

# #056

## Resequencing and multi-environmental phenotyping of 1650 accessions of Rapeseed (*Brassica napus* L.)

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With the rapid development of next generation DNA sequencing technologies, genomic assisted selection is a feasible tool in commercial breeding. However, characterization has so far been limited to sparse core sets of *Brassica napus*, only limited phenotypic and genotypic data are accessible by breeders. With an aim to provide systemic detailed information of potentially useful germplasm, a large scale phenotyping and genotyping project was conducted, which was supported by Chinese National key research and development program. A total of 1650 accessions of elite rapeseed were selected for phenotyping and genotyping, which consist of cultivars, breeding parents, resynthetic *Brassica napus*, elite and stable hybrids from wide hybridization. To obtain the genotyping of the 1650 lines, the whole genomes were re-sequenced with a mean sequencing depth of 15 × per individual. All the SNP locations were obtained by mapping the resequenced reads onto the Darmor-bzh reference sequence. Multi-environmental phenotyping were arranged in seven ecological regions, namely Jiangsu, Anhui, Hunan, Guizhou, Sichuan, Yunan and Shannxi corresponding to the major rapeseed production areas in China. More than 35 traits, including yield, quality, disease resistance, phenological and physiological, has been identified in the two successive growing seasons. Based on the phenotyping and genotyping data, the genetic background and utilizability of each accession will be interpreted, and a database will be set up to facilitate molecular breeding of rapeseed.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS