

# Our daily bread – new insights into the bread wheat genome and its significance for the global food supply

Neuherberg, 18.07.2014. Scientists at the Helmholtz Zentrum München (HMGU) have conducted research in frame of the International Wheat Genome Sequencing Initiative. They gained new insights into the composition and structure of the wheat genome and the complex interplay of genes that form the basis for regulating a polyploid\* genome. In the process they discovered bread wheat's great potential for adapting to environmental conditions and shed new light on the evolution of bread wheat. The findings have now been collated in four research publications in the renowned research journal Science.



Source: Fotolia/ Irina Tischenko

Bread wheat (*Triticum aestivum* L.) is the most widely cultivated cereal crop in the world and provides 20 percent of the food calories consumed by humans. A polyploid species, hexaploid bread wheat contains six duplicated copies of its genome and is more than five times larger than the human genome. This makes genome research in wheat particularly difficult.

Dr. Klaus Mayer, Head of the Research Unit Plant Genome and Systems Biology at HMGU, in collaboration with his colleagues Matthias Pfeifer, Dr. Karl Kugler and Manuel Spannagl, succeeded in gaining insights into complex gene-regulatory interactions: for example, how genes can be transcribed at different stages of grain development. "Our studies help us to understand how a polyploid genome is regulated and orchestrated. It revealed that for different purposes different sub-genomes are favored and used. This will have impact on future breeding, agricultural cultivation and industrial properties of bread wheat," Mayer says.

### Understanding as a basis for breeding

The highly specific intra- and inter-chromosomal activities of bread wheat enable it to adapt to the environment in many different possible ways. "The better we understand the organization, function and evolution of the large polyploid genome, the more easily we can identify the genes that are important for breeding," explains Mayer. "This will make it possible to breed the most suitable plant for different locations."

### Long evolutionary history – many opportunities for development

The scientists can now trace a common ancestor of the wheat types "A" and "B" back to about seven million years. From this another third type ("D") evolved one to two million years later.

“We have discovered that the present-day bread wheat genome is the result from a series of polyploidisation and hybridization events during the evolution of wheat. That is why we must understand it as a multilevel phylogenetic mosaic,” explains Mayer.

“The newly gained insights into the biology of the bread wheat genome will enable us to isolate genes faster and speed up the development of genetic markers for breeding. These are the building blocks that will enable us to successfully meet the challenge of satisfying the world’s growing demand for food at a time of stagnating yields, plant diseases and climate change,” Mayer says.

Further research findings relating to the wheat genome:

Major breakthrough in deciphering bread wheat’s genetic code

## Further information

\*If more than two sets of chromosomes are present, this is referred to as a polyploid genome

Original publications:

International Wheat Genome Sequencing Consortium/ Mayer et al.(2014), A chromosome-based draft sequence of the hexaploid bread wheat genome, Science, doi: 10.1126/science.1251788

[Link to publication](#)

Marcussen, T. et al (2014), Ancient hybridizations among the ancestral genomes of bread wheat, Science, doi: 10.1126/science.1250092

[Link to publication](#)

Pfeifer, M. et al. (2014), Genome interplay in the grain transcriptome of hexaploid bread wheat, Science, doi: 10.1126/science.1250091

[Link to publication](#)

Choulet, F. et al. 2014), Structural and Functional Partitioning of Bread Wheat Chromosome 3B, Science, doi: 10.1126/science.1249721

[Link to publication](#)

The Helmholtz Zentrum München, the German Research Center for Environmental Health, pursues the goal of developing personalized medical approaches to the prevention and therapy of major common diseases such as diabetes and lung diseases. To achieve this, it investigates the interaction of genetics, environmental factors and lifestyle. The Helmholtz Zentrum München has about 2,200 staff members and is headquartered in Neuherberg in the north of Munich. It is a member of the Helmholtz Association, a community of 18 scientific-technical and medical-biological research centers with a total of about 34,000 staff members.

The main focus of the Research Unit Plant Genome and Systems Biology (PGSB) is plant genome and systems-oriented bioinformatics. It has a focus towards analyzing genomic encryption, expression patterns, functional and systems biology of plants. PGSB also maintains a large data set of plant genomes in databases, which it makes available to the public along with comparative analyses.

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