

# MEDIA KIT

“Shifting the limits in wheat research and breeding using a fully annotated reference genome”

by the International Wheat Genome Sequencing Consortium

Science, 17 August 2018



## SUMMARY

1. The article presents the reference genome sequence of bread wheat. It is a detailed description of the DNA of the 21 wheat chromosomes.
2. The work is the result of 13 years of collaborative interdisciplinary research coordinated by the International Wheat Genome Sequencing Consortium (IWGSC).
3. Having a reference sequence is essential for breeding more resilient wheat varieties to feed a growing world population and address food security in the context of climate change.

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EMBARGO DEADLINE: Thursday 16 August 2018, 2PM US EDT

## THE WHEAT CODE IS FINALLY CRACKED

### THE WHEAT GENOME SEQUENCE WILL CONTRIBUTE TO GLOBAL FOOD SECURITY

Bethesda, Maryland, USA – August 16, 2018

The International Wheat Genome Sequencing Consortium (IWGSC) published today in the international journal *Science* a detailed description of the genome of bread wheat, the world's most widely cultivated crop. This work will pave the way for the production of wheat varieties better adapted to climate challenges, with higher yields, enhanced nutritional quality and improved sustainability.

The research article – authored by more than 200 scientists from 73 research institutions in 20 countries – presents the reference genome of the bread wheat variety Chinese Spring. The DNA sequence ordered along the 21 wheat chromosomes is the highest quality genome sequence produced to date for wheat. It is the result of 13 years of collaborative international research.

A key crop for food security, wheat is the staple food of more than a third of the global human population and accounts for almost 20% of the total calories and protein consumed by humans worldwide, more than any other single food source. It also serves as an important source of vitamins and minerals.

To meet future demands of a projected world population of 9.6 billion by 2050, wheat productivity needs to increase by 1.6 per cent each year. In order to preserve biodiversity, water, and nutrient resources, the majority of this increase has to be achieved via crop and trait improvement on land currently cultivated rather than committing new land to cultivation.

With the reference genome sequence now completed, breeders have at their disposal new tools to address these challenges. They will be able to identify more rapidly genes and regulatory elements underlying complex agronomic traits such as yield, grain quality, resistance to fungal diseases, and tolerance to abiotic stress – and produce hardier wheat varieties.

"The wheat genome sequence lets us look inside the wheat engine," said Rudi Appels, University of Melbourne and Murdoch University Professor, and AgriBio Research Fellow. "What we see is beautifully put-together to allow for variation and adaptation to different environments through selection, as well as sufficient stability to maintain basic structures for survival under various climatic conditions."

It is expected that the availability of a high-quality reference genome sequence will boost wheat improvement over the next decades, with benefits similar to those observed with maize and rice after their reference sequences were produced.

"How do you thank a team of scientists who persevered and succeeded in sequencing the wheat genome and changed wheat breeding forever?" said Stephen Baenziger, University of Nebraska–Lincoln Professor and Nebraska Wheat Growers Presidential Chair. "Perhaps it is not with the words of a scientist, but with the smiles of well-nourished children and their families whose lives have been changed for the better."

Sequencing the bread wheat genome was long considered an impossible task, due to its enormous size – five times larger than the human genome – and complexity – bread wheat has three sub-genomes and more than 85% of the genome is composed of repeated elements.

"The publication of the wheat reference genome is the culmination of the work of many individuals who came together under the banner of the IWGSC to do what was considered impossible," explained Kellye Eversole, Executive Director of the IWGSC. "The method of producing the reference sequence and the principles and policies of the consortium provide a model for sequencing large, complex plant genomes and reaffirms the importance of international collaborations for advancing food security."

The impact of the wheat reference sequence has already been significant in the scientific community, as exemplified by the publication on the same date of six additional publications describing and using the reference sequence resource, one appearing in the same issue of *Science*, one in *Science Advances* and four in *Genome Biology*. Moreover, more than 100 publications referencing the reference sequence have been published since the resource was made available to the scientific community in January 2017.

In addition to the sequence of the 21 chromosomes, the *Science* article also presents the precise location of 107,891 genes and of more than 4 million molecular markers, as well as sequence information between the genes and markers containing the regulatory elements influencing the expression of genes.

The IWGSC achieved this result by combining the resources it generated over the last 13 years using classic physical mapping methods and the most recent DNA sequencing technologies; the sequence data were assembled and ordered along the 21 chromosomes using highly efficient algorithms, and genes were identified with dedicated software programs.

All IWGSC reference sequence resources are publicly available at the IWGSC data repository at URGI-INRA Versailles and at other international scientific databases such as GrainGenes and Ensembl Plant.

The *Science* article is entitled "Shifting the limits in wheat research and breeding using a fully annotated reference genome".

