

A Brief Note on Plant Transcriptomics

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DESCRIPTION

Transcriptomics has been accustomed to studying 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 of the foremost widespread topics in biology in recent times. Transcriptome sequencing (RNA-Seq) may be a high-throughput, high-sensitivity, and high-resolution technique that may be accustomed to studying the model and non-model organisms [1]. 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 analyze functional genes and regulatory mechanisms of medicative plants and improve breeding choices 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 [2]. We are going to concentrate 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 analyses are used to study the evolution and diversification method of plant species. In 2014, the 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 characterizing and quantifying gene phenomena in mature pollen. Genes concerned with cell wall metabolism and cytoskeleton were found to be overexpressed [3]. Transcriptome approaches also allowed tracing 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 plant 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 contaminated 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 [4]. We have a tendency to show that sometimes errors and inaccuracy can turn beneficial, revealing insect and arthropod pests once analyzing plant transcriptomes.

We have got found a 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 find 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 the 3 categories of proteins to the insect or arthropod species responsible for the contamination.

REFERENCES

1. Ghorbel M, Brini F. Hormone mediated cell signaling in plants under changing environmental stress. *Plant Gene*. 2021;28:100335.
2. Dos Santos NR, Rodrigues JL. Manganese exposure and association with hormone imbalance in children living near a ferro-manganese alloy plant. *Environ res*. 2019;172:166-74.
3. Jin Y, Li J. GhAPC8 regulates leaf blade angle by modulating multiple hormones in cotton. *Int J Biol Macromol*. 2022;195:217-228.
4. Lau OS, Deng XW. Plant hormone signaling lightens up: integrators of light and hormones. *Curr Opin Plant Biol*. 2010;13:571-577.

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