and effects on an individual ("**WHO definitions of genetics and genomics**") (Geschwind and Flint 2015). Genomics is considered as one of the developing, emerging, evolutionary and revolutionary discipline which consists of various sophisticated tools and techniques that can be used in different disciplines especially in plants to program the internal mechanisms of an organism. It has been used in different areas of agriculture such as plant protection, plant pathology, plant genetics, plant breeding, molecular genetics, biotechnology, animals, livestock, biochemistry and many more (Bustamante et al. 2011).

Accurate and appropriate methodologies for marker assisted selection and molecular breeding, provision of approaches based on knowledge to plant biotechnology are provided by genomics, in order to accelerate the synthesis of novel plant cultivars. Functional gene products are recognized by the studies of gene expression that provides phenotypes and this data can be used for the crop improvement process. The specific addition of genes inside the plant can give rise to desirable phenotype rapidly as compared to conventional plant breeding methods (Lander 1996).

The interrelationship of genes of an individual is very much necessary for continuity of bodily activities. Important economical traits are incorporated into agricultural crops through the advanced genomic technologies, thus helps in designing of crops of desirable characteristics which fulfill the food demands of people. Molecular level analysis, genomic sequencing of plants are being exploited by researchers in different areas of plant sciences (Shalini et al. 2018).

Advanced genomic technologies have paved the way forward to produce qualitative foods along with different beneficial objectives such as high grain yield of rice and drought tolerant cultivars in maize, grain quality in wheat, etc. (Ashikari et al. 2005), as well as shelf life longevity in banana cultivars (Mehrotra and Goyal 2013).

SNPs and SSR which are the discoveries of genome sequencing technologies are being provided to improve qualitative traits in economical crops (Salgotra et al. 2014). Marker-assisted selection is also used to select progeny with desirable traits. Mutation breeding is also used to produce desirable crops having certain targeted economic characters by exposure to mutagenic reagents (Fleming 1983).

The prior identification of desirable traits in an individual has become easy through the application of molecular markers. The genetic diversity can be amended and accessed of the economical characters of crop plants by the help of such DNA markers (Collard and Mackill 2008). Generations of genetical as well as physical mapping have been done through the appropriate use of these DNA markers. They are also use to recognized areas which are needed for the crop environmental adaptation against different harsh circumstances (Varshney et al. 2009). The process of cosegregation is needed to create genetic maps which represent the position of markers in the group of linkage. Greater marker densities of genetic maps have been provided by next-generation sequencing (NGS) technologies. The mapping technology of quantitative trait loci (QTL) has been replaced by these enhanced maps technology. As molecular tool of characterization, the association maps are more accurate and detailed (Perez-de-Castro et al. 2012).

The transition of gene study from a single hereditary unit to a complete genome is a revolutionary step of genomics. It is helpful in understanding of gene interrelationships inside the genome. Such genomic modernization and technology would helpful in exploitation of evolutionary hierarchy of edible crops and reorganization of their ancestry that from where these present modern-day crops have been evolved. These genomic tools are equipping scientists to produce genetically engineered crops which provide sustainability of the food system and equal distribution of qualitative food among the global population. Furthermore, these genomic studies performs better to explore and understand the functional properties of genes in order to exploit better-off hereditary information for sustainable use(Shalini et al. 2018).The whole mechanisms of Genome sequence are as sculptured in Fig. 8.3.

8.2.1 Proteomics

The large-scale study of proteins is known as proteomics. Proteins comprise 50% dry weight of the cell, and it is an important part of an individual and consider as the main hub of various bodily activities. Meanwhile, the complete set of proteins produced by an organism is considered a proteome. Proteomics concern the handling of proteins at the molecular level (Anderson 1998; Blackstock and Weir 1999).

