

IPK research team unlocks potential of barley's closest wild relative, *Hordeum bulbosum*

Gatersleben, 09.07.2025 **Wild plants can contribute valuable genes to their domesticated relatives. Fertility barriers and a lack of genomic resources have hindered the effective use of crop-wild introgressions. An international research team led by the IPK Leibniz Institute constructed a pangenome of barley's closest wild relative, *Hordeum bulbosum*. Today, the study was published in the journal "Nature".**

Wild relatives of cultivated plants are a vital source of genetic diversity for improving crops and provide a valuable reservoir of resistance against biotic and abiotic stressors. Although their value has been recognised for decades, technological obstacles have long hindered their exploration. Thanks to advances in high-throughput genomic research, the same tools can now be used in crops and their wild relatives.

An international research team led by the IPK Leibniz Institute studied structural genome evolution in barley (*Hordeum vulgare*) and *Hordeum bulbosum*. For this study, Dr. Frank Blattner collected *H. bulbosum* genotypes in natural populations all over the Mediterranean, which, combined with accessions from genebanks, resulted in a panel of 263 diverse genotypes. This collection comprises both diploid and tetraploid cytotypes. After analysing their population structure, the research team assembled and annotated ten reference-quality chromosome-scale genomes of bulbous barleys.

"The tetraploid forms have two origins, one in Greece and one in southwestern Asia. In Asia they originated already between one and two million years ago, while in Greece tetraploids arose only within the last 100,000 years", explains Jia-Wu Feng, first author of the study. "We found evidence that both types are now interbreeding, which provides a way for polyploids to enrich their genomic diversity through multiple origins", Dr. Frank Blattner adds.

Although *H. bulbosum* is barley's closest wild relative, with an estimated divergence time of 4.5 million years, the species has evolved quite differently genetically. The most obvious difference is the expansion of the barley genome. "Quite surprising, we showed that this expansion did not occur uniformly across the genome, but mainly at the ends of the chromosomes", says Jia-Wu Feng.

A common way of transferring genes from wild relatives into domesticated plants is through introgression lines. These are derived from crosses between crops and their wild relatives and contain a small proportion of the wild parent's genes within a cultivated genomic background. Based on the reference genomes, the research team has decoded the Ryd4 resistance locus's structure approximately 40 years after its introgression from *H. bulbosum* into barley. "This is without question the most promising crop-wild introgression in barley to date, and the only one close to being deployed in commercial varieties. It provides qualitative resistance to the devastating barley yellow dwarf virus, which affects several cereal crops", explains Dr. Martin Mascher, head of IPK's "Domestication Genomics"

Press Release

Scientific Contact

Dr. Martin Mascher

Phone: +49 39482 5243

mascher@ipk-gatersleben.de

Media Contact

Christian Schafmeister

Phone: +49 39482 5461

schafmeister@ipk-gatersleben.de

research group and a member of the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig.

“Having genome sequences for crop wild relatives will be useful for more targeted introgression breeding in the future”, says Dr. Martin Mascher. “The systematic genomic characterisation of crop plants and their wild relatives is important foundational research to make plant genetic resources better accessible for crop improvement”, emphasises Prof. Dr. Nils Stein, head of the Federal *Ex situ* Genebank for agricultural and horticultural crops at IPK Leibniz Institute, “and it is the driver to evolve the genebank from a seedstore into a biodigital resources centre”.

Original publication:

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Photo:



A spike of *Hordeum bulbosum* in Israel
Photo: Amir Sharon, Tel Aviv University