

# #032

## Whole-genome resequencing reveals *Brassica napus* origin and genetic loci involved in its domestication and improvement

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*Brassica napus*, an important allopolyploid crop derived from interspecific crosses between *Brassica rapa* and *Brassica oleracea*, does not occur in the wild, and the processes underlying its origin, domestication and improvement are unknown. To gain insight into its origin, we resequenced 588 *B. napus* accessions at ~5× depth. Our results suggest that the *B. napus* A subgenome evolved from the ancestor of European turnip, and that the *B. napus* C subgenome might have evolved from the common ancestor of kohlrabi, cauliflower, broccoli, and Chinese kale, with recent migration into *B. napus* ~1000 years ago. Winter oilseed might be the original form of *B. napus*. A subgenome-specific selection of defense-response genes contributed to environmental adaptation after formation of the species, and that of other genes contributed to seed quality, whereas asymmetrical subgenomic selection led to ecotype change. By integrating genome-wide association studies, selection signal identification, and transcriptome analyses, we identified genes associated with improved stress tolerance, oil content, seed quality, and ecotype as candidates for further functional characterization. These results provide insight into the evolution of *B. napus* and present a valuable resource for future genetic improvements to *B. napus* and other *Brassica* crops.

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