Identification and characterization of complete set of proteins' received from a genome can be done through the applications of proteomics (Wilkins et al. 1996). Amino acids are the building blocks of proteins. The determination of the concentration of amino acid sequences and different post-translational changings can be determined through proteomics (Barbier-Brygoo and Joyard 2004). In order to maintain the structure and the necessary regulatory mechanisms of proteins, its code

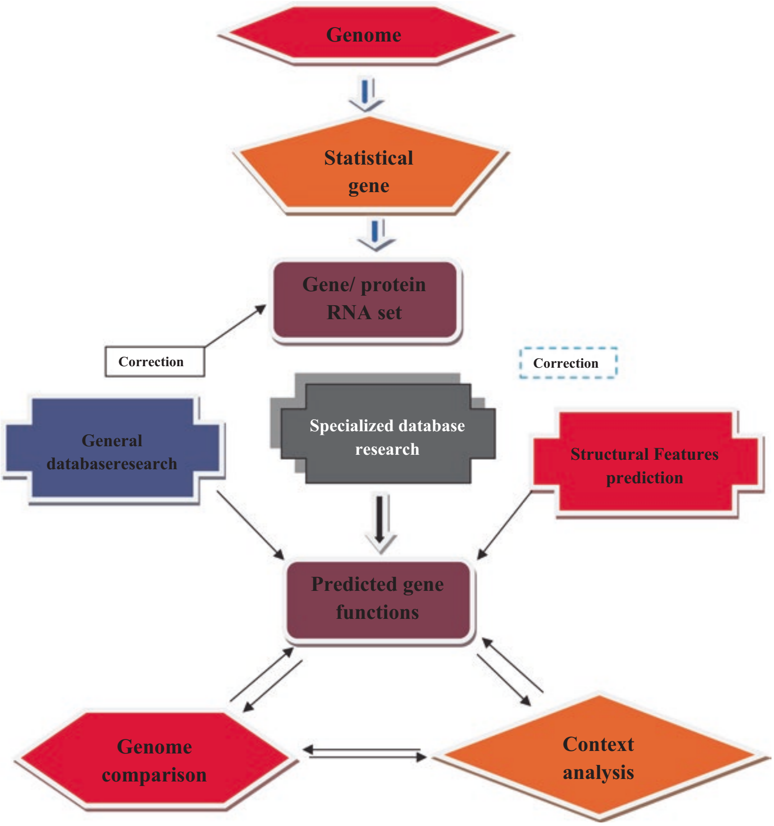


Fig. 8.3 Flowchart indicating the mechanism of genome sequence

of the genome is needed (Whitelegge 2002). Proteomics explains us the complex life processes and functional responses of a cell against environmental issues. The balancing of homeostasis inside the cells and networks of cell signaling for structural adjustment of cell are the main functions of proteins and these are all can be appropriately controlled by proteomics(Renaut et al. 2006).

The protein needed for MS traits has been identified for the hybrid selection and detection of male sterility traits in the hybrid by the help of proteomics (Yu et al. 2002). For the development of transgenic crops, proteomics can be applied (Gong and Wang 2013). To increase the photosynthetic mechanisms and abiotic stress tolerance of plants, certain efforts have been made in this regard. C4 plants are more workable relative to energy conversion because they contain two kinds of chloroplasts in their cell. In order to recognize the proteins responsible for the process of light fixation, proteomic study was conducted for both C3 and C4 plants respectively(Zhao et al. 2013).

The diversified functions of bio-molecules inside the body, their roles and interrelationship in metabolism of cell can be determined through advanced technology of proteomics and bioinformatics. The information of omics has been updated and advanced through the involvement of proteomics applications, and it provides in-depth of various biological mechanisms that take place inside the living organisms. The interaction between proteins and post-translational modifications can be known by the applications of proteomics. Probably, the development of protein-based bio-synthetic fungicide can be synthesized through the techniques of proteomics. Simultaneously, such protein based biosynthetic herbicides and pesticides as well fertilizers would be developed by utilizing the proteomics technology(Shalini et al. 2018). The flowchart proteomics protocol is as shown in Fig. 8.4.

8.2.2 Transcriptomics

The gene sequences which are expressed in a specific cell at a specific period are provided by the applications of transcriptomics. The nature of transcriptome is dynamic because the cell's transcriptome continuously changes due to different internal conditions. The function of genes, level of transcription and processes of molecules can be understood by the study of transcriptome (Borevitz and Chory 2004). Enzymes are the major players of metabolic activities. Analysis of expression of genes help in identification of particular gene controlling specific character, thus helpful in identification of main enzymes of that metabolic network (Poole et al. 2007).

