

HelmholtzZentrum münchen

German Research Center for Environmental Health

PGSB Plant Genome and
Systems Biology



How complex can it be? The bread wheat genome and its implications for wheat intolerance

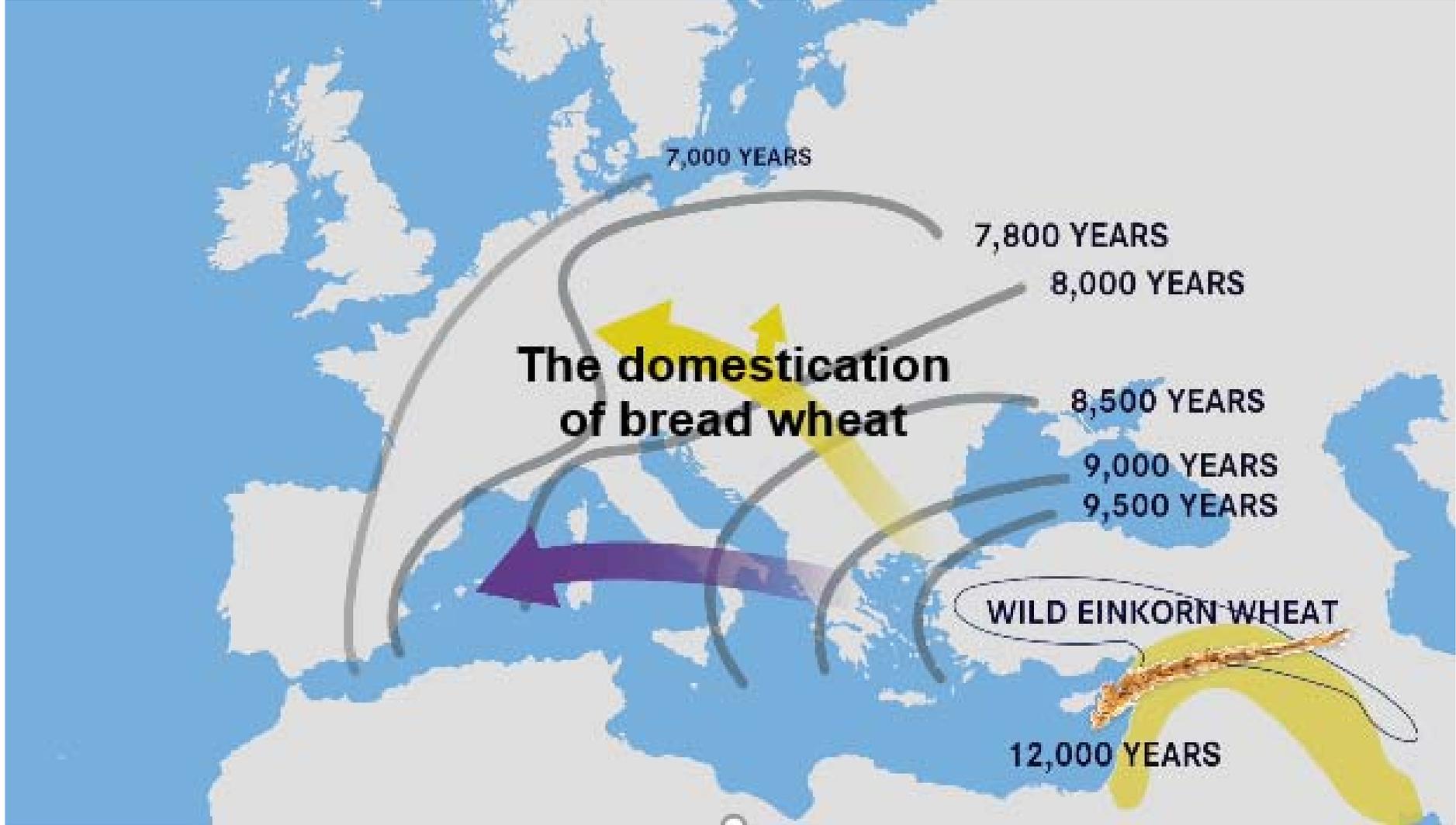
Manuel Spannagl

PGSB, March, 29th 2019

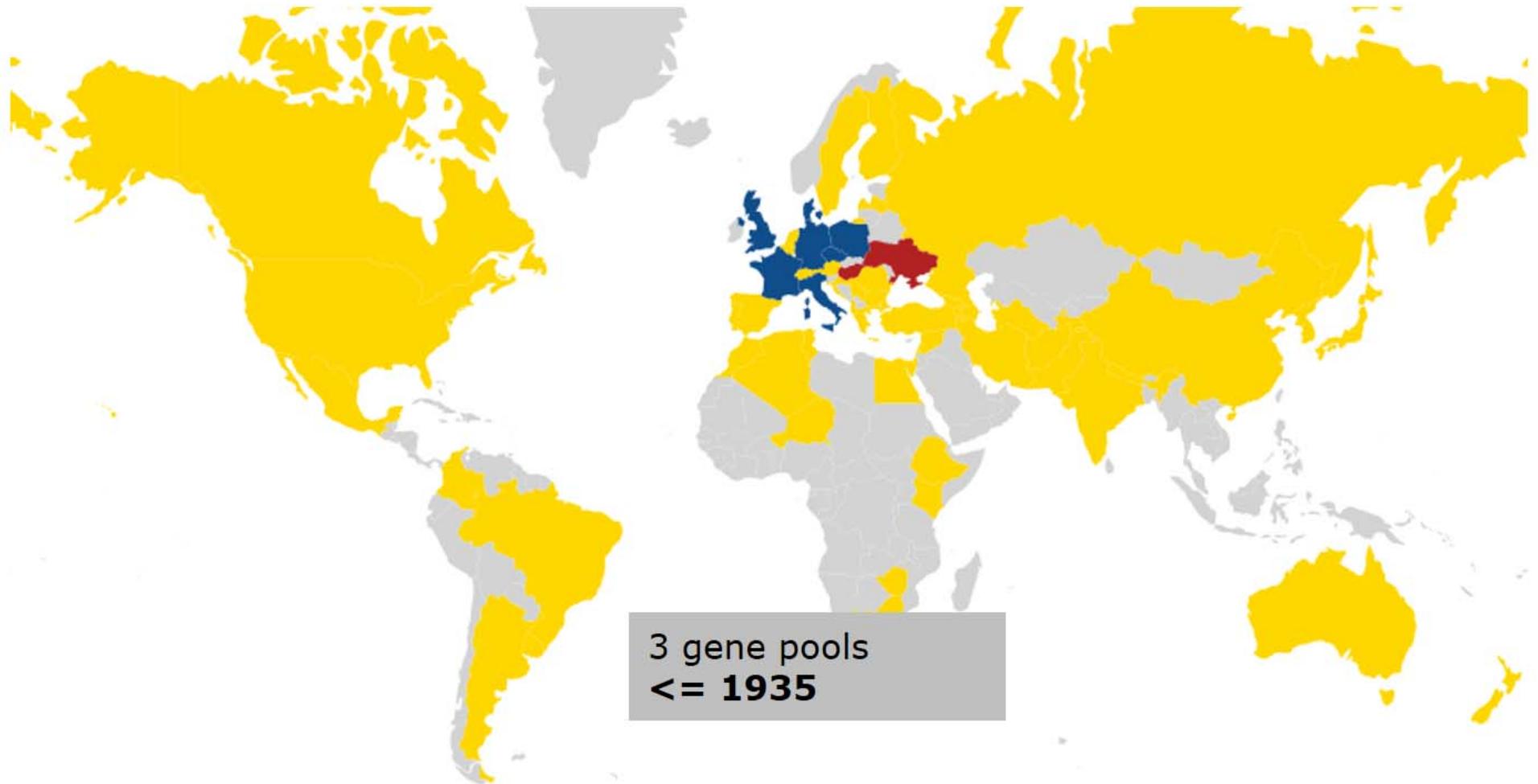
Outline

- Introduction – what makes the wheat genome so special aka complex?
- Previous wheat WGS/survey sequences
- The bread wheat reference genome sequence
- The Wheat prolamin map
- What's next?





Humans & even politics shape the gene pools of wheat



Nature Genetics, 2019

A photograph of a combine harvester working in a vast field of golden wheat. The harvester is positioned in the middle ground, moving from left to right. A large plume of dust or chaff is being kicked up behind it, partially obscuring the machine. The sky is a pale, clear blue. The foreground shows the texture of the wheat stalks and the ground.

**Wheat (yield) is threatened
by climate change**

Wheat is not good for everyone



Celiac disease

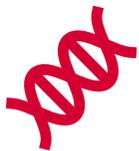
Wheat insensitivities

Wheat allergy

Baker's asthma

>60% of world's food:

