

Eruca sativa* accessions as resistance donors against pollen beetle (*Brassicogethes aeneus*) - metabolite profiling of secondary plant defence in green flower buds and genetic mapping in *E. sativa

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Brassica napus is facing immense infestation by pesticide-resistant pollen beetles (*Brassicogethes aeneus*) and, given the large economic losses, resistance breeding to improve natural plant defense against insects is of great importance. Previous studies demonstrated that *Eruca sativa* is the least damaged by pollen beetles of many crucifers. Five *E. sativa* accessions were identified as resistance donors, and an introgression study was initiated. The aims of the presented study are A) support the identification of the phytochemical base of resistance in *E. sativa* and B) develop a genetic map of *E. sativa*, which will help to identify introgressed chromosomes from *E. sativa* in intergeneric hybrids with *B. napus*.

A non-targeted metabolomics approach using LC-ESI-TOF (liquid-chromatography-electrospray ionization-quadrupole-time-of-flight mass spectrometry) was conducted in *E. sativa* by extracting semi-polar compounds from green flower buds and analyzed in positive or negative ion mode. Selection of features for metabolite identification was conducted by correlating all features against feeding damage on buds. Certain features showed up quantitatively more often in some *E. sativa* accessions than in the standard *B. napus* cultivar ‘Express’.

A genetic map of *E. sativa* will be developed using SSR (simple sequence repeat) markers. The PCR protocol to detect markers is established and polymorphic markers between two *E. sativa* accessions will be identified to be applied on a segregating mapping population. The F2 mapping population is derived from two accessions that show slight differences for their feeding damage. Using GISH (Genomic In Situ Hybridization) chromosomes from *E. sativa* will be visualized in backcross progenies of the intergeneric hybrids.

Metabolome profiling of *E. sativa* could reveal potential antifeedants such as glucosinolates or their hydrolysis products. The genetic mapping of *E. sativa* could support locating regions with resistance genes against pollen beetles on chromosomes in Brassicaceae. The combination of metabolites and genetic mapping will support the breeding of resistance against pollen beetles in *B. napus*.