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## Investigation on glandular trichome transcriptome of Artemisia annua L

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A rtemisia annual L. is a common type of wormwood that grows throughout the world. Artemisinin, a terpene compound in Artemisia annua L., has recently been recognized as the most promising antimalaria drug. Artemisinin and other types of terpenoids are synthesized and accumulated in glandualr trichomes that appear on the surface of leaf, stem and flower bud. To understand the molecular basis of terpene biosynthesis in Artemisia annual L., a normalized glandular trichome cDNA collection was sequenced by Roche GS FLX pyrosequencing system. Two sequencing runs generated totally 85M nucleotides which were further assembled into 160000 unigenes (40000 contigs and 120000 sigletons). Putative functions were assigned to the unigenes based on Blast search against GeneBank database. Many terpene biosynthesis pathway genes were identified from the pyrosequencing ESTs, Among them, three putative sesquiterpene synthases SQS02039, SQS16267 and SQS14765 were identified and functional characterization are being carried out. Together with other identified Artemisia annual L. terpene pathway genes, a global view of terpene biosynthesis in glandular trichomes of Artemisia annual L. were re-established. Meanwhile, two putative transcriptional factors, namely, bHLH35994 and WD24501 were identified. These two genes showed high sequence similarity at amino acid level with their Arabidopsis orthologs, which play key roles in determining trichome morphogenesis. Results from this research will shed lights on the molecular mechanism of glandular trichome morphogenesis and metabolic function in Artemisia annual L.

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