

Finding hidden genetic treasure: Study uncovers untapped diversity in historic wheat collection

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Watkins Landraces in the field. Credit: John Innes Centre

A decade-long collaborative study has discovered huge genetic potential that is untapped in modern wheat varieties. The international study which [appears](#) in *Nature* reveals that at least 60% of the genetic diversity found in a historic collection of wheat is unused, providing an unprecedented opportunity to improve modern wheat and sustainably feed a growing global population.

To make this discovery, a cross-institutional collaboration led by Dr. Simon Griffiths, at the John Innes Centre and Professor Shifeng Cheng at the Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences (CAAS), studied the A.E. Watkins Landrace Collection, a historic collection of local varieties of wheat which are no longer grown anywhere in the world and compared this with modern wheats.

The achievement is the result of a consortium joint effort. Cheng says, "We built a collaborative and complementary consortium with full openness, making resources in germplasm, genomic and phenotypic datasets, publicly available through the Watkins Worldwide Wheat Genomics to Breeding Portal (<https://www.wg2b.com/>). Our effort has facilitated and accelerated many existing projects both in fundamental research and in breeding practices."

One of the key factors that contributed to the success is the in-depth phenotyping, covering experimental stations from the UK (three locations) and field evaluation (five locations) from northern to southern China. In total, 137 traits were surveyed in this study. This work was particularly underpinned by Rothamsted Research, who worked as a phenotyping hub to add understanding of the qualities and characteristics of the wheat, to connect the crop to the genetic sequence.

The team built a wheat genomic variation map, a haplotype-phenotype association map. The landrace-cultivar comparison revealed that modern wheat varieties only make use of 40% of the [genetic diversity](#) found in the Watkins Collection.

The remaining diversity represents a goldmine of potential to improve modern wheat, says Dr. Griffiths, group leader at the John Innes Centre, and an author of the paper, "This missing 60% discovered in this study is full of beneficial genes that we need to feed people sustainably. Over the last ten thousand years, we've tended to select for traits which increase yield and improve disease resistance.

"We've found that the Watkins landraces are packed full of useful variation which is simply absent in modern wheat, and it is imperative to deploy this into modern breeding. What's exciting is that genes and traits are already being discovered using the data and tools developed over the past decade."

The A.E. Watkins landrace collection of bread wheat (Watkins collection) assembled in the 1920s and 1930s from 32 countries, represents the most comprehensive collection of historic wheat anywhere in the world.

The collection provides a snapshot of the diversity of cultivated wheat before the advent of modern, systematic plant breeding and shows how the genetic variation is dispersed in clusters, or ancestral groups, around the world.

"We can retrace the novel, functional and beneficial diversity that were lost in modern wheats after the 'Green Revolution' in the 20th century, and have the opportunity to add them back into elites in the [breeding programs](#)," says Professor Cheng.

Genomics and bioinformatics analysis completed by researchers at the Agricultural Genomics Institute at Shenzhen, allowed the consortium to see where modern wheat came from. They discovered that globally, wheat varieties originate from central and western Europe, with just two of the seven ancestral groups in the Watkins collection being used in modern plant breeding.

Using three complementary association genetics approaches (QTL mapping, GWAS and NAM GWAS), the team discovered hundreds of Watkins-unique haplotypes that can confer superior traits in modern wheats, informing breeders to know what accessions carry what useful genetic loci or alleles in their breeding programs.

Key traits already found in this untapped diversity include [nitrogen use efficiency](#), slug resistance and resilience to pests and diseases.

Dr. Griffiths adds, "There are genes which will enable plant breeders to increase the efficiency of nitrogen use in wheat. If we can get these into modern varieties that farmers can grow, they will need to apply less fertilizer, saving money and reducing emissions."

Fertilizer use in agriculture is expensive and contributes to emissions of greenhouse gases, reducing its use could help agriculture to move towards net zero. Enhancing nitrogen use efficiency in crops and reducing agriculture's nitrogen footprint is currently a big challenge globally, especially for countries like China.

To achieve this unprecedented research feat, the team developed a core set of 119 landraces which represented the breadth of the genetic variation within the Watkins collection. This diverse set was then crossed and back crossed into modern wheat to make a collection of 12,000 lines of wheat that are now stored in the Germplasm Resource Unit at the John Innes Centre.

This means that for the first time in 100 years these lost traits have been incorporated into modern wheat, and the data and tools are already being used to improve crops.

This research establishes a framework for wheat whole-genome design pre-breeding by connecting genomics to phenomics and to breeding practice. "We implemented a pre-breeding strategy to decode, discover, design and deliver progress in breeding," says Dr. Griffiths.

"Indeed, the genomics revolution is leading to the genetic revolution and a breeding revolution," says Cheng. This study was truly a collaborative, long-term, endeavor and couldn't have been completed without international cooperation.

In collaboration with UK commercial plant breeders, the team have created the freely available [breeder's toolkit](#), a set of online resources which are open source and accessible globally for anyone to use. The toolkit provides an integrated set of tools for the research and breeding communities, allowing others to access and use new, beneficial diversity to deliver sustainable, resilient wheat now and into the future.

These germplasms, the resources and toolkits developed in this study, are still under further investigation in various experimental stations in China. These efforts are expected to significantly contribute to [wheat](#) genetic improvement and breeding in China.

More information: Cheng S. et al. Harnessing landrace diversity empowers wheat breeding, *Nature* (2024). [DOI: 10.1038/s41586-024-07682-9](https://doi.org/10.1038/s41586-024-07682-9), www.nature.com/articles/s41586-024-07682-9

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