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Genome Bioinformatics at GDEC

Frédéric Choulet

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Genome Bioinformatics at GDEC

Frédéric Choulet



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Clermont
Auvergne



GDEC

Université Clermont Auvergne Campus des
Stade des eaux

Clermont-Ferrand

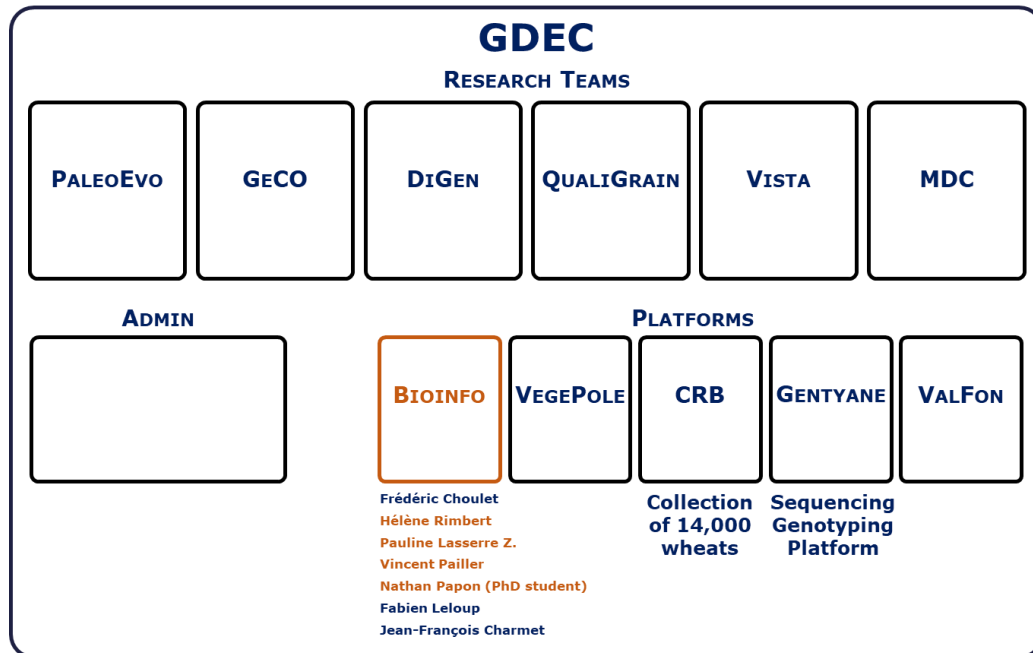
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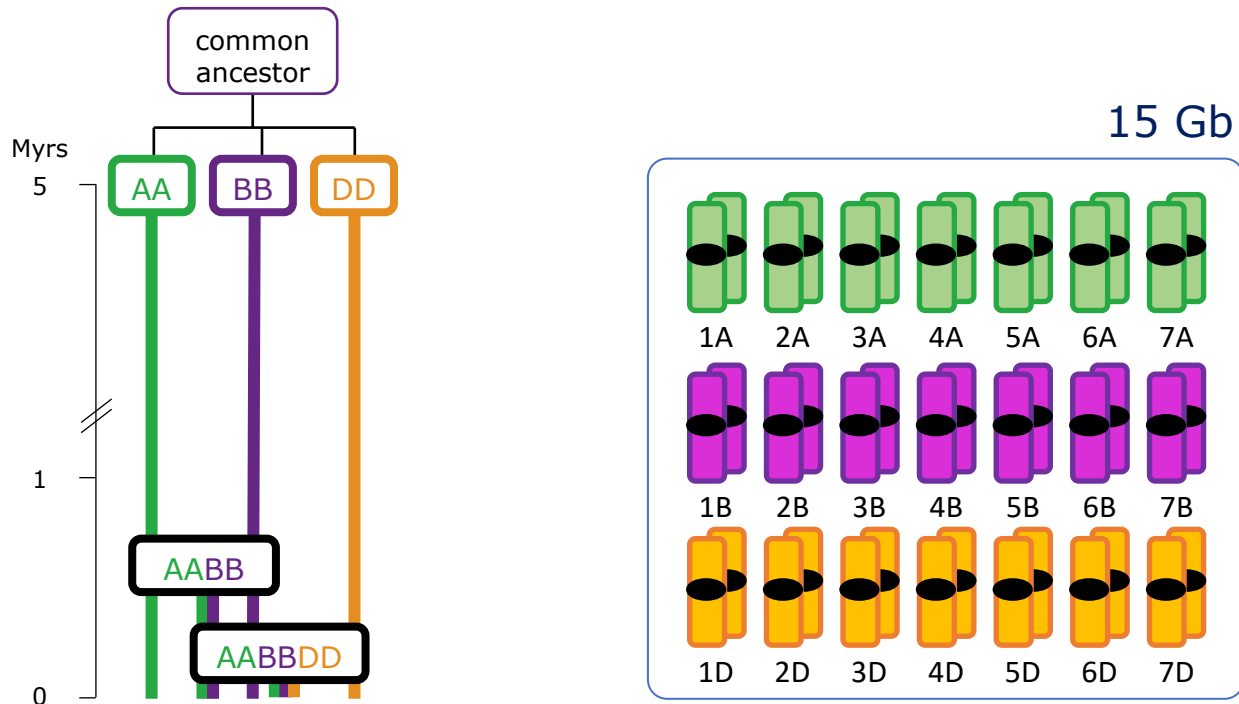
- Bioinfo for bread wheat and *Triticeae* (pan)genomics



