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Short Communication

Metabolomics Research is Crucial for Understanding Plant Biology: Melanoidin Coloration Changes in the Bacterial Extracellular Supernatant when Silver Nanoparticles (AgNPs) are Biosynthesized

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Abstract

In plant biology, metabolomics is important for growth, development, and stress resistance. Plants create a wide variety of metabolites, ranging from 200,000 to 1,000,000, hence metabolomic research is crucial for understanding plant biology. Plants have a wide variety of metabolites, making it difficult to accurately identify and measure them. Plant metabolomics has advanced significantly, yet it is still difficult to consistently annotate metabolite signals in databases and with worldwide standardised informatics. The improvement of separation efficiencies and the identification of specific metabolites are key factors in the development of metabolomics. In plant metabolomics, the fluxome and metabolomic QTL (mQTL) constitute a critical gap.

Nowadays, system biology includes metabolomics, and using metabolomics in conjunction with a system biology approach will enable the objective capture of mass spectrometric data from a wide range of samples. The improvement of technology for metabolite detection and identification in complex plant tissue as well as the distribution of metabolomics research data would be highly beneficial in overcoming various obstacles (German JB et al., 2002).

INTRODUCTION

The main goal of "OMICS" technology is the identification of all gene products (transcripts, proteins, and metabolites) without any specific targeting. The final challenge in functional genomics is metabolomics, which follows the development of tools for high-throughput DNA sequencing (genomics), gene expression analysis (transcriptomics), and protein analysis (proteomics).

The word "metabolism" was created to describe practically all high-throughput, unbiased investigations of complex metabolite combinations seen in plant extracts. The objectives of functional genomics research and recent developments in mass spectrometry technology are the main driving forces behind this potentially comprehensive approach to metabolome study (Mendes P, 2006).

A multidimensional, completely integrated approach must be established for the best sample extraction, metabolite separation, detection, automated data collection, processing, analysis, and eventually quantification in order to achieve the largest overview of metabolic composition.To accomplish these aims, both analytical and computational improvements are crucial.

METABOLIC DIVERSITY AND DATABASE

At least 270,000 plant species are known to exist, and researchers estimate that there may be as many as 400,000 plant species in the globe. Estimates place the total number of metabolites in the plant kingdom at 200,000 and 1,000,000. Numerous substrate specificities for numerous

enzymes, rather than the presence of 20,000 to 50,000 genes, are what contribute to the metabolic richness.

Thus, the biggest obstacle to large-scale, comprehensive metabolite profiling is overcome—an obstacle that spurs cutting-edge technical advancement. The chemical identification of a plant metabolite is now being determined using a variety of experimental methods. The relative concentration and chemical complexity of the analytical techniques used varies. Usually, authenticated substances found in spectrum libraries are compared with metabolites to identify them. The NIST, Wiley, and Sigma-Aldrich libraries are a few of the frequently used spectrum libraries (Weckwerth W, 2003). Despite having more than 350000 items, the majority of these libraries' entries lack information on chromatographic activity and aren't biologically complicated.

Metabolomic research will show to be a very useful instrument for producing data that is very important in many sectors. Fast-track approaches that utilise metabolomics investigations of tagged lines or unidentified mutants are anticipated to yield priceless information for functional genomics initiatives. In addition to helping to establish a deeper understanding of the intricately interconnected metabolic network of plants and how they respond to genetic and environmental change, metabolomic information will also offer a rare window into the fundamental characteristics of plant phenotypes in relation to growth, physiology, tissue identity, resistance, biodiversity, etc.

Currently, metabolomics is being used in several biological investigations, from research on the relationships between carbon and nitrogen in plants to the creation of personal metabolomics for the evaluation of the next generation of a person's nutritional needs. The real objective of all functional genomics approaches will be to gain a better understanding of the relationship between genes and functional phenotypes of an organism.

PRESENT STATUS OF METABOLOMICS

Monitoring an organism's reaction to a conditional perturbation at the transcriptome, proteome, and metabolome levels is crucial. With the use of these three levels of expression profiling, one may create models that quantitatively characterize the dynamics of biological systems, infer meaningful associations between macromolecules, and find functional links between phenotypic expressions. If we want to go from gene function prediction to experimental validation, broad phenotypic assessments are crucial. Therefore, to research the dynamics of the metabolome, to examine fluxes in metabolic pathways, and to understand the function of each metabolite in response to varied stimuli, the simultaneous identification and quantification of metabolites is required. Finding alterations in the metabolomic network that are functionally associated with the physiological and developmental phenotype of a cell, tissue, or organism is one of the problems of metabolomics. Visualizing the functional genomics repertoire of an organism requires the linking of functional metabolomic data to data on mRNA and protein expression (Saito K et al., 2010).

METABOLITE PROFILING TECHNIQUES

Because the genes in plants' genomes perform such a wide range of tasks, they may synthesise a tremendous variety of compounds. The fast developing area of post-genomic study is metabolomics. A cell's final phenotype, as determined by changes in gene expression and protein activities, is represented by its metabolome. The metabolome can also affect how genes are expressed and how proteins work. As a result, metabolomics is crucial for understanding biological processes and decoding gene activities.

Metabolite analysis is confounded by the significant fluctuations (106) in the relative amounts of metabolites. Therefore, utilising several parallel complementary extraction and detection methods with careful experimental design is the only way to obtain complete coverage. A combination of different analytical techniques, such as gas chromatography (GC), liquid chromatography (LC), capillary electrophoresis (CE)-MS, NMR, and rapid scanning time-of-flight (TOF), is typically used to detect the greatest number of compounds in plants or other organisms because there is currently no technology available to do so.

MISSING LINK

To take into account the dynamic characteristics of plant metabolism, a third layer of omics called the "Fluxome" is necessary between the proteome and metabolome levels. These metabolic interconversion rates within live cells are steady-state rates. They have a major role in cellular phenotype, regulating the rates of growth and product production. The steady-state flux distribution is calculated primarily using flux balance analysis. According to the fluxbalance analysis concept, a collection of metabolic fluxes in the network, such as substrate intake or product excretion, must be empirically quantified. Flux-balance analysis has the drawback of being unable to quantitatively anticipate how much individual enzyme activities need be changed in order to produce a desired outcome, such as an increase in a product's specific production rate (Dixon RA et al., 2003).

A potent method for identifying genes linked to metabolic illness markers and unravelling the genetic component of metabolic profiles is quantitative trait locus mapping (mQTL) of metabolic phenotypes. The mQTL mapping entails a genetically diverse cohort, a contemporary genotyping platform, hypothesis-free metabolic profiling using high throughput nuclear magnetic resonance (NMR)

spectroscopy or mass spectrometry (MS), generating up to 20,000 metabolic traits per sample, and the statistical tool necessary to map these traits on to the genome of the experimental population. mQTL research' biological interpretation can be improved by network and system biology approaches.

CONCLUSION

The study of metabolomics is particularly relevant in the field of plant biology since plants create a wide variety of different metabolites. A single analytical method cannot fully identify and quantify these metabolites, but many simultaneous complimentary technologies will be highly beneficial.

To decipher the co-occurrence principle of transcripts and metabolites, information from the transcriptome co-expression network will be crucial. Therefore, identifying and evaluating genetically engineered crops can be highly useful.

Understanding plant systems and the subsequent development of biotechnological applications will be largely dependent on metabolomics and system biology. For crop breeding, metabolome QTL (mQTL) in combination with gene expression and agronomical characteristic will be extremely beneficial.

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