



Using *Brassica oleracea* in breeding of *B. napus* canola

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Ph.D. student Azam Nikzad (first author of the paper) crossing canola while Habibur Rahman (su

Ph.D. student Azam Nikzad (first author of the paper) crossing canola while Habibur Rahman (supervisor and corresponding author of the paper) looks on.

The narrow genetic base of *Brassica napus* L. (AACC) canola is an impediment for continued improvement of this crop. This crop species evolved from the progenitor species *B. rapa* (AA) and *B. oleracea* (CC). The wide genetic variation present in the *B. oleracea* gene pool makes this species a valuable resource for use in the breeding of *B. napus* canola as well as to broaden the genetic base of this oilseed crop, especially its C genome.

Authors of a recent article in *Crop Science* studied six *B. napus* canola populations. They were derived from *B. napus* × *B. oleracea* interspecific hybridization involving six accessions of *B. oleracea* belonging to four variants of this species and a single *B. napus* canola line. The lines were used to to investigate the potential of the *B. oleracea*

gene pool for the improvement of agronomic and seed quality traits of *B. napus* canola. Among these, populations derived from the broccoli-derived cross gave the greatest seed yield while those derived from cauliflower had the highest seed oil. Several lines exceeded seed yield of the *B. napus* parent and also had acceptable agronomic and seed quality traits.

Thus, the study demonstrates that the use of *B. oleracea* can improve the performance of spring *B. napus* canola as well as broaden the genetic base of this crop.

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Nikzad, A., Kebede, B., Pinzon, J., Bhavikkumar, J., Yong, R., & Rahman, H. (2019). Potential of the C genome of different variants of *Brassica oleracea* for the improvement of agronomic and seed quality traits of *B. napus canola*. *Crop Science*, 59(2608–2620). <https://doi.org/10.2135/cropsci2019.05.0304>

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