



Category: Plant Genomics

De novo assembly of transcriptome and draft chloroplast genome from RNAseq data of *Bacopa monnieri* L. (Bramhi)

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Abstract

Medicinal plant naming services have recorded at least 28,187 plant species as being of medicinal use. Only 16% (4,478) of these plants have been cited in medicinal regulatory publications and even a lesser proportion of it has ready-to-use transcript sequence information available in public data bases. *Bacopa monnieri* L. or Bramhi is a widely used medicinal herb mentioned in ancient ayurvedic scripts as a part of medhya rasayanas (brain rejuvenating nutraceuticals). In spite of being an extensively studied plant, it has very little genetic resources in public databases, thereby limiting extensive molecular studies based on genetics. In this study we sequenced the whole transcriptome of *B. monnieri* L. using Illumina Hiseq 2500 producing ~78 million high quality reads, followed by the *de novo* assembly generating a transcriptome size of ~88Mb and 111,290 clustered unigene transcripts. Plant non-redundant database, pfam and uniprot database were used as reference databases and a total of 59,260 (53.25%) transcripts were annotated based on similarity searches. Pathway mapping of the unigenes using Kyoto encyclopedia of genes and genomes revealed 14,816 transcripts involved in 143 pathways. The triterpenoid and sesquiterpenoid biosynthesis pathway was selected to validate the assembled transcripts as the bioactive compounds in *B. monnieri* L. are reported to be triterpenoids. Simple sequence repeat (SSR) analysis excluding mono-nucleotide repeats showed the presence of 10,556 SSR's in a total of 8892 transcripts. An attempt was made to assemble the draft chloroplast genome from the assembled transcriptome data and ~65% of chloroplast genome has been assembled and in progress. The draft chloroplast genome will also help in shedding light towards the evolution of *B. monnieri* L. The current study will provide information about key enzymes involved in various biosynthetic pathways and also a resource for comparative genomic and transcriptomic studies in future.

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