## WHO PARTICIPATED?

The work is the result of a collaborative interdisciplinary project involving teams from 73 research institutes and private companies in 20 countries.

The article itself has 202 authors, with the International Wheat Genome Sequencing Consortium (IWGSC) being the main author. All authors have contributed directly to the generation, assembly and/or analysis of the data.

## WHY IS IT IMPORTANT TO SEQUENCE THE WHEAT GENOME?

Wheat is essential for global food security.

It is the most widely grown crop in the world, being grown on all continents except Antarctica and is adaptable to a wide range of climate and cultivation conditions. It is the staple food for one third of the global human population and contributes more to the daily calorie and protein intake than any other human food source.

The world is currently facing enormous challenges with a human population projected to rise to over 9.6 billion by 2050. The FAO predicts that food production will need to increase by over 60% to meet demand. The increase in production also must be achieved sustainably, without expanding land use, with minimal use of fertilizers, water and pest treatments, and in the context of climate change.

To produce sufficient wheat for the human population in the future, there is an urgent need to develop new wheat varieties with higher yield, better resistance to diseases and pests, and tolerance to abiotic stresses such as drought, high salinity or high mineral content of the soils.

With the reference genome sequence, breeders have at their disposal tools to identify genes and regulatory elements underlying complex traits and accelerate improvement through genomics assisted breeding and biotechnology.

Using the information provided in the genome sequence, breeders will be able to produce more rapidly new wheat varieties with higher yields and improved sustainability to meet the demands of a growing world population in a changing environment.

## WHAT IS THE ARTICLE ABOUT?

The article presents a high-quality reference genome sequence of the bread wheat variety Chinese Spring. This is essentially a highly detailed map of the wheat genome DNA ordered along the 21 wheat chromosomes. This genome sequence is the most complete and best ordered sequence that has been produced for wheat, the most widely grown crop in the world.

The article also reports the precise location of 107,891 genes and more than 4 million molecular markers along the 21 chromosomes. The genes and markers are identified "in context", meaning that they have been positioned on their specific sub-genomes and the sequence information in between the genes and markers is also described, providing a comprehensive view of the organization of the genes and the regions important for their regulation.

Furthermore, the article also presents information on where and when the nearly 108,000 genes are active (or expressed) under different conditions that include different growth stages of the wheat plant and under certain stress conditions.

## WHAT IS A REFERENCE SEQUENCE?

A reference sequence is the full DNA sequence information of one representative of a species, in this case *Triticum aestivum* cv Chinese Spring. All subsequent wheat genome-related research will refer to this resource as if it was a dictionary.

It is considered to be a reference because it meets high quality standards, representing over 90% of the genome in sequence blocks that are organized along chromosomes and are highly representative of the wheat DNA. Previous versions of the wheat genome sequence were considered to be drafts because they did not present the information in the full linear order context of the 21 chromosomes. The cultivar, Chinese Spring was chosen for the reference because it had been used to develop many genetic resources widely used by wheat scientists.

The wheat reference sequence published here represents 94% of the wheat genome assigned to the 21 wheat chromosomes and presents the location and order of 107,891 genes, as well as more than 4.7 million molecular markers on the 21 chromosomes.

## WHAT DOES HIGH-QUALITY MEAN AND WHY IS IT IMPORTANT?

Building a genome sequence is like cartography. The IWGSC genome sequence can be likened to a roadmap with several layers of detail: major highways, smaller roads, little paths, rivers, landmarks and houses. The more details there are in a map, the higher its quality. This is essentially the same for a genome sequence.

The IWGSC genome sequence maps out all the little roads, contains more than 4 million landmarks (markers) and gives the precise addresses of more than 100,000 houses (genes). Having this detailed information about the location of markers and genes is absolutely critical to researchers and breeders using the sequence to develop improved wheat varieties.

High-quality also means that a very high proportion of the sequence information between the 100,000+ genes is known. It is crucial to have this information because 80% of the wheat genome is composed of long stretches of repeated DNA sequences that are not genes. It is not yet fully understood what the role of this non-gene information is, but it is suspected that it plays a role in controlling when and how a gene is expressed.

## WHY DID IT TAKE SO LONG?

The whole project took 13 years.

From the start, obtaining a high-quality reference sequence of the genome of bread wheat has been a scientific challenge because of the size and structure of the wheat genome. The wheat genome is huge – more than five times larger than the human genome – and comprises 21 chromosomes originating from three highly similar sub-genomes (A, B and D). Each sub-genome is larger than the human genome and contains 7 chromosomes.

Also, over 80% of the wheat genome is made of repeated elements that are grouped in long stretches that are nested within each other (like a Russian doll).

