

High-density mapping of QTL for domestication related traits in field cress (*Lepidium campestre*) - a novel oil crop for Northern Sweden and beyond

BACKGROUND

Field cress (*Lepidium campestre*), a close relative of *Arabidopsis thaliana* has been targeted for domestication because it holds high agronomic potential as a biennial/perennial oilseed crop due to its many good characteristics of a high-yielding winter-hardy crop. Unlike other oilseed crops on the market, field cress can be highly productive in the northern parts of temperate regions, yielding correspondingly 3.3 tons of seed per hectare 40 km south of the Arctic circle in 2018. The domestication of field cress has progressed rapidly during the last decade and one of the potential end-uses for the oil is as raw material for the production of hydrated vegetable oil (HVO) diesel while the seed cake could be used as a high-value animal feed.

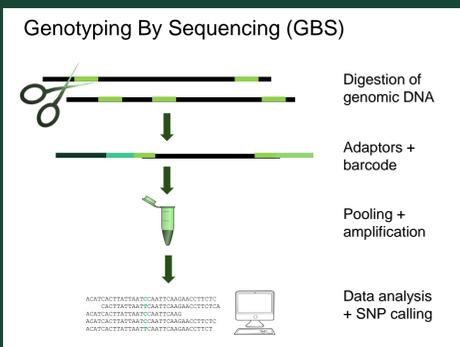


20 years of domestication at SLU

QTL MAPPING OF FIELD CRESS (*LEPIDIUM CAMPESTRE*)

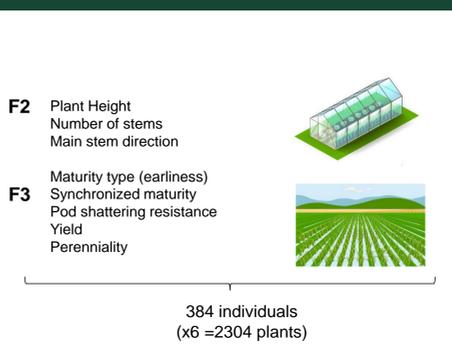
To speed up the domestication process a significant effort has been made to develop the genomic tools and resources for field cress. For this purpose a mapping population was generated through crossing pairs of field cress (*L. campestre*) and *L. heterophyllum* of divergent phenotypes measured for a range of relevant traits including plant height, number of stems, main stem direction, earliness, synchronized maturity, pod shattering resistance, yield and perenniality. By back crossing F_1 an F_2 interspecific hybrid population was obtained which was genotyped and used as a mapping population for genetic linkage mapping and QTL mapping.

GENOTYPING



Genotyping by Sequencing (GBS) was used to genotype a F_2 mapping population of 384 individuals resulting in 3.7 million unique aligned tags to the previously generated whole genome sequence and the identification of 26 800 SNPs.

PHENOTYPING

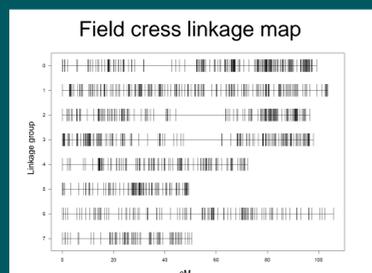


Due to problematic field conditions in the year of 2016, phenotyping for pod shattering resistance (PSH), maturity type (MT), perenniality (PE) and yield was made on the F_3 generation, where each plant in the F_2 population were represented by six plants in the F_3 generation planted at three field site in Sweden. However main stem direction (MSD) number of stems (NS) plant height (PH) were measured in greenhouse on the F_2 population. The data derived from phenotyping the F_2 generation was analyzed separately from that generated from phenotyping the F_3 generation

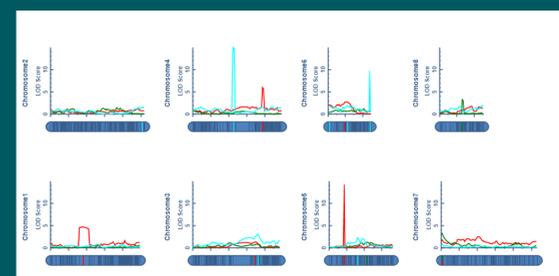
RESULTS



A genetic linkage map composed by of eight linkage groups containing 2331 SNP markers derived from 10302 contigs, 1044 mapped by SNPs and 9258 mapped by haplotype, was constructed based on the GBS data.



The preliminary analysis of the phenotypic F_2 data detected five different QTLs, two for Plant height (PH, turquoise), two for number of stems (NS, red) and one for direction of main stem (MSD, green). Through comparative analysis of the *Lepidium* and *Arabidopsis* genomes, candidate genes underlying some of these QTL have been identified. The QTL on chromosome 6 (or linkage group 6) for PH is associated with the genes *XDH1* and *XDH2* which has been shown to regulate this trait in *Arabidopsis*. The analysis of the phenotypic F_3 data is currently ongoing.



Cecilia Gustafsson
Department of Plant breeding,
Swedish University of
Agricultural Sciences, Alnarp
cecilia.gustafsson@slu.se



Ganapathi Varma Saripella
Department of Plant breeding,
Swedish University of
Agricultural Sciences, Alnarp
ganapathi.varma.saripella@slu.se



Mulatu Geleta
Department of Plant breeding,
Swedish University of
Agricultural Sciences, Alnarp
mulatu.geleta.dida@slu.se