

Whole Genome Sequence of
Aegilops sharonensis Reveals
Inconsistency in the *Sitopsis*
Section Taxonomy

Burkhard Steuernagel

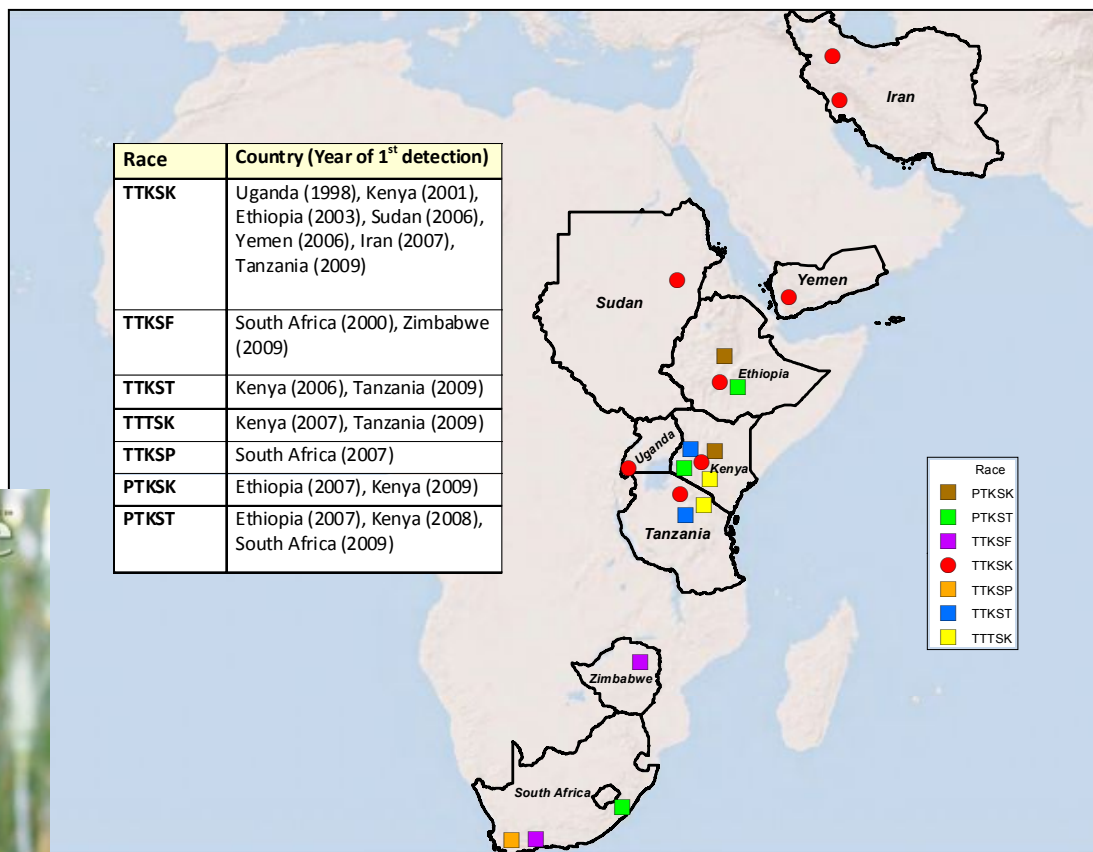
2014-01-11

What has stem rust got to do with a liger?