These two features present problems for assembling the genome sequence from the short pieces that are the product of sequencing machines, and for assigning the sequences to the correct chromosome and sub-genome.

Because of these issues, the IWGSC decided that the only approach that would deliver a high-quality reference was to reduce the complexity and follow a strategy similar to that used for other high-quality reference genomes – such as human, mouse, zebrafish, Arabidopsis and rice – namely, sequencing each chromosome separately. This took a long time, but the end result is of high quality and can directly be used by breeders to improve wheat.

## ARE THE DATA PUBLICLY AVAILABLE?

Yes.

All IWGSC data are available at a central IWGSC repository in France at URGI-INRA. The repository provides public access to wheat sequence data and other IWGSC resources, such as physical maps and marker data. All data related to the reference genome were released to the scientific community as soon as they became available, in January 2017.

While the IWGSC team continued to work on the analysis of the genome and prepared the present publication, other scientists have had access to the information so that they could advance their work more rapidly. Consequently, already more than 100 scientific articles have been published referencing the IWGSC reference genome.

The wheat reference sequence data are also available in other international database such as Ensembl Plants, Graingenes, NCBI, and have been deposited in the European Nucleotide Archive (ENA).

## WHAT WILL BE THE IMPACT FOR SCIENTISTS?

Bread wheat is a very good model for studying complex genomes. The reference sequence provides a unique resource for studying and understanding the biology of the wheat genome, in particular understanding how wheat evolved, why some parts of the genome were conserved over time, and how genes are regulated, to name only a few areas of research.

Scientists will also use the reference genome tool to study wheat diversity, i.e. the differences between the genomes of different wheat varieties that are associated with specific characteristics, such as resistance to pests and diseases, or adaptation to drought or climate extremes. These differences can be studied at the level of single genes, sub-genomes, or whole genomes and new tools will be developed to speed up the process of screening for markers of interest.

For example: even though wheat is not a major crop in Japan in terms of acreage cultivated, the varieties that are grown there are very well adapted to high humidity and temperatures. Studies of the differences between the sequence of those varieties and the reference genome sequence could help identify genes responsible for those desirable characteristics. Once identified, these genes could be introduced in commercial varieties that could be grown in hot and humid climates, such as in Southeast Asia, therefore contributing to food security in the region.

## WHAT WILL BE THE IMPACT FOR BREEDERS?

The reference sequence provides breeding companies and public breeders with a tool to speed up the development of new improved varieties.

They will be able to use the information provided in the reference genome sequence to more rapidly identify and locate genes, or markers close to genes, responsible for agronomic characteristics (called "traits") of interest, such as high yield, stress tolerance, quality, and disease resistance. They can then isolate those genes, study how they function and introduce them into commercial varieties.

In the past, the time between "finding a gene" and commercialization of a variety containing an interesting gene was about 12 to 15 years, now, with a high-quality reference sequence available, this could be reduced by a third, to between 3 and 5 years.

## WHAT WILL BE THE IMPACT FOR FARMERS?

Farmers will benefit from the new varieties developed by breeders that will be better adapted to specific field conditions and agronomical practices. For example, the new varieties could be more resistant to drought, need less nitrogen input, or be resistant to diseases, hence requiring less fertilizers or fungicide applications.

Farmers will be able to produce better quality seeds, with less impact on the environment, leading to more sustainable production.

## WHAT WILL BE THE IMPACT FOR CONSUMERS?

Ultimately, consumers will benefit by having access to higher quality food that meets more stringent requirements for agricultural sustainability and impact on the environment.

Also, breeders will be able to develop refined varieties containing characteristics to meet specific markets. This could, for example, be wheat varieties with higher protein content or less gluten to address gluten intolerance.



## WASN'T THE WHEAT GENOME ALREADY SEQUENCED?

Several draft versions of the wheat genome have been generated over the last years by different groups using different approaches. What sets them apart is the extent and the quality of the information provided.

From the start, the IWGSC goal was to produce resources to accelerate wheat improvement, i.e., to produce a reference sequence that could be used by breeders. Unlike genome sequences that are used mostly for scientific research, this requires a very precise map of the genome with information on markers and genes ordered along the 21 wheat chromosomes.

The IWGSC reference genome is the best quality genome sequence produced to date for wheat. It not only presents the genetic code of wheat, it also provides the precise location and sequence of more than 100,000 genes, as well as more than 4 million markers, on the 21 wheat chromosomes.

## HOW DID THEY DO IT?

To overcome the size and complexity problems of the wheat genome, the IWGSC set out a roadmap in 2005 to produce physical maps of individual chromosomes that positioned physical bacterial clones (bacterial artificial chromosomes (BACs), around 200 kilobases long) and genetic markers to specific chromosomes.

