Accelerating the domestication of a new oil crop through genomics application

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The importance of replacing fossil oils with a renewable source has been emphasized for many years. For this purpose vegetable oil is central, and meeting the growing demands and coping with the changing climate necessitate the development of more productive and resilient oilseed crops. Field cress *(Lepidium campestre),* a close relative of *Arabidopsis* 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. 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).

Recently, great efforts have been made to speed-up fast-track the domestication process through the use of genomics tools and resources by developing genomics based breeding techniques. A first draft of the whole genome sequence of field cress has been generated and was used as a reference genome for GBS analysis. The genome size of field cress was determined to be about 533 Mbp, and of this 219 Mbp was assembled. A genetic linkage map consisting of eight linkage groups containing 2331 SNP markers derived from 1044 contigs, and spanning 881 cM, was constructed based on the GBS data. In addition, 24 homologues of *Arabidopsis* genes regulating various desirable traits have been mapped. The effect of variation within these genes on the traits they regulate is being studied to develop genetic molecular markers for their use in marker assisted selection. These studies have shown a high level of collinearity between field cress linkage groups and *Arabidopsis* chromosomes providing an additional interesting insight into the evolution of *Brassicaceae* genomes.