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Omics-based optimisation of hybrid performance and heterosis in winter oilseed rape

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Background:

During the past two decades, breeding of European winter oilseed rape has switched almost entirely from pedigree breeding to hybrid breeding. To efficiently exploit heterosis, it is essential to separate strongly intermixed breeding populations into effective heterotic pools with high general combining ability. Omics data combined with novel prediction strategies can help to develop heterotic pools and better understand and exploit heterosis.

Objective:

A fast-track chain crossing scheme, optimised by genome-wide SNP marker data and simulation studies, was implemented to maximise recombination and pool separation within an elite winter oilseed rape breeding population. Using multi-omics data associated to the pool founders, we dissected functional differences between two diversified pools and implemented machine-learning methods to optimize predictive breeding for hybrid performance.

Methods:

Two sets of 50 elite winter oilseed rape breeding lines were selected as founders for fast-track creation of novel genetic pools. For 100 founder lines we collected whole-genome sequences, whole-genome bisulphite sequences, seedling mRNA and miRNA profiles along with long-read resequencing and additional genome-wide methylation data for 30 representative lines from each pool. This data was used to index genome-wide haplotypes with functional information, employing deep-learning autoencoders to reduce genomic features and functional information to predictors that could be used for pool definition and hybrid prediction.

Results:

We identified striking, conserved differences in chromosomal patterns of methylation between different genetic pools, indicating that methylation patterns may play a role expression of heterosis. Furthermore, we found that genome-wide presence-absence variants alone can clearly discriminate genetic and heterotic pools, underlining the role of dominance effects caused by presence-absence on hybrid vigour on rapeseed. Consolidation of omics data into functional features using deep-learning autoencoders provided a computationally efficient way to integrate large-scale regulatory data associated with heterotic pool pedigrees into hybrid predictions. By comparing genome assemblies of related parental combinations from elite hybrids with high and low hybrid performance, respectively, we shed light on complementary genome features and heterotic haplotype patterns that may have particular importance for hybrid yield in winter oilseed rape.

Conclusions:

As the cost for generation of omics datasets and genome-wide marker profiles continues to drop, a combination between high-resolution characterisation of genome-wide sequence patterns and regulatory features in breeding founder lines with high-throughput genotyping and haplotype analysis in heterotic pool offspring can provide an interesting basis for omics-based predictions of oilseed rape hybrid performance. Comparative whole-genome assemblies and characterisation of regulatory features underlying heterotic haplotypes can provide a basis to better understand and exploit heterosis in genome-based breeding strategies.