Maize



Rice



Soy

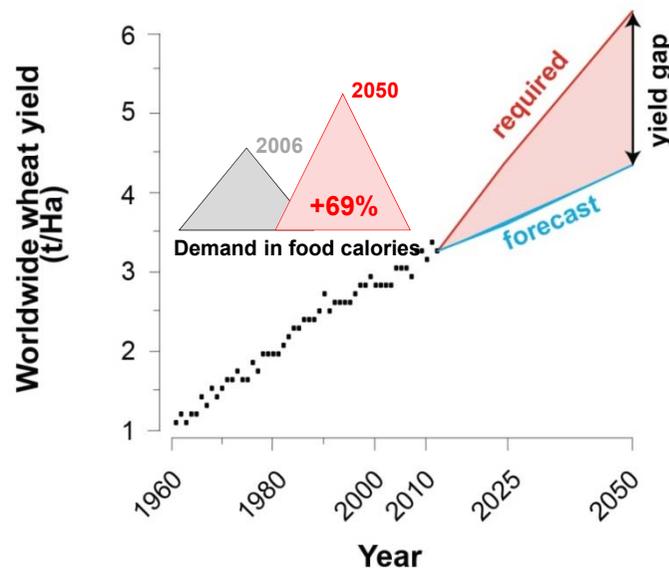


Wheat

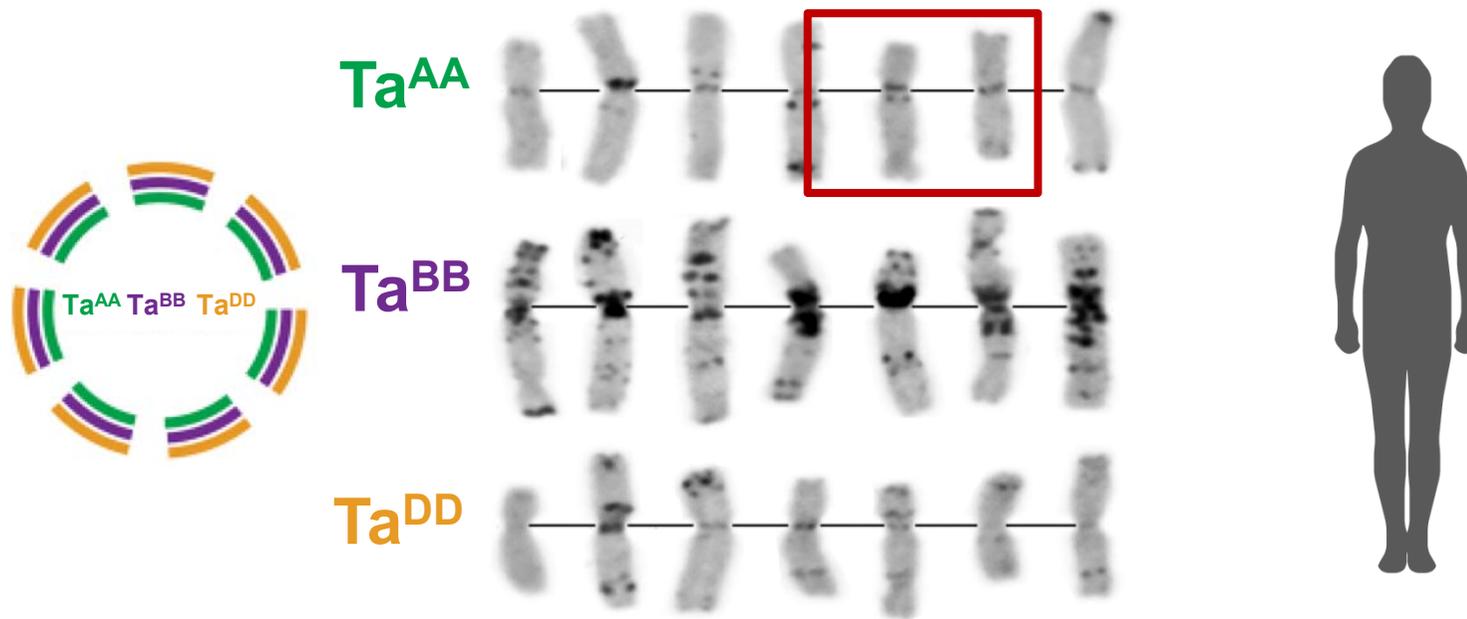


Filling the yield gap – a challenge for agricultural research

- Staple food source for 30% of the world's population
- ~20% of human's daily consumed calories
- 620 million tonnes harvested (2012)
- US\$200 billion trade volume



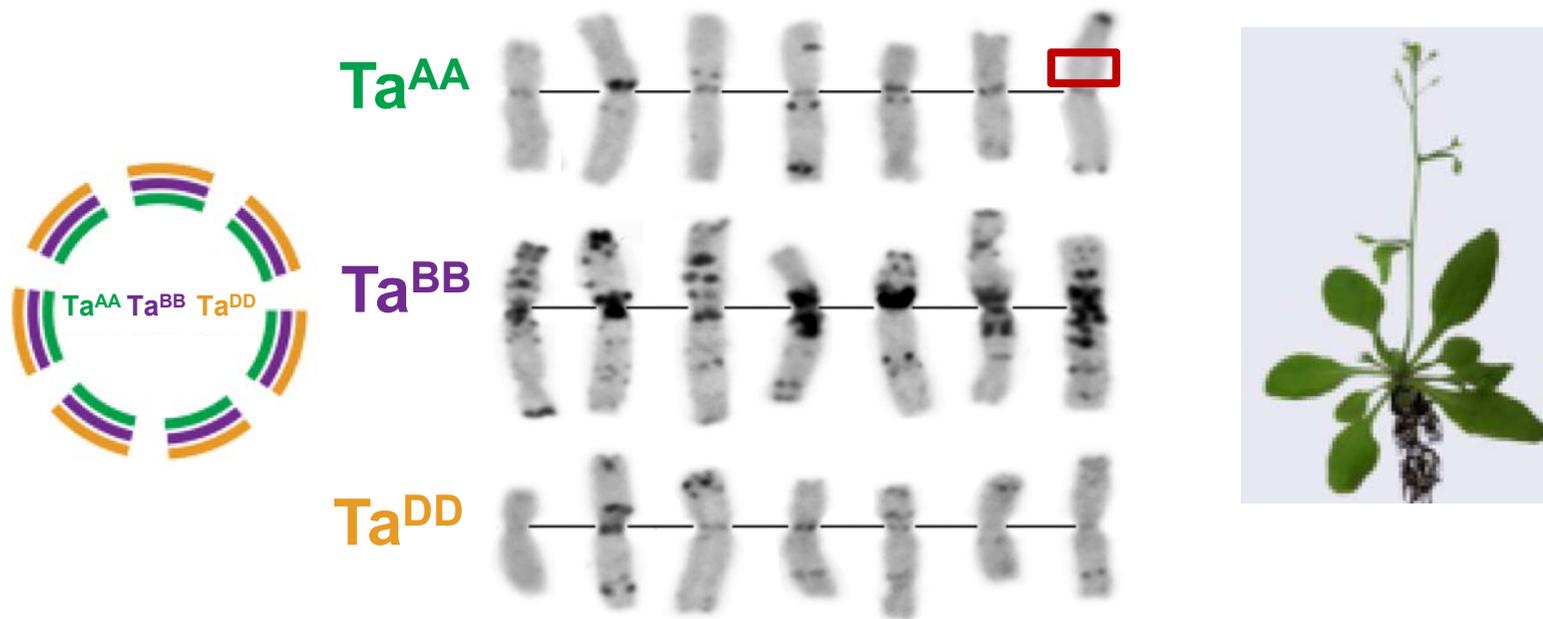
The genome of bread wheat (*T. aestivum*) is ...



...large and complex!

- allohexaploid: three “diploid-like” ($2n = 6x = 42$)
- ~17Gb genome size; > 80% repeat content
- Highly similar genomes (>97% identity)

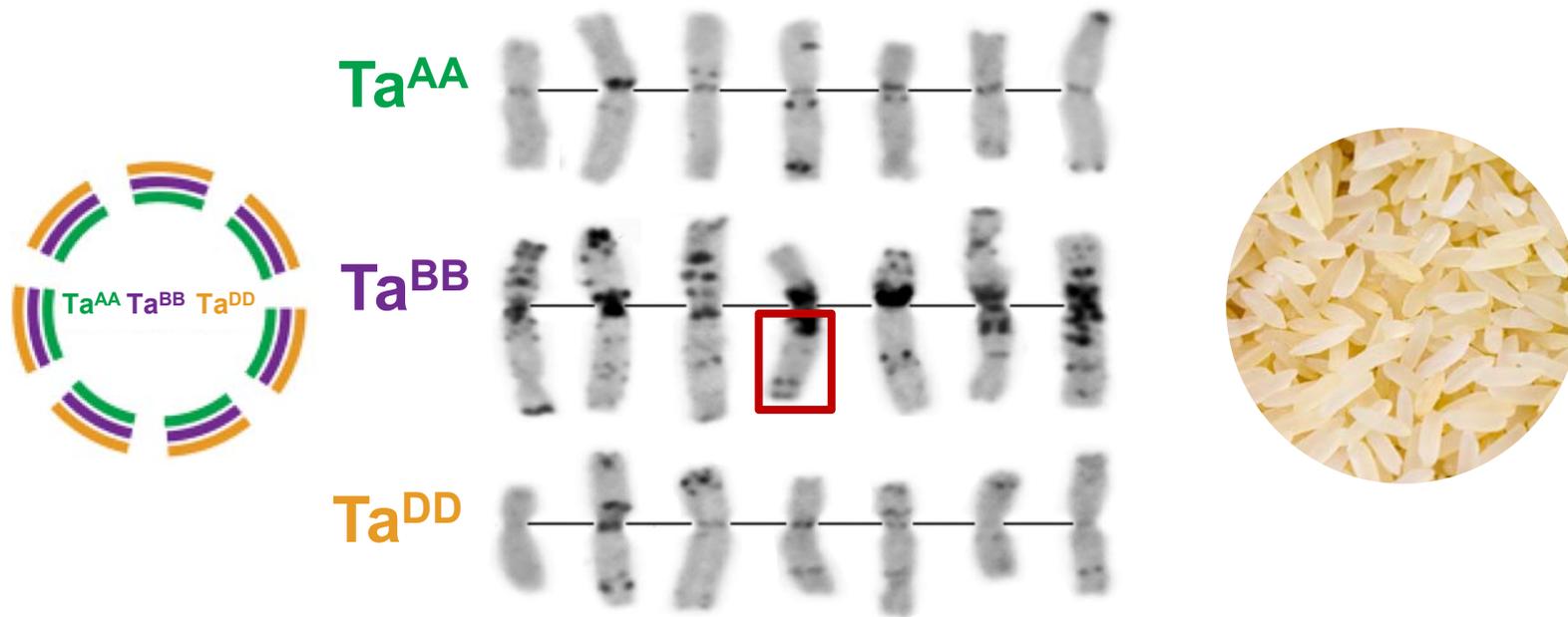
The genome of bread wheat (*T. aestivum*) is ...



...large and complex!

- allohexaploid: three “diploid-like” ($2n = 6x = 42$)
- ~**17Gb** genome size; > **80% repeat** content
- Highly **similar genomes** (>97% identity)

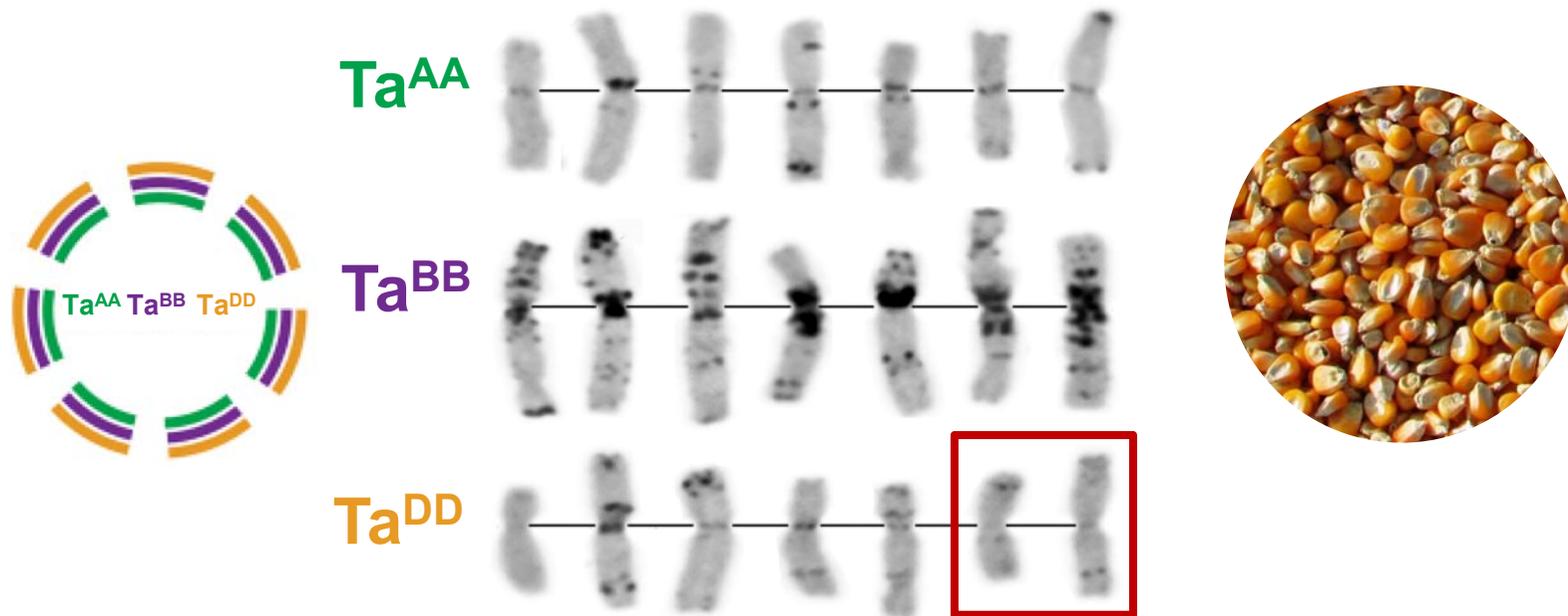
The genome of bread wheat (*T. aestivum*) is ...