❖ Research area and questions

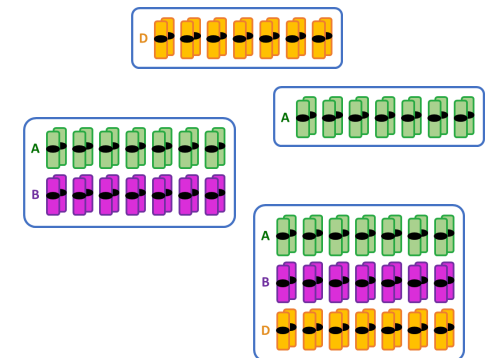
- Methodologies
 - Gene and transposon prediction in genomes
 - Comparative genomics
 - How to compare “complex” genomes?
- Genome Biology
 - What is the extent of diversity? Pangenomics
 - What is the dynamics of transposons?
 - What is the impact of polyploidy on transposon activity?
 - ...

❖ Hexaploid genome



Triticum/Aegilops

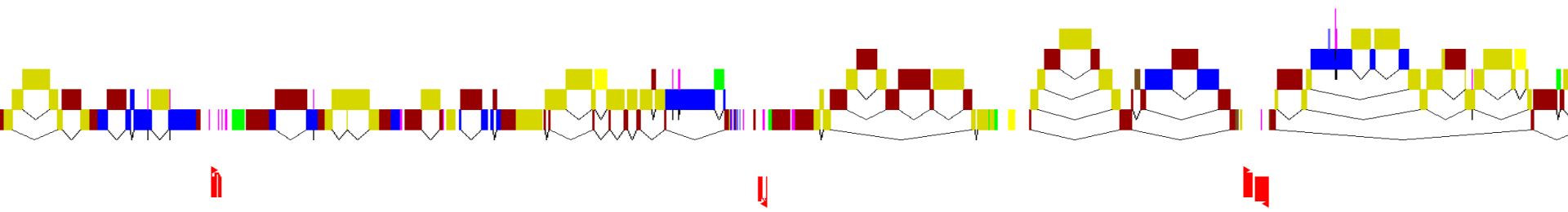
- Wild **diploids** (AA, BB, DD, SS, UU, NN, ...)
- Wild & cultivated **tetraploids** (AABB, DDNN, ...)
- Cultivated **hexaploids** (AABBDD)



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❖ Genome composition

- Transposons (85%)
- Genes (2%)

