

THE ROLE OF OMICS RESEARCH IN GERmplasm CONSERVATION

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ABSTRACT

The word omics refers to a field of study in biological sciences that ends with -omics, such as genomics, transcriptomics, proteomics, or metabolomics. The ending -ome is used to address the objects of study of such fields, such as the genome, proteome, transcriptome, or metabolome, respectively. In relation to the conservation of germplasm, genomics-based plant germplasm research has been carried out and has been proven to be able to conserve germplasm. Recently, to conserve germplasm using only genomics-based plant germplasm research, it is felt to be incomplete, because not all genes can be expressed under certain conditions. For this reason, other omics such as proteomics and metabolomics play an important role in the conservation of germplasm. In this paper, the role of other omics research, especially metabolomics is described.

Key words: germplasm conservation, metabolomics, omics.

INTRODUCTION

Germplasm conservation is very important and it has a valuable natural resource that provides knowledge about the genetic composition of a species and is crucial for conserving plant diversity. Germplasm protection strategies not only involve rescuing plant species threatened with extinction, but also help preserve all essential plants, on which rests the survival of all organisms (Priyanka et al., 2021). Moreover, the successful use of genetic resources necessitates their diligent collection, storage, analysis, documentation, and exchange. Slow growth cultures, cryopreservation, pollen and DNA banks, botanical gardens, genetic reserves, and farmers' fields are a few germplasm conservation techniques being employed.

Biotechnology that includes molecular biology and genetic engineering requires germplasm. What can we engineer if there is no germplasm sources? Thus, the preservation or conservation of germplasm is absolutely necessary. So that in turn, molecular biology or genetic engineering can optimize the preservation of germplasm. Germplasms acts as both raw material and a source of natural variation. As a way of shaping and using genetic information, biotechnology has implication for germplasm conservation and use. Although biotechnology is commonly thought of as recombinant DNA (deoxyribonucleic acid) technology or genetic engineering, it is used here in a broader sense to include tissue culture, cryopreservation, plant micropropagation, and animal regeneration from early embryos. Biotechnology influences germplasm conservation in several ways. First, it provides alternatives in some cases to conserving whole organisms. Second, it can assist with the exchange of germplasm. Third, the techniques of molecular biology can be applied to the problems of managing and using germplasm. The fourth influence results from the increased demand for germplasm and conservation services by the biotechnologists themselves (Peter et al., 1993).

Moreover, molecular biology provides a scientific framework that describes the elements of the genetic system as sequences of four nucleotide bases that make up DNA. Knowledge of how these DNA sequences are expressed and how expression is regulated and coordinated during development is growing rapidly. It is now commonplace to introduce

foreign gene constructs into an organism, and the ability to add regulatory sequences that determine when and how strongly the introduced genes will be expressed to alter the phenotype of the recipient is often possible. The numbers of genes that have been isolated, cloned, and sequenced increase daily, and the information thus obtained already represents a genetic resource of considerable and growing scientific and commercial value (Peter et al., 1993).

However, there are so many genes that can only be expressed under certain conditions, so that a study based on genomics alone is still not perfect. For this reason, it is not enough just to conserve germplasm with research based on molecular biology or genetic engineering, but other omics studies such as metabolomics are needed.

METABOLOMICS

What is Metabolomics?

Many experts define metabolomics, briefly metabolomics is the scientific study of the set of metabolites present within an organism, cell, or tissue. Moreover, metabolomics is the large-scale study of small molecules, commonly known as metabolites, within cells, biofluids, tissues or organisms. Collectively, these small molecules and their interactions within a biological system are known as the metabolome. Thus, metabolomics can be defined as an analytical profiling technique for measuring and comparing large numbers of metabolites present in biological samples.

Metabolites are considered to “act as spoken language, broadcasting signals from the genetic architecture and the environment”, and therefore, metabolomics is considered to provide a direct “functional readout of the physiological state” of an organism (Roessner and Bowne, 2018). A range of analytical technologies has been employed to analyze metabolites in different organisms, tissues, or fluids. Mass spectrometry coupled to different chromatographic separation techniques, such as liquid or gas chromatography or NMR, are the major tools to analyze a large number of metabolites simultaneously. Although the technology is highly sophisticated and sensitive, there are still a few bottlenecks in metabolomics. Due to the huge diversity of chemical structures and the large differences in abundance, there is no single technology available to analyze the entire metabolome. Therefore, a number of complementary approaches have to be established for extraction, detection, quantification, and identification of as many metabolites as possible (Roessner and Bowne, 2018).

