

# #030

## Genomic and epigenomic patterns in novel heterotic pools of winter rapeseed (*Brassica napus*)

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Exploitation of hybrid vigour in crops is simplified by distinct heterotic pools and breeding methods that facilitate effective prediction and use of heterosis. In crops which have traditionally been bred as open-pollinated inbred line varieties, like oilseed rape/canola (*Brassica napus*), heterotic pools generally do not exist and systematic exploitation of heterosis is challenging. Using winter oilseed rape as a case study, we are investigating how genome-wide patterns of genomic and epigenomic variation may help distinguish and develop new heterotic pools. We sequenced two pools of 50 elite, winter type oilseed rape lines, and catalogued the genomic and epigenomic variants of each genotype. As expected from the breeding history, single nucleotide polymorphisms and methylation patterns were found to largely overlap between pools. However, variants unique to pools were detected at the genomic level, indicating strong potential for genomics-assisted separation of heterotic pools. By tracing these divergent variants throughout a breeding program in intercrossed pool offspring, we are generating a catalogue of genomic and epigenomic patterns which will serve as a basis for hybrid performance prediction once recombinants are successfully fixed in individual pools through genomics-assisted crossing designs. Our approach introduces a novel exploitation of heterotic patterns to enhance breeding process which bypasses the need for direct association of each variant to the trait performance.

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