In order to study variation in transcriptome information during growth, stresses, development, seed germination, the technology of microarray has been utilized successfully (Poole et al. 2007). For the successful improvement of plant cultivars

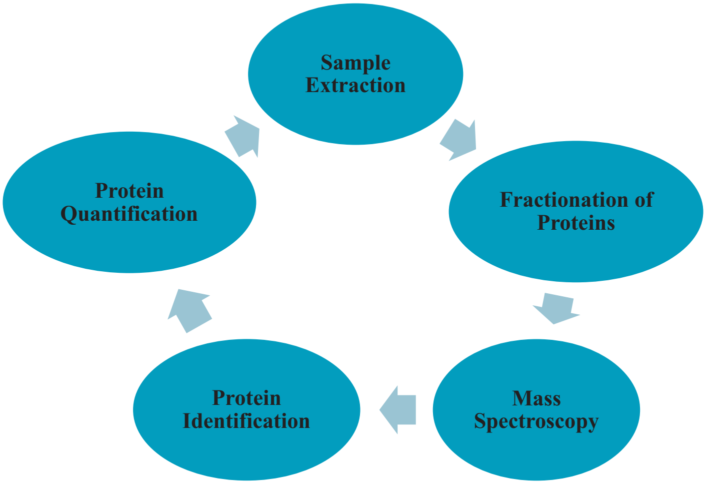


Fig. 8.4 Flowchart indicating proteomics protocol

incorporation of QTLs specific to resistance against biotic and abiotic stresses and grain development have been mapped on plant genomes (Saha et al. 2010). For the purpose of refinement of economical plants, functional tools like mutagenesis, epigenetics and RNA interference can be applied to gene silencing. For the recognition of chromosomal region related with expression of agricultural crop traits, bulk segregate analysis technique of genome mapping is used efficiently. For the development of disease resistant pigeon pea, this BSA technique was used successfully (Wei et al. 2009).

Significant data about genes involved in specific metabolic process is given by the gene expression analysis of mutant varieties. Generation of expression profile information depends on developmental stage of an individual, physiological circumstance and cell types can be developed through the application of transcriptomics. For comparing the relative DNA expression sequences of different species can be done by the evaluation of various information sets simultaneously. The relationship between plants and their wild relatives can be revealed through the analysis and assessment of molecular and expression diversity of an organism (Shalini et al. 2018).

8.2.3 Metabolomics

Living body is full of chemical reactions. The food we eat, the water we drink, they all have their own mechanisms in body to run bodily activities. The scientific study of these chemicals and their by-products, smaller molecules and metabolites is known as metabolomics. Basically, it is the study of unique finger print characteristics associated with it or the patterns of finger print metabolites that we leave behind (Daviss 2005).

The linkage between genotypes and phenotypes is known through the study of metabolomics. The major difference between proteomics and metabolomics is that metabolomics find out metabolically active expression of proteins, recognize biochemical processes and different metabolites roles that comes after result. The internal and environmental circumstances are subjected to dynamic metabolome. It involves continuous observation of associated changes caused in metabolic pathways; such changes are due to abiotic and biotic stress respectively. This dynamic monitoring helps in the development of improved cultivars and provides foundation mechanism to know about the biology of systems (Aliferis and Jabaji 2011). The manipulations occur in the metabolome proves helpful in the discovery of novel pesticides by the information comes from the studies of distinction of the pesticides action mode consequently. By the observation of manipulations of metabolite sequences, it will be helpful and easy to cause changes in plant health and qualitative changes in its nutrition simultaneously (Dixon et al. 2006). The profiling of metabolic pathways is helpful by providing data about what activities are going on inside the cell. For instance, during seedling stage, identification of activities inside the seed (Dunn and Ellis 2005).

The sign of similarity in composition between traditional and manipulated plants can be provided by metabolomics and it can find out the unwanted changes caused in the whole composition of metabolite. Mass spectrometry and nuclear magnetic resonance are the two analytical tools used in metabolic profiling. These techniques can be utilized in herbicides to find out their metabolic responses, examine and observe metabolic regulations and manipulations occur in metabolites in relation to environmental and genetic conditions respectively (Aliferis and Jabaji 2011).

