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Genomic analyses of rapeseed dissect selective signatures and genetic networks underlying plant architecture and yield traits

ADDRESS

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Rapeseed (*Brassica napus* L.) is the second largest oil-producing crop in the world. Nevertheless, genome-wide patterns of the genetic basis for rapeseed genome and the genetic changes that occurred during the short period domestication remained largely unknown. Here, we resequenced 418 diverse rapeseed accessions to generate a map of genome variations and to elucidate the genetic basis of plant architecture (PA) and yield (PY). Selective signatures between winter and semi-winter type rapeseeds were identified, suggesting their roles in broad adaptation to different latitudes and climatic environments. We phenotyped 56 agronomic traits in six different areas from 2013 to 2017, identifying many large-effect loci related candidate causative genes for PA and PY traits as well as pleiotropic loci for them. We found a nonsynonymous substitution (phenylalanine to cysteine) of the gene on chromosome A09 encoding an E3 ubiquitin-protein ligase, which was confirmed to affect seed weight. Association network analysis demonstrated that 17 traits could be linked through the linkage disequilibrium of 23 associated loci with phenotypic correlation and Hi-C data analysis also validated the high interaction frequency of these loci. This study provides insights into the genomic basis for improving rapeseed varieties and for further evolutionary and adaptation analysis of allotetraploid crops.

PLENARY TALKS

ORALS

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