Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
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More yield through heterosis: IPK research team decodes gene interaction

Press Release

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Gatersleben, 10.12.2025 **A research team at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) has developed a new method that improves our understanding of why crosses between homozygous parent plants - known as hybrids - are often significantly more productive than their parents. This phenomenon, known as heterosis, is crucial for increasing the yield of important crops such as wheat and maize. The results of the study have now been published in the journal "Nature Communications".**

When two homozygous plant lines with different characteristics are crossed, the resulting offspring are often more robust and productive than their parents. This phenomenon is called heterosis. It can be caused by positive variants of genes that dominate negative ones, or by complex interactions among numerous genes that 'communicate' with each other and influence one another. The research team has developed a new statistical method that can analyse these gene interactions more quickly and accurately.

Rather than testing billions of possible gene combinations individually, the new method, hQTL-ODS (Heterotic Quantitative Trait Locus - One-Dimensional Scan), evaluates the overall contribution of each gene through its interactions. In a large-scale study of wheat involving over 5,000 hybrids, the researchers identified relevant loci that contribute most to heterosis. Various mathematical techniques were implemented in hQTL-ODS to make it feasible for whole-genome sequencing data.

The advantages of the new method are clear. "Using conventional methods, it would have taken us years to complete the same analysis," explains Dr. Guoliang Li, first author of the study. "With our new approach, however, we were able to complete the evaluation in just a few days. It's as if we were suddenly looking at the genome through a telescope instead of a magnifying glass."

"We have seen that heterosis is caused by genes that talk to each other," Guoliang Li continued. "It's like an orchestra, where the conductor leads by communicating with the musicians. With heterosis, however, there isn't just one conductor that increases the final yield." Thus, the researchers show that it is the combined effect of many gene interactions that determines heterosis, rather than the effect of a few very dominant genes.

The method reveals previously hidden genetic patterns. "Our method can also detect weak signals that were previously overlooked," Guoliang Li explains. "It's like suddenly seeing the entire network of cables that controls the plant beneath the surface." "This study demonstrates the importance of developing advanced mathematical/ statistical tools for understanding complex biological mechanisms", says Dr. Yong Jiang, researcher in the research group "Quantitative Genetics" and also one of the leading authors of the study.

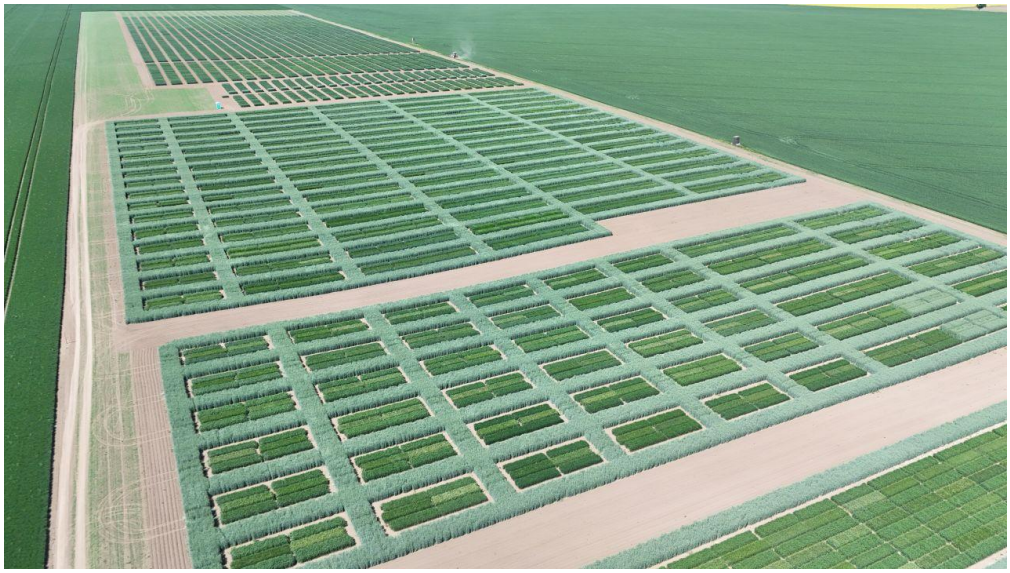
The new model offers a novel approach to deciphering the genetic basis of heterosis in the era of whole-genome sequencing and can be applied to other plants, such as maize and rice. Potentially, hQTL-ODS may assist breeders to identify plant varieties with robust hybrid

vigour. This would accelerate yield increases, which is an essential contribution to securing food supplies in times of climate change and a growing world population.

Original publication:

Li *et al.* (2025): Powerful one-dimensional scan to detect heterotic quantitative trait loci. Nature Communications. DOI: 10.1038/s41467-025-65563-9

Photo:



Field trials of hybrid wheat at IPK Leibniz Institute Photo: IPK Leibniz Institute