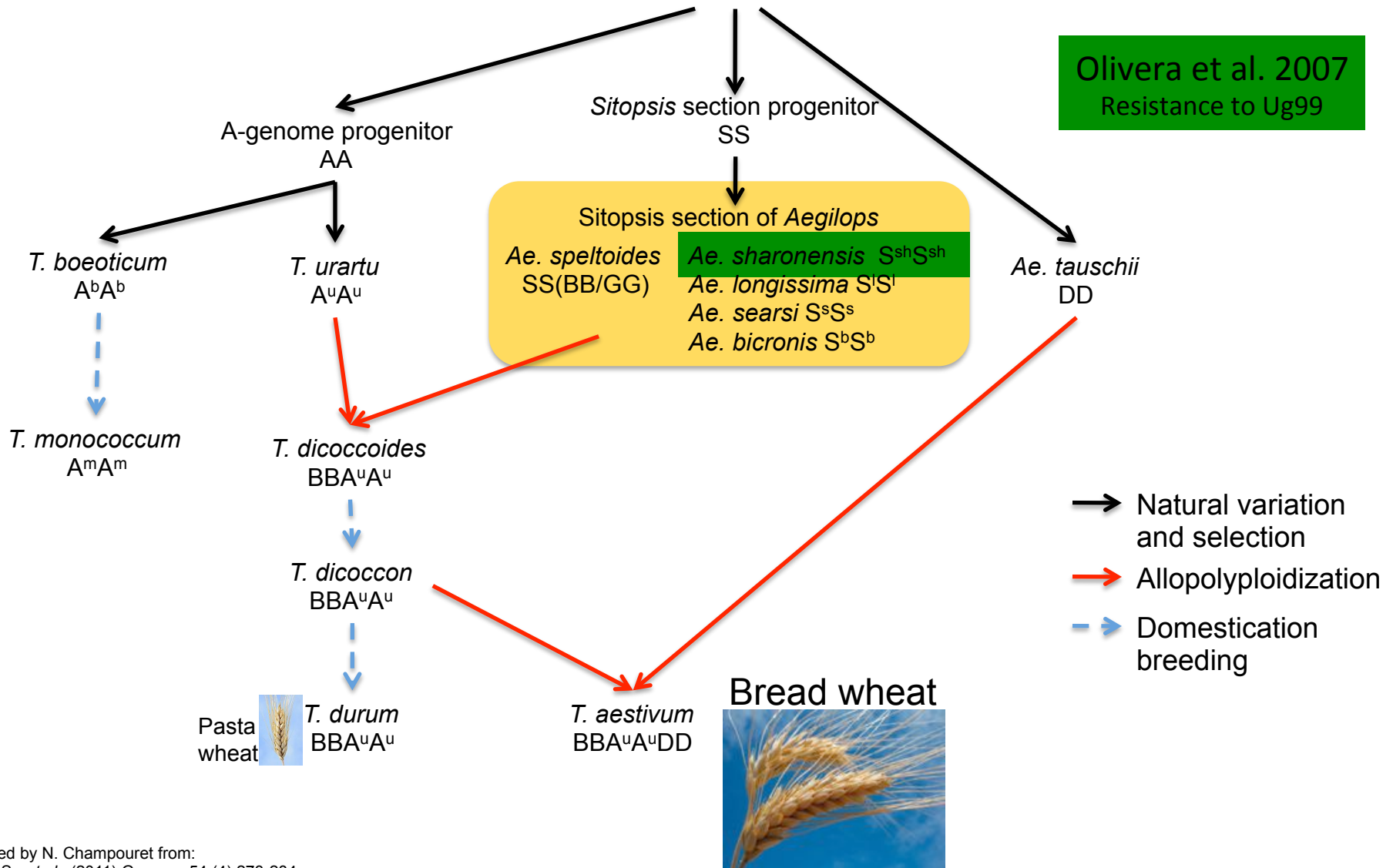


Wheat Stem Rust – A threat from Ug99

- Major *R*-genes from green revolution overcome by isolates from the Ug99 family
- Need for new major *R*-genes



Wheat Related Germplasm



Olivera et al. 2007
Resistance to Ug99

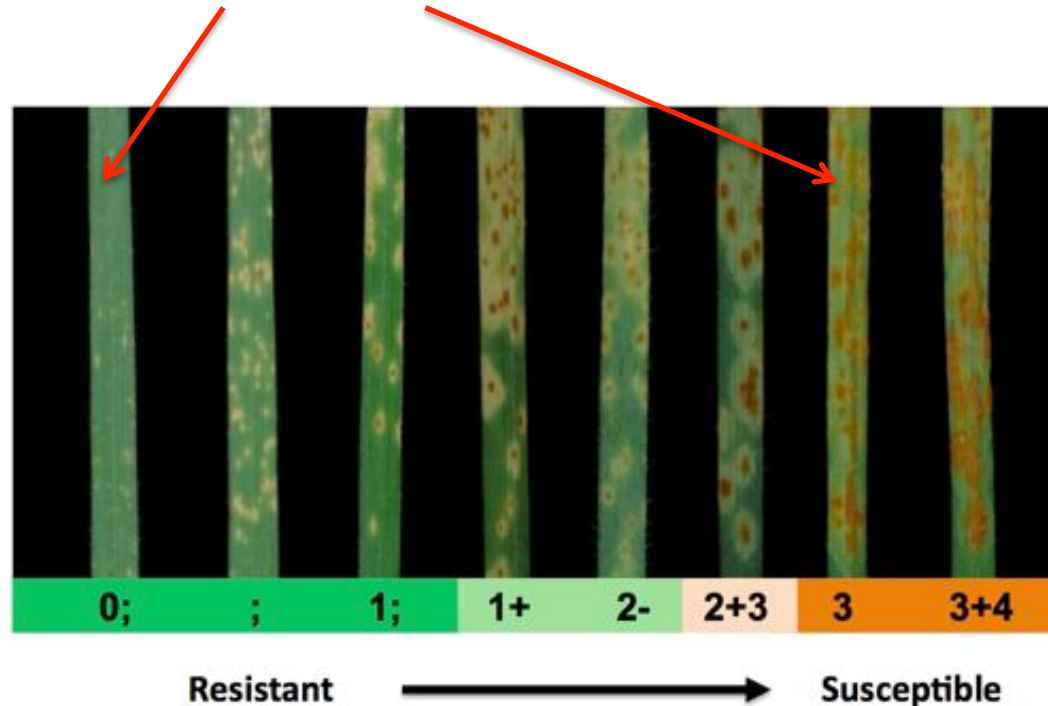
- Natural variation and selection
- Allopolyploidization
- > Domestication breeding



Adapted by N. Champouret from:
Wang S., et al., (2011) Genome 54:(4) 273-284.
Wild Crop Relatives: Genomic and Breeding Resources: Cereals; By Chittaranjan Kole.

