



## Unraveling the biosynthetic pathway of triterpenoid saponins in *Barbarea vulgaris*

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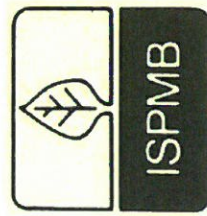
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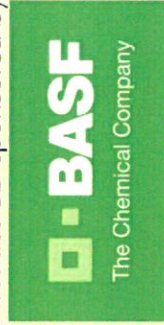
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## UNRAVELING THE BIOSYNTHETIC PATHWAY OF TRITERPENOID SAPONINS IN *BARBAREA VULGARIS*

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**Presenter:** Mr. Jörg Augustin

Plant defense mechanisms often include the production of specific secondary metabolites either in prior (phytoanticipins) or in direct response (phytoalexins) to pathogenic or herbivorous attack. One class of phytoanticipins are the amphiphilic saponins, which confer resistance against a vast array of pathogens and insect herbivores by inducing cell membrane penetrating effects.

Although the ability to produce saponins is widespread among plants, the biosynthetic pathway has not been elucidated. To uncover the impact of saponins against pathogens and herbivorous insects, we have developed a model system based on the wild crucifer *Barbarea vulgaris*, which is phylogenetically positioned between *A. thaliana* and the crop *Brassica napus* (oil seed rape). An unbiased LC-MS metabolomic approach based on a segregating population of a cross between a resistant and susceptible line identified four saponins as the main anti insecticidal compounds. Pyro-sequencing (454) of the *B. vulgaris* transcriptome generated 262,843 reads which could be assembled into 29,369 contigs and 33,708 singlets. Data mining identified several gene candidates for biosynthesis of saponins as well as many SSR to be used for QTL mapping. The QTL mapping indicates that biosynthesis of saponins in *B. vulgaris* is affected by mutations in a limited number of genes. Oxidosqualene synthases, cytochromes P450 and family 1 glycosyltransferases (UGTs) are key candidate enzymes for biosynthesis of saponins. Biochemical characterization of a UGT identified the enzyme that glucosylates the saponin aglycone.

Knowledge of the saponin pathway can be exploited for bioengineering or molecular breeding of crop plants with increased antifungal and anti insecticidal properties.