

## Plant Transcriptomics and Developmental Mechanisms in Medicinal Plants

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### DESCRIPTION

Transcriptomics has been accustomed to study the variations in gene expression in medicinal plants under abiotic stress and to spot genes that have an effect on the expansion and development of medicinal plants and resistance to external stress. Transcriptomics is one among the foremost widespread topics in biology in recent times. Transcriptome Sequencing (RNA-Seq) may be a high-sensitivity, and high-resolution technique that may be accustomed to study model and non-model organisms.

Transcriptome Sequencing is a very important technique for learning the genomes of medicinal plants; a subject on that limited information is available. The study of medicinal plants through transcriptomics will help researchers to analyze functional genes and regulatory mechanisms of medicative plants and improve breeding choice and cultivation techniques. This commentary analyzes and compares the applications of transcriptome sequencing in medicinal plants over the past decade and briefly introduces the ways of transcriptome sequencing and analysis, their applications in medicative plant analysis, and potential development trends. We concentrated on the research and application progress of transcriptome sequencing within the following four areas: The mining of functional genes in medicative plants, development of molecular markers, biosynthesis pathways of secondary metabolites, and biological process mechanisms of medicative plants which can give ideas for the mining of functional genes of medicative plants and breeding new varieties.

Transcriptome analysis is used to study the evolution and diversification method of plant species. In 2014, 1,000 plant genomes project was completed within which the transcriptomes of 1,124 plant species from the families *viridiplantae*, *glaucophyta* and *Rhodophyta* were sequenced. The protein coding sequences were later compared to infer phylogenetic relationships between plants and to characterize the time of their diversification within

the process of evolution. Transcriptome studies are accustomed to characterize and quantify gene phenomenon in mature pollen. Genes concerned in cell wall metabolism and cytoskeleton were found to be overexpressed. Transcriptome approaches also allowed tracing the changes in gene phenomenon through completely different biological process stages of pollen, starting from microspore to mature spore grains; such stages may be compared across species of various plants including *Arabidopsis*, rice and tobacco.

- Many odorant-binding and chemosensory proteins are found in plants transcriptomes.
- Such genes originate from insect contamination throughout feeding and ovipositing.
- We have additionally found an oversized variety of Niemann-Pick proteins from ticks.
- Plant samples contamination by insects could shed light on insect-plant relationships.

With the wide adoption of transcriptome sequencing an ever increasing amount of information is becoming available, together with spurious data originating from contamination. We have a tendency to show that sometimes errors and inaccuracy can turn beneficial, revealing insect and arthropod pests once analysing plant transcriptomes.

We have got found large number of soluble olfactory proteins, Odorant-Binding Proteins (OBPs) and Chemosensory Proteins (CSPs), in plant databases, likely due to contamination by guest insects. In fact, each category of proteins is solely expressed in insects, with few CSPs also present in other arthropods. Additionally, we have a tendency to found several sequences of the Niemann-Pick (NPc2) family, proteins dedicated to cholesterol transport in vertebrates and hypothesized to be concerned in chemical communication in insects, however absent in plants. In many cases we have a tendency to trace down members of these categories of proteins to the insect or arthropod species responsible for contamination.

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