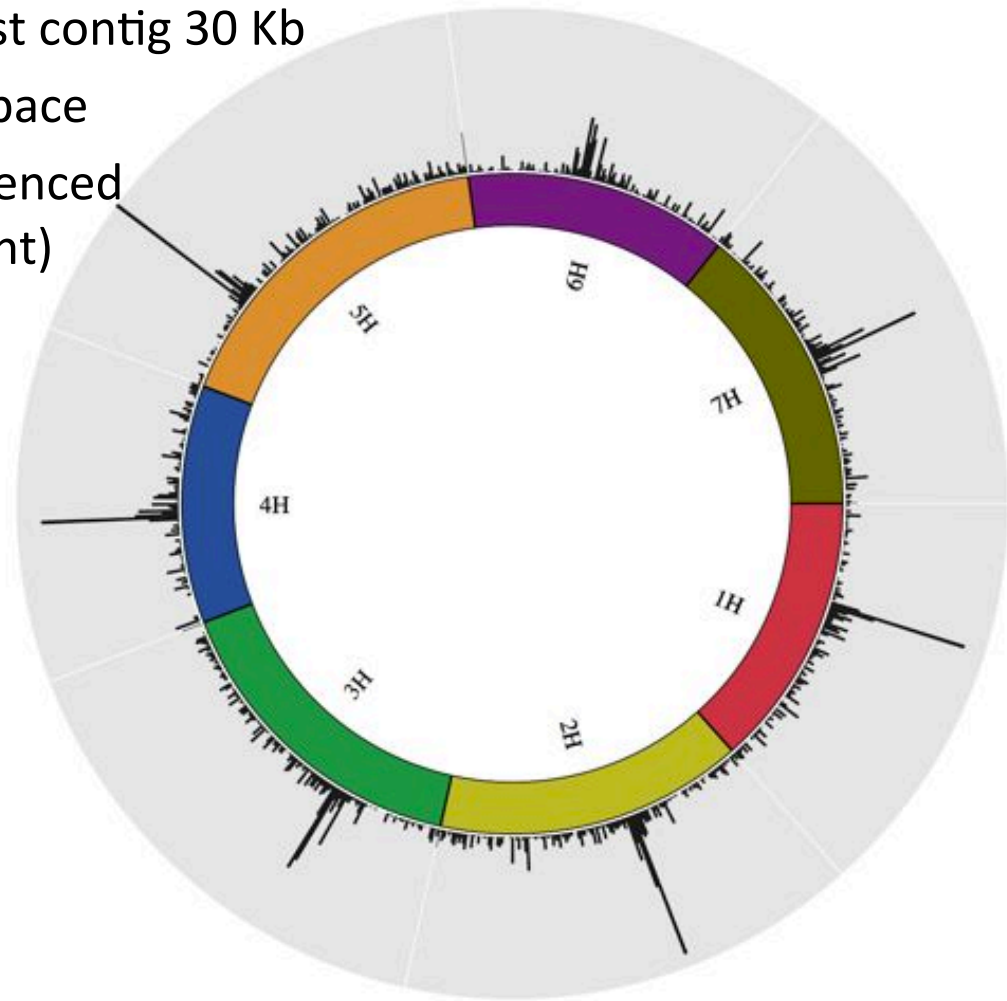
Sequencing of *Aegilops sharonensis*

- 7.3 Gb genome, diploid, 7 chromosomes
- Sequencing Genomes of two accessions
 - each ~30x coverage
 - Accessions: 1644 and 2189



Sequencing of *Aegilops sharonensis*

- Assembly
 - 1.5 Gb; very fragmented; largest contig 30 Kb
 - Good representation of gene space
 - Millions of SNPs between sequenced accessions (marker development)
- Anchoring
 - Genetic map in development
 - Synteny to barley

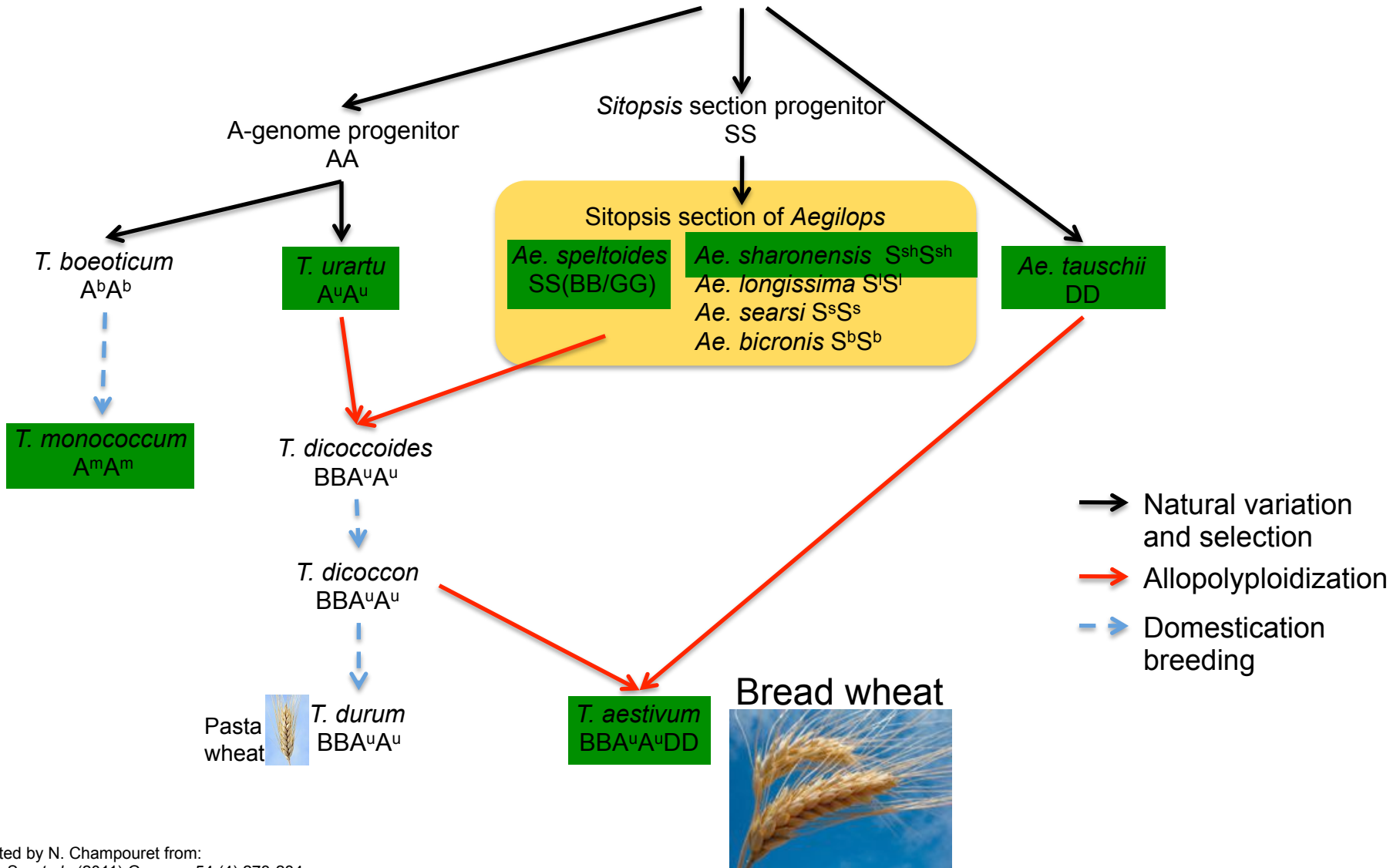


Comparative wheat genomics



- Flow sorting and sequencing of each chromosome arm of hexaploid bread wheat
Sequencing and assembly of individual chromosome arms
- Whole Genome Sequencing of “progenitors”
T. urartu, *T. monococcum*, *Ae. speltoides*,
Ae. tauschii, *Ae. sharonensis*

