Science Societies

Genomic predictions identify superior soybean crosses

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Soybean genomicists and co-authors of the Crop Science article Martine Jean (right) and François Belzile are working with Canadian soybean breeders to assist in the identification of the most promising combinations of parents to maximize yield potential within the *different maturity groups grown in Canada. Photo by Caroline Labbé.*

Yield improvement is critical for the commercial success of new cultivars. Choosing the pairs of lines to cross to achieve this is a daunting exercise, and the number of possible crosses vastly exceeds the number that can be handled. Although progeny performance can be predicted solely based on genetic makeup, the implementation of genomic selection awaits the demonstration that superior crosses can be efficiently identified using computer-simulated predictions.

In a *Crop Science* study, researchers report having predicted the performance of 60,000 soybean crosses, comparing the predicted performance of 101 of these to their success in producing improved lines for commercialization. The team found that all but two of the 22 crosses identified as superior by conventional selection had been predicted to display above-average yield. They also noted that 96.2% of all crosses predicted to produce below-average progeny had been eliminated during selection.

This study therefore indicates that genomic predictions of cross performance could help make cultivar development more efficient by either performing fewer crosses and achieving the same yield improvement with fewer resources or, alternatively, investing the same resources on a more promising set of crosses and thereby achieving greater improvement.

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Jean, M., Cober, E., O'Donoughue, L., Rajcan, I., & Belzile, F. (2021). Improvement of key agronomical traits in soybean through genomic prediction of superior crosses. *Crop Science*. **https://doi.org/10.1002/csc2.20583** (in press).