The BACs were then used as a substrate for sequencing (this method was also used to generate the reference human genome sequence and for wheat chromosome 3B), or to produce sequence tags that could be combined with sequences assembled from a whole genome sequencing approach to position the sequence pieces on the correct chromosomes.

A whole genome sequence was produced from short sequence fragments (average 150 bases) using algorithms developed specifically to handle wheat by the company NRGene and chromosome-specific resources (physical maps, chromosome and BAC sequence tags, genetic markers and chromosome conformation data (ChIP) were used to assign and position sequence fragments on the chromosomes.

The ultimate result of combining all of these approaches is a high-quality reference genome sequence of bread wheat.

## WHAT IS THE NEXT STEP?

The IWGSC will now focus on producing a genome-sequence based toolbox for breeders and scientists to use for wheat improvement.

It will involve several projects, such as maintaining and improving the current reference genome to ultimately produce a "Gold Standard" reference genome sequence that is manually and functionally annotated; sequencing other varieties of wheat in order to represent the worldwide diversity of wheat; and continuing to develop a database for the wheat community to access all these genomic resources.

## FOR MORE INFORMATION



### — infographics

- The origin of wheat
- The bread wheat genome
- Importance of wheat for food security
- How breeders use a reference sequence

### — article on why the wheat genome is an essential key to feeding the planet

- New Food Economy, 21 June 2016: Harry Potter and the gigantic genome

### — news articles on the effects of the current heat wave in Northern Europe, America and Asia on wheat production this year

- Reuters, 2 August 2018: Heatwave ravages European fields, sending wheat prices soaring
- Reuters, 26 July 2018: IGC cuts forecast for world wheat crop to five-year low
- Bloomberg 25 July 25 2018: The Global Heatwave Is About to Hit Your Wallet
- Bloomberg, 15 July 2018: Europe's Blistering Heatwave Is Ruining This Year's Harvest
- Gro Intelligence, 26 June 2018: Chinese Wheat Production Expected to Drop

# QUOTES FROM AUTHORS OF THE ARTICLE



"The genome sequence of each of the 21 wheat chromosomes lets us look inside the wheat engine. What we see is beautifully put-together to allow for variation and adaptation to different environments through selection as well as sufficient stability to maintain basic structures for survival under various climatic conditions."

— **Rudi Appels**  
Professor, University of Melbourne and Murdoch University, AgriBio Research Fellow, Victoria, Australia

"The publication of the wheat reference genome is the culmination of the work of many individuals who came together under the banner of the IWGSC to do what was considered impossible. The method of producing the reference sequence and the principles and policies of the consortium provide a model for sequencing large, complex plant genomes and reaffirms the importance of international collaborations for advancing food security."

— **Kellye Eversole**  
IWGSC Executive Director



"The sequence resources reported here will and have already changed our way of generating knowledge on wheat crop biology and crop performance. I am sure this will stimulate many more young scientists all over the world to take advantage of this new information and make their contributions towards sustained and maybe even increased global wheat yields in a changing world. This current achievement has also set the start now to an even bigger endeavor: to gather a complete catalog of natural genetic diversity available to modern wheat breeding "

— **Nils Stein**  
Group Leader, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

"I am really thrilled, because after 13 years of efforts with the whole wheat community we have reached our major milestone. The vision we had is now becoming concrete, we have a high quality reference sequence that can be used to accelerate wheat research and breeding. I'd wish I'd be at the beginning of my career again because the fun is really starting now and we can efficiently decipher the biology of our favorite crop. Having this sequence and combining it with other advances in science and technologies is fundamental to enable us understanding how wheat plants perform in their environments and boost our ability to improve wheat production worldwide."

— **Catherine Feuillet**  
Chief Scientist Officer, Inari Agriculture, USA

"Genomic knowledge of other crops has driven progress in selecting and breeding important traits. Tackling the colossal wheat genome has been a Herculean challenge, but completing this work means we can identify genes controlling traits of interest more rapidly. This will facilitate and make more effective the breeding for traits like drought or disease resistance. Where previously we had a broad view and could spot areas of interest, we can now zoom into the detail on the map."

— **Cristobal Uauy**  
Project Leader, John Innes Centre, UK

"The wheat reference sequence will be a game changer for wheat research; for gene discovery projects, like finding genes under QTL, development of molecular markers, but also for genetic diversity studies and the pan-genome."

— **Ute Baumann**  
Group Leader, Plant Genomics Centre, University of Adelaide, Australia

"With the availability of the wheat reference sequence, it is now a great time to play wheat gene(s) and genome(s) to increase wheat yield to meet increasing demand"

— **Hikmet Budak**  
Professor, Montana State University, USA

"For me, as a functional genomics and genetics researcher, having a continuous and fully annotated sequence for each of the 21 wheat chromosomes is of paramount importance. This will greatly speed up our efforts on identification of agriculturally important wheat genes, including those that would help to combat major fungal diseases. This will also be hugely and immediately beneficial for wheat breeders, accelerating development of new elite varieties."