Wheat Related Germplasm



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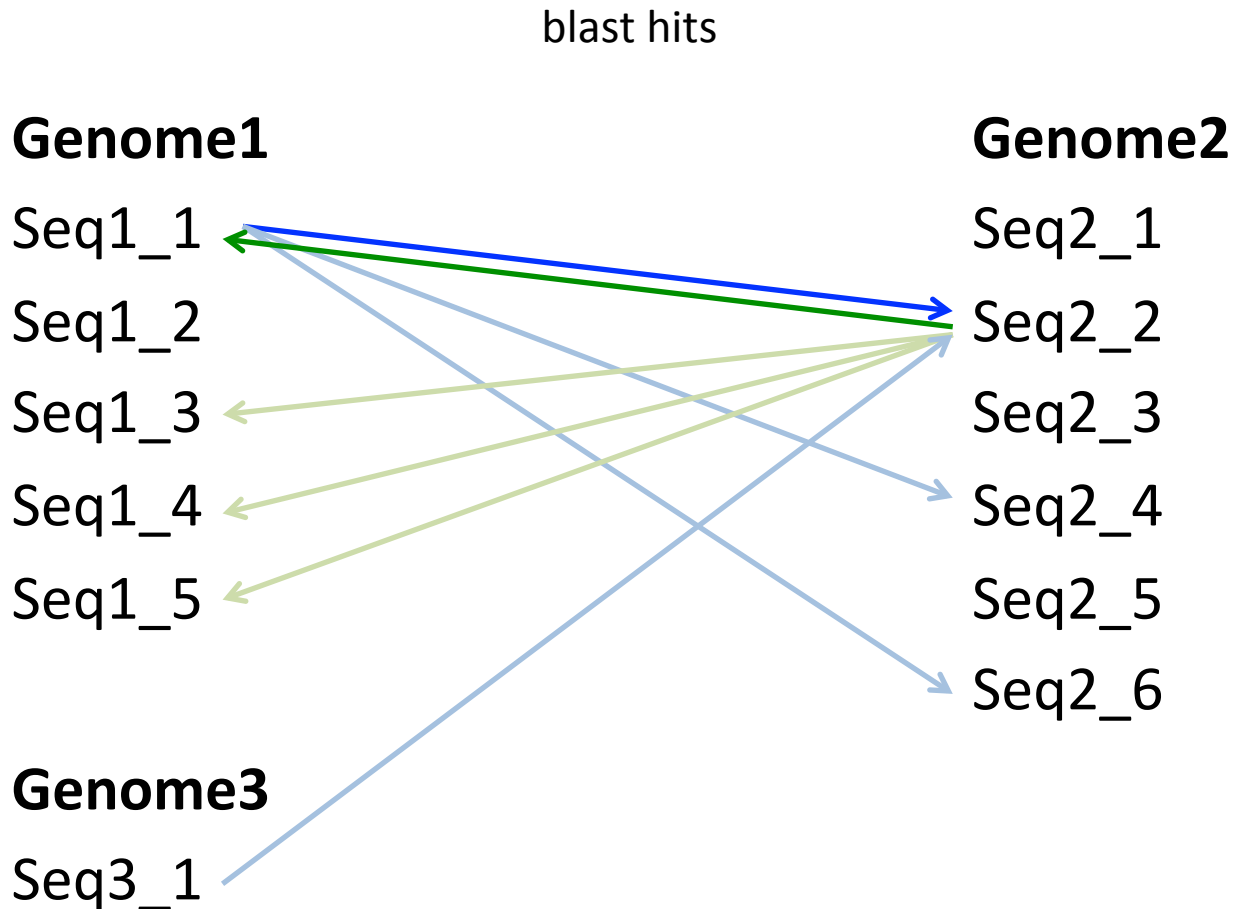
Comparative wheat genomics



