



Global genomic population structure of wild and cultivated oat reveals signatures of chromosome rearrangements

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Summary:

The genus *Avena* comprises 30 or so cultivated and wild oat species, but only a few of the latter have been made use of in breeding better oats for food or feed. In this work, more than 9,000 wild and cultivated hexaploid oat accessions of global origin were characterised using genotyping-by-sequencing.

Population structure was explored using multidimensional scaling and population-based clustering methods. Twenty-nine of the lines sequenced as part of the [PanOat project](#) were also projected onto the diversity plots. Other analyses revealed chromosomal regions associated with local adaptation, some of which resulted from large-scale chromosomal rearrangements.

Four distinct genetic populations within the wild species *A. sterilis* were identified, along with a distinct population of cultivated *A. byzantina* and multiple populations within cultivated *A. sativa*. Some chromosomal regions associated with local adaptation were also associated with confirmed structural rearrangements on chromosomes 1A, 1C, 3C, 4C, and 7D.

This work provides evidence suggesting multiple origins for polyploid oats, as well as the occurrence of multiple domestication events. It also confirms the existence of reproductive barriers amongst *Avena* populations caused by differences in chromosome structure.



Data and tools resulting from the project can be found on [the Global Oat Genomic Diversity Project page](#) on the GrainGenes website. One tool of particular interest is the '[Shiny](#)' app created so that the relationships among the different lines and populations can be viewed in 3-D.