

## IPK scientists find the key to the comprehensive gene pool of rye

Gatersleben, 18.03.2021 Rye is a distinctly climate-resistant cereal plant that is of considerable importance for Germany and north-eastern Europe. Despite its large and complex genome, an international research team led by the IPK Leibniz Institute has now succeeded in completely decoding the genome of rye. All data is open to the general public. This means that the extensive genetic diversity of barley and wheat's "little brother" can be systematically discovered and used by breeders in a more targeted approach.

Rye shares a close and long evolutionary history with barley and wheat. However, its career as an important crop is much shorter. While barley and wheat were domesticated about 10,000 years ago in the so-called Fertile Crescent of the Near East, rye initially spread to Northern Europe as a weed growing in barley and wheat fields, gradually adopting the characteristics of its two "big brothers" until rye also became a purely cultivated species 5,000 - 6,000 years ago providing a major important food source in Northern Europe in the meantime. The reason for this are important biological differences between rye and its two relatives.

Rye is fertilized through cross-pollination, thus individual genetic traits cannot be fixed as easily as in a self-fertile plant species. In addition, the rye genome is highly complex, which is mainly due to the large number of highly repeated DNA segments. "The comparatively low economic importance on a global scale, combined with the great complexity of the genome, interfered with rye getting into the focus of the international research community and thus its genome sequence has been revealed only recently," explains Prof. Dr. Nils Stein, lead of the research group Genomics of Genetic Resources at IPK and holder of a joint professorship at the University of Göttingen. At the same time, the genetic diversity of rye holds great promise for breeding.

Based on their experiences in decoding the genomes of wheat (IWGSC 2018) and barley (Mascher et al. 2017), the Gatersleben scientists now decided to create a reference sequence for rye as well. Therefore, they used homozygous seeds from the plant breeding company KWS SAAT SE & Co. KGaA. "The technical prerequisites for sequencing such a complex genome are available today," emphasises Prof. Dr. Nils Stein, who was able to convince many national and international partners for the financing of the project, a kind of crowd funding initiative.

The results published today in the journal Nature Genetics are promising for science and breeding. Rye, for example, offers access to a diverse wild gene pool, not only for rye breeding but also for wheat breeding in particular. "For example, resistance genes from rye can be transferred to wheat through classical cross-breeding, which has already been used repeatedly in the past," explains Prof. Dr. Nils Stein. "So the significance of our research extends far beyond rye." Knowing the reference sequence makes it easier to transfer



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positive properties of rye, such as resistances, to wheat without negatively affecting baking properties, for example.

But KWS also hopes that the new findings will lead to progress in breeding. "The new genome sequence of our inbred line Lo7 is a great technological achievement and an important step forward towards a more comprehensive genetic characterisation of this crop," says Dr. Andres Gordillo, lead of rye breeding at KWS. "It will considerably enhance breeding progress and, therefore, the attractiveness of rye. More specific, it will substantially improve our ability to link resistance traits observed in the field with their underlying genes and their location on the rye genome."

Parallel to the work of the international research team led by Prof. Dr. Nils Stein, Chinese researchers created a reference sequence of a Chinese landrace. "We worked very well with our Chinese colleagues, which ultimately brought great added value for rye breeding and research. We were able to use two different methods to study two very different rye varieties, of which the complete reference sequences are now available," explains the IPK scientist.

"With these two studies, rye has caught up with barley and wheat and is in the middle of the genome research era," says Prof. Dr Nils Stein. This means that the IPK Leibniz Institute now has a leading role in the elucidation of genome sequences for all three cereals, which are of particular importance in Germany and Europe.

**Original publications:** Rabanus-Wallace et al. (2021), Chromosome-scale genome assembly provides insights into rye biology, evolution, and agronomic potential. Nature Genetics. DOI: 10.1038/s41588-021-00807-0

Li et al. (2021), Analysis of rye genome sequence sheds new light on its genome expansion and agronomically important genes. Nature Genetics. DOI: 10.1038/s41588-021-00808-z

Figures (for free use): <https://ipk-cloud.ipk-gatersleben.de/s/G2zMARf32m4q5Fc>



Rye only became a pure cultivated species 5,000 - 6,000 years ago and has a complex genome that has now been fully decoded for the first time. Photos: KWS Lochow GmbH, 2020