An insight study of metabolites' and their appropriate analysis is helpful in decline the utilization of pesticide and synthesis of new pesticides, enhancing nutritional content, and provides better nourishment to the main traits of interest. Metabolomics possess a great potential to study the small molecular patterns specifically associated with different molecules to alter the genetic adjustment of plants (Idle and Gonzalez 2007).

8.3 Application of Foodomics in the Safety, Security, and Sustainability of Food

Foodomics is an emerging discipline which combines omics technologies of advanced level to make better health and consumer's well-being. It integrates tools like food chemistry and biology of food to utilize technology in a proper way (Cifuentes 2009). Foodomics and its processing mechanisms are as listed in Table 8.2.

It aims to focus on provision of better qualitative food along with a sufficient quantity to fulfill the requirements of rapidly growing global population. As it is already mentioned that world population is about to reach 9 billion in 2050 and now breeders, scientists, researchers, and food scientists are on the way to overcome the scarcity of food all over the world. In this whole scenario, advanced technologies like omics have been proved helpful to revolutionize the world with the efficient quantity of food for safety, security and sustainability of food. Foodomics was officially emerged as a discipline in the first international conference held in 2009 at Cesena, Italy (García-Cañas et al. 2012). Due to high throughput analysis

Table 8.2 Foodomics and its processing mechanisms

Foodomics			
Bioactivity	Safety	Quality	Traceability
Microbial growth	Assessment and evaluation of food	Assesses and evaluates the quality and life of food	Identification of sources
Identify pathogens	Transgenic food	Food	Food
Adaptation of pathogens	Contaminants	New food	Ingredients
Impacts of molecules on health	New ingredients	Processing	Plant breeding and crop improvement

requirement of foodomics, it is still bounded in sense of research and developmental progress. Foodomics based upon four major disciplines of omics namely (Balkir et al. 2020):

(a) **Genomics:** It concerns the detailed examination of genomic structures (Brennan et al. 2020).
(b) **Transcriptomics:** It uses different tools of analysis, including microanalysis, to explain genomic sets and recognizes differences among various conditions and individuals (Dong and Chen 2013).
(c) **Proteomics:** It concerned with the structure and physiological functions of protein. it is the large-scale study of the proteome (set of proteins) present in organisms. (Graves and Haystead 2002).
(d) **Metabolomics:** It is particularly concerns with the comprehensive study of metabolites in a biological system and their effects cellular behavior(Clish 2015).

All these abovementioned disciplines have been previously discussed in depth. The Foodomics utilizes the applications of these four major areas in order to design and synthesis food of its own choice that meets the demands of global community. Foodomics has various advantages for the welfare of human beings. It provides easy data access to scientists to arrange food analysis and its effects on health living organisms. It is a forward step towards progress and growth of food and technology to better understand them. It also leads to nutrional genomics which is the further extention of foodomics and helpful to analyze the interaction among genetics, food and human health studies. Foodomics is really an emerging field whose applications are using to check food effects on human, plants and animals, in order to cure the diseases genetically and on time. It ensures safer provision of food and paves the way for sustainable food development (Capozzi and Bordoni 2013). The overlapping of the different omics disciplines in foodomics is shown in Fig. 8.5.

