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TRANSCRIPTOMIC ANALYSIS OF WHOLE PISTILS AND OVULE CELLS TO IDENTIFY GENES RELATED TO APOSPORY IN *HYPERICUM PERFORATUM* L.

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St. John's wort (*Hypericum perforatum* L.) is a medicinal plant that produces important metabolites with antidepressant and anticancer activities. Beside the pharmaceutical interest, recently gained information has shown that *H. perforatum* is also an attractive model system for the study of aposporous apomixis, that is a reproductive strategy, which, unlike sexual reproduction, permits the inheritance of the maternal genome over generations without genetic recombination events. This asexual mode of seed formation is believed to be a trait with enormous economic and social potential in agriculture. Its innovative use in this area relies upon the idea that indefinitely fixing highly complex genotypes, including hybrid cultivars, through apomixis would have tremendous advantages in plant breeding, biomass and seed production. During the last decades, the understanding of the molecular basis of apomixis in this species has been complicated by the lack of biological data, *e.g*. genomic or even transcriptomic sequences. The aim of our research project was the sequencing, annotation and comparative investigation of the *H. perforatum* flower transcriptome, as critical steps toward a better understanding of the genetic control of aposporic and sexual reproduction in the facultative apomict *H. perforatum*. To this end, next generation sequencing technologies have been used to sequence the flower transcriptomes of obligate sexual and unrelated apomictic *H. perforatum* genotypes. This approach has enabled the assembly and annotation of large cDNA repositories and their exploitation to design a custom array to be used in flower expression studies. Global gene expression analysis of *H. perforatum* was initially performed on ovaries collected from sexual and aposporic plant accessions for the purpose of identifying genes and processes potentially associated with apomixis in this model species. Overall, across two selected developmental stages, 224 and 973 unigenes were found to be significantly up- and down-regulated. Ontological annotation of differentially expressed genes indicated that terms related to cell cycle, single-organism cellular process DNA (cytosine-5-)-methyltransferase activity, among others, were significantly enriched. In a following step, a laser-capture microdissection approach was adopted in combination the RNA-seq technology with the aim of identifying genes differentially expressed in the ovule cell types primarily involved in the differentiation of the megaspore mother cells and aposporous initials. On the whole, our data suggest that phenotypic expression of apospory is concomitant with the modulation of key genes involved in the sexual

reproductive pathway and the responsive to hormonal stimuli. Annotation of all identified flower transcripts as well as their qualitative and quantitative expression data will be presented and critically discussed as they prove a far better understanding of molecular bases of pistil development, embyo sac and egg cell formation in sexual and apomictic *H. perforatum*.