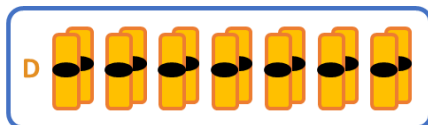
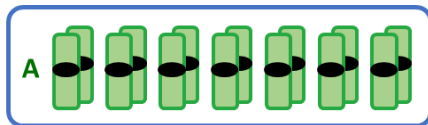
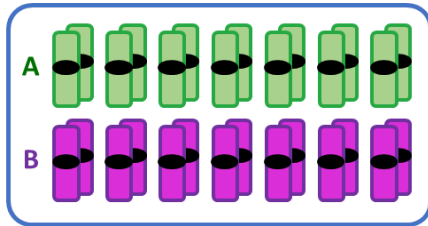
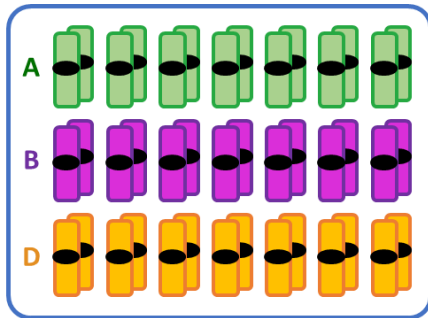


1st genome seq assembled:

Chinese Spring (*IWGSC Science 2018*)

- 4 million TEs
- ~107,000 genes

❖ Pangenomics



- *T. aestivum*

- **Chinese Spring** (Illumina)
- 10 other varieties (Illumina)
- Zang1817 (Illumina)
- Fielder (Pacbio)
- Kariega (Pacbio)
- Renan (ONT)
- Attraktion (Pacbio)

