Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
Foundation under Public Law

The genetic diversity of wild barley opens up new avenues for research and breeding

Press Release

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Gatersleben, 18. November 2026 **For the first time, an international research team coordinated by the IPK Leibniz Institute has characterised genomic diversity across the agriculturally important genus Hordeum. The study reveals how the genomes of barley and its wild relatives have evolved. These findings open up new avenues for systematically investigating this diversity and, in the long term, utilising it for plant breeding. The results were published in the science magazine "Nature".**

The wild relatives of our crops harbour extensive genetic diversity. This diversity can help us understand how plants adapt to different environmental conditions and develop new approaches to plant breeding. For barley, an international research team led by the IPK Leibniz Institute is now making this diversity accessible across species boundaries. The researchers compared 27 plant accessions representing 25 species of the genus *Hordeum*, including all recognised diploid species and selected polyploid representatives. To do so, they used high-quality genome assemblies that resolve the genetic material at the level of individual chromosomes.

Previous pangenome studies focused on cultivated barley and its wild relatives within *Hordeum vulgare*, as well as the closely related species *Hordeum bulbosum*. A pangenome brings together the genetic information of multiple plants, revealing both shared and variable components. The newly published resource extends this approach across the genus *Hordeum*, providing a comprehensive view of barley's evolutionary history and that of its wild relatives.

A key finding concerns the interplay between genes and their regulation. While the DNA sequences that encode proteins are highly conserved across species, many regulatory regions evolve more rapidly. These regions determine when, where and to what extent genes are active. "Our findings show that the genomes of closely related plant species differ not only in their genes, but also in the DNA sequences that regulate gene activity," explains Dr. Martin Mascher, who coordinated the study at the IPK. "The genomes of wild barley species therefore offer new opportunities to understand the evolution of important traits and investigate previously unexplored genetic diversity."

The analysis of flowering time, a trait that plays an important role in determining yield, illustrates the potential effects of these differences. Winter barley requires a prolonged period of cold before it can flower. Some wild *Hordeum* species, however, can flower without this cold stimulus. In *Hordeum cordobense*, the international research team identified a distinctive arrangement of gene copies that gives rise to small RNA molecules. These may help to silence a gene that normally represses flowering. Together with further changes in a key flowering gene, this finding illustrates how wild species use the same genetic control points that also play a role in cultivated spring and winter barley.

Chromosome structure also changes substantially over the course of evolution. Particularly striking is that central chromosome regions undergo much more extensive structural change than outer regions. The team discovered large-scale rearrangements and inversions, stretches of DNA in reverse orientation, near the centromeres, which play a crucial role in chromosome segregation during cell division. Other regions retain traces of past

hybridisation between species. The genus's history resembles a network in which different evolutionary lineages have repeatedly exchanged genetic material.

The researchers also identified 611 genes that appear to have entered wild barley genomes through horizontal gene transfer from millet-related grasses. Horizontal gene transfer occurs outside the usual parent-to-offspring inheritance process. The team showed that many of these genes are transcribed in the recipient plants, suggesting that they may also fulfil biological functions. Whether they confer advantages on the plants remains to be determined.

Differences in genome size between species can largely be explained by varying levels of transposon accumulation. These DNA elements, also known as "jumping genes", can leave additional copies of themselves in the genome and account for an average of 86 percent of the genomes analysed. A further case study identified EOG1 as a regulator of glume development, demonstrating that comparisons between wild species can help to elucidate gene functions in crops.

The expanded barley pangenome enables the systematic investigation of genetic and regulatory variants. For breeding research, it provides a basis for identifying previously unexplored genetic variants, including those potentially affecting flowering time or disease resistance. Further functional studies and breeding trials are needed to determine whether and how individual variants can be used in cultivated barley.

Original publication: Jia-Wu Feng *et al.* (2026). Structural and regulatory evolution across the genus *Hordeum*. Nature. DOI: 10.1038/s41586-026-11332-7

Image caption: The glumes of different wild barley species vary markedly in shape and size. Comparing their genomes helps researchers understand which genes are involved in the development of these plant structures. Among its findings, the study identified EOG1 as an important regulator of glume development.

