

ASL 3: Use of genotyping by sequencing (GBS) in chamomile (*Matricaria recutita* L.) to enhance breeding



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Abstract

German chamomile (*Matricaria recutita* L.) is an important medicinal plant with a wide range of medical uses. Genotyping by Sequencing (GBS) was performed for this non-model organism on a panel of 33 different origins (varieties, populations, accessions; in total 91 plants with 2-4 plants per origin), and for 2 accessions of *M. discoidea* as outgroup. High-quality SNP identification (single nucleotide polymorphisms) was done using the pyRAD pipeline, and genetic diversity was analysed with STRUCTURE and CLC Genomics Workbench 8.5.

The analysis revealed one group with low genetic differentiation (14 origins with 39 plants), whereas clear differences could be identified between the remaining 19 origins (52 plants). Single plants of the same origin were mostly genetically similar, although elevated genetic diversity could be identified between single plants of 13 origins.

Phenotypic traits (flowering time, chemical compounds, powdery mildew infection) and ploidy were also measured. Ongoing work includes the identification of associations between genetic data (SNPs) and these traits. These data will be used to improve the exploitation of genetic resources in chamomile (e.g. utilization of heterosis, generation of cytoplasmic male sterility, facilitation of breeding of varieties with improved traits).

To summarize, we have applied next generation genomics methods to medicinal plants as a basis to improve the breeding process. The efforts to perform such an analysis are manageable, especially regarding the decreasing costs and increasing availability of bioinformatic pipelines for the GBS-analysis.