International research teams decode the pangenome and origin of oats

Press Release

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Gatersleben, 29.10.2025 **Oats are considered particularly healthy. They provide fibre, lower cholesterol levels and are gluten-free. However, the genetic makeup of oats has been difficult to understand until now, mainly because it is particularly large and complex. An international research team led by the IPK Leibniz Institute has succeeded in creating a pangenome of oats and has also investigated when and where the genes are active in different parts of the plant. In a further study, another research team investigated the origin of oats. Today, the results were published in the journals Nature and Nature Communications.**

The pangenome is central to our understanding of cultivated plants such as oats, as it maps their entire genetic diversity. It encompasses not only genes that occur in all plants, but also those that are only present in certain species, serving as a kind of map. In turn, the pantranscriptome shows which genes are active in different tissues, such as leaves, roots and seeds, and at different stages of development. It serves as a gene expression atlas. However, understanding how genetic differences influence individual plant traits is challenging, particularly in the case of oats. The oat genome is very complex because oats are a hexaploid plant with six sets of chromosomes originating from three different ancestors.

In their journey towards the pangenome, the team sequenced and analysed the genomes of 33 oat lines, encompassing cultivated varieties and their wild relatives. To create the pantranscriptome, they examined the gene expression patterns in six tissues and developmental stages of 23 of these oat lines. State-of-the-art sequencing technologies were used for this purpose. The aim was to identify possible structural variations. These can involve changes in the arrangement of chromosomes, such as inversions (i.e. sections that have been rotated) or translocations (i.e. sections that have been moved to a different location).

“With our pangenome, we demonstrate the true extent of the genetic diversity in oats. This helps us to better understand which genes are important for yield, adaptation, and health,” says Dr. Raz Avni, first author of the study. The research team also came across some surprising details in their work. “For instance, we found that many genes had been lost in one of the three subgenomes. However, the plant remains productive because other gene copies apparently take over the corresponding tasks.”

“Decoding the oat pangenome shows how modern genomics can advance basic research and have a direct impact on health, agriculture, and breeding,” explains Dr. Martin Mascher, head of the “Domestication Genomics” research group at the IPK. He immediately gives an example. “We have also found that structural variation in the genome affects genes responsible for controlling flowering time,” says Dr. Mascher, who is also coordinator of the international PanOat consortium.

In another study, an international research team led by Agriculture and Agri-Food Canada (AAFC) involving the IPK investigated the genetic structure of wild and cultivated oats, with a particular focus on the hexaploid Avena species. There are around 30 Avena (diploid, tetraploid and hexaploid) species worldwide. The researchers analysed approximately 9,000 accessions. Their aim was to identify population structures and genome regions associated with local adaptation. For their study, the team used genotyping-by-sequencing. This method enables genetic variation in thousands of samples to be characterised comprehensively.

"Our study has shown that the wild oat species Avena sterilis has not just one, but four different genetic populations, some of which are linked to specific regions of the Mediterranean and the Middle East," explains Dr. Raz Avni, one of the study's authors. "We were also able to clearly distinguish an independent population of the cultivated oat species Avena byzantina, as well as various populations within the widespread species Avena sativa. This confirms earlier indications that these two cultivated oat types are genetically very different," says Dr. Martin Mascher, explaining another of the study's findings, which was published in the journal Nature Communications today.

It is particularly interesting that some regions of the oat genome associated with adaptation to the environment show structural rearrangements. In these cases, certain sections of the chromosome are either reversed (inversion) or moved to a different location (translocation). "This suggests that different chromosome structures may have played an important role in the emergence of various oat lines, their domestication, and the formation of 'reproductive barriers' - obstacles that hinder gene exchange between populations," explains the IPK scientist.

Original publications:

Avni *et al.* (2025): A pangenome and pantranscriptome of hexaploid oat. Nature.
DOI: 10.1038/s41586-025-09676-7

Bekele *et al.* (2025): Global genomic population structure of wild and cultivated oat reveals. Nature Communications. DOI: 10.1038/s41467-025-57895-3

Information about the project:

https://graingenes.org/GG3/PanOat

Photo:

Ripe oat ripens Photo: Edyta Paczos-Grzęda, University of Life Sciences, Lublin