IWGSC 2018

Walkowiak et al. 2020

Guo et al. 2020

Sato et al. 2021

Athiyannan et al. 2022

Aury et al. 2022

Kale et al. 2022

- *T. durum* **AABB**

- *T. dicoccoides* **AABB**

- *T. urartu* **AA**

- *Ae. tauschii* **DD**

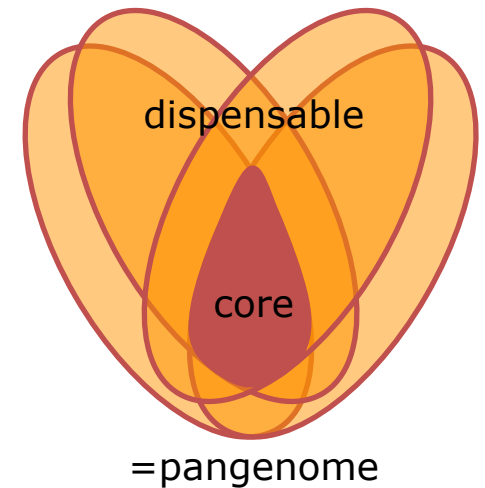
- *Ae. searsii* **DD**

- *Ae. bicornis* **DD**

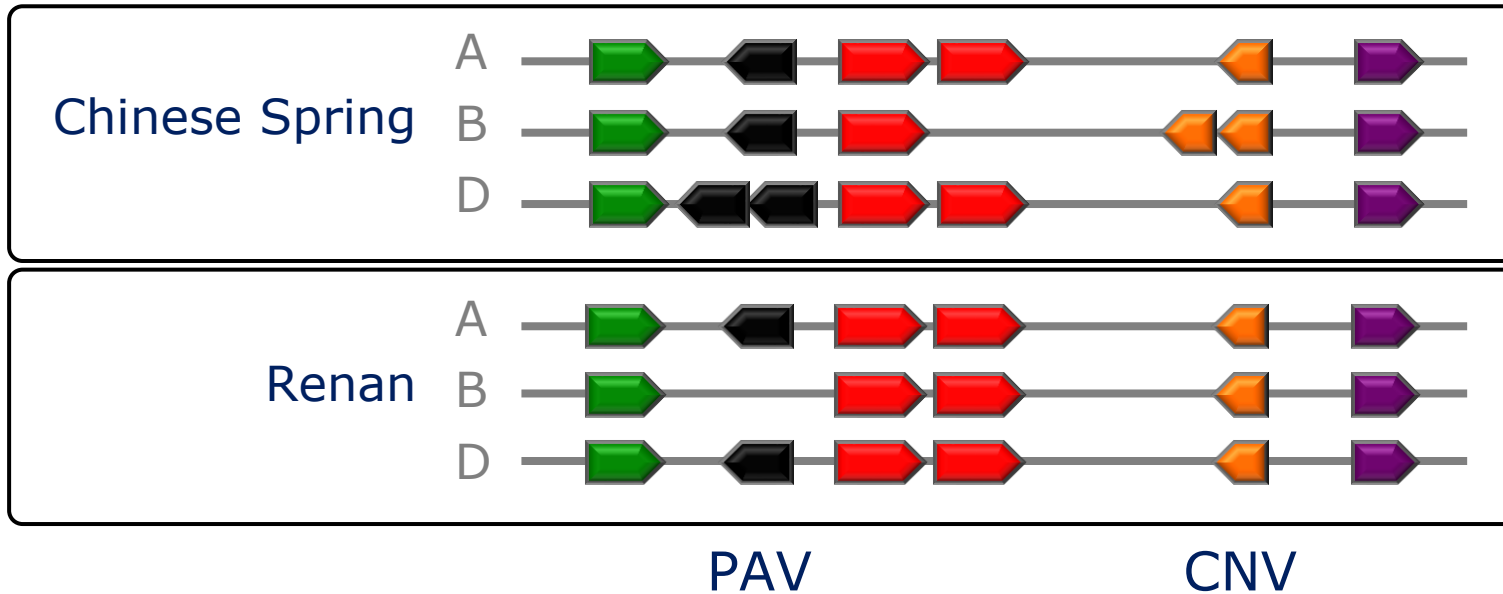
- *Ae. longissima* **DD**

- *Ae. sharonensis* **DD**

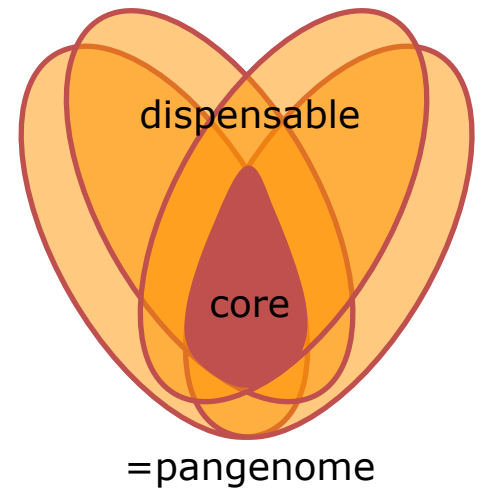
- *Ae. speltoides* **SS**

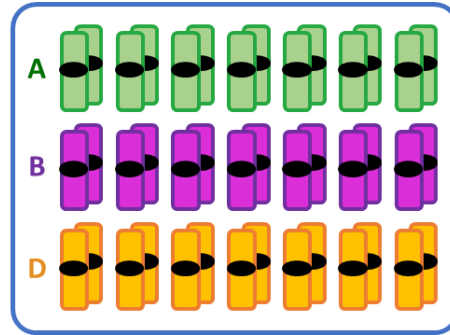


❖ Pangenomics

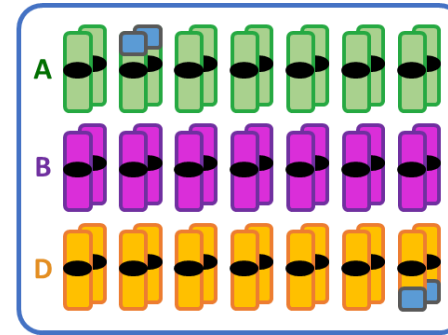


- Chromosome-scale assemblies required
