

Barley genome sequence cracked

The researchers of the International Barley Genome Sequencing Consortium (IBSC) including scientists from the Danish Carlsberg Research Laboratory have successfully finalized the genome sequence of barley and report the outcome of their joint work in the April 27 issue of the prestigious scientific journal “Nature”.

Barley was one of the first grains to be cultivated. Today barley is a major cereal crop especially in temperate regions of the world. In Denmark for instance it was grown on more than 700,000 hectare of farm land in 2016. Barley is mainly used as animal fodder and serves as the raw material for producing malt from which beer and whiskey are made. In fact, alcoholic beverages made from malted barley have been known since the Stone Age and some even consider these as one of the reason why humankind adopted plant cultivation.

With their work on the barley genome the IBSC has succeeded in producing the first high-quality reference genome for a member of the Triticeae, a group of plants including –beside barley - such important cereal crops like rye and wheat. Now scientists have for the first time access to all genes in the barley genome and can further locate all of them precisely in the genome.

Sequencing the barley genome – an international research collaboration

However, sequencing the barley genome has been a challenging task for the scientists in the sequencing consortium. The genome of this crop plant is almost twice as large as the human genome and 80 percent consist of highly complex repetitive structures, often referred to as “selfish DNA”. Sequencing and stitching the genome together has hence kept teams of researchers with different expertise in Germany, United Kingdom, China, Finland, Australia, USA, Switzerland, Sweden, Czech Republic and Denmark, busy for a decade. Still, the past years saw many advances in sequencing technology and computational algorithms that helped the consortium to produce a nearly complete high-quality reference sequence of the barley genome.

“Sequencing and assembling the barley genome was a truly international collaboration”, says Nils Stein, researcher at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany.

Stein has been coordinating the IBSC since 2008 and is grateful for the support the consortium has received:

“Our thanks go to the public and private funders who believed in the success of our project and have sustained our research over the past ten years”.

The research undertaken by the Carlsberg Research Laboratory has been supported financially by The Carlsberg Foundation, one of the world’s oldest industrial foundations supporting basic scientific research. Chairman of the board of the Carlsberg Foundation, Professor Flemming Besenbacher, says:

“We are very proud and happy that the Carlsberg Research Laboratory together with the international colleagues of the IBSC-consortium have succeeded in sequencing the barley genome. I see it as the latest example of scientific breakthroughs from the Carlsberg Research Laboratory since its establishment in 1876, like the purification of yeast and the definition of the pH scale. It is at the foundation’s heart to support research like the barley reference genome project and at the same time enable scientists to address global challenges to benefit society in general. This scientific achievement will not only benefit the brewing process and the development of better beer but also science at large.”

Ilka Braumann, the scientist who has coordinated the consortium related research at Carlsberg Research Laboratory, the only Danish member in the initiative, adds:

“We are very grateful for the generous funding we have received from the Carlsberg Foundation, which allowed us to join the IBSC.”

Sequencing the genome of barley reveals detailed information on the location, structure and function of its genes. This knowledge will help plant breeders to continuously improve crop plants with novel and improved traits for the benefit of the farmer and the consumer. For instance, the current key challenge of plant breeding is certainly to develop climate-smart and disease-resistant crops. Plants tolerant to extreme weather conditions like heat or drought will help farmers to maintain a stable yield while saving resources. Also due to the changing climate, new pathogens and diseases are emerging in the Nordic countries. Breeding barley plants with resistance to those would allow reducing pesticides, which benefits farmers, consumers and most importantly the environment. In addition, the barley genome sequence is also a valuable source of information to continuously improve and breed barley with a better nutritional quality for human food as well as for animal feed. The barley genome is now accessible for the scientific community and private plant breeding companies for genetic analyses.

Genes related to malt and beer quality

The value the new reference genome has for barley breeding is also of great importance for the Carlsberg Research Laboratory, where breeding high quality novel malting barley varieties is the main goal of the local barley research and breeding program. Here researchers do not only focus on agronomic traits but also have a special interest in the genes related to barley-, malt- and beer quality. They believe that through the reference genome they will gain novel insights that can help to improve beer quality and taste.

“Access to the full barley genome sequence allows us for the first time ever to study all barley genes that are relevant throughout the whole process of making beer, including malting, mashing and fermentation.” says Ilka Braumann and adds as an example that she was intrigued by the unexpected dynamics that was found in a key family of malting-related genes named amylases. These are important for the production of fermentable sugars during malting. “It came as a great surprise to us that there is lots of structural variability in the largest amylase gene cluster, even between elite malting barleys.”

“It has been known for over twenty years that that there are many genes in the barley genome that encode for amylases, but until now, we were unable to determine the exact number because some copies are very similar to each other,” explains Chengdao Li, IBSC member and Director of Western Barley Genetics Alliance at the Murdoch University in Perth, Australia. “Only with the help of the genome sequence could those individual copies be compared.”

The barley reference genome is a huge data set

The single unit of the DNA molecules that compose an organisms genome is called a base. For the barley reference genome the consortium initially produced a final raw data set of 2.5 terabases (tera = 10^{12}) in the form of short sequence reads. These pieces were then put together to construct the fully ordered sequence assembly using bioinformatics. Martin Mascher, a scientist at IPK Gatersleben and lead author of the *Nature* paper names

the novel methods applied: “We used chromosome conformation capture and Bionano optical mapping, two new technologies that can reconstruct the linear order of sequences from the three-dimensional structure of the genome in the nucleus or images of labelled long DNA molecules”. All datasets and computational methods are available to the scientific community and have been deposited in public archives and described in a Data Descriptor in the journal *Scientific Data*.

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