

Barley pan-genome: IPK scientists reach milestone on the way to “transparent” barley

Gatersleben, 25.11.2020 An international research team led by the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) has reached a milestone on the way to the “transparent” barley plant. With the complete sequencing of 20 different genotypes, the scientists completed the first step in decoding the genetic information of the entire species “barley” - the barley pan-genome. Breeders will greatly benefit from these new findings, which have today been published in the renowned magazine Nature.

In order to record all genetic information of an individual, its genome must be completely decoded. IPK scientists and international partners for barley already succeeded in doing this three years ago (Mascher *et al.* 2017). But to understand the genetic information of the entire barley species, much more is required. An international team, again led by IPK scientists, has now come a significant step closer to deciphering this so-called pan-genome of barley, as the science magazine Nature reports in today's issue.

What is astonishing, individual genomes sometimes differ considerably in their number of genes and in the arrangement and orientation of large parts of individual chromosomes, the carriers of genetic information. These “structural” changes in the barley genome can present an insurmountable barrier for recombining important plant characters in crossbreeding.

The starting point of this research was the attempt of characterising by sequencing all approximately 22,000 barley seed samples from the Federal Ex-situ Gene Bank at IPK (Milner *et al.* 2019). This identified twenty highly diverse genotypes, which have now been selected for complete sequencing. “Criteria for the selection included the greatest possible differences in their genetic diversity, geographical origin and biological traits such as winter or spring type, grain hull, row-type,” says Prof. Dr. Nils Stein, head of the Genomics of Genetic Resources research group at IPK and holder of a joint professorship at the University of Göttingen.

Besides the observation that two barley varieties can differ substantially in their total gene content, the scientists found amazing differences in the linear order of the genetic information in the chromosomes - so-called structural genome differences. Two of these structural variations, inversions (the opposite arrangement of genetic information in two genomes), attracted the particular interest of the scientists: in one case, a link could be established to mutation breeding in the 1960s; the inversion since then spread unnoticed through breeding to present-day varieties. In the second case, the observed structural variation got potentially selected during environmental adaptation while the range of barley production in early agriculture expanded to northern latitudes in Europe. “The description of such large genomic inversions in barley is new”, says Prof. Dr. Nils Stein. “They can play a decisive role in the breeding process as they might prevent recombination, thus making cross-breeding for desired trait combinations impossible.” But in general: “These naturally



Scientific Contact

Prof. Dr. Nils Stein
Tel.: +49 39482 5522
stein@ipk-gatersleben.de

Dr. Martin Mascher
Tel.: +49 39482 5243
mascher@ipk-gatersleben.de

Media Contact

Christian Schafmeister
Tel. +49 39482 5461
schafmeister@ipk-gatersleben.de

occurring or artificially induced inversions are evidence of a considerable dynamics in the genome organisation of this important crop species."

The new findings have a great impact on science and breeding. "We have created a new knowledge-base and opened up a treasure trove of new information for breeding", confirms Prof. Dr. Nils Stein. Molecular markers could now be used to specifically take into account structural variation for barley breeding.

The project, including scientists from Australia, Canada, USA, China, Japan and Scotland, was initiated and coordinated at IPK. The IPK has been funded by the Federal Ministry of Education and Research in the field of cereal genome research for more than ten years.

Despite current progress, researchers still face major challenges. "We have not yet recorded the entire diversity of barley," explains Dr. Martin Mascher. "To do so, we need to fully sequence and decode additional genotypes," says the head of the independent Domestication Genomics Research Group at IPK. In a next step, the researchers want to take a closer look at wild barley, the direct ancestor of today's cultivated crop. "We still lack wild barley as an important gene pool," explains Dr. Martin Mascher. "And I am quite sure that we are discovering diversity that could be of considerable value for future barley breeding and research."

Original publication: Jayakodi, Padmarasu *et al.* (2020), The barley pan-genome reveals the hidden legacy of mutation breeding. *Nature*. DOI: 10.1038/s41586-020-2947-8

Figures (for free use):

<https://ipk-cloud.ipk-gatersleben.de/s/WmgrAM6ZMb6mPxB>



The photo shows a spectrum of diversity in wheat and barley.
Photo: IPK Leibniz Institute/
Andreas Bähring

