

The barley genome unravelled... and it's bigger than yours

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Barley has more genes than humans. Credit: Alexander von Halem

(Phys.org)—As part of an international consortium, scientists led by UA plant sciences professor Rod Wing have helped decipher the genetic alphabet of the barley plant. This is the largest plant genome to be sequenced and paves the way for tackling the wheat genome, the last frontier in the world's most important cereal crops.

Higher yields, improved pest and disease resistance and enhanced nutritional value are among potential benefits of an international scientific research effort that has resulted in an integrated physical, genetic and functional sequence assembly of the barley genome, as described in a paper published in the journal *Nature*.

"If you think of all the barley genes as a giant puzzle, you could say we can now see what picture the puzzle shows, how many pieces there are, what they look like and where they go," explained Rod Wing, Regents' Professor of Plant Sciences in the University of Arizona College of Agriculture and Life Sciences and director of the UA Arizona Genomics Institute.

Wing and several members of his lab are part of the International Barley Sequencing Consortium, or IBSC, a consortium comprised of many researchers at many institutions across the world. Wing's group is part of the UA BIO5 Institute.

According to the IBSC, the new resource will facilitate the development of new and better barley varieties able to cope with the demands of climate change. It should also help in the fight against cereal crop diseases, which cause millions in losses every year.

"The barley genome will help us in our quest to help solve the '9 billion-people' question: How to feed two more billion mouths in less than 40 years," Wing said.

Knowing the entire sequence helps plant breeders select lines that contain desirable genes more rapidly than the conventional method of repeated crossing of strains followed by evaluation, Wing explained.

First cultivated more than 10,000 years ago, barley belongs to the Triticeae family – which includes wheat and rye – and that together

provides around 30 percent of the calories consumed worldwide. It is the world's fourth most important cereal crop both in terms of area of cultivation and in quantity of grain produced.



Sequencing the barley genome helps scientists tackle the largest genome of the cereal crops: wheat. Credit: Dag Endresen

At 5 billion nucleic acid base pairs (the genetic "letters"), the barley genome is almost twice the size of that of humans, and determining the sequence of its DNA has presented a major challenge. This is mainly because its genome contains a large proportion of closely related sequences, which are difficult to piece together.

"The larger the genome, the more repetitive its sequence is," Wing said. "If you perform a whole genome shotgun sequencing approach, 90 to 95 percent of the genome sequence you get consists of almost the same sequence over and over, with no order or orientation."

Wing's group laid an important piece of the groundwork for the sequencing project by constructing a library containing the genetic sequences of large chunks of the genome. Built in 2000, that library was the largest of its kind at the time. In the current effort, those pieces helped the consortium determine the locations of the genetic sequences obtained by the participating centers so they could construct a map of the barley genome.

"With these big genome projects you have different groups that are specialized in different tasks," Wing said. "This project has been going on for a long time and finally culminated with a high-quality genome sequence."

By developing and applying a series of innovative strategies that allowed them to circumvent these difficulties, the IBSC has succeeded in positioning the DNA sequences of the majority of barley genes into a linear order along each individual chromosome. This is an important milestone toward eventually unravelling a full barley genome sequence.

"Here, we have a physical map and a draft sequence," Wing said. "We know where most of the genes reside in the barley genome. If the sequence were a text, we'd have almost all the words in the right order, but every 100 words or so, there'd be one that's missing."

Their publication in Nature provides a detailed overview of the functional portions of the barley genome, revealing the order and structure of most of its 32,000 genes and a detailed analysis of where and when genes are switched on in different tissues and at different

stages of development. They describe the location of dynamic regions of the genome that carry genes conferring resistance to diseases.

"Plants carry genes that make them resistant to certain types of bacterial, fungal and viral diseases," Wing said. "Once we know where all the resistance genes are in the most important crop cereals, we can do comparative genomics – a great tool for plant pathologists to dissect the molecular pathways used by the plants in fighting pathogens."

"The genome sequence shows you where all the potential disease resistance genes are, and that makes it easier to track them and select the ones you want by conventional breeding approaches," Wing added.

Wing said the sequenced barley genome would serve as a guide for wheat, the last of the world's most important cereal crops yet to be sequenced, with a genome about three times larger than barley.

After having played instrumental roles in sequencing rice, corn, soybean, tomato, cacao and the 12 genomes of the fruit fly *Drosophila*, Wing's lab is now embarking on playing a role in the wheat genome sequencing project, in addition to his ongoing rice genome work. His consortium is getting close to completing the genomes of 12 wild rice varieties and is now working on determining the functions and evolutionary history of the rice genes with the iPlant consortium, which is led by the UA.

According to the IBSC, the barley sequence highlights with unprecedented detail the differences across a range of barley cultivars and provides a springboard for the development of innovative approaches for the use of abundant genetic resources kept in gene banks around the globe.

In addition, access to the assembled catalogue of gene sequences will streamline efforts to improve barley production through breeding for

varieties better able to withstand pests and disease and deal with adverse environmental conditions such as drought and heat stress.

More information: *Nature* paper: [DOI: 10.1038/nature11543](https://doi.org/10.1038/nature11543)

The genome sequence and related resources are [freely accessible online](#).

Provided by University of Arizona

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