...large and complex!

- allohexaploid: three “diploid-like” ($2n = 6x = 42$)
- ~**17Gb** genome size; > **80% repeat** content
- Highly **similar genomes** (>97% identity)

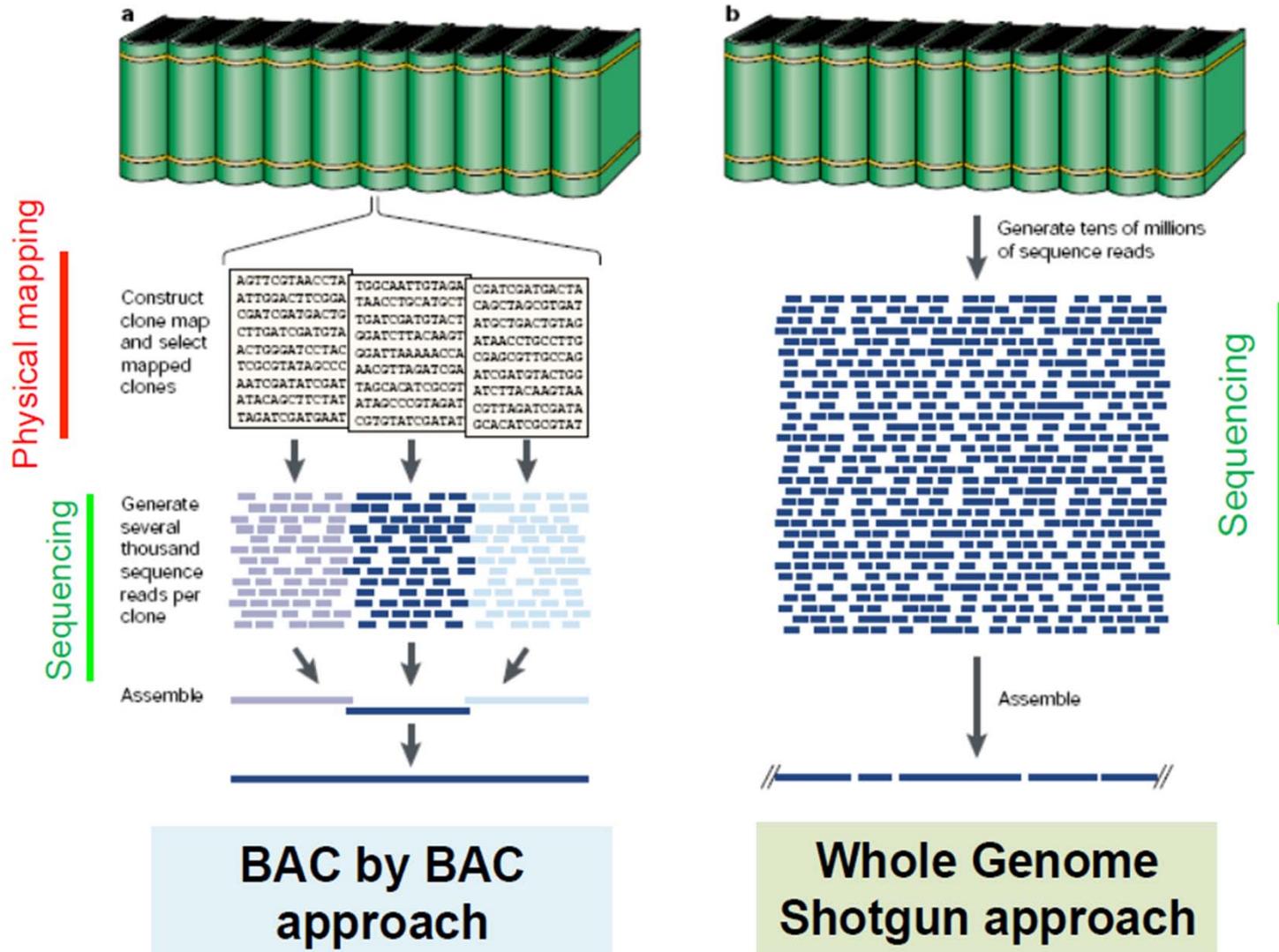
The genome of bread wheat (*T. aestivum*) is ...



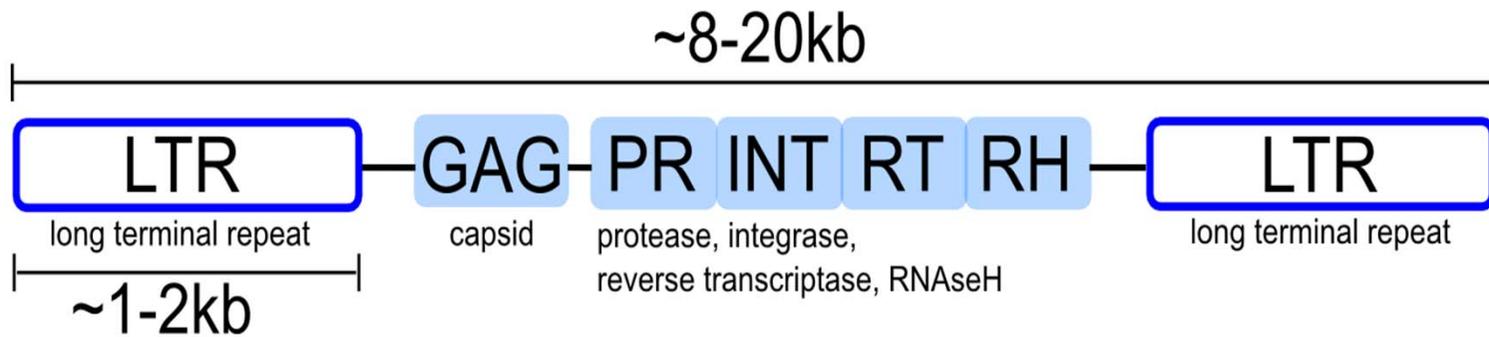
...large and complex!

- allohexaploid: three “diploid-like” ($2n = 6x = 42$)
- ~**17Gb** genome size; > **80% repeat** content
- Highly **similar genomes** (>97% identity)

Sequencing complex cereal genome - strategies



Why is the assembly so complicated?



Wheat genome sequencing efforts



- **2014:** Chromosome-sorted WGS assembly
- ~100,000 gene models identified (highly similar A,B,D homeologous)
- BUT: highly fragmented, little inter-genic sequence available
- Newer assembly by:

TGAC 
The Genome Analysis Centre™

The International Wheat Genome Sequencing Consortium



2015

COUNTRIES

55



MEMBERS

1100



INSTITUTES/COMPANIES

372

SPONSORS

21



Board of Directors
 Role: Overall strategy and organization
 Up to 10 directors including at least 1 Outside Director

Leadership Team
 Role: Daily management
 Members: Appels, Eversole, Feuillet, Keller, & Rogers

Coordinating Committee
 Role: Scientific strategy
 Members: Sponsors & Leaders of IWGSC Projects & Initiatives

Members
 Role: Participation & Input
 Members: Open to Anyone



www.wheatgenome.org

Sequence Assembly Breakthrough!

NRGene

De**Novo**MAGIC™ 2.0

- **Novel algorithm for (genome) sequence assembly**
 - Uses standard **Illumina short reads** (at high coverage)
 - Some specific insert library sizes needed
 - **Long scaffolds** even in presence of high repetitivity and large genome sizes
 - **Fast:** 14 days for hexaploid wheat genome (17 Gb!)
-

The tragic ripples of
an epic fraud *p. 636*

Insect pest profits from
maize defenses *pp. 642 & 694*

Photoredox activation
of methane *pp. 647 & 668*

Science

\$15
17 AUGUST 2018
sciencemag.org

AAAS



ROAD MAP FOR WHEAT

Ordered sequence will
speed research *pp. 635, 661, & 662*

- Pseudo-chromosome assembly
- ~108,000 HC gene models
- ...still with gaps and missing sequence

