#024

Genomics-led radiation mutagenesis in rapeseed

Lenka Havlickova
Zhesi He, Ian Bancroft

University of York, United Kingdom, York, UK

Rapeseed is the most agronomically important crop type of the species B. napus, a recently formed allotetraploid (2n=38, AACC) with short evolutionary history and limited genetic diversity. Both diploid progenitors, Brassica rapa (AA) and Brassica oleracea (CC) underwent whole-genome triplication (WGT) event prior to rediploidization caused by extensive genomic rearrangements, gene losses and homoeologous exchanges (HE). Polyploid redundancy supports the viability of genome structural variation frequently occurring in rapeseed as result of natural non-homologous translocations, duplications and deletion events as well as sustains vitality in artificially mutagenized plants with high mutation rates. The advent of Next Generation Sequencing (NGS) technology allowed us to revise our understanding of the impacts of ionizing radiation on plant genomes. We developed a radiation mutagenesis panel of M2 rapeseed lines derived from a current cultivar and re-sequenced the genomes (to ~12x redundancy) for ~600 lines. The range of mutations induced, including single nucleotide variants, frame shift-inducing InDels and segmental duplications, as well as a broad range of structural deletions, will be described. The resource represents a powerful genomics-led reverse genetic platform for predictive mutation breeding.