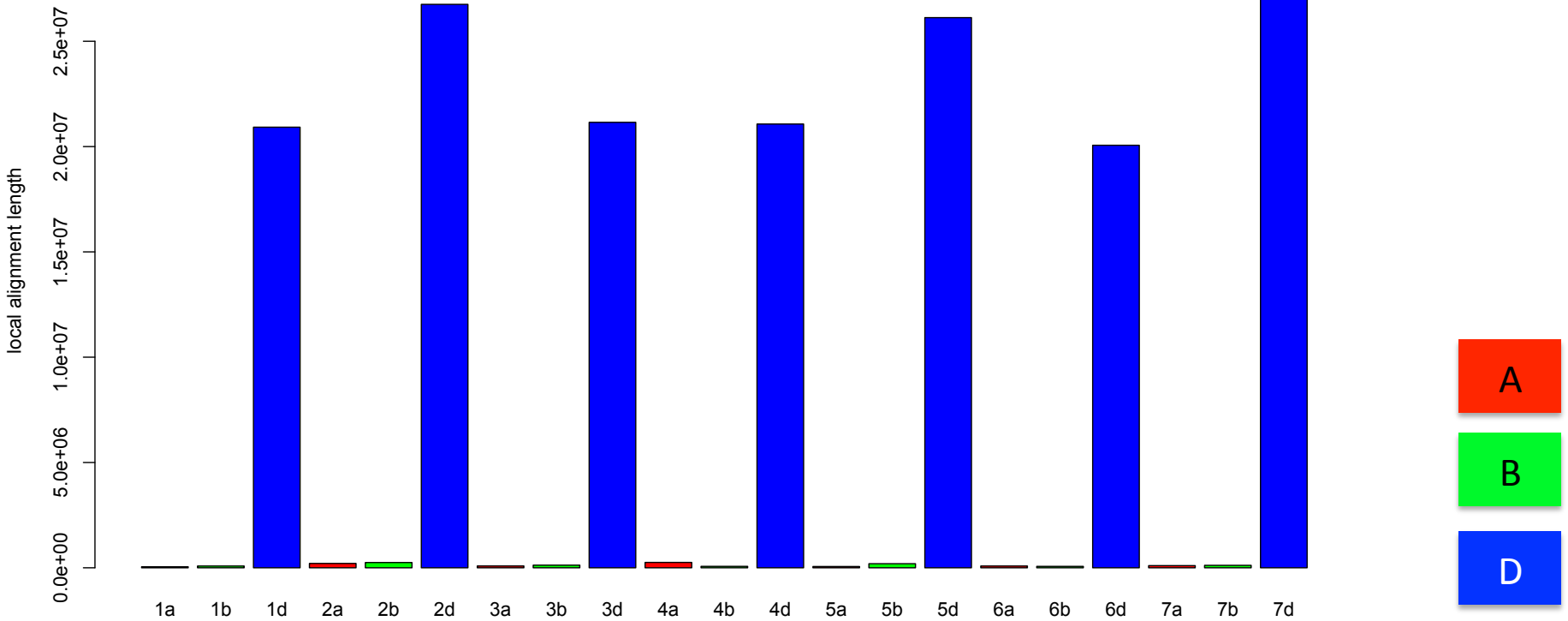
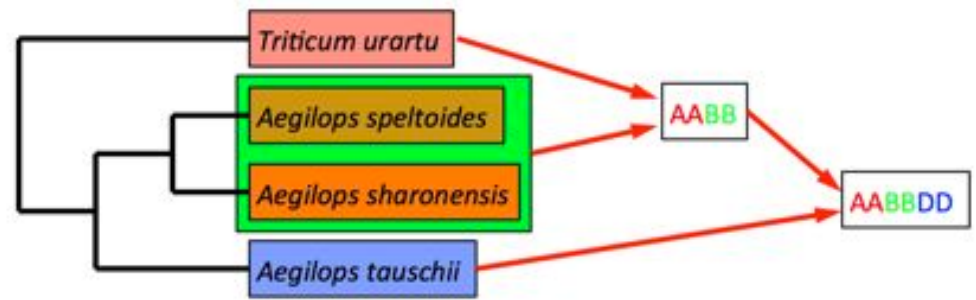
- Flow sorting and sequencing of each chromosome arm of hexaploid bread wheat
Sequencing and assembly of individual chromosome arms
- Whole Genome Sequencing of “progenitors”
T. urartu, *T. monococcum*, *Ae. speltoides*,
Ae. tauschii, *Ae. sharonensis*
- Compare diploid species by alignment to wheat chromosome arms

What is the relation of *Ae. sharonensis* to wheat?

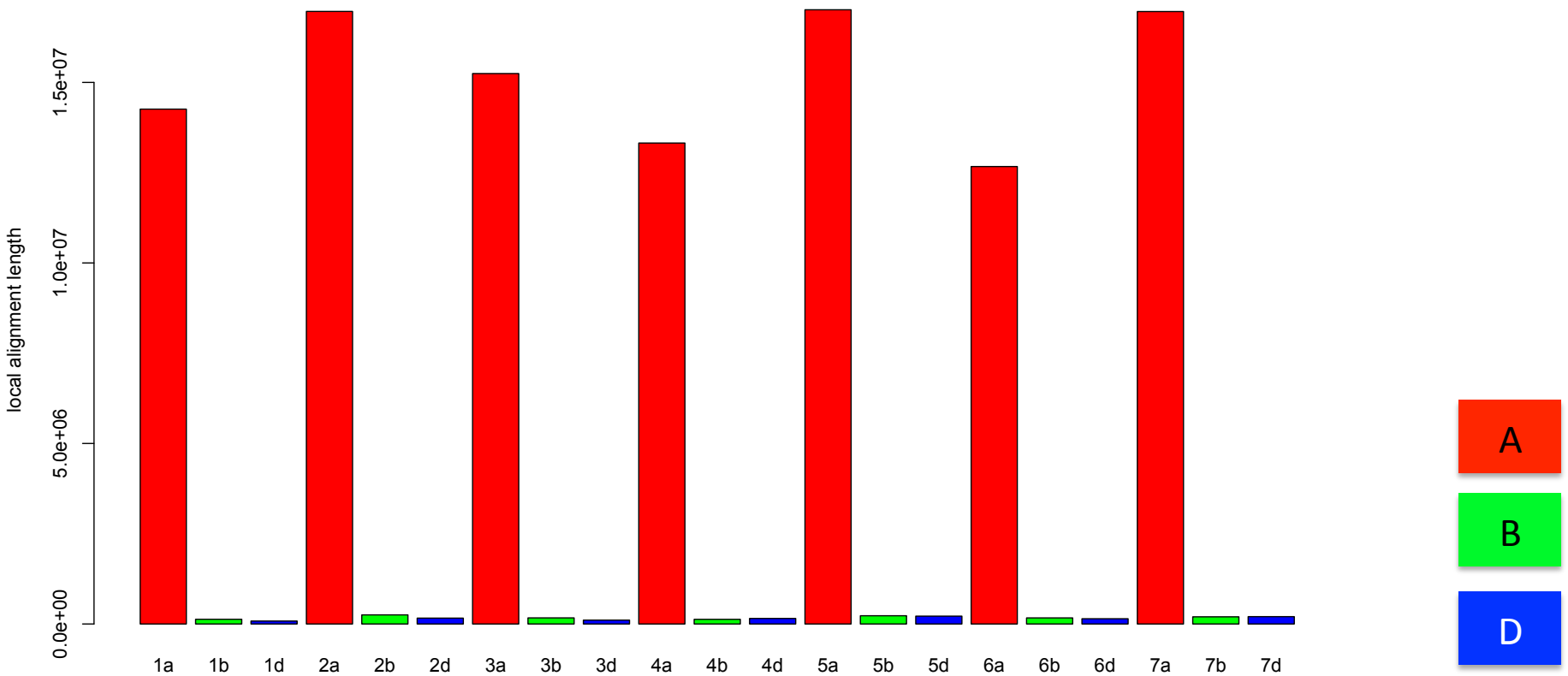
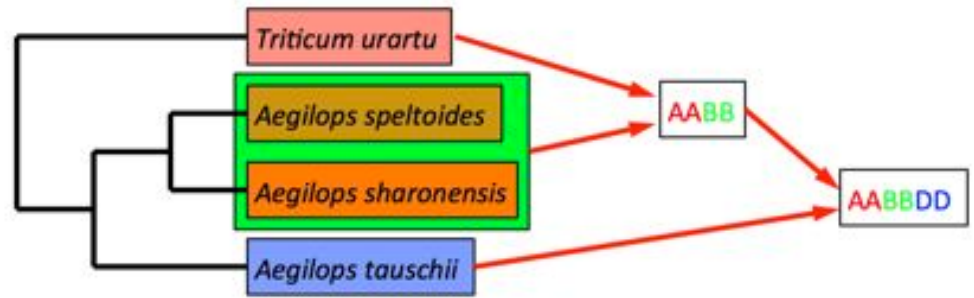
Bidirectional Best (blastn) Hits



