Transcriptome analysis of apical and sub-apical cells of *Artemisia annua* trichomes with next-generation-sequencing

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Artemisinin is the basis for the method of choice in the treatment of resistant malaria. In addition to this, artemisinin is also active against cancer, hepatitis and schistosomiasis [1]. The increasing demand for artemisinin has led to shortages. Because chemical synthesis of artemisinin is impossible for a reasonable price, *Artemisia annua* is the only commercial source. Unfortunately, this plant produces small amounts of artemisinin. Therefore, attempts were made for engineering heterologous plants and microbes to produce artemisinin, but only the production of artemisinin precursors was achieved [2]. This is due to an incomplete knowledge of the biosynthetic pathway of artemisinin. Artemisinin is produced in specialized 10-celled glandular trichomes on the leaves, stems and inflorescences. Transcripts for enzymes involved in the artemisinin synthesis, were detected exclusively in the apical trichome cells [3]. This suggests that only apical cells are producing artemisinin.

By comparing transcripts of apical and sub-apical cells, there is a possibility to discover new genes that are involved in the biosynthesis of artemisinin. Therefore, the whole transcriptome of apical and sub-apical cells will be analyzed with next-generation sequencing.

Apical and sub-apical cells of the trichomes were isolated with laser microdissection and pressure catapulting (LMPC). Thereafter, a procedure was optimized for linear amplification of mRNA to prepare the samples for next-generation-sequencing. Sequencing will be performed with the Illumina Genome Analyzer II platform.

References

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