The tragic ripples of
an epic fraud *p. 636*

Insect pest profits from
maize defenses *pp. 642 & 694*

Photoredox activation
of methane *pp. 647 & 668*

Science

\$15
17 AUGUST 2018
sciencemag.org

AAAS



ROAD MAP FOR **WHEAT**

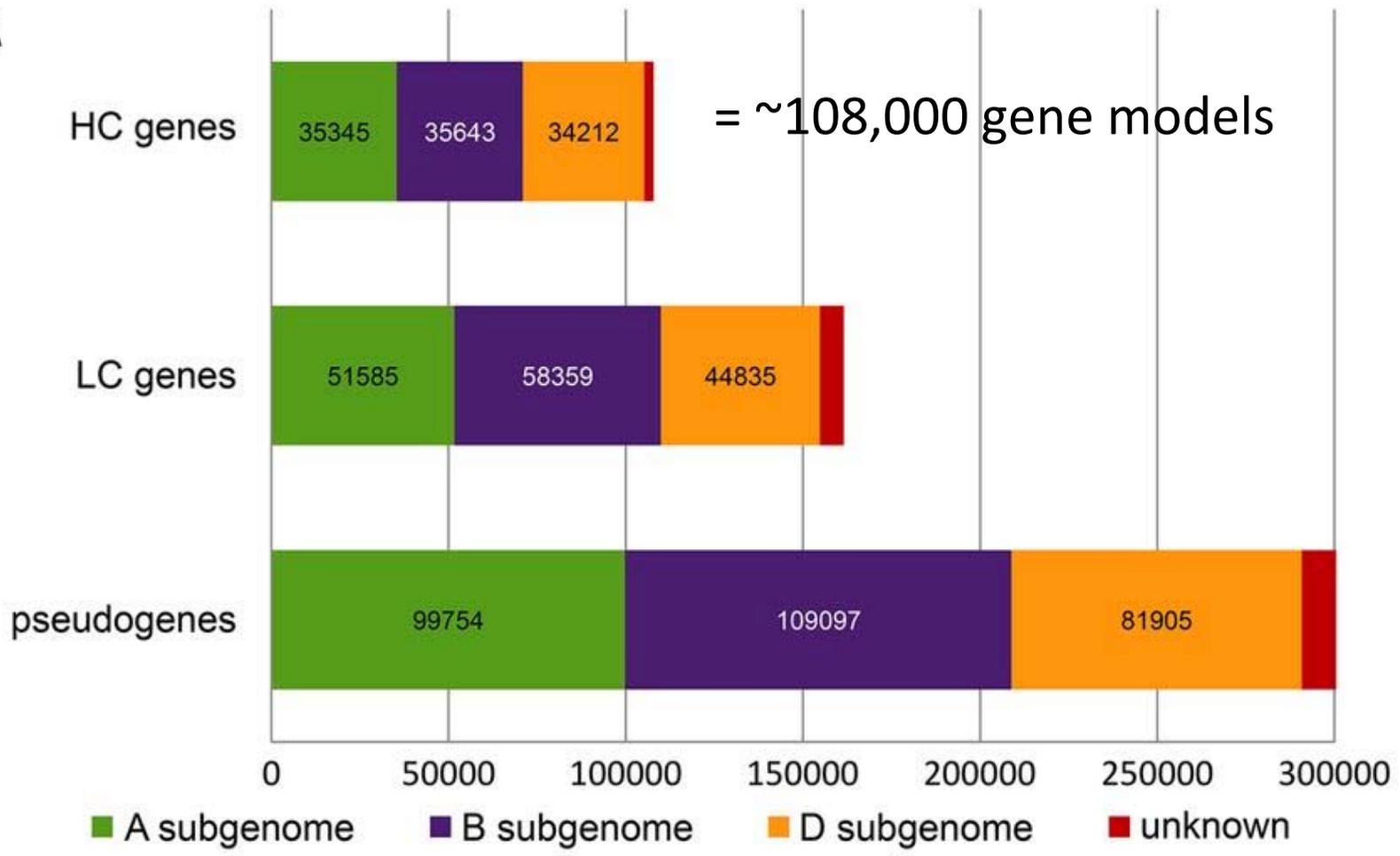
Ordered sequence will
speed research *pp. 635, 661, & 662*

Finally!!

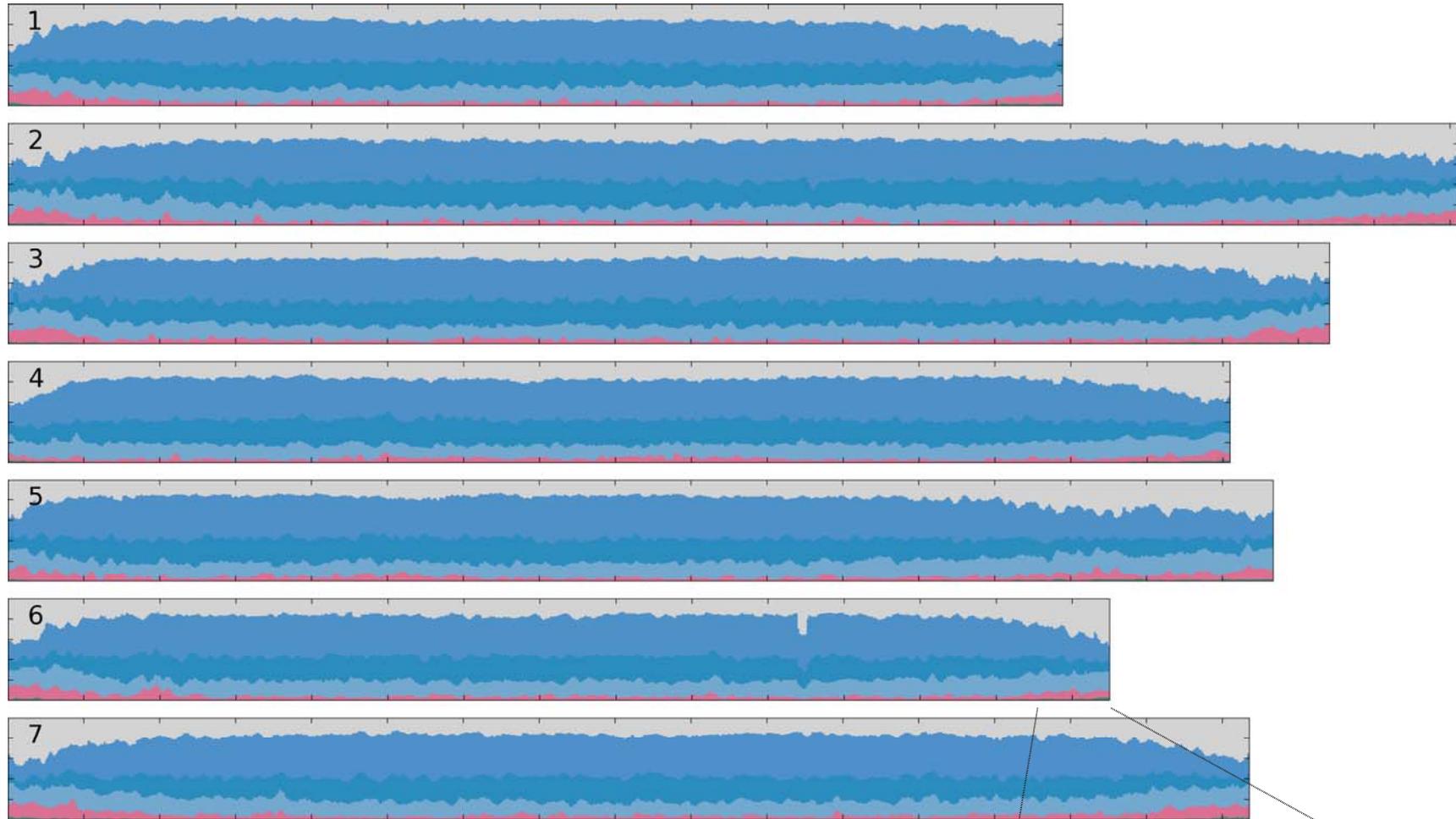
**A true reference
genome sequence for
bread wheat**

The genes of bread wheat

A



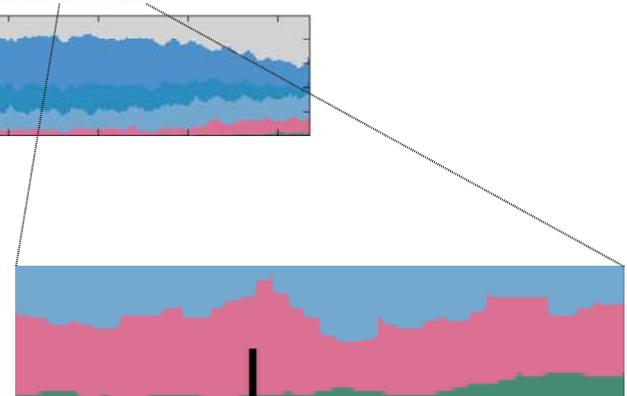
Genes = "needles in the haystack"



LTR-retrotransposons

- unassigned LTR-retrotransposons
- Gypsy LTR-retrotransposons
- Copia LTR-retrotransposons

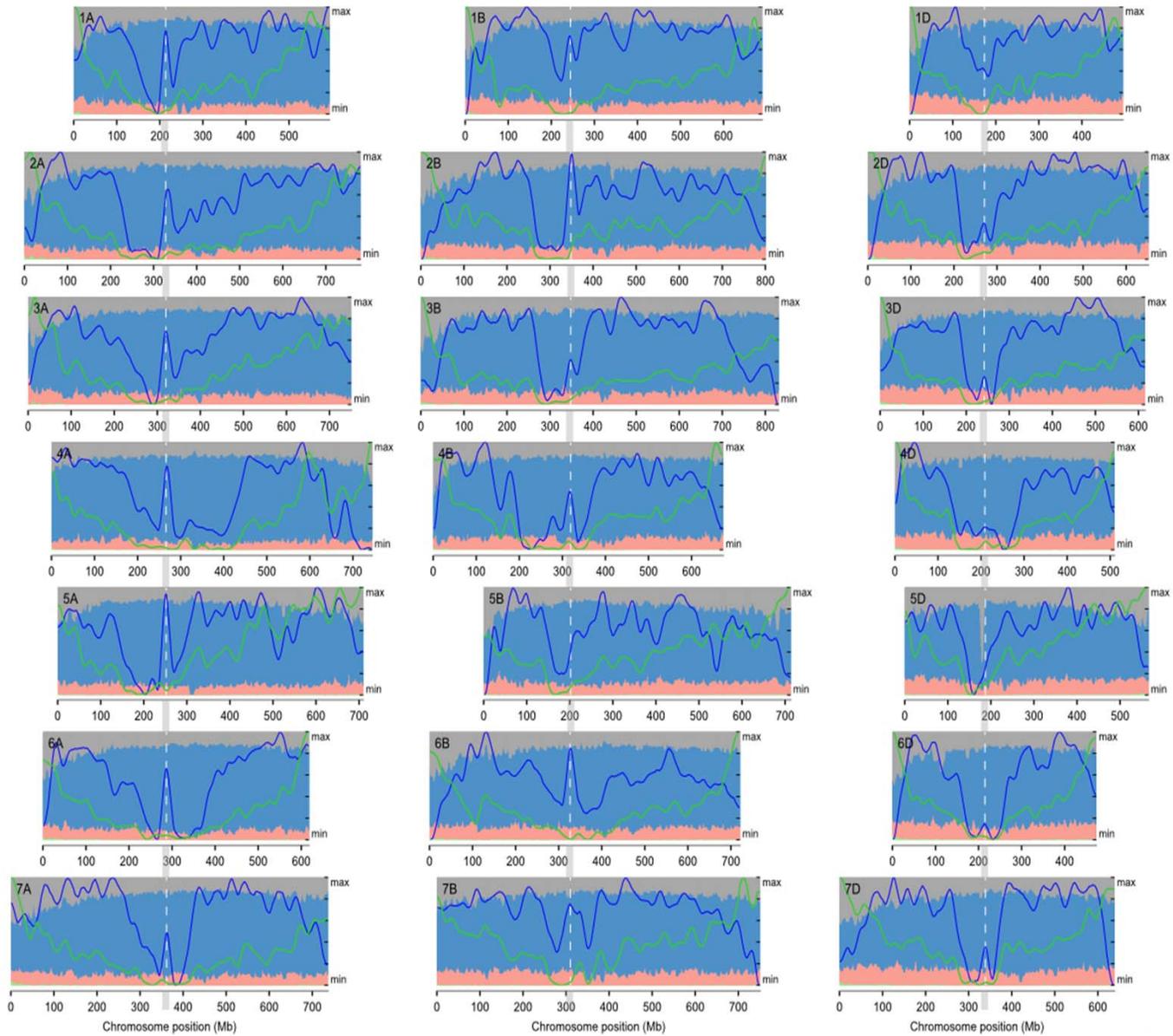
- DNA-transposons
- Genes (cds)

