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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 (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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