



## A pangenome and pantranscriptome of hexaploid oat

Raz Avni, Nadia Kamal, Lidija Bitz, Eric N. Jellen, Wubishet A. Bekele, Tefera T. Angessa, Petri Auvinen, Oliver Bitz, Brian Boyle, Francisco J. Canales, Craig H. Carlson, Brett Chapman, Harmeet Singh Chawla, Yutang Chen, Dario Copetti, Samara Correia de Lemos, Viet Dang, Steven R. Eichten, Kathy Esvelt Klos, Amit M. Fenn, Anne Fiebig, Yong-Bi Fu, Heidrun Gundlach, Rajeev Gupta, Georg Haberer, Tianhua He, Matthias H. Herrmann, Axel Himmelbach, Catherine J. Howarth, Haifei Hu, Julio Isidro y Sánchez, Asuka Itaya, Jean-Luc Jannink, Yong Jia, Rajvinder Kaur, Manuela Knauff, Tim Langdon, Thomas Lux, Sofia Marmon, Vanda Marosi, Klaus F.X. Mayer, Steve Michel, Raja Sekhar Nandety, Kirby T. Nilsen, Edyta Paczos-Grzęda, Asher Pasha, Elena Prats, Nicholas J. Provart, Adriana Ravagnani, Robert W. Reid, Jessica A. Schlueter, Alan H. Schulman, Taner Z. Sen, Jaswinder Singh, Mehtab-Singh, Nick Sirijovski, Nils Stein, Bruno Studer, Sirja Viitala, Shauna Vronces, Sean Walkowiak, Penghao Wang, Amanda J. Waters, Charlene P. Wight, Weikai Yan, Eric Yao, Xiao-Qi Zhang, Gaofeng Zhou, Zhou Zhou, Nicholas A. Tinker, Jason D. Fiedler, Chengdao Li, Peter J. Maughan, Manuel Spannagl, and Martin Mascher

Nature (2025)

<https://doi.org/10.1038/s41586-025-09676-7>

**Contacts:** Martin Mascher (IPK), [mascher@ipk-gatersleben.de](mailto:mascher@ipk-gatersleben.de); Manuel Spannagl (HZM), [manuel.spannagl@helmholtz-muenchen.de](mailto:manuel.spannagl@helmholtz-muenchen.de); Jeff Maughan (BYU), [jeff\\_maughan@byu.edu](mailto:jeff_maughan@byu.edu); Chengdao Li (Murdoch U.), [c.li@murdoch.edu.au](mailto:c.li@murdoch.edu.au); Jason Fiedler (USDA-ARS), [jason.fiedler@usda.gov](mailto:jason.fiedler@usda.gov); and Nick Tinker (AAFC, retired), [nick.tinker@agr.gc.ca](mailto:nick.tinker@agr.gc.ca)

### Summary:

Hexaploid oats (AACCDD) have large genomes rich in repeated sequences that have been shaped by subgenome (A, C, or D) exchanges over millennia. The work done in this study resulted in the chromosomes of 33 wild and domesticated oats being sequenced, assembled, and annotated with the locations of possible genes. Three of the lines represent diploid species (2 AA and 1 CC) and one represents a tetraploid species (CCDD). The other 29 lines represent hexaploid species, including *Avena sativa* (24 lines), *A. sterilis* (2 lines), *A. byzantina* (1 line), *A. occidentalis* (1 line), and the synthetic line ‘Amagalon’.

Through comparative analysis of the genome assemblies and annotations, the team catalogued which genes were shared among all oat lines and which were unique to specific oat lines (the pangenome). The lines used in this study cover most of the diversity space identified by [Bekele, et al. \(2025\)](#), which gives the results even greater meaning.

An atlas of the genes expressed in six different tissues at different stages of development in 23 of the 33 accessions was also produced. The diversity of gene expression across subgenomes,



accessions, and tissues (the pantranscriptome) was then analyzed. The results indicated that the loss of functional genes in hexaploid oats is compensated for by the up-regulation of the remaining homoeologues on other subgenomes, but this process is affected by differences between those subgenomes.

Chromosomal rearrangements have had a large impact on recent oat breeding. A large pericentric inversion associated with early flowering explains distorted segregation on chromosome 7D and a homoeologous sequence exchange between chromosomes 2A and 2C in a semidwarf mutant has risen to prominence in Australian elite varieties.

In addition to the information available in the supplementary files and figures accompanying the original published article, the genome sequence information is available on the [GrainGenes PanOat Data Download Page](#). The genome browsers can also be found on the [GrainGenes Pangenome Resources page](#). Sequences can be searched using the [GrainGenes BLAST tool](#). The sequences are also available from the INSDC databases ([ENA](#), [NCBI](#), and [DDBJ](#)).

This work will promote the adoption of genomic approaches to understand the evolution and adaptation of domesticated oats and help accelerate their improvement through breeding.