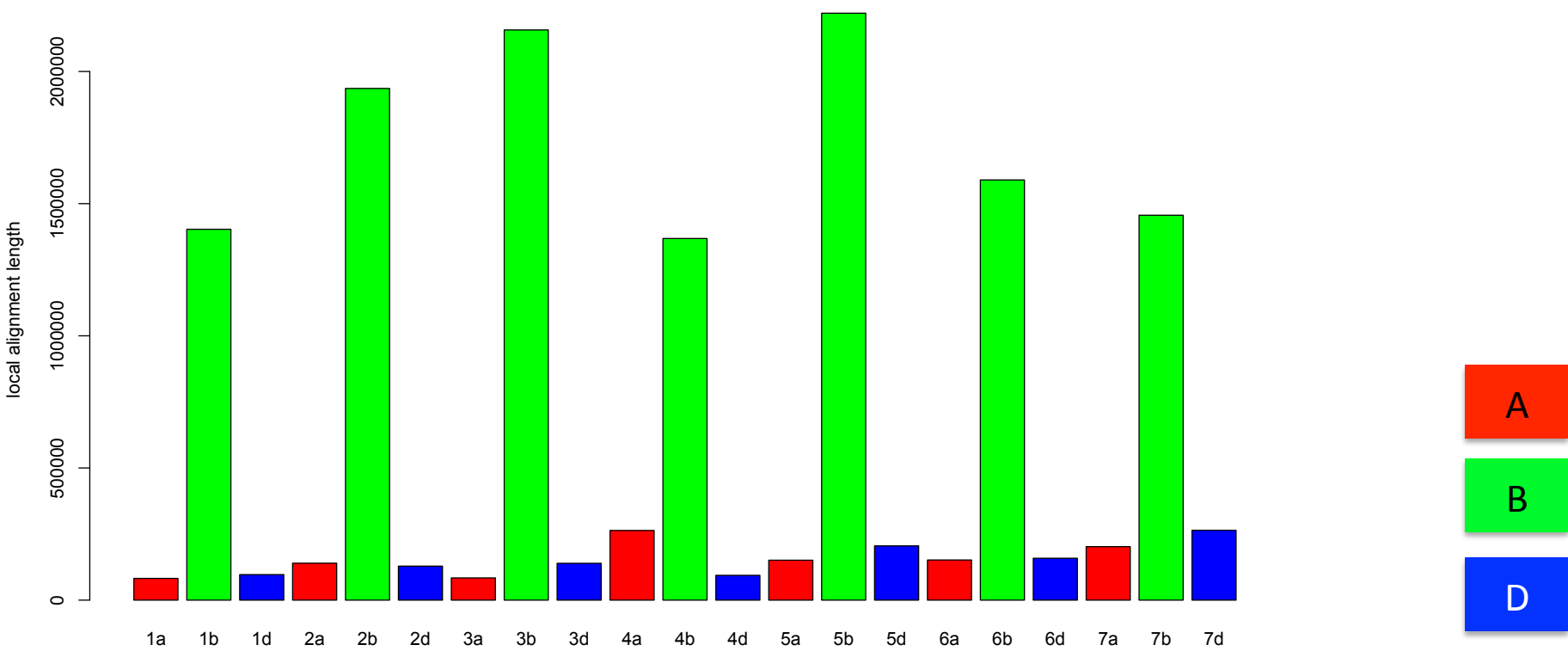
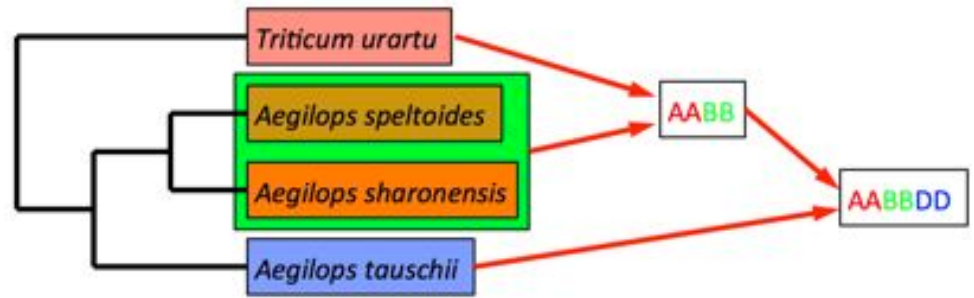
Aegilops tauschii vs. *Triticum aestivum* arms



