

#169

Exploring the genetic variation of the mustard *Sinapis alba* using a new reference genome

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Sinapis alba (yellow mustard) is an important condiment crop for the Canadian Prairies. Although seemingly better adapted, with enhanced drought and heat tolerance, and resistance to pod shatter and common Brassica pests and pathogens, as a crop *S. alba* suffers from inconsistent and low yields compared to its related Brassica mustard types. Improvements to *S. alba* yields have been slow, predominantly due to its obligate outbreeding nature, which favours recurrent selection as a breeding strategy. Current molecular techniques provide robust and relatively inexpensive opportunities to further crop improvement, yet there has been limited application of such techniques in *S. alba*. To facilitate the exploitation of modern breeding techniques to *S. alba*, a reference genome sequence was generated based on an established Illumina sequence assembly approach with chromosome-scale scaffolds facilitated through the application of Hi-C chromosome conformation data and genetic mapping. A comparison of the genome structure of *S. alba* with its closest Brassica relative, *B. nigra* (black mustard) will be discussed. Further, the genome reference was used to map genotype-by-sequencing data from the collection of *S. alba* genotypes along with those of its wild relative *S. arvensis* housed at the Plant Gene Resources Canada. These data provide a picture of the available genetic variation within *S. alba* and a resource for future breeding efforts.

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