

IPK-led research team provides insights into the pangenome of barley

Gatersleben, 13.11.2024 **Pangenomes are collections of annotated genome sequences of multiple individuals of a species. The structural variants uncovered by these datasets are a major asset to genetic analysis in crop plants. An international research team led by the IPK Leibniz Institute reports a pangenome of barley comprising long-read sequence assemblies of 76 wild and domesticated genomes and short-read sequence data of 1,315 genotypes. An expanded catalogue of sequence variation in the crop includes structurally complex loci that are rich in gene copy number variation and that control certain traits. Today, the results were published in the journal "Nature".**

Reliable crop yields fueled the rise of human civilizations. As people embraced a new way of life, cultivated plants, too, had to adapt to the needs of their domesticators. There are different adaptive requirements in a wild compared to an arable habitat. Crop plants and their wild progenitors differ, for example, in how many vegetative branches they initiate or how many seeds or fruits they produce and when.

A common concern among crop conservationists is dangerously reduced genetic diversity in cultivated plants. But crop evolution needs not be a unidirectional loss of diversity. "Our panel of 1,000 plant genetic resources and 315 elite varieties allowed us to compare pangenome complexity in the crop and its wild progenitor", explains Dr. Murukarthick Jayakodi, joint first author of the study. "And we have shown that valuable diversity can arise after domestication."

The recently published human draft pangenome demonstrated how contiguous long-read sequences help make sense of reams of sequence data. This current study on the barley pangenome sheds light on crop evolution and breeding. The shortcomings of previous short-read assemblies made it all but impossible to see patterns that now emerge from their long-read counterparts. "We were able for the first time to study the evolution of structurally complex loci and detected 173 of them with nearly identical tandem repeats and genes", explains Dr. Martin Mascher, head of IPK's research group "Domestication Genomics".

To demonstrate the utility of the pangenome, the researchers focused on a few loci - *Mla*, *HvTB1*, *amy1_1*, *HvSRH1* - and the traits they control: disease resistance, plant architecture, starch mobilization and the hairiness of a rudimentary appendage to the grain. And taking a broader view of the environment as a set of exogenous factors that drive natural selection, barley provides a fascinating, and economically important example.

The process of malting involves the sprouting of moist barley grains, driving the release of enzymes that break down starch into fermentable sugars. Only the long-read based high-quality pangenome revealed the copy-number differences and haplotype diversity of the starch-degrading alpha-amylase1_1 family of genes and makes this information accessible to breeding. "Novel allelic variation is illustrative of the power of pangenomics", emphasises Prof. Dr. Nils Stein, head of IPK's department "Genebank". "Our findings indicate that much

Press Release

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of the allelic diversity we see at structurally complex loci in the pangenome may have helped crop plants adapt to new selective regimes in agricultural ecosystems.”

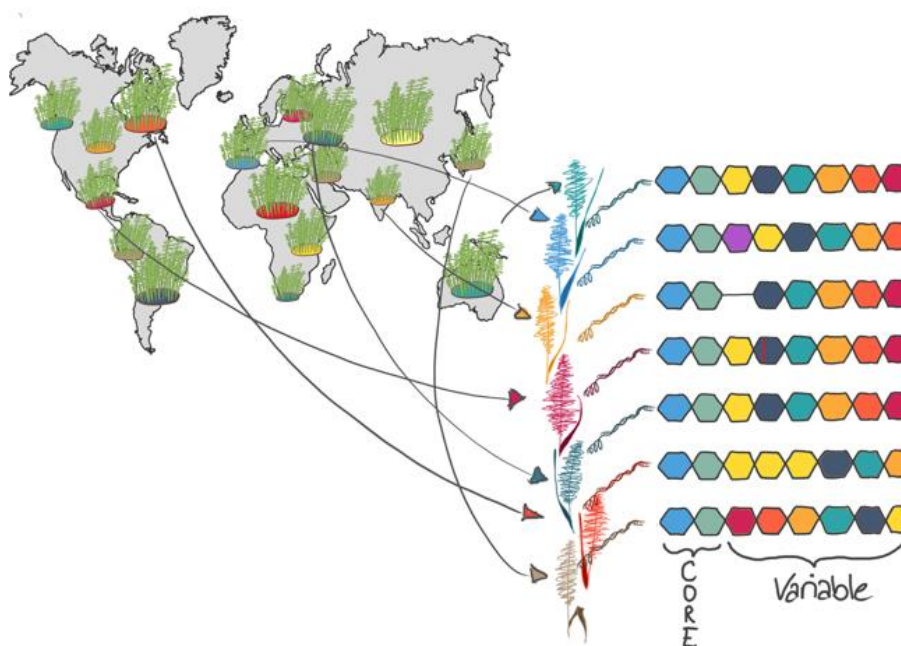
Barley is among the top five crops globally today. Its importance may increase in the future because barley tolerates harsh and marginal environments and can adapt to dry climates. Allelic diversity at structurally complex loci may help fulfill the needs of both farmers and breeders. “More diverse crop pangenomes will help us understand how the counteracting forces of past domestication bottlenecks and newly arisen structural variants influence future crop improvement in changing climates”, says Prof. Dr. Nils Stein.

With this study the IPK emphasises its role as a leading institution in the area of crop and genebank genomics with a coordinating role in genome sequencing and earlier pangenome studies of barley, wheat, rye and oats and their wild relatives. The barley pangenome project brought together 80 scientists from 12 different countries and was initiated and coordinated at IPK.

Original publication:

Jayakodi *et al.* (2024): Structural variation in the pangenome of wild and domesticated barley. Nature. DOI: [10.1038/s41586-024-08187-1](https://doi.org/10.1038/s41586-024-08187-1)

Graphic (for free use):



Representative genotypes are chosen from genetically diverse populations based on genome-wide genotypic data for ex situ germplasm collections. Chromosome-scale genome assemblies are built for a small, but representative core set. The pan-genome compartments such as core (i.e. genomic sequences present in all individual of a species) and variable (i.e. sequences found in some/few individuals) are identified from the de novo assemblies.