Alkaloid biosynthesis in the opium poppy

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Plant natural products form an enormous reservoir of chemical biodiversity. The structures of more than 200,000 secondary metabolites have been elucidated to date. In comparison to primary metabolites, secondary metabolites are not essential to the growth and development of a plant, but rather function in the communication of the plant with its environment. The dynamic interactions between competing organisms are reflected in the diversity of secondary metabolites.

It is presumed that the genes of secondary metabolite formation have been recruited from primary metabolism; there is evidence accumulating to support this view. Alkaloids, in particular, appear to function in the chemical defense of the plant as anti-feedants and toxins. Specifically in our research, we investigate how selected plant systems synthesize alkaloids at the enzyme and gene levels. The study of the formation of plant alkaloids has greatly advanced in recent years, such that a number of genes are now available from (*S*)-reticuline-derived tetrahydrobenzylisoquinoline alkaloid biosynthetic pathways from *Berberis spp*. (berberine), *Argemone mexicana* (sanguinarine) and *Papaver somniferum* (morphine). These species share a central biosynthetic pathway that leads from L-tyrosine to (*S*)-reticuline and the cDNAs encoding the enzymes of the central pathway have been identified. The biosynthetic pathways branch after (*S*)-reticuline to form the classes of alkaloids that are characteristic of a given species.

Regulation of these pathways at the gene and enzyme level is complex; multiple cell types can be required for synthesis and for storage. When we perturb cellular physiology through metabolic engineering, metabolite homeostasis and intra- and intercellular partitioning can be affected in still unpredictable ways.

An update will be given on what we understand today about enzymes, genes and spatial organization of alkaloid biosynthesis in the opium poppy *P. somniferum*.