

Improved reference genome supports the breeding of rye and wheat

Gatersleben, 19.08.2026 Rye is not only a hardy and high-yielding crop, but also possesses a valuable gene pool for wheat breeding. An international research team led by the IPK Leibniz Institute has significantly improved the foundations for research and breeding by publishing a high-quality reference genome sequence. For the first time, the sequence includes the complete centromeres of all seven chromosome pairs. Centromeres are important for the correct distribution of genetic information during cell division. The results of the study have now been published in the journal 'Nature Communications'.

Rye shares a close and long evolutionary history with barley and wheat. However, its history as a major crop is considerably shorter. Whilst barley and wheat were 'domesticated' 10,000 years ago in the so-called Fertile Crescent of the Near East, rye initially spread as a field weed. In the process, rye gradually adopted some characteristics of its two 'big brothers and sisters', until, 5,000–6,000 years ago, it too became a cultivated species in its own right, and, in the Middle Ages, emerged as the most important bread grain in Northern Europe.

However, rye's large, complex genome poses challenges for science. Not only is the genome significantly larger than the human genome, but it also consists of almost 90 per cent repetitive DNA sequences. Previous reference sequences, such as the one produced at the IPK in 2021, represented very useful and important advances for research and breeding. However, these remained incomplete and too imprecise. They contained gaps, misaligned sections, collapsed regions and, not least, incompletely mapped centromeres. The latter are fundamental during cell division to ensure that daughter cells receive the same genetic information and can function properly.

To create the improved reference sequence, the research team used state-of-the-art sequencing technologies available at the IPK, funded by the federal and state governments. First, the team sequenced long DNA molecules from the Lo7 line. This line is an established reference genotype in rye research. Long reads make it possible to bridge regions of the genome that are difficult to decode more efficiently. The DNA fragments were then arranged in the correct order across the seven chromosomes. The researchers then verified the new reference sequence using several independent methods, and confirmed the high quality of the genome sequence.

"The new reference sequence represents a quantum leap for rye research and breeding," explains Dr. Erwang Chen, first author of the study. "It is more complete than previous versions, corrects earlier assembly errors and provides access to regions of the genome for further analysis and utilisation," says the IPK researcher. In these regions, there are identical sections in direct repetition which, in earlier versions, were only present in a collapsed state and could not be correctly resolved. The correct composition of the centromeres, in particular, represents a breakthrough. "These regions have been particularly difficult to decipher until now. With the new sequence, we can now see how these central regions of the chromosomes are structured and which DNA elements characterise them," explains Dr. Erwang Chen. Furthermore, the IPK research team showed that certain mobile DNA elements, known as transposons, were active in rye centromeres until very recently. "This

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proves that centromeres can evolve differently between closely related cereal species.” This is because transposons drive variation, and that variation can lead to different functions.

Of particular interest to plant breeding are the new findings regarding the ‘short’ arm of rye chromosome 1R, known as 1RS. This has already been transferred to several wheat varieties through cross-breeding, and improves traits such as disease resistance, stress tolerance and yield. Particularly well-known are resistance genes against plant-pathogenic fungi, such as rust or powdery mildew. The study indicates that the 1RS segments utilised in wheat are all more or less identical, or at least very closely related to one another. However, when this segment is compared across the various rye genotypes that have been sequenced, it becomes apparent that this region exhibits much greater variability in rye.

“This means that there is still a great deal of untapped potential in rye diversity,” emphasises Prof. Dr. Nils Stein, head of the ‘Genebank department’. “With the new standard we have achieved in rye genome sequencing, we can now take the next step. As part of the ‘RyeHub’ research project, funded by the Federal Ministry of Research, Technology and Space (BMFTR), we have already begun sequencing many rye genomes to create what is known as a rye pan-genome. This serves as the basis for the systematic exploration of rye’s genomic diversity for research and breeding.” Researchers use the term ‘pangenome’ to refer to the totality of all genes or DNA sequences of a species.

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An international research team has produced a new, high-quality reference genome sequence for rye. It provides a sound basis for breeding progress in rye and wheat. Photo: IPK Leibniz Institute/ N. Stein