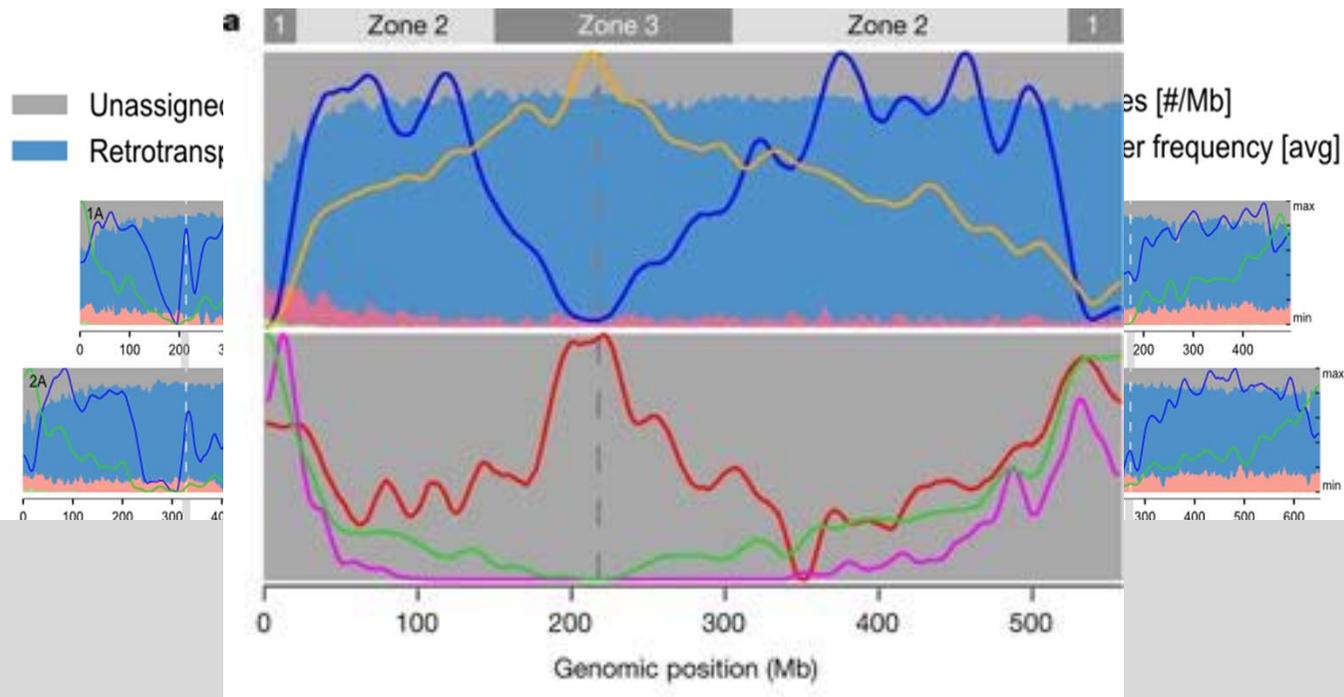


Unassigned
Retrotransposons

DNA transposons
Genes (CDS)

Genes [#Mb]
20mer frequency [avg]





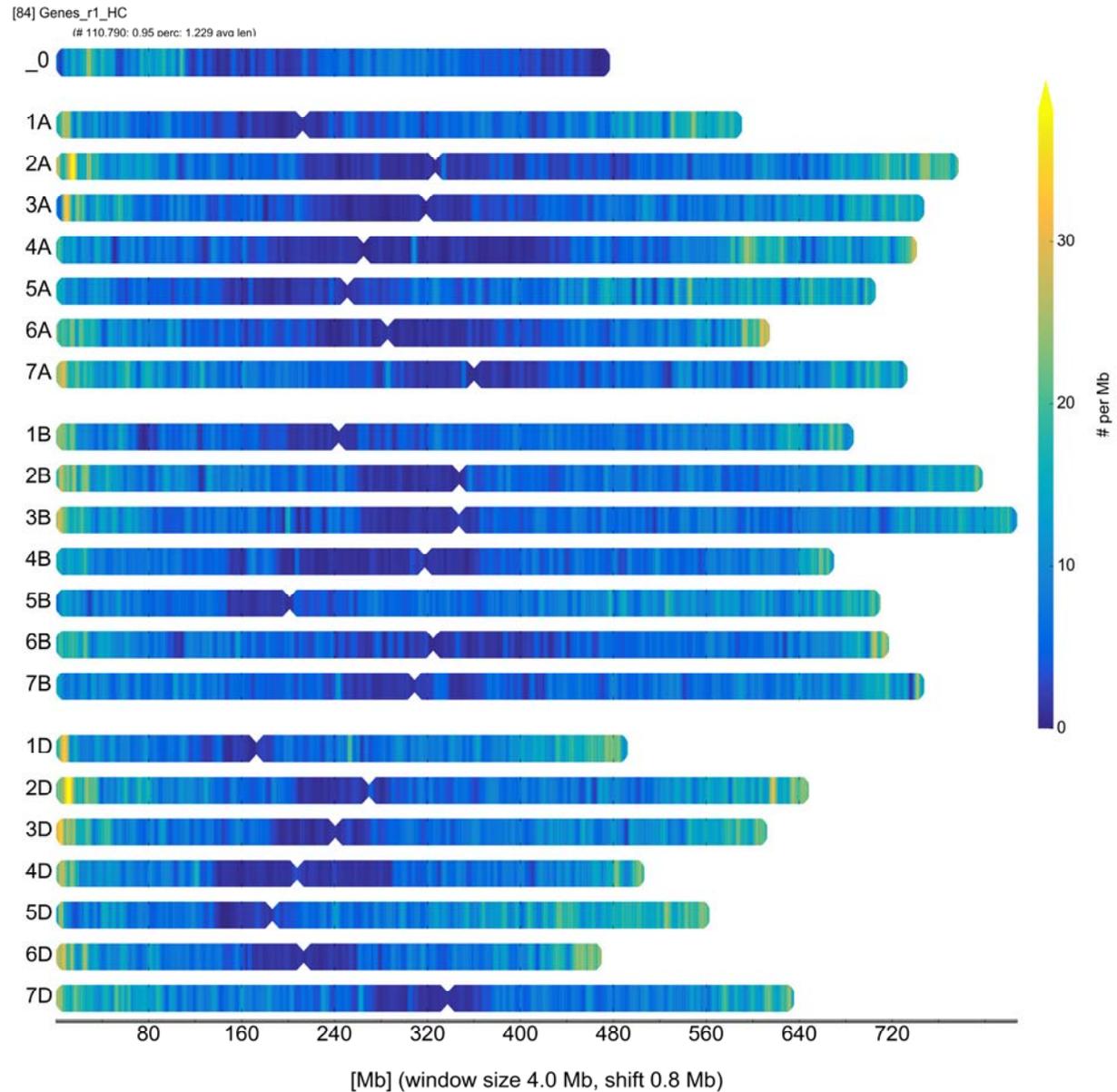
Distinct chromosomal compartments:

Zone 1: the „quite“ neighborhood:
centromer/housekeeping

Zone 2: the „industrial area“: middle parts

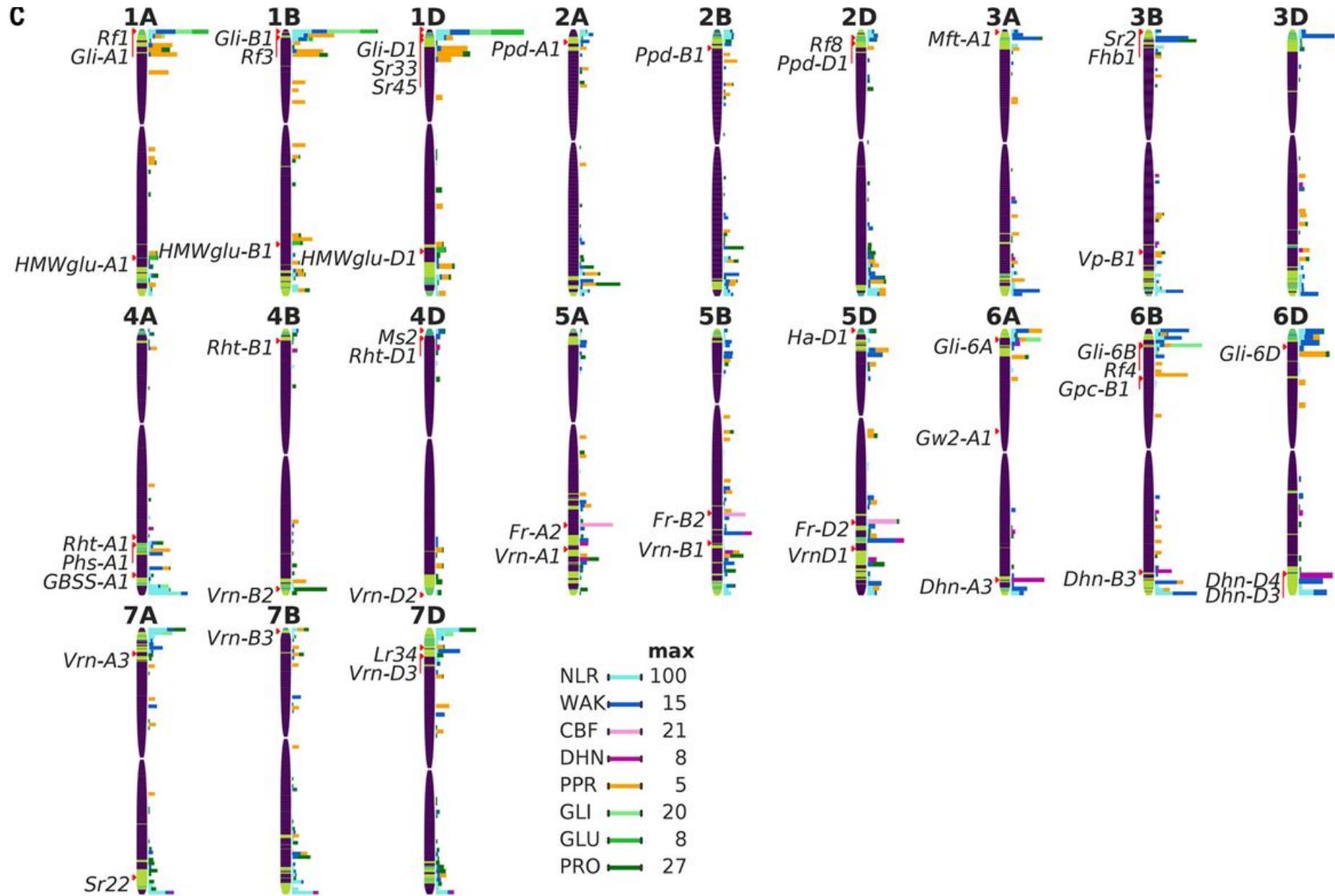
Zone 3: the „innovation quarter“: chromosome
ends/high recombination

Genomic distribution of genes



What is it good for?