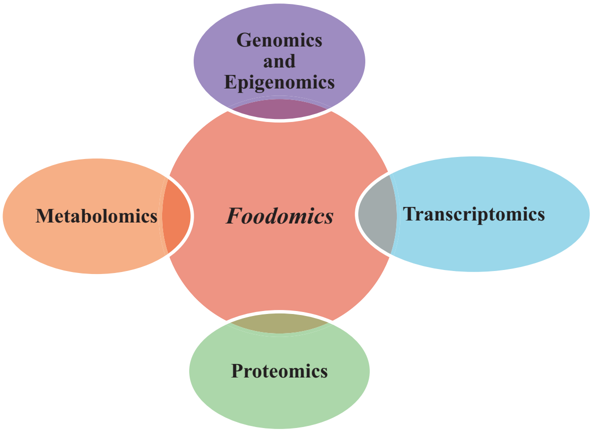


Fig. 8.5 Shows the overlapping of different omics disciplines in foodomics

8.3.1 Cryobionomics

As an emerging, evolutionary and developing discipline, cryobionomics provides an ultimate solution to preserve germplasm stock better-off. The process of cryopreservation of in vitro germplasm material for the purpose of long-term conservation results in the exposition of tissues to physical, physiological and chemical stresses resulting cryo-injury. However, the impacts of cryo-injury on the genome are rare; any DNA polymorphisms' accumulation would not be induced by cryopreservation itself, but the consequence of complete cryo-protection culture regeneration mechanism. It is desirable to evaluate the complete genetics of plants surviving cryogenic storage to find out either they are 'true to type' after cryopreservation. It can be approached at the phenotypic, biochemical, cytological, histological, and molecular level (Kaviani 2021) (Kaviani 2021) (Kaviani 2021).

To obtain a sophisticated picture of the basic biological mechanisms that consist of cryopreservation of whole systems, scientists are now capable to work on the same sample through the complete access of omics technologies (Morrison et al. 2006). Generally, high-throughput tools of omics such as genomics, transcriptomics, proteomics, metabolomics, and all other omics technologies can be applied to the same sample, following a detailed examination into biomolecular manipulations which combine the plant materials cryopreservation. Contemporary research in plant cryopreservation is now advocated by omics technologies that prepare a new knowledge foundation that will help in growth to resolve some of the more complex cryobiological issues (Basu 2008; Carpentier et al. 2005, 2007, 2008a, b; Volk 2010).

This whole process requires standard operating procedures to achieve a profound recovery that takes decades of collaborative examination using docile model systems to understand the complexity of the species and specific genotype responses to cryopreservation (Johnston et al. 2007, 2009, 2010). Necessary advancements have been marked in the last decade (Normah et al. 2013; Reed 2008), but there remained some instances where cryopreservation is restricted by scarcity of process where its utilize is highly desirable for the valued material preservation (Häggman et al. 2008). As progress in cryopreservation growth towards recalcitrant non model individuals, an increasing number of hurdles have been stumbled on with low levels of post-storage survival (Reed et al. 2013).

It is an evolving phenomenon that deals with the two aspects of cryopreservation viz. the linkage present between genetic stability and cryo-injury and secondly, the functionality and behavior of plant species in relation to their re-introduction in natural habitats environments and atmospheres (Harding 2004). The applications of omics disciplines in cryobionomics are as shown in Fig. 8.6.

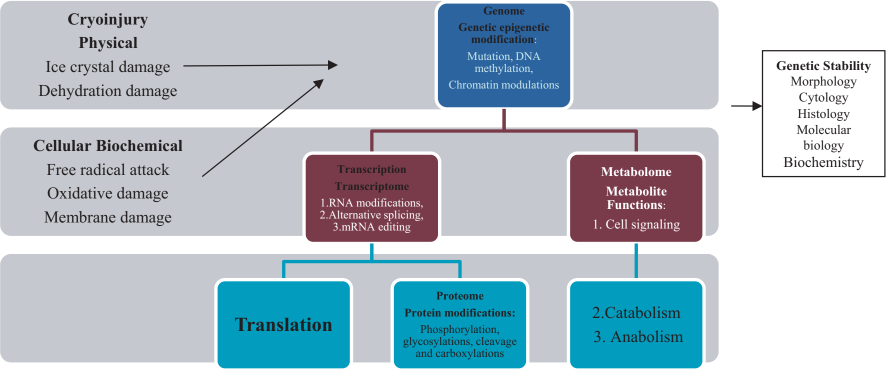


Fig. 8.6 Indicates the application of omics disciplines in cryobionomics

8.4 Conclusion and Future Perspectives

The science of omics contains great potential to alter the genetic make-up of plants, to achieve desirable objectives in plants, vegetables and crops respectively. It aims to bring such productive changes inside the genes, DNA, RNA, macro and micro-molecules at the highest level. The genuine issue which the world is facing today is the shortage of qualitative and healthy food, continuous change in climatic patterns and environmental stress. The Food and Agriculture Organization is working on strategies to overcome this barrier; fulfill the needs of the population all over the world, with the objective of producing novel cultivars with higher yield, less pesticide consumption, and higher thermo tolerance; and develop sustainable food production practices. Other national and international organizations are also working on formulating sustainable food production policies to ensure food and health safety among the masses. The recent inventions of modern molecular and nanotechnologies have overcome various issues related to the safety and sustainability of food. Their revolutionary contribution to plant production can never be ignored. Disciplines like omics can give us a genetic map to yield possibly the deepest-red apple easily. Its scientific results are beyond imagination, if one reveals its mysterious phenomena.