- Quality of annotation matters



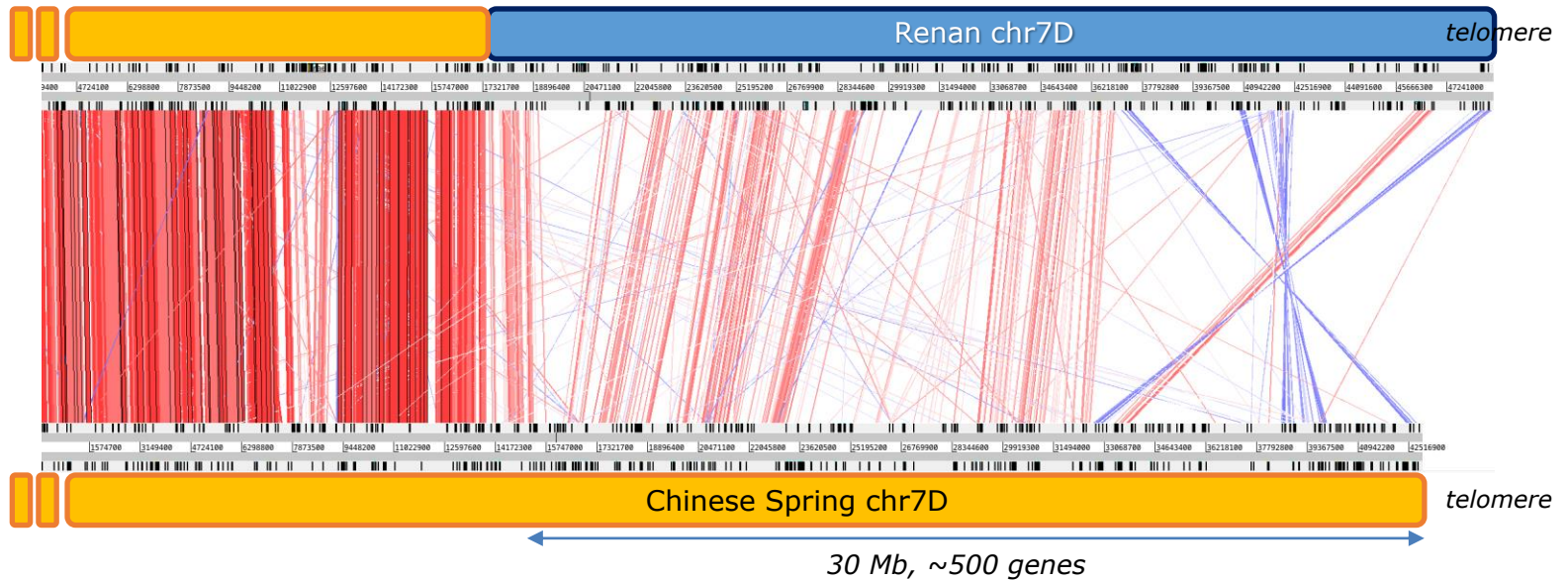


Chinese Spring



Renan

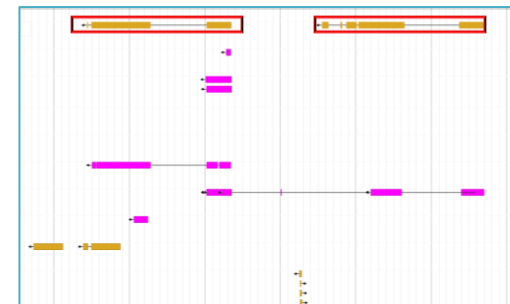
- ✓ Nanopore
- ✓ Illumina
- ✓ Bionano
- ✓ HiC



❖ **Genes**

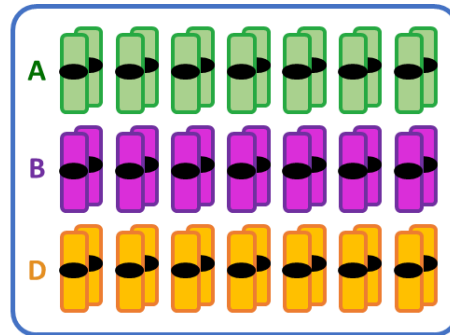
❖ Gene annotation

- Predicting genes is not trivial
 - *de novo* gene prediction not adapted to pangenomics

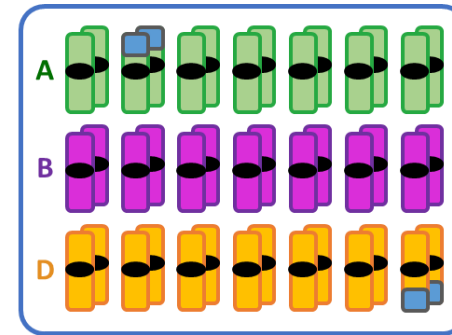


❖ Gene annotation


- Predicting genes is not trivial
 - *de novo* gene prediction not adapted to pangenomics
- Mapping a reference gene set sounds better
 - Develop **MAGATT** (*H. Rimbart*)



Chinese Spring



Renan

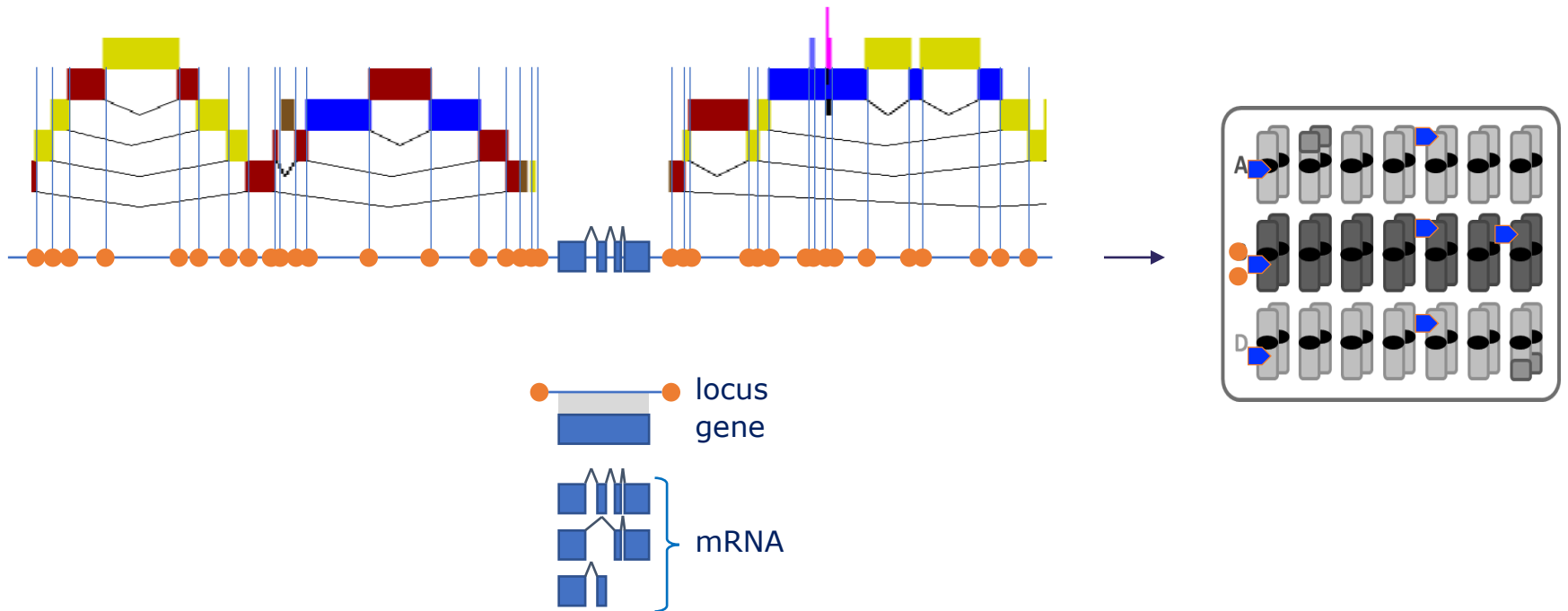

107k genes

Gmap
→

**88% of genes
mapped
unambiguously**

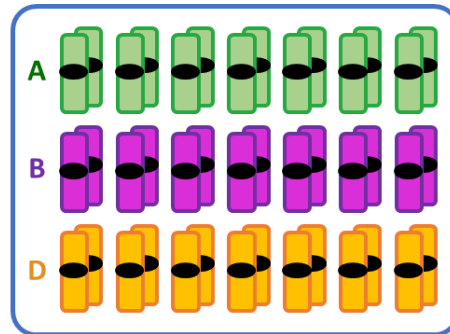
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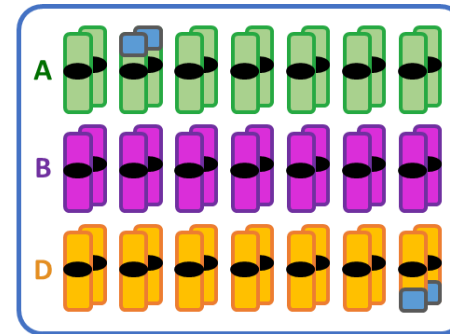


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Chinese Spring



Renan


107k genes

Gmap
→

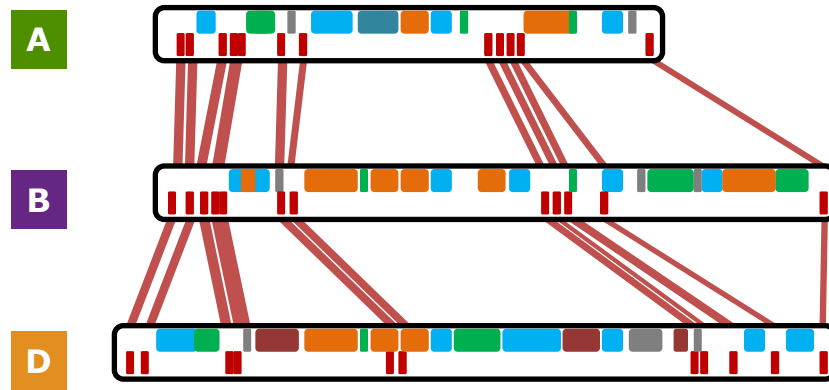
88% of genes
mapped
unambiguously

MAGATT
→

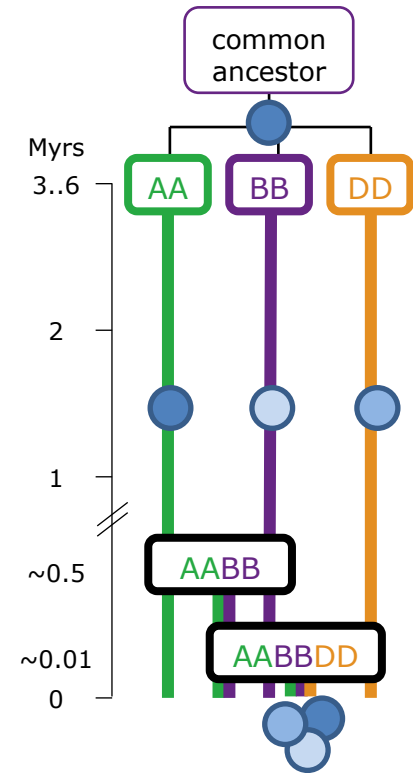
**98% of genes
mapped
unambiguously**

❖ **Transposons**

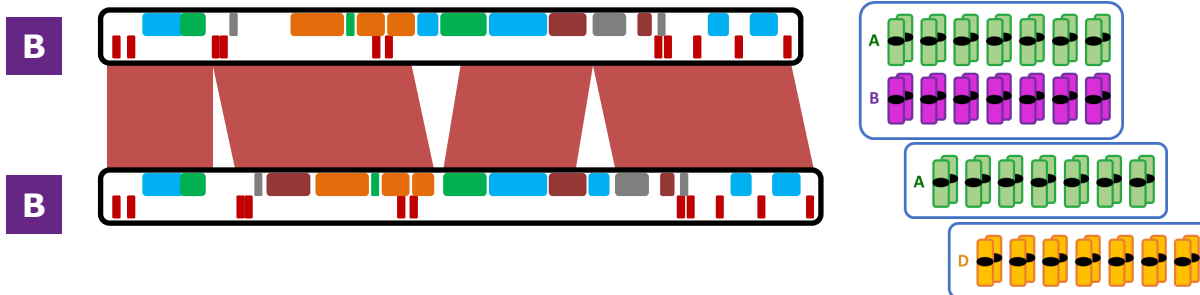
❖ Transposon dynamics



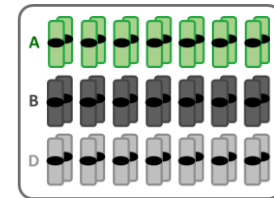
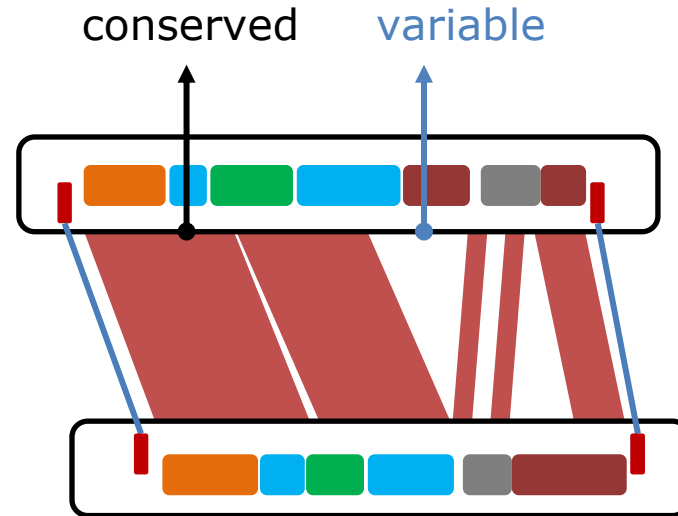
➤ **Equilibrium** model of evolution



PhD Nathan Papon (2019-2023)



❖ Transposon dynamics



- **Method: bp-resolved gene anchored whole-genome**

- How variable is the TE space? ➤ 5 .. 15%
- Which TE families are active? ➤ ~ all
- Impact of polyploidization? ➤ none

➤ **Transposition highly regulated; transposons may be a key role in shaping a functional genome architecture**

CSH Cold Spring Harbor Laboratory

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New Results [Follow this preprint](#)

All families of transposable elements were active in the recent wheat genome evolution and polyploidy had no impact on their activity

Nathan Papon, Pauline Lasserre-Zuber, H  l  ne Rimbart, Romain De Oliveira, Etienne Paux, Fr  d  ric Choulet
doi: <https://doi.org/10.1101/2022.11.25.517938>
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ABSTRACT

Bread wheat (*Triticum aestivum* L.) is a major crop and its genome is one of the largest ever assembled at reference-quality level. It is 15 Gb, hexaploid, with 85% of transposable elements (TEs). Wheat genetic diversity was mainly focused on genes and little is known about the extent of genomic variability affecting TEs, transposition