— **Kostya Kanyuka**  
Project Leader, Rothamsted Research, Harpenden, UK

"Sequencing the wheat genome has long been considered as impossible. But as Oscar Wilde said : "Shoot the moon. Even if you miss, you'll land among the stars". With the IWGSC RefSeq, not only have we reached the moon, but we have paved the way to a new galaxy of exciting basic and applied research projects."

— **Etienne Paux**  
Senior Researcher, National Institute for Agricultural Research (INRA), France

"The IWGSC RefSeq revolutionizes gene cloning in wheat, which has been extremely difficult in the past. Now, the large repertoire of disease resistance genes in the bread wheat gene pool becomes available for molecular characterization."

— **Beat Keller**  
Professor, University of Zürich, Switzerland

# QUOTES FROM USERS OF THE WHEAT SEQUENCE

"It's such a great work; it brings a great deal of convenience to all the researchers around the world working on wheat. I appreciate all the contributions you have made to the world wheat research."

— **Rui Hu**  
Ph.D candidate, Huazhong University of Science and Technology, China

"Having access to IWGSC RefSeq helped us a lot to improve the annotation of hundreds of PPR genes"

— **Joanna Melonek**  
Research Fellow, University of Western Australia, Australia

"Having access to a high quality chromosome-level assembly for wheat was a hugely valuable resource for my PhD project, which involves cloning stripe rust resistance genes. I was able to retrieve physical positions for markers that were genetically linked to our targets, define new markers spanning the region and confirm their linkage with newly identified candidate genes. This information is now being used by breeders to develop varieties with improved disease resistance. "

— **Clémence Marchal**  
PhD student, John Innes Centre, UK

"Thank you once again for pre-publication access to the RefSeq v1.0. This gave us the opportunity to support our mapping results with information about the physical positions of markers linked to detected QTL."

— **Manuel Geyer**  
Institute for Crop Science and Plant Breeding, Freising, Germany

"How do you thank a team of scientists who persevered and succeeded in sequencing the wheat genome and changed wheat breeding forever? Perhaps it is not with the words of a scientist, but with the smiles of well-nourished children and their families whose lives have been changed for the better."

— **Stephen Baenziger**  
Professor, University of Nebraska-Lincoln  
Wheat Growers Presidential Chair, USA

"The key enablers for this PhD were the availability of the wheat genome sequence and the creation of novel I mutants in wheat by CSIRO."

— **In: Van De Velde, Karel, Philip Ruelens, Koen Geuten, Antje Rohde, and Dominique Van Der Straeten. "Exploiting DELLA signaling in cereals." Trends in Plant Science 22, no. 10 (October, 2017): 880-893**

"The USDA regional genotyping labs are using the IWGSC reference sequence to facilitate marker-assisted breeding. The IWGSC assembly has accelerated trait mapping and development of highly diagnostic assays suited to high-throughput genotyping. We are now able to quickly cross-reference trait associated markers from independent studies, rapidly associate QTL regions with candidate genes, and use reference based pipelines for SNP discovery and genotyping. "

— **Gina Brown-Guedira**  
Research Geneticist, USDA-ARS, Raleigh, NC, USA



The wheat IWGSC resources help us develop genomic breeding tools on a daily basis. Through these resources our accuracy and speed is at a much higher level now. [...] To further investigate this Rht24 genomic region, we aligned the sequences of the markers from this region with the wheat reference genome (IWGSC RefSeq v1.0). This revealed that almost all of the significantly associated markers are located in an approximately 50-Mbp region between 400 and 450 Mbp."

— **Willmar Leiser**  
Head of Biotechnology Group, University of Hohenheim, Germany

"We have been using the IWGSC Data in our (phospho)proteomics data analyses, and this increases our identification with ~25%. We are very thankful for this genome data set."

— **Ive De Smet**  
Group leader, VIB & Ghent University, Belgium



# ABOUT THE IWGSC

## AN INTERNATIONAL, COLLABORATIVE RESEARCH CONSORTIUM



Established in 2005 by a group of wheat growers, plant scientists, and public and private breeders

### MISSION

Make a high quality genome sequence of bread wheat publicly available

### VISION

Lay a foundation for basic research that will enable breeders to develop improved wheat varieties

2,400  
MEMBERS  
IN  
68  
COUNTRIES



### ROADMAP

The IWGSC uses a milestone-based, adaptable strategy to ensure the immediate availability of significant outputs for wheat breeders and the wheat industry in parallel to continued advancements in basic research on the wheat genome.

