

Next Generation Sequencing: A Step toward Unraveling of Biosynthetic Pathways in Plants

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Editorial

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Editorial

Plant science is largely driven by DNA sequence data, which has been fundamentally changed in last decade due to the development and emergence of next-generation sequencing (NGS) technologies. NGS has played a vital role in the advancement of plant genomics, which has opened the opportunities for genetic improvement of crop plants and identification of biosynthetic pathways of important pharmaceutical biomolecules (tanshinones, forskolin, artemisinin etc.). Improved NGS technologies (Roche 454 pyro-sequencing, Illumina, Ion Torrent and PacBio) produce a huge amount of data, which are needed to be assembled and curated by the computational biologists using various tools (Cufflinks, Trinity, CLC genomics workbench etc). Further, genome information of 4739 plants is available at NCBI database till date. Among plants, *Arabidopsis thaliana* (a model plant) was the first plant whose genome (125 Mb, consisting of 25,489 genes) was sequenced in 2000 [1]. Thereafter, the number of genome sequence data is increasing exponentially. Plant Genomics has opened the avenues of understanding and elucidating the biosynthetic pathways in plants. The Arabidopsis Information Resource (TAIR) contains the information of various biosynthetic pathways for the model plant *Arabidopsis thaliana*, which could be possible only after decoding its genome. Plant genome decoding has also laid down the path for the biofortification of crop plants such as; *Triticum aestivum* (wheat), *Oryza sativa* (Rice), *Musa acuminata* (Banana), *Phaseolus vulgaris* (common beans) etc.

Genomics & Transcriptomics: An Emerging Tool for Elucidation of Biosynthetic Pathway of Pharmacologically Important Molecules in Medicinal Plant

The genomic and transcriptomic data of medicinal plants deposited at NCBI database is far less than data available

for model plants and important crop plants (wheat, rice, beans, banana etc.). Plant Genomics provide crucial information of genome diversity and chemo-diversity (especially various secondary metabolites with potential bioactivities) that exists in medicinal plants. These medicinal plants are the rich source of large number of structurally diverse pharmacologically active metabolites (taxol, forskolin, Artemisinin, vincristine and vinblastine etc.) collectively called as secondary metabolites. The *de novo* transcriptome study of medicinal plants has opened the new gateways for understanding and decoding of the important metabolic pathways in these plants. Repository of Sequence Reads Archive (SRA) data of medicinally important plants (*Salvia miltiorrhiza*, *Artemisia annua*, *Cassia angustifolia*, *Coleus forskohlii*, *Centella asiatica*, *Catharanthus roseus* and *Ocimum* species, etc.) at NCBI database is growing exponentially [2-8]. These SRA data are becoming a vital key for identification of biosynthetic pathways of important secondary metabolites in these medicinal plants. Comparative genomic and transcriptomic study in neem (*Azadiracta indica*) reveals many key steps involved in its secondary metabolic pathways [9]. *Coleus forskohlii*, an imperative medicinal plant known for its bioactive molecule forskolin. The unraveling of forskolin biosynthesis in *Coleus forskohlii* was possible due to the transcriptomic study of oil bodies present on roots of the herb [10]. In another natural laxative medicinal plant (*Cassia angustifolia*) Illumina MiSeq platform was used for prediction of the biosynthetic pathway of sennosides (a pharmaceutically important molecule) [2]. Recently, in Tibetan medicinal plant (*Swertia mussotii*), NGS proved to be an important tool for the identification of genes involved in secoiridoid biosynthesis [11]. Medicinal plant genome database (<http://medicinalplantgenomics.msu.edu/>) has further proved to ease out the understanding and mining of metabolic pathways of important medicinal plants (*Camptotheca acuminata* and *Catharanthus roseus*). Genome decoding of *Catharanthus roseus* has laid down the foundation for understanding the complete

biosynthetic pathway of vincristine and vinblastine (a key anticancer molecule) in the plant [11]. The quick emergence and adoption of plant genomic technologies have enabled researchers to answer the fundamental questions about genome biology, nutritional enrichment, improving the agronomic traits of crop plant, and the unraveling and understanding of the biosynthetic pathways of the pharmaceutically important secondary metabolites in plants.

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