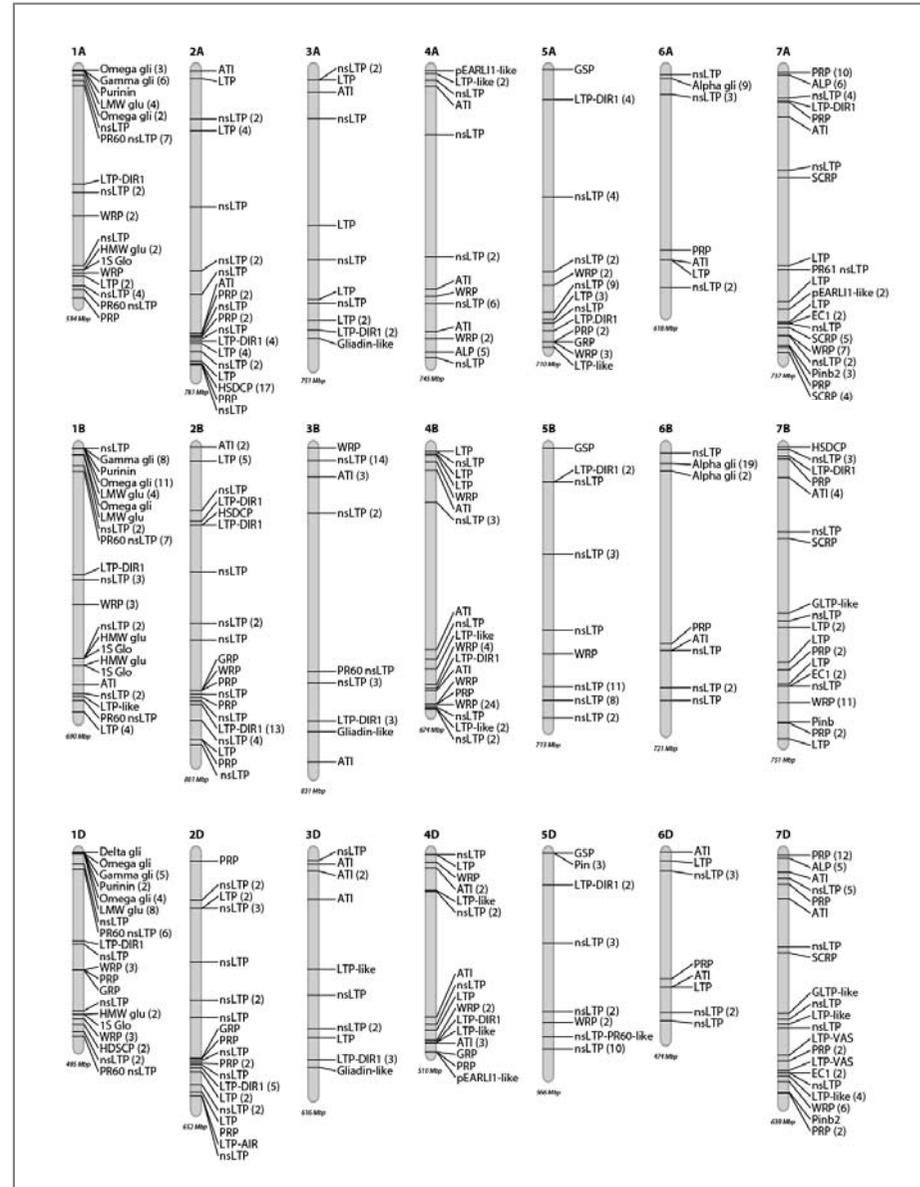




First comprehensive map of wheat prolamins

IWGSC, Science 2018

- Within the IWGSC RefSeq v1 annotation, 731 proteins were manually corrected, including 135 proteins that were added as a completely new sequence
- Expressed everywhere e.g. in roots, leaves, spike, pollen or grain



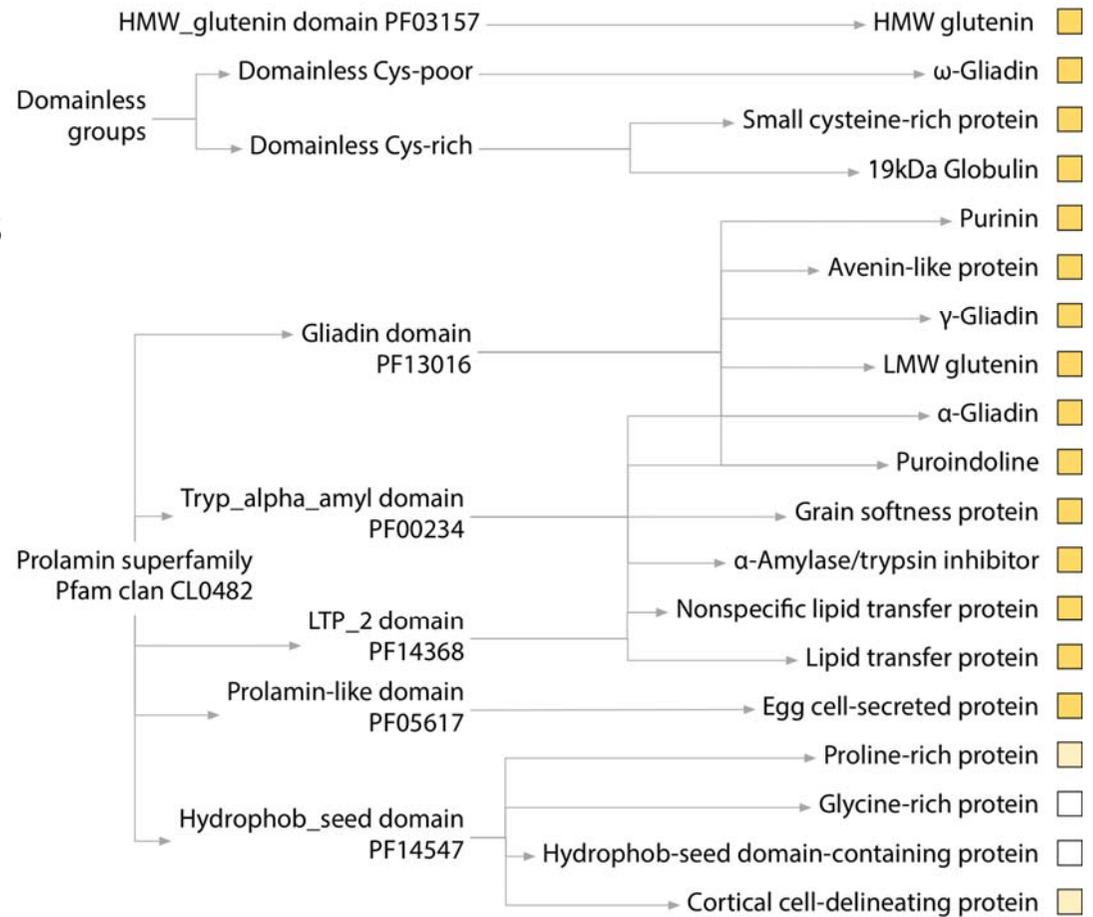
The wheat prolamins superfamily

Juhasz et al., Science Advances, 2018

Pfam domains – Prolamin clan CL0482

- Gliadin
- Tryp-alpha-amyl
- LTP2
- Hydrophob_seed
- Prolamin-like

- HMW glutenins
- Domainless protein groups
- omega gliadins
- small cysteine-rich proteins

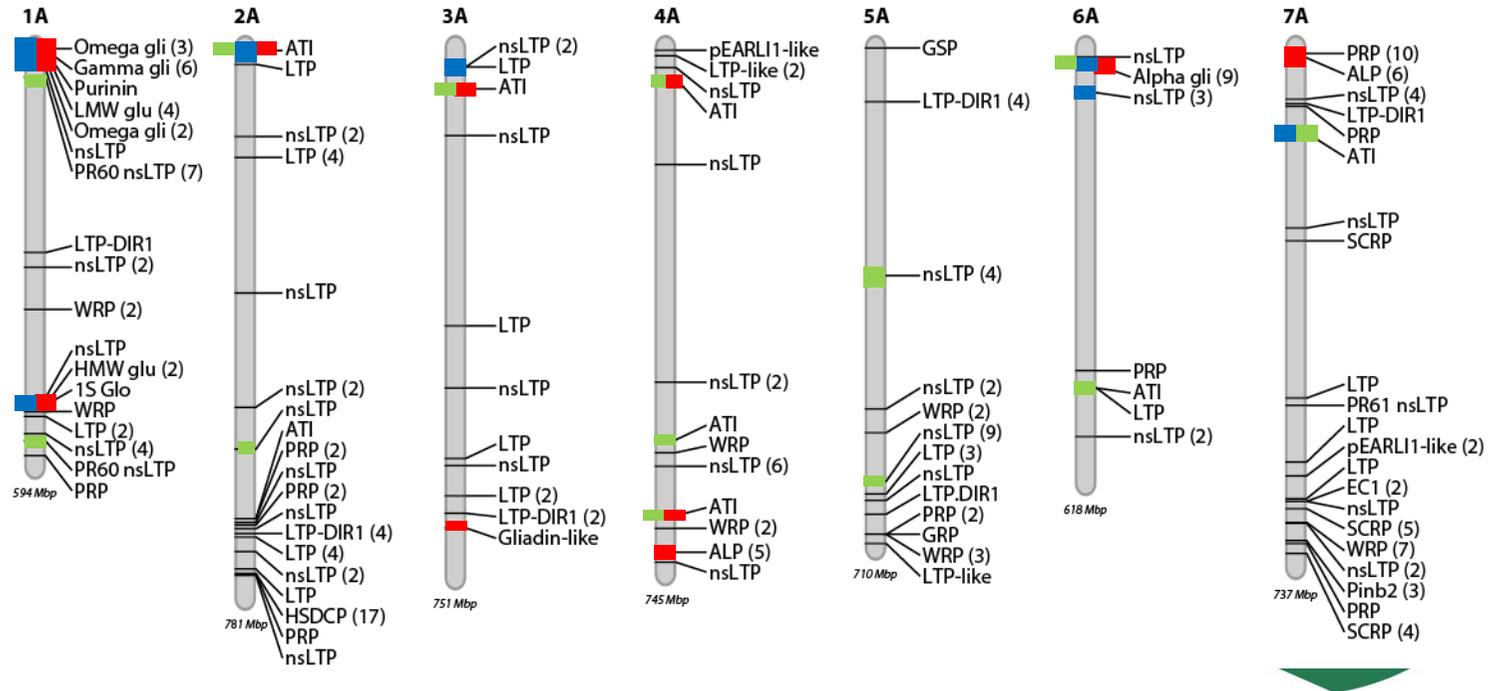


The classic prolamins as immune reactive proteins

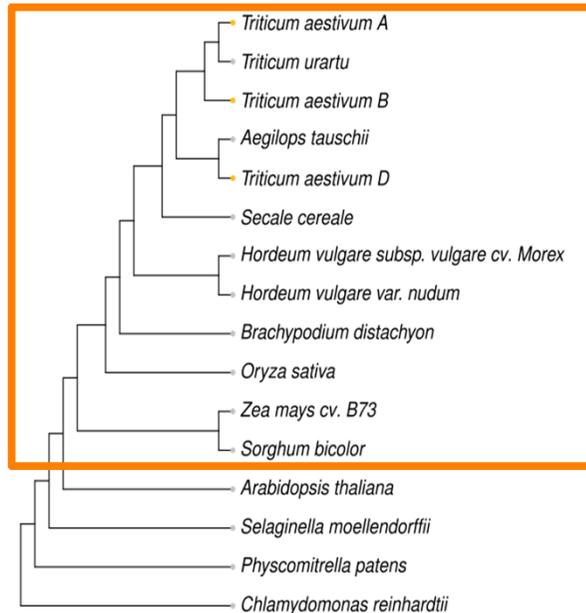
Juhasz et al., Science Advances, 2018

A genome

- Celiac disease
- Wheat allergy
- Baker's asthma



The Prolamin Clan in Grasses



Creation of gene family dataset:

