

#059

Genome reshuffling revealed by mapping and genome sequencing of progenies from interspecific crosses involving *B. carinata*, *B. rapa* and *B. napus*

Yikai Zhang

Xiangxiang He, Huaiqi Zhang, Huiying Xue, Dandan Hu, Han Qin, Meng Wang, Qingyong Yang, Jinling Meng, Jun Zou

College of Plant Science & Technology of Huazhong Agricultural University, Wuhan, China

To broaden the gene pool and exploring intersubgenomic heterosis for rapeseed, a novel dynamic gene pool of *B. napus* (ArArCcCc) has been constructed with introgression of the Ar and Cc subgenome from hundreds of accessions of *B. rapa* (ArAr) and *B. carinata* (BcBcCcCc) in our previous studies. With aim to dissect the genome changes in these resynthesized lines and their impacts on important traits, three homozygous new-type *B. napus* lines bred from this gene pool were selected as mapping parents according to their special seed quality traits and heterosis potential when crossed with two sequenced *B. napus* cultivars (Europe cultivar Tapidor and Chinese cultivar Ningyou7). Six DH mapping populations derived from the F1 crosses among the new-type *B. napus* parents, Tapidor and Ningyou7, were developed, which shared one parent with each of the other populations. Three of them were genotyped by whole-genome wide sequencing. Complex genetic variation pattern were observed in the mapping populations, and classified for genetic mapping with consideration of individual genome variation. High density genetic maps were constructed, integrated and compared. QTL accounting for flowering time, seed yield components and seed quality traits were analyzed. The new-type *B. napus* parents were also deep sequenced. Rich allelic and genome structural variation were investigated in the new-type *B. napus* parents by sequence analysis and was further analyzed through multiple parents-based genetic mapping using their derived DH populations. Several small segment of B genome introgression were also detected in the sequenced new-type *B. napus* lines. These results would provide insights for understanding the rapid genome reorganization of *B. napus* from interspecific crosses, and rewriting the genome of rapeseed with favorable exotic introgression.

ADDRESS

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS