#037

Quantitative disease resistance and structural genome variation

Christian Obermeier
Iulian Gabur, Harmeet S. Chawla, Paul Vollrath, Rod Snowdon

Justus Liebig University, Department of Plant Breeding, Giessen, Germany

Structural genome variation including copy number variation (CNV) and presence-absence variation (PAV) have been discovered in selected gene families in most crop species. However, the global prevalence of these polymorphisms in most complex genomes is still unclear and the magnitude of their effects on quantitatively inherited agronomic traits is still largely unknown.

We analyzed the association of long-range and short-range structural variation including gene PAV with resistance of oilseed rape against the important fungal pathogens Leptophaeria maculans, Sclerotinia sclerotiorum and Verticillium longisporum, as examples for complex quantitative disease resistances in the strongly rearranged genome of the recent allopolyploid B. napus crop species.

Using Single Nucleotide absence Polymorphism (SNaP) markers to efficiently trace PAV in biparental and multi-parental breeding populations, we significantly increased the resolution of loci influencing resistance against all three pathogens in biparental quantitative trait loci (QTL) analyses and in multi-parental GWAS. Deletions confirmed by long-range Bionano optical mapping, Oxford Nanopore sequencing and short-range PCR analyses of mapping parents were found to be commonly associated with disease susceptibility as well as with disease resistance against L. maculans. S. sclerotiorum and V. longisporum. Short-range gene PAV, assayed by Illumina resequencing of mapping parents, was observed, e.g. in about 50% of all genes harboured within confidence intervals of QTL for V. longisporum resistance, and high-priority candidate genes identified within QTL regions were all affected by PAV.

The results demonstrate the prominent role of long-range and short-range gene PAV in determining disease resistance and putatively other agronomic traits, suggesting that this important class of polymorphism should be exploited more systematically in future oilseed rape breeding.