- Protein sequences screened for known domains using HMMER3
- protein sequences were clustered by similarity NCBI blast+
- “gene families” were constructed in the form of orthologous groups using OrthoFinder
- All protein sequences with a HMW glutenin or a Prolamin clan domain were extracted → **1783 sequences**

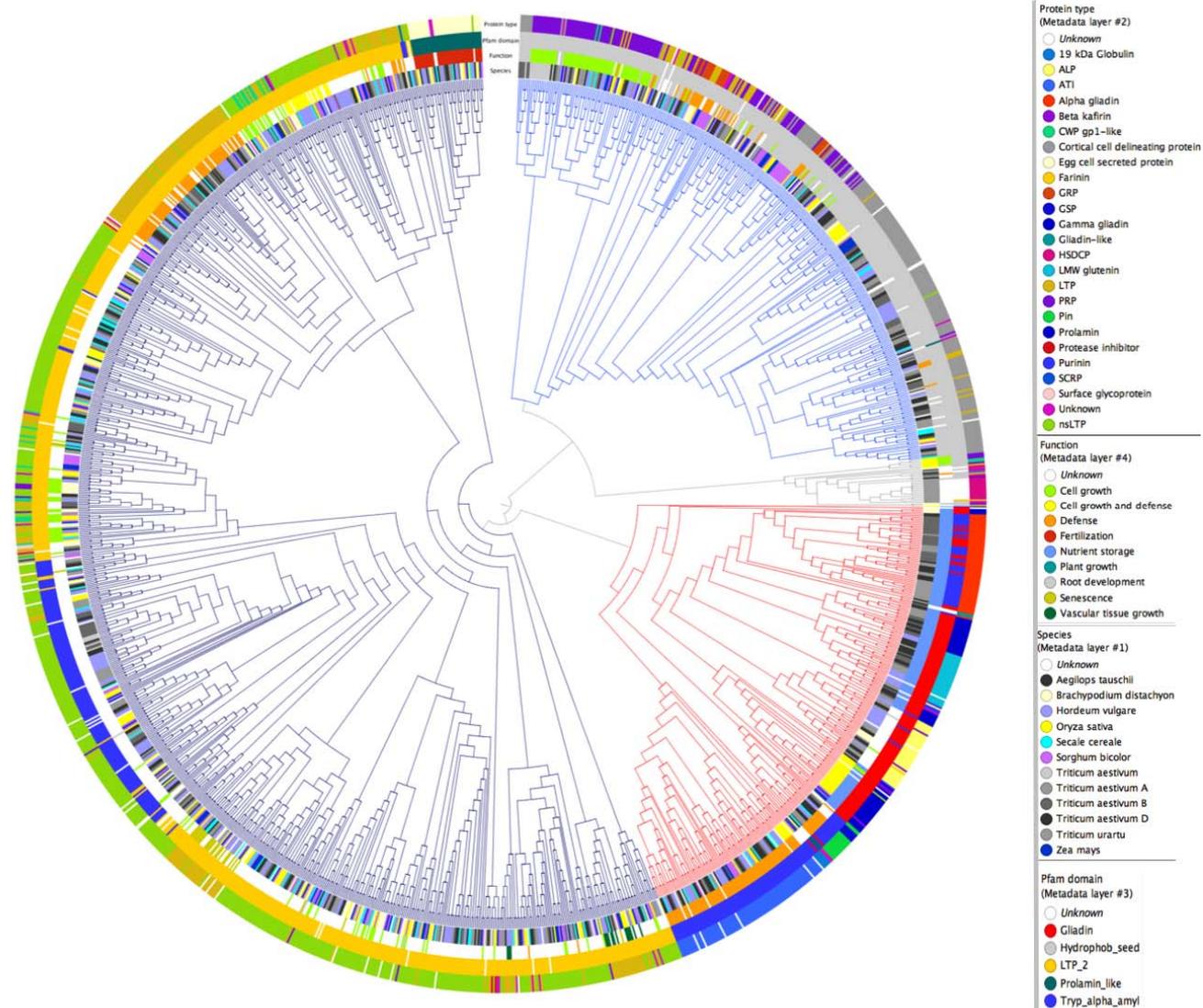
Juhász et al. 2018, Sci. Adv.

Tree of Prolamin Clan sequences

Hydrophob seed:
Cell growth, Root
development, defense

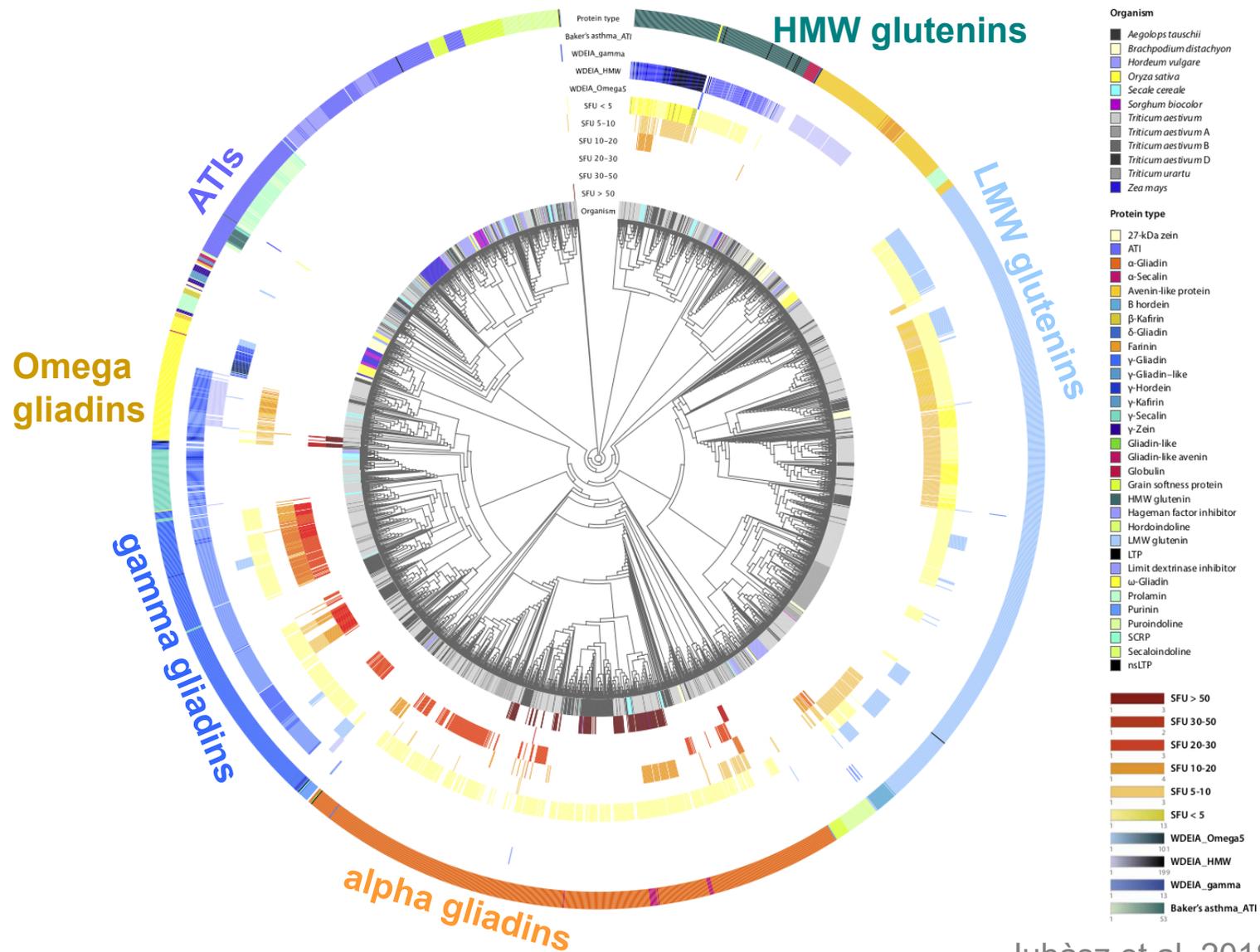
LTP_2,
Tryp_alpha_amy:
Cell growth,
Senescence
Prolamin-like :
Fertilization

Gliadin,
Tryp_alpha_amy:
Nutrient storage,
defense



Juhász et al. 2018, Sci. Adv.

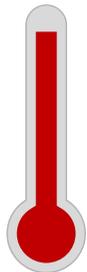
Celiac disease & Baker's asthma epitopes



Juhász et al. 2018, Sci. Adv.