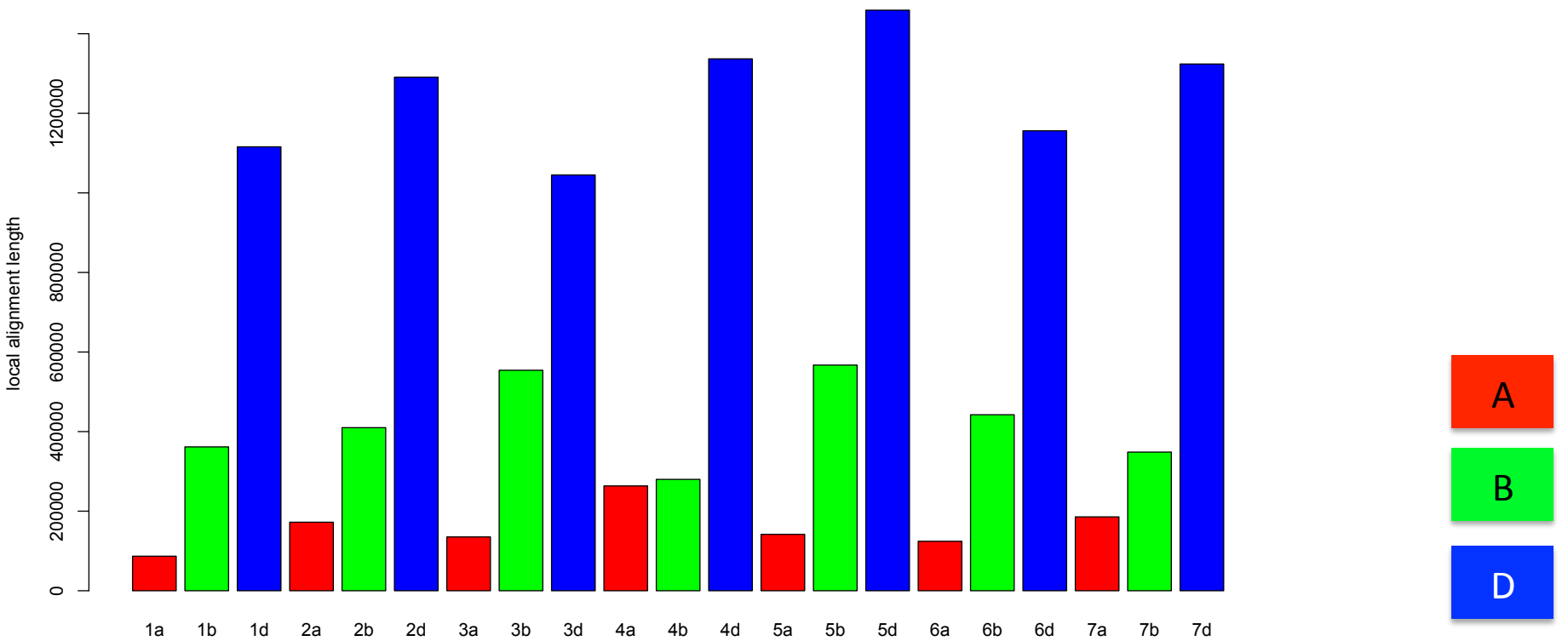
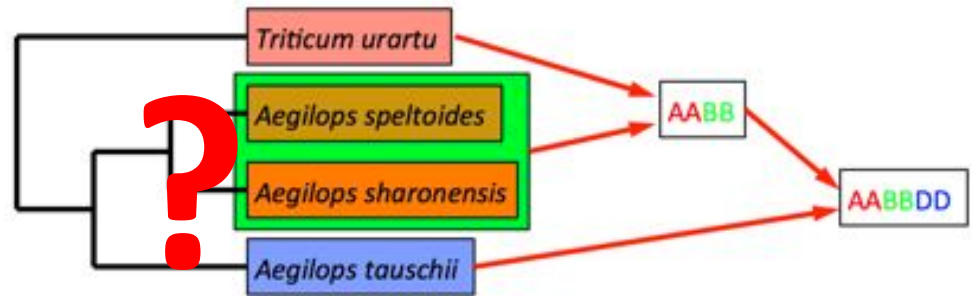
Triticum urartu vs. Triticum aestivum arms