The four key milestones of the IWGSC roadmap:

- (1) use of survey sequences of the 21 bread wheat chromosomes to assign gene sequences to individual chromosomes – reached in July 2014: Science, DOI: 10.1126/science.1251788
- (2) develop physical maps to provide resources for sequencing – reached end 2015
- (3) deliver a reference sequence for each of the chromosomes – reached in August 2018: Science, DOI: 10.1126/science.aar7191
- (4) produce a gold standard genome sequence – expected by 2025

### BOARD MEMBERS

- Kellye Eversole (Eversole Associates, USA), Chair of the Board and Executive Director
- Rudi Appels (Murdoch University, Australia)
- Ute Baumann (University of Adelaide, Australia)
- Hikmet Budak (Montana State University, USA)
- Catherine Feuillet (Inari Agriculture, USA)
- Beat Keller (University of Zurich, Switzerland)
- Etienne Paux (INRA, France)
- Sebastien Prud (Biogemma, France)

[WWW.WHEATGENOME.ORG](http://WWW.WHEATGENOME.ORG)



@wheatgenome



wheat.genome

All resources generated are publicly available at the IWGSC data repository at URGI-INRA Versailles.

### MORE ABOUT THE IWGSC

- fact sheet
- timeline
- video



# MEDIA CONTACTS

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# IWGSC YOUTUBE CHANNEL

Click on the images to access the videos

## EXPLAINER VIDEO



The Bread Wheat Genome Sequence - A Tool for Breeders to Improve Wheat and Contribute to Food Security

