

Hypericin is an important natural product which renders antidepressant, neuroprotective, anticancer, wound healing and several other pharmacological properties of *Hypericum* species (Acar et al 2014, Straub et al 2014, Walbroel et al 2014, Galeotti et al 2014). Hypericum extracts are equally effective as most advanced antidepressant drugs (Prozac®, Zoloft® and Paxil®), while it displays almost no to much less adverse effects than conventional antidepressants (Rahimi et al 2009, Linde et al 2015). Currently, hypericin is considered as an important multifunctional lead drug molecule in new therapies (Karioti and Bilia 2010; Zhu et al 2014). Additionally, being a light sensitive molecule, photoexcitation properties of hypericin are under exploitation for use as fluorescent diagnostic tool and to treat tumours *via* photodynamic therapy (Kleeman et al 2014, Straub et al 2014, Liu et al 2015, Laffers et al 2014). In spite of several applications in the pharmaceutical industry and medical field, the biosynthesis of hypericin is not understood yet, mainly due to the lack of information about the genes involved in this pathway.

Screening of differentially expressed transcripts and identifying putative genes involved in hypericin biosynthesis is the primary task of this project. Genes that are differentially expressed between the *Hypericum* plant materials with and without the dark glands/hypericin production will be identified and isolated. The functions of these genes will be validated through functional genomics approaches such as gene silencing and overexpression. The phenotypes of these manipulations will be evaluated at the level of dark gland development and hypericin production in these plants.

With this straightforward approach we are certain to elucidate hypericin biosynthesis pathway, which not only benefits the basic research but also the applied sciences. Since *H. perforatum* is one of the most consumed medicinal plants in the world and would contribute to the knowledge-based bio economy, it is worth investing in the characterization of its biosynthesis pathways.