Transcriptome landscaping for gene mining and SSR marker development in Coriander (Coriandrum sativum L.)

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Abstract:

Coriander (Coriandrum sativum L.) is an aromatic herb, widely used as a spice and is of great pharmaceutical interest. Despite high medicinal and economic value, there is a dearth of genomic information about profiling as well as the expressed sequence-based genic markers. In this study, transcriptome was sequenced from seeds, leaves, and flower for gene mining and identification of SSR markers. A total of 9746 SSR containing loci were identified, the most abundant type of SSR identified were the di-nucleotide repeat motifs (45.5%), followed by tri- (34.6%), tetra- (4.5%), penta- (1.5%) and hexanucleotide repeats (1%). A total of 3795 primers were designed, out of which 120 randomly selected were validated in 14 accessions of coriander cultivated in India. The current study provides useful information about preliminary transcriptome sketch and genic markers, which can be useful in breeding and genetic diversity estimation of coriander.

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