## INTERVIEWS

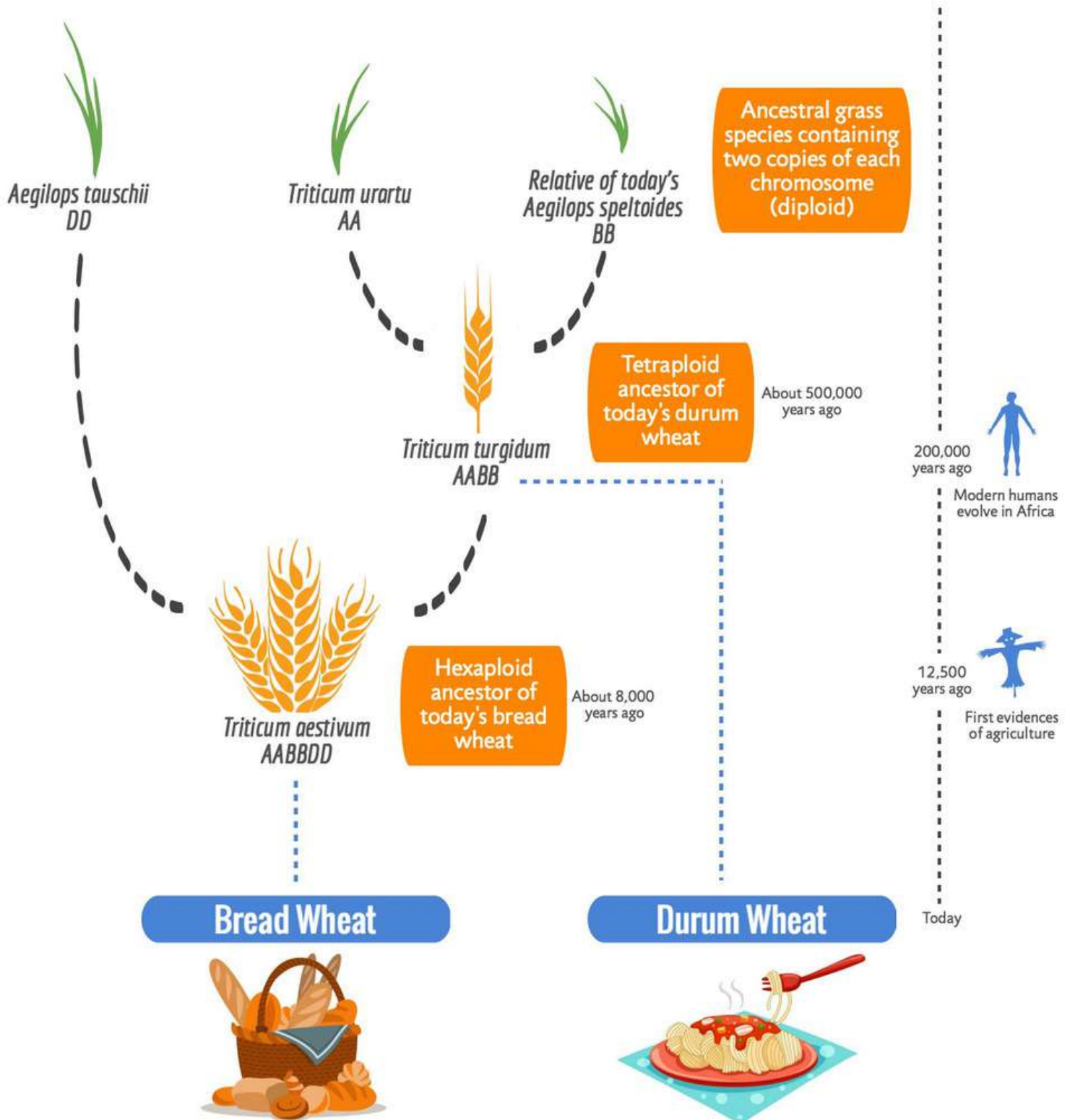


The Reference Sequence of Bread Wheat



# The Origin of Wheat

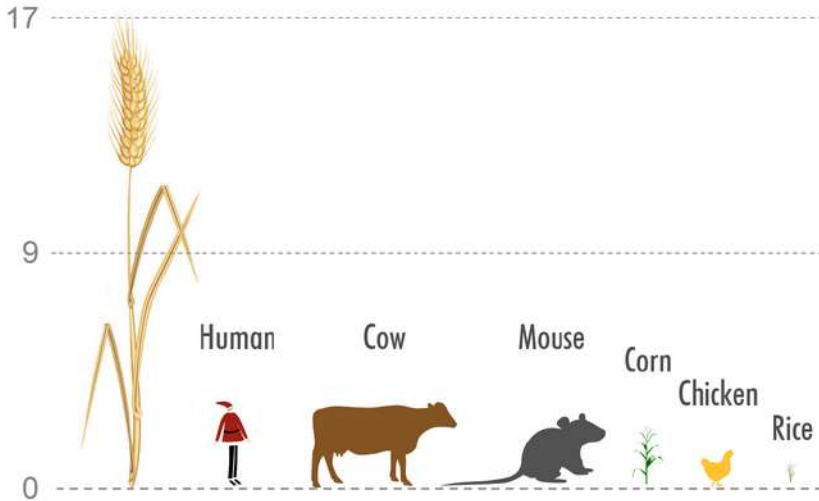
Today's bread wheat originates from three ancestral grass species and results from two consecutive hybridizations



# THE BREAD WHEAT GENOME



## Five times larger than the human genome

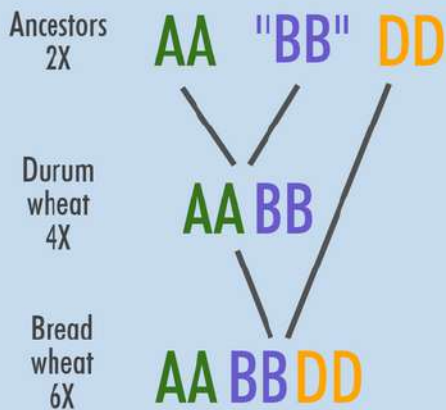


16 Gb !!

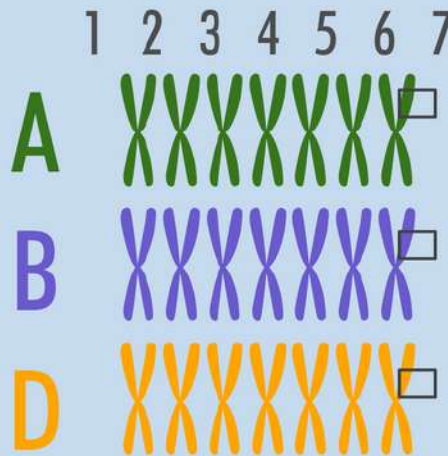
35 times larger than the rice genome



## Three genomes combined



2X = two copies of each chromosome



Three sets of chromosomes

21 chromosomes in 2 copies = 42 chromosomes

110,000 to 150,000 genes



## Similar genes and a lot of repetitions

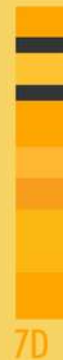
- the three sets of chromosomes have highly similar gene contents
- more than 80% of the genome is made of repetitive elements
- genes represent only 2% of the genome



7A



7B



7D

genes

repetitive elements

[www.wheatgenome.org](http://www.wheatgenome.org)





# WHEAT

## A KEY CROP FOR FOOD SECURITY



**10,000**  
years old

Humans have cultivated and consumed wheat since the beginning of civilization

Wheat is produced all over the world

**6**  
continents

**749**  
million tons  
produced in 2016

**220**  
million hectares  
planted in 2016

The main producing countries are the European Union, China, India, Russia, and the United States.

Most of the wheat produced is consumed by humans

**67%**

of the wheat produced worldwide is used for human consumption

Wheat is especially critical for the

**2.5**

billion people who live on less than US \$2 per day.