The wide-ranging dump of omics tools are increasing the taste, quality, and nutritional composition of major food crops, enhancing agricultural yield for food, feed, and fiber, playing a vital role in plant protection, and consequently impacting agricultural economics. Through the appropriate utilization of genomics, proteomics, transcriptomics, and metabolomics, the predictability, uniformity and consistency in plant breeding have been improved, reduction in time occurs and expenses of producing best qualitative major edible crops which possess resistance against biotic and abiotic stresses, but still possess high nutrition. Omics has given depth to the molecular processes of insect resistance to pesticides, and the tolerability in plants towards herbicides for better management of a pest. Linking genes to characters provides extra scientific assurance leading to improved varieties and lines and understanding the processes of insect and weed resistance. Omics provides a systems' biological approach in order to understand the complex interrelationships between proteins, genes and metabolites within the resulted phenotype. This integrated approach depends heavily upon chemical analytical methodologies, computational analysis, bioinformatics and various biological disciplines, leading to plant protection and trait improvement. The application omics technologies in plant science is shown in Fig. 8.7.

Omics can be applied in agriculture research expansion in different sectors like health and food sector, energy division, animal feed, and special preparation of chemicals while it can be helpful in enhancement, preservation and remediation of the environment. Technologies of the omics are focusing on important target characters along with accuracy. It can enhance traits of nutrition of food for the advantage of a consumer, such as tomato which contains high lycopene concentration, fruits which contain delayed trait of ripening, as well as yield along with potential antioxidant capacities. Omics potential targets, focus and outcomes are as shown in Table 8.3.

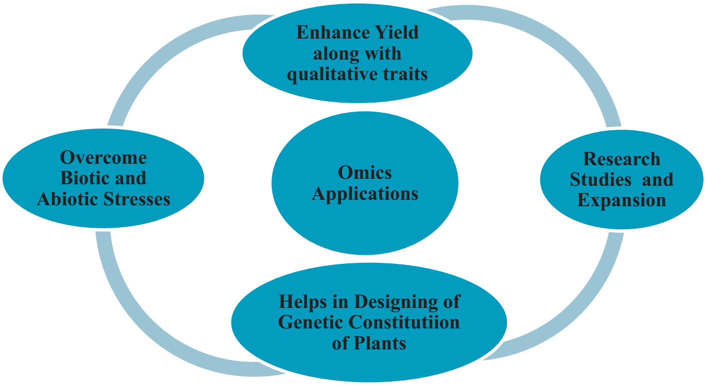


Fig. 8.7 Some applications of omics technology in plant sciences

Table 8.3 Omics potential targets, focus, and outcomes

Approach	Target molecule	Focus	Potental influence and outcomes
Metagenomics	DNA	Whole community taxonomic and functional analysis	Novel organisms, processes, and bioactive compunds
Metabolomics	Small molecules (metabolomics/ metabolites)	Elucidating composition, diversity, and richness of metabolomes	Characterization of novel metabolomes (metabolites)
Proteomics	Amino acids, peptides, and protein molecules	Expressed protein composition and quantification	Highlights the differences between protein translation and degradation in food waste
Transcriptomics	RNA (total RNA, rRNA, or mRNA)	Elucidating the composition, diversity, and richness of transcriptomes (expressed genes)	Gene expression profiling, identification, and characterization uncovers novel RNA species

Abiotic stresses affect plant growth as plants are the earth's basic producers and potential of yield in an individual. Stress conditions at certain times, plant species adjust per se to temporarily adaption to the present status by manipulating the expression design of metabolites, proteins, genes. In order to recognize such manipulations, many techniques such as transcriptomics, genomics, metabolomics, genomics and glycomics have been designed to appropriately tackle the genetic constitution of plants and their succession in adaptability under stressed conditions. Hence, there are uncountable applications of omics are available which can be utilized to take various benefits in plants, to create food sustainability and safety for the welfare of human beings.

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