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Natural and induced genome structural variation in oilseed rape

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The Brassica species are undergoing a process termed diploidization, which stabilizes genomes following polyploid formation. We are learning that the most recent naturally occurring polyploidy events, as exemplified by the formation of *B. napus*, have resulted in an unexpectedly high rate of genome structural variation and that this variation is tolerated in the germplasm of oilseed rape and other crop types. Extensive variation in gene content, dosage and arrangement complicates the analysis of the genetic basis of trait variation. To address this in a unified way, we have adopted an approach that uses high-resolution linkage mapping, comparative genomics and novel computational approaches to develop pan-genomes for each of the Brassica A, B and C genomes, linked to reference genomes: those of the closely related *Thellungiella parvula* and extensively studied *Arabidopsis thaliana*. These pan-genomes form the basis for a unified Brassica gene naming convention and system for describing genome structural relationships across all cultivated Brassica species. The use of the resource (and interim stages of development) will be described for the analysis of genome structural variation in rapeseed arising from breeding and radiation mutagenesis.

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