Wheat is used to make breads, biscuits, couscous, flatbreads, cookies, cakes, breakfast cereals, noodles...



Wheat is the number one food crop consumed in the world

**65 kg**  
of wheat are consumed per person per year

The highest consumption per person per year is in Central Asia (143 kg), followed by North Africa (139 kg), Western Asia (138 kg) and Europe (109 kg).

Wheat is the main source of calories and proteins in human diets

**19%**

of all calories consumed

**20%**

of all proteins consumed

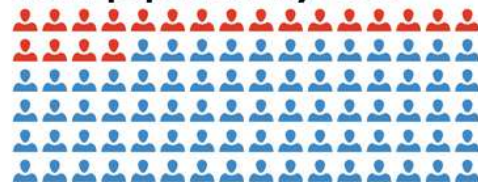
In Central & Western Asia and North Africa, wheat provides more than one third of all calories and proteins consumed.

Wheat production needs to increase by



**60%**

to feed the projected 9.6 billion world population by 2050



## International Wheat Genome Sequencing Consortium

[www.wheatgenome.org](http://www.wheatgenome.org)

Sources:  
FAO, [www.fao.org/faostat/en/#data/FBS](http://www.fao.org/faostat/en/#data/FBS) - data year: 2013 & 2016  
[www.wheatfoods.org/resources/72](http://www.wheatfoods.org/resources/72)  
CGIAR: [wheat.org/wheat-in-the-world](http://wheat.org/wheat-in-the-world)  
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# The Wheat Genome Reference Sequence

## — HOW BREEDERS USE IT —

The availability of a reference genome for a crop helps plant breeders to speed up the development of new improved varieties

### Gene discovery

CTGCA  
TCTGA  
CTCCT  
GAGAA  
GT TCA

Plant scientists use the information provided in a reference genome sequence to identify and locate genes responsible for desirable agronomic traits (such as high yield, stress tolerance and disease resistance), isolate those genes and study how they function.

Once a gene is known, this information can – for example – be utilized to tap into the natural diversity of the crop to discover new versions of the gene with more favorable features than those found in the variety used to produce the reference sequence and use those to introduce improved traits into commercial varieties.

### Gene improvement

TGGCC  
ATTCTT  
CCCATT

The information provided in a reference genome sequence can also be used to look for modified and improved versions of the genes into mutant collections and /or create modified and improved versions by genetic engineering.

### Marker-assisted breeding



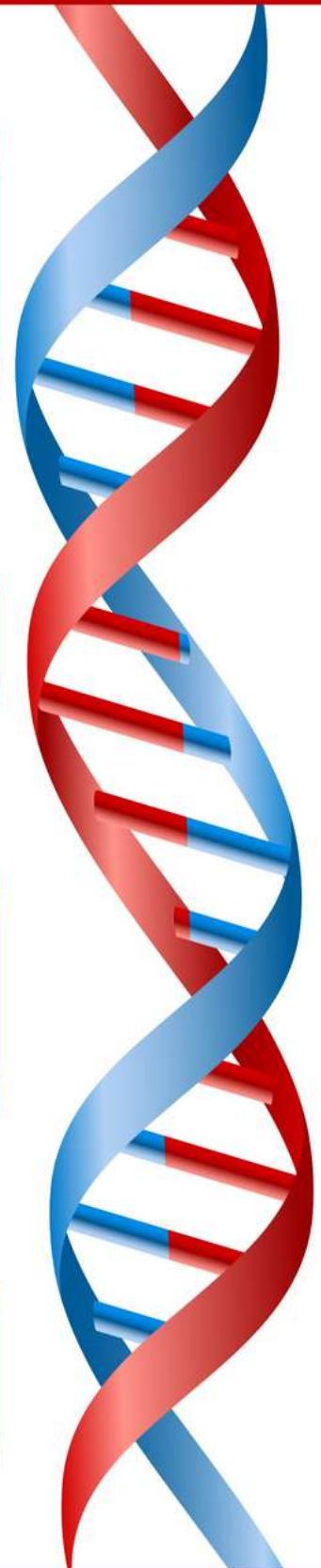
Molecular markers are easily identifiable fragments of DNA sequence that are located close to a specific gene. With a reference sequence in hands, breeders have an unlimited source of molecular markers close to or within the genes of interest.

They can use these markers to identify suitable parents containing the traits of interest for new crosses and track down the presence of the genes of interest in the descendants during the selection process.

### New varieties breeding



Ultimately, breeders use markers and genes to speed up the development of new varieties with specific characteristics such as higher yield, tolerance to a stress (heat, water scarcity, high salt content in soil) or resistant to a specific disease (such as rust diseases and Fusarium head blight disease).



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