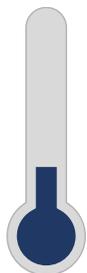
Seed allergen expression in different environments

Juhasz et al., Science Advances, 2018



High temperature

Increasing effect on the celiac disease associated gene expressions – gliadins and glutenins

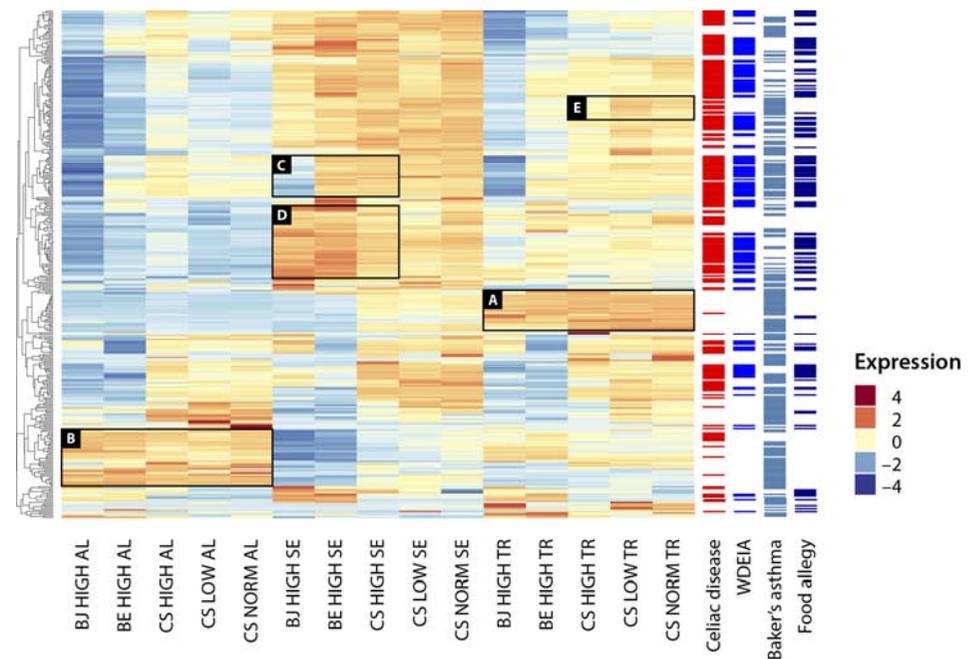


Low temperature

Increasing effect on baker's asthma and food allergy genes

Chinese Spring
Bjarne
Berserk

Low: 15/10°C day/night
Normal: 20/16°C day/night
High: 26/20°C day/night

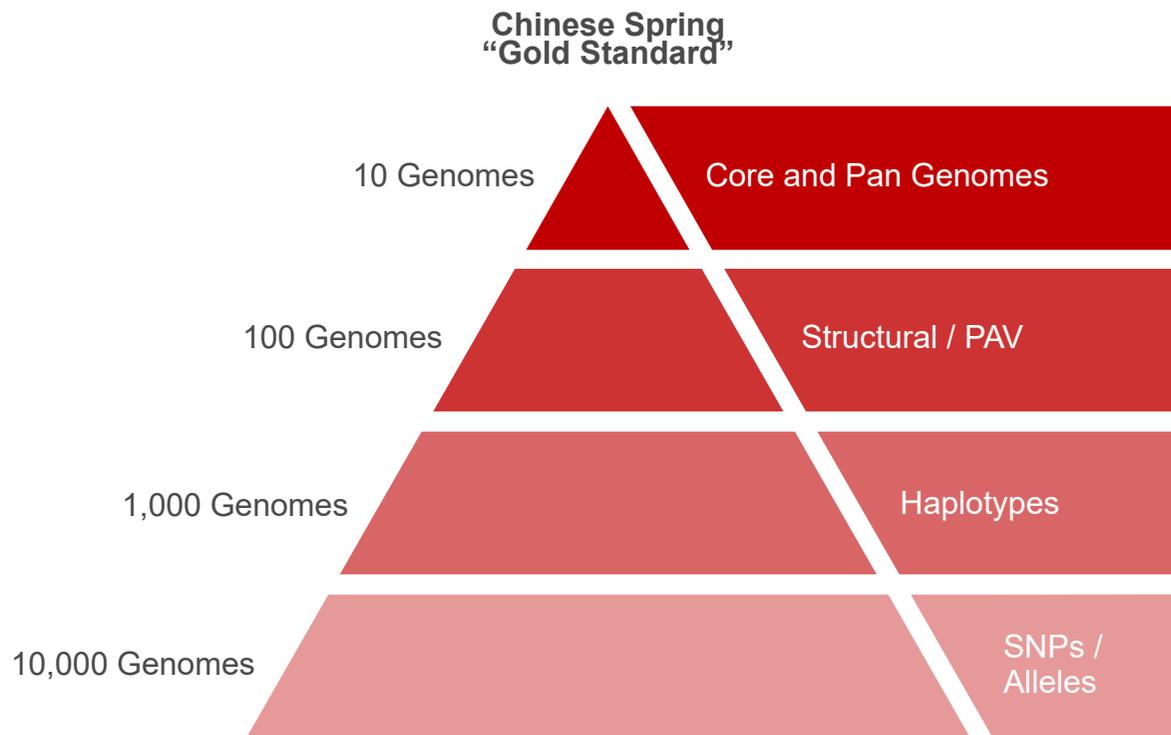


What's next??



One reference genome is not enough!





The Ten+ Genomes Project

NRGene
RefSeq
Assemblies

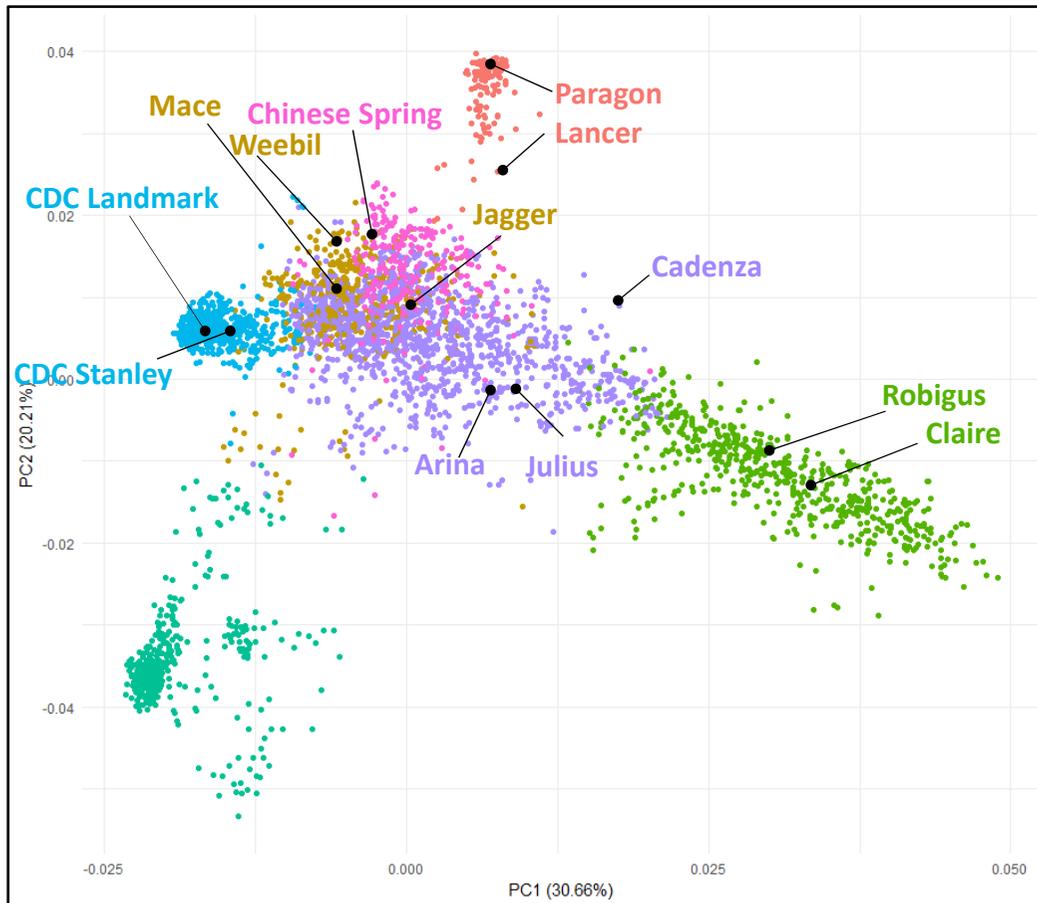


- 2 Canadian spring wheat (**CDC Landmark, CDC Stanley**)
- 1 USA (**Jagger**) - J. Poland, G. Muehlbauer
- 1 German winter wheat variety (**Julius**) – N. Stein, K. Mayer
- 1 Swiss winter wheat variety (**Arina**) – B. Keller
- 2 Australian varieties (**Mace, Lancer**) – P. Langridge
- 1 Japanese variety (**Norin61**) – K. Shimizu
- 2 Chinese varieties (**Kenong 9204***) HongQing Ling
- Syngenta – (**SY Mattis**)

W2RAP
Assemblies

Cadenza, Paragon, Kronos, Robigus, Claire

Harnessing the diversity from global breeding programs



Genomic Diversity Analysis:

- 3,819 samples (mostly hexaploid)
- 1,779 SNP markers from the 35K and 90K arrays, distributed across all chromosomes
- PCA transformed and clustered using k-means

Tetraploid wheats – the wild and the domesticated



wild emmer wheat

T. turgidum ssp. *dicoccoides*



Durum (pasta) wheat

T. turgidum ssp. *durum*

- A and B subgenome, genome size ~10 Gb
- plus diploid wheats and ancestors + Rye & Spelt

Perspectives...what else is it good for?

- ✓ Gene and marker discovery!
 - ✓ Predictive Breeding/genomic selection
 - ✓ Accessing variation
 - ✓ Reduced genetic variation in modern breeding lines;
 - ✓ Only 10% of genetic variation in wheat has been captured in modern varieties
 - ✓ Comparative Triticeae Genomics – the non-recombining part of the genome, gene regulation/networks
 - ✓ Towards a less allergenic wheat...
-

Meet the team...



PGSB

Daniel Lang
Heidrun Gundlach
Thomas Lux
Iris Fischer
Michael Seidel
Verena Prade
Nadia Kamal
Georg Haberer
Sven Twardziok
Klaus Mayer

Murdoch University

Angela Juhasz
Rudi Appels

Norwegian Academy of Lifesciences

Tetiana Belova
Odd-Arne Olsen



www.wheatgenome.org



Acknowledgements Wheat

IWGSC Sponsors



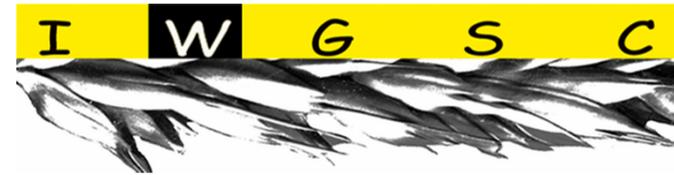
MONSANTO



I W G S C



Acknowledgements Wheat



IPK
Nils Stein
Martin Mascher

IPK BIT
Sebastian Beier
Uwe Scholz

IEB Olomouc
Hana Simkova
Jaroslav Dolezel

INRA
Fred Choulet
Etienne Paux
Michael Alaux
et. al.

PGSB
Heidrun Gundlach
Thomas Lux
Iris Fischer
Daniel Lang
Verena Prade
Georg Haberer
Michael Seidel
Sven Twardziok
Klaus Mayer

Murdoch University
Angela Juhasz
Rudi Appels

Norwegian Academy of Lifesciences
Tetiana Belova
Odd-Arne Olsen

IWGSC: Kellye Eversole, Jane Rogers
Bayar: Catherine Feuillet
Univ. of Zurich: Thomas Wicker & Beat Keller
Univ. of Udine: Michele Morgante et al.
KWS: V Korzun
CNRGV: H Berges, A Bellec
Haifa: A Korol, Z Frenkel
KSU: Jesse Poland
TGAC: Mario Caccamo et al.
USASK: Curtis Pozniak
U.Tel Aviv: Assaf Distelfeld
John Innes Center: Cristobal Uauy et al
Earlham Institute: Anthony Hall et al.

WheatScan partners
Katharina Scherf



Bundesministerium für Ernährung und Landwirtschaft



Bundesministerium für Bildung und Forschung





Thank you for your attention!