A metabolomic study should, in theory, be able to detect, identify and quantify all the metabolites present in a given sample at a given moment; the metabolomic map that is obtained is the representation of biological processes which, in turn, are influenced by individual tissue genetic features, regulation of gene expression, protein abundance and environmental influences.

Potential and Applications of Metabolomics

There are four conceptual approaches in metabolomics: target analysis, metabolite profiling, metabolomics, and metabolic fingerprinting. First, target analysis has been applied for many decades and includes the determination and quantification of a small set of known metabolites (targets) using one particular analytical technique of best performance for the compounds of interest. Secondly, metabolite profiling, on the other hand, aims at the analysis of a larger set of compounds, both identified and unknown with respect to their chemical nature. This approach has been applied for many different biological systems using GC-MS, including plants, microbes, urine, and plasma samples. Third, metabolomics employs complementary analytical methodologies, for example, LC-MS/MS, GC-MS, and/or NMR, in order to determine and quantify as many metabolites as possible, either identified or unknown compounds. The fourth conceptual approach

is metabolic finger-printing (or footprinting for external and/or secreted metabolites). Here a metabolic “signature” or mass profile of the sample of interest is generated and then compared in a large sample population to screen for differences between the samples. When signals that can significantly discriminate between samples are detected, the metabolites are identified and the biological relevance of that compound can be elucidated, greatly reducing the analysis time (Roessner and Bowne, 2018).

Even farther, metabolites are so closely linked to the phenotype of an organism, metabolomics can be used for a large range of applications, including phenotyping of genetically modified plants and substantial equivalence testing, determination of gene function, and monitoring responses to biotic and abiotic stress. Metabolomics can therefore be seen as bridging the gap between genotype and phenotype, providing a more comprehensive view of how cells function, as well as identifying novel or striking changes in specific metabolites. Analysis and data mining of metabolomic data sets and their metadata can also lead to new hypotheses and new targets for biotechnology (Roessner and Bowne, 2018).

The role of Metabolomics Studies on Germplasm Conservation

To date, most research in germplasm conservation is not only based on technology to store germplasm but also based on sequences of genomes, genes, mRNA, and/or proteins. However, the correlation of gene and protein expression is low and that between gene expression and metabolites even lower. However, metabolites, especially secondary metabolites, are extremely important for most organisms to defend themselves from stressful environments or predators. Although primary metabolites involved in central metabolism can be used to determine nutritional and growth status, secondary metabolite profiles may better reflect the differentiation of species and their complex response to environmental factors and other organisms. The suite of secondary metabolites in an organism can be astonishingly complex, and while certain compounds may be found in different organisms, a vast number of compounds are very species-specific. Secondary metabolites are therefore considered as potential markers for taxonomy and phylogenetic (Roessner and Bowne, 2018).

Nowadays, metabolomics is being increasingly used in many crop species irrespective of the availability of transgenic system (Daygon and Fitzgerald, 2013; Simó et al., 2014). The metabolomics has the potential to facilitate selection of superior traits and improvement of breeding materials (Zivy et al., 2015). In conjunction with the advances in metabolomics, the availability of whole genome sequence, genome-wide genetic variants and cost-effective genotyping assays opens exciting opportunity to effectively integrate metabolomics in crop breeding programs (Kumar et al., 2017). Based on the information above, it is clear that the study of metabolomics has an important role in germplasm conservation.

CONSLUSION

The role of metabolomics studies with germplasm conservation, metabolomics technology will be able to complement the existing germplasm conservation technology, because metabolomics is a collection of powerful tools for the analysis of phenotype, both by hypothesis generation and by hypothesis testing. Building on the strengths of the “omics technologies that came before, metabolomics uniquely comprises analytical technologies that can provide diagnostic patterns via fingerprinting, absolute quantitation of targeted metabolites via pool analysis, relative quantitation

of large portions of the metabolome using metabolite profiling, and tracing of the biochemical fate of individual metabolites through a metabolic system via flux analysis. Metabolomics research technology can make a very significant contribution to the conservation of germplasm.

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