Integrating Genetics and Genomics in *Brassica* Breeding

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Abstract

The genus *Brassica* constitutes one of the world's most diverse and economically important plant groups. Three diploids i.e. *B. rapa* (AA, n=10), *B. nigra* (BB, n=8) and *B. oleracea* (CC, n=9), and three amphidiploids i.e. *B. juncea* (AABB, n=18), *B. napus* (AACC, n=19) and *B. carinata* (BBCC, n=17) are cultivated for producing vegetables, vegetable oils, condiments and fodders. Although extensive studies were done in the past two decades using molecular markers to find genetic loci/QTL governing economically important traits in vegetable and oilseed Brassicas, only handful of those studies could be used in breeding program as those studies used mostly anonymous markers, markers linked to QTL are not close enough with gene of interest and presence of multiple QTL in a short chromosomal region. Our work on different *Brassica* species tried to address some of the reasons behind bottlenecks in conventional *Brassica* breeding, structural and functional evolutionary interrelationships between different *Brassica* genomes besides identifying crucifer building blocks harboring the most important QTL/ candidate genes for yield traits, leaf traits, quality traits, disease and insect resistances in *Brassica* genomes. We used conventional genetic analysis, different molecular markers and recently developed NGS technology to find some of the candidate genes, and developed genome wide gene specific SNP markers for genomics-assisted precision breeding of Brassicas.

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