Aegilops speltoides vs. *Triticum aestivum* arms



Aegilops sharonensis vs. *Triticum aestivum* arms



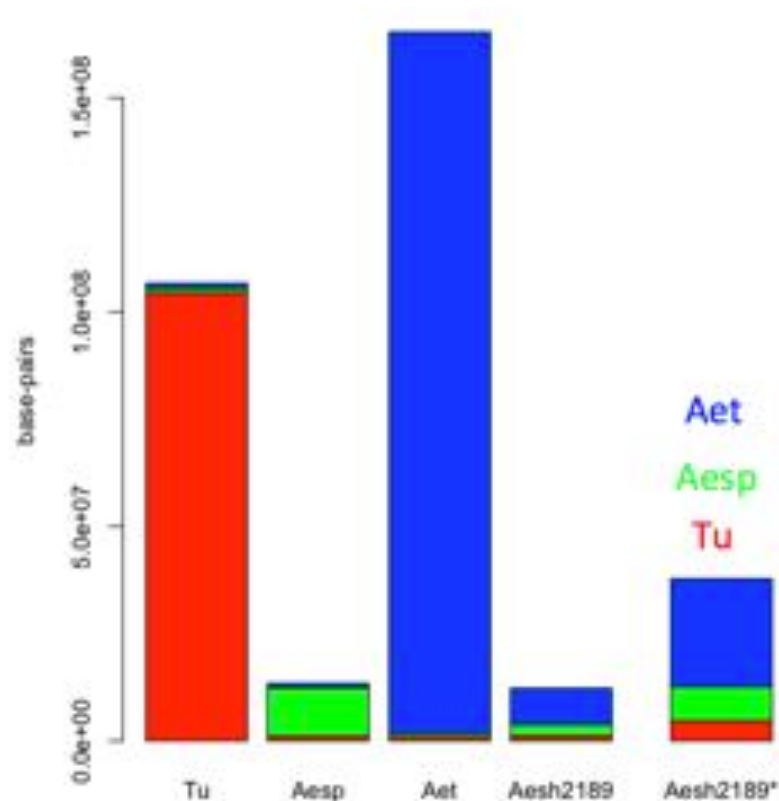
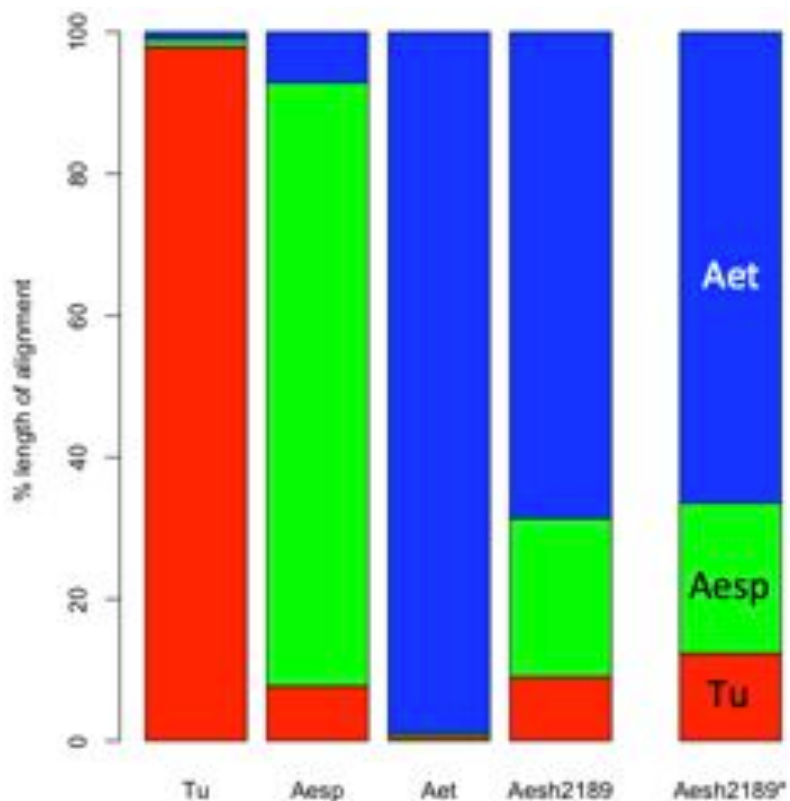
Inconsistency in taxonomic classification of *Sitopsis*

A

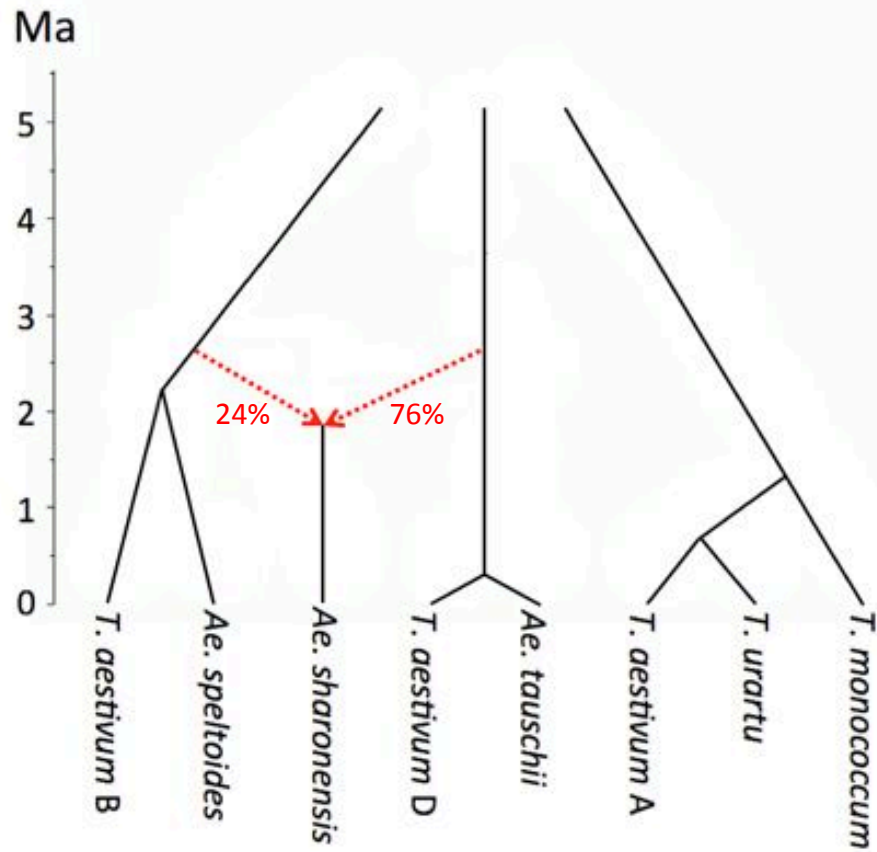
B

D

- (*Ae. sharonensis* is clearly not BB progenitor)
- *Ae. sharonensis* is closer related to *Ae. tauschii* than to *Ae. speltoides*.
→ *Sitopsis* Section????



~~Aegilops~~ *sharonensis* is a hybrid species



- Homoploid hybrid speciation
 - progenitor of B and *Ae. speltoides*
 - *Ae. tauschii*
- Taxonomy is man-made

Thomas Marcussen
Simen Rød Sandve
Lise Heier

Summary

- *Ae. sharonensis* sequence resource available
- Enabling comparative genomics for wheat family
 - *Ae. sharonensis* is closer related to *Ae. tauschii* than to *Ae. speltoides*.
→ Inconsistency in *Sitopsis* section
- *Ae. sharonensis* is a hybrid species

Acknowledgements

2Blades Group

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2Blades

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Thomas Marcussen

Simen Rød Sandve

Lise Heier

Eitan Millet

Jon Wright

Sarah Ayling

Mario Caccamo

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