Statistical model predicts performance of hybrid rice

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Genomic prediction, a new field of quantitative genetics, is a statistical approach to predicting the value of an economically important trait in a plant, such as yield or disease resistance. The method works if the trait is heritable, as many traits tend to be, and can be performed early in the life cycle of the plant, helping reduce costs.

Now a research team led by plant geneticists at the University of California, Riverside and Huazhong Agricultural University, China, has used the method to predict the performance of hybrid rice (for example, the yield, growth-rate and disease resistance). The new technology could potentially revolutionize hybrid breeding in agriculture.

The study, published online this week in the *Proceedings of the National Academy of Sciences*, is a pilot research project on rice. The technology can be easily extended, however, to other crops such as maize.

"Rice and maize are two main crops that depend on hybrid breeding," said Shizhong Xu, a professor of genetics in the UC Riverside Department of Botany and Plant Sciences, who co-led the research project. "If we can identify many high-performance hybrids in these crops and use these hybrids, we can substantially increase grain production to achieve global food security."

Genomic prediction uses genome-wide markers to predict future individuals or species. These markers are genes or DNA sequences with known locations on a chromosome. Genomic prediction differs from traditional predictions in that it skips the marker-detection step. The method simply uses all markers of the entire genome to predict a trait.

"Classical marker-assisted selection only uses markers that have large effects on the trait," Xu explained. "It ignores all markers with small effects. But many economically important traits are controlled by a large number of genes with small effects. Because the genomic prediction model captures all these small-effect genes, predictability is vastly improved."

Without genomic prediction, breeders must grow all possible crosses in the field to select the best cross (hybrid). For example, for 1000 inbred parents, the total number of crosses would be 499500.

"It is impossible to grow these many crosses in the field," Xu said. "However, with the genomic prediction technology, we can grow only, say, 500 crosses, then predict all the 499500 potential crosses, and select the best crosses based on the predicted values of these hybrids."

Xu noted that genomic prediction is particularly useful for predicting hybrids because hybrid DNA sequences are determined by their inbred parents.

"More cost-saving can be achieved because we do not need to measure the DNA sequences of the hybrids," he said. "Knowing the genotypes of the parents makes it possible to immediately know the genotype of the hybrid. Indeed, there is no need to measure the genotype of the hybrid. It is fully predicted by the model."

When the researchers incorporated "dominance" and "epistasis" into their prediction model, they found that predictability was improved. In genetics, dominance describes the joint action of two different alleles (copies) of a gene. For example, if one copy of a gene has a value of 1 and the other copy has a value of 2, the joint effect of the two alleles may be 4, indicating that the two alleles are not additive. In this case, dominance has occurred. Epistasis refers to any type of gene-gene interaction.

"By incorporating dominance and epistasis, we took into account all available information for prediction," Xu said. "It led to a more accurate prediction of a trait value."

Genomic prediction can be used to predict heritable human diseases. For example, many cancers are heritable and genome prediction can be performed to predict disease risk for a person.

Xu was joined in the research by Qifa Zhang and his student Dan Zhu at

Huazhong Agricultural University, China.

Next the research team, led by Xu and Zhang, will design a field experiment to perform hybrid prediction in rice.

Provided by University of California - Riverside

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