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## **Plant Metabolomics: An Overview**

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### **Authors' contributions**

*This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.*

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### **ABSTRACT**

The term metabolomics was coined by Oliver and his group in 1998. It is a study of biochemical profile and regulation of functions in whole organism by analyzing a metabolite pool present in organism. Researchers believe that more than 400,000 plant species exist worldwide. Total number of metabolites in the plant kingdom are about 2,00,000 to 10,00,000. With the availability of highly sensitive and selective analytical techniques, metabolic changes in plant systems can be followed in a comprehensive way. This technology is useful in assessing gene function and relationships to metabolites. The nutritional values of food and concentration of pharmaceuticals in plants can be improved by using metabolomics study and its functional genomic strategies. Metabolomics analysis is comparatively fast, cheaper and reliable, but simultaneous identification of all metabolites in a crop plant remains a challenge.

*Keywords: Genomic strategies; metabolomics; plant kingdom; fingerprinting.*

### **1. INTRODUCTION**

The term metabolomics was coined by Oliver and his group in 1998 [1]. It is a study of biochemical profile and regulation of functions in whole organism by analyzing a metabolite pool present in organism.

Researchers believe that more than 400,000 plant species exist worldwide [2]. Total number of metabolites in the plant kingdom are about 2,00,000 to 10,00,000. Metabolites are intermediates or product of metabolism having less than 1 kDa size. There are two types of metabolites:

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## 1.1 Primary Metabolites

(carbohydrates, proteins and fats) required for energy, normal growth development & reproduction.

## 1.2 Secondary Metabolites

(phenols, alkaloids etc.) are important for ecological functions.

A metabolome represents the ultimate phenotype of cells and play a key role in understanding cellular systems and decoding functions of gene. Therefore, metabolome analysis is a valuable tool for inferring gene functions. Metabolomics provides most functional information of the "omics" technologies. It provides primary effect of genetic mutation, and or product of encoded protein, and elucidated the functions of a whole metabolic pathway. Metabolites are complex by nature; hence adequate tools are needed to analyze and interpret it.

## 2. METABOLOME ANALYSIS

There are four types of strategies to analyze metabolome viz., (1) Metabolite target analysis, (2) Metabolite profiling, (3) Metabolomics, (4) Metabolic fingerprinting [3]. To analyze metabolome, most utilized techniques include chromatography coupled to MS and NMR spectroscopy are LC-MS, GC-MS, HPLC, TOFMS, CE-MS, FTICR-MS, NMR [4].

### 2.1 Applications of Plant Metabolomics

Cook et al. [5] studied a prominent role for the carbon repeat dehydration responsive element binding factor (CBF3) in *Arabidopsis* and observed changes in CBF3 cold response pathway. Total 102 metabolites were found to increase in *Arabidopsis* in response to over expression of CBF3 [6]. Reported the over expression of HQT gene by GC-MS analysis in tomato. They found that HQT gene caused plants to accumulate higher level of chlorogenic acid, with no side effects on the levels of other soluble phenolics, and showed improved antioxidant capacity and resistance to bacterial infection. Tomatoes with elevated chlorogenic acid levels could be used in foods with specific benefits for human health [7] found  $\alpha$ -Tomatine in tomato for resistance against root-knot nematode, *Meloidogyne incognita*. They studied role to  $\alpha$ -Tomatine as resistant biomarker of root-knot nematode in tomato and enhanced functional food quality. However, [8] gave the

general outline for plant metabolomics. It adds a compilation of work in plant metabolomics to give an overview about the breadth and scope for which metabolomics is used to understand the plant metabolism.

Dixon et al. [9] studied *Medicago truncatula* for different pathways of isoflavonoid and triterpene metabolism. They found new information on pathway regulation by transcription factors and control of vacuolar storage of secondary metabolites [10] reviewed crop studies employing metabolite profiling. They indicated identification of the natural variation on metabolites level in 70 rice varieties, revealed large metabolic differences between the cultivars.

### 2.2 Metabolic Engineering

Many major crops lack the ability to synthesize the special osmoprotectants that are naturally accumulated by stress tolerance organism. Therefore, [11] hypothesized that installing the osmoprotectant synthesis pathways is a potential route to breed stress tolerant crops. Indeed, he studied metabolic engineering for stress tolerance and found glycine betaine was metabolite marker for water stress. [12] examined enhancement of folates in plants through metabolic engineering. The expression of bacterial GTP cyclohydrolase-1 in transgenic *Arabidopsis* resulted in a 1250-fold and 2 to 4-fold enhancement of pterins and folates, respectively. These results helped to identify other potential factors, regulating the folate synthesis suggesting the ways to further enhance folate levels in food crops. The Table 1 show metabolomics Database and function,

#### 2.2.1 Advantages

1. Sample complexity is reduced.
2. It is the downstream product of gene expression.
3. Metabolic fluxes are regulated by gene expression environmental stresses.
4. Experimental cost two to three times less than proteomic and transcriptomics.

#### 2.2.2 Limitation

1. Limitations of analytical approaches/ techniques.
2. Chemical complexity of the Metabolome.
3. Inherent biological diversity of living organisms.
4. Uncertainty about the number of primary and secondary metabolites in a species.

**Table 1. Metabolomics database and function**

No.	Database	Function
1.	AraCyc	Tool to visualize biochemical pathways of Arabidopsis.
2.	ArMet	Design and code allow the detailed description of each step in the experiment and define detailed sub-components.
3.	Database DOME (a of MEs)	Composed of various sub-sections that contain metadata, raw data, analysis results and an ontology describing the known molecular biology of the plant species of interest.
4.	MetaCyc	Describes metabolic pathways, reactions, enzymes and substrate compounds that were gathered from a variety of literature and on-line sources and contains citations to the source of each pathway.
5.	MapMan	Displays large datasets onto diagrams of metabolic pathways or other processes
6.	MetNet	Metabolic and regulatory network map that contains a growing map of Arabidopsis entities and the catalytic and regulatory interactions between them

In summary, plants "inform" the environment of their clinical status, specifically indicating whether they are being attacked by insects [13], nematodes, microorganisms [14,15,16], or affected by some abiotic stress [17,18,19]. In this regard, said "chemical language" occurs through the constitutive production of secondary metabolites, and the subsequent emission of Biogenic Volatile Organic Compounds (BVOC) into the atmosphere [20, 21].

Generally, plants that grow in environments with low rainfall develop additional defenses to mitigate the effects of high temperatures [22,23,24], ultraviolet rays, meteorological drought [25,26,27,28], climate variability [29,30,31,32], and salinity [33], results evidenced in crops such as corn [34], tomato [35]; Onion [36] and potato [37]. In relation to this, there is little information related to these phenomena, which have an immeasurable potential to be investigated within the context of innovation and generation of new biotechnological products of natural origin, coming from different agroecosystems. Different methodological approaches have allowed the progressive characterization of individual genes and the identification of pathways associated with inter and intracellular signaling induced by water deficit stress. Although many of the components involved in responses to water deficit are still missing, in recent years there has been notable progress in understanding the molecular bases of these responses in plants.

### 3. CONCLUSION

With the availability of highly sensitive and selective analytical techniques, metabolic

changes in plant systems can be followed in a comprehensive way. This technology is useful in assessing gene function and relationships to metabolites. The nutritional values of food and concentration of pharmaceuticals in plants can be improved by using metabolomics study and its functional genomic strategies. Metabolomics analysis is comparatively fast, cheaper and reliable, but simultaneous identification of all metabolites in a crop plant remains a challenge.

### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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