rate, and the impact of polyploidy. Multiple chromosome-scale assemblies are now available for bread wheat and for its tetraploid and diploid wild relatives. In this study, we computed base pair-resolved, gene-anchored, whole genome alignments of A, B, and D lineages at different ploidy levels in order to estimate the variability that affects the TE space. We used assembled genomes of 13 *T. aestivum* cultivars (6x=AABBDD), *T. durum* (4x=AABB), *T. dicoccoides* (4x=AABB), *T. urartu* (2x=AA), and *Aegilops tauschii* (2x=DD). We show that 5 to 34% of the TE fraction is variable, depending on the species divergence. Between 400 and 13,000 novel TE insertions per subgenome were detected. We found lineage-specific insertions for nearly all TE families in di-tetra- and hexaploids. No burst of transposition was observed and polyploidization did not trigger any boost of transposition. This study challenges the prevailing idea of wheat TE dynamics and is more in agreement with an equilibrium model of evolution.

Competing Interest Statement

The authors have declared no competing interest.

❖ Acknowledgments

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Jonathan Kitt
Marion Ranoux
Florence Exbrayat
François Balfourier
Etienne Paux
Pierre Sourdille
Sophie Bouchet

○ *Collaborators*

Jean-Marc Aury's team (Genoscope)
Arnaud Bellec (INRAE CNRGV)
Michael Alaux (INRAE URGI)
Thomas Wicker (U Zurich)
Heidrun Gundlach (PGSB Munich)
Manuel Spannagl (PGSB Munich)

○ *IWGSC*

Kellye Eversole, et al.



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○ *Funding*



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