HelmholtzZentrum münchen
German Research Center for Environmental Health

PGSB Plant Genome and Systems Biology

www.wheatgenome.org

Reference gene prediction in the hexaploid wheat genome

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PAG 2017

HELMHOLTZ ASSOCIATION

Objectives (I)

- **Single, high quality gene annotation for the IWGSC v1.0 Chinese Spring reference assembly**
  - Based on automated, efficient gene modeling tools
  - Compatible with future releases and manual curation
  - Agreed and “useful” gene identifiers
  - Classification of gene models based on their supporting evidence

Objectives (II)

- **Functional annotation of the wheat gene models**
  - Assign potential function to as many gene models as possible
  - Only assign reliable functional descriptors

  Automated functional annotation <-> experimentally verified functions

  - How to transfer existing knowledge on wheat gene functions to now available genomic resources?
  - Controlled vocabulary?

IWGSC gene prediction strategy

Two annotation teams

- PGSB
- INRA - Frederic Choulet, Helene Rimbert, Phillipe Leroy

One quality and consolidation team

- Earlham Institute (formerly TGAC) – David Swarbreck, Luca Venturini

Pipeline comparison and gene model consolidation is currently ongoing!!

Data for structural gene annotation – reference annotations / protein sequences

- *Arabidopsis thaliana* version ARAPORT11
- *Brachypodium distachyon* version 3.1
- Rice version MSU7
- *Sorghum bicolor* version 2.1
- *Seteriaca italica* version 3.1
- All triticeae protein sequences from UniProt (filtered for complete gene models, downloaded 16.10.2016)

Data for structural gene annotation – RNA-seq data sets

ID	#samples	#reads	#mapped	ratio	Availability	Source
E-MTAB-1729	60	2.27E+09	2.03E+09	0.90	public	EBI arrayexpress
E-MTAB-2137	30	2.10E+09	1.92E+09	0.91	public	EBI arrayexpress
E-MTAB-3103	9	5.21E+07	4.22E+07	0.81	public	EBI arrayexpress
NBS-LRRs	17	8.10E+08	7.46E+08	0.92	not public	JIC - Steuernagel
SRP045409	14	2.11E+09	1.76E+09	0.83	public	Sequence Read Archive
INRA 2014	30	3.47E+09	3.14E+09	0.90	Public	https://urgi.versailles.inra.fr
Earlham 2016	6	1.55E+09	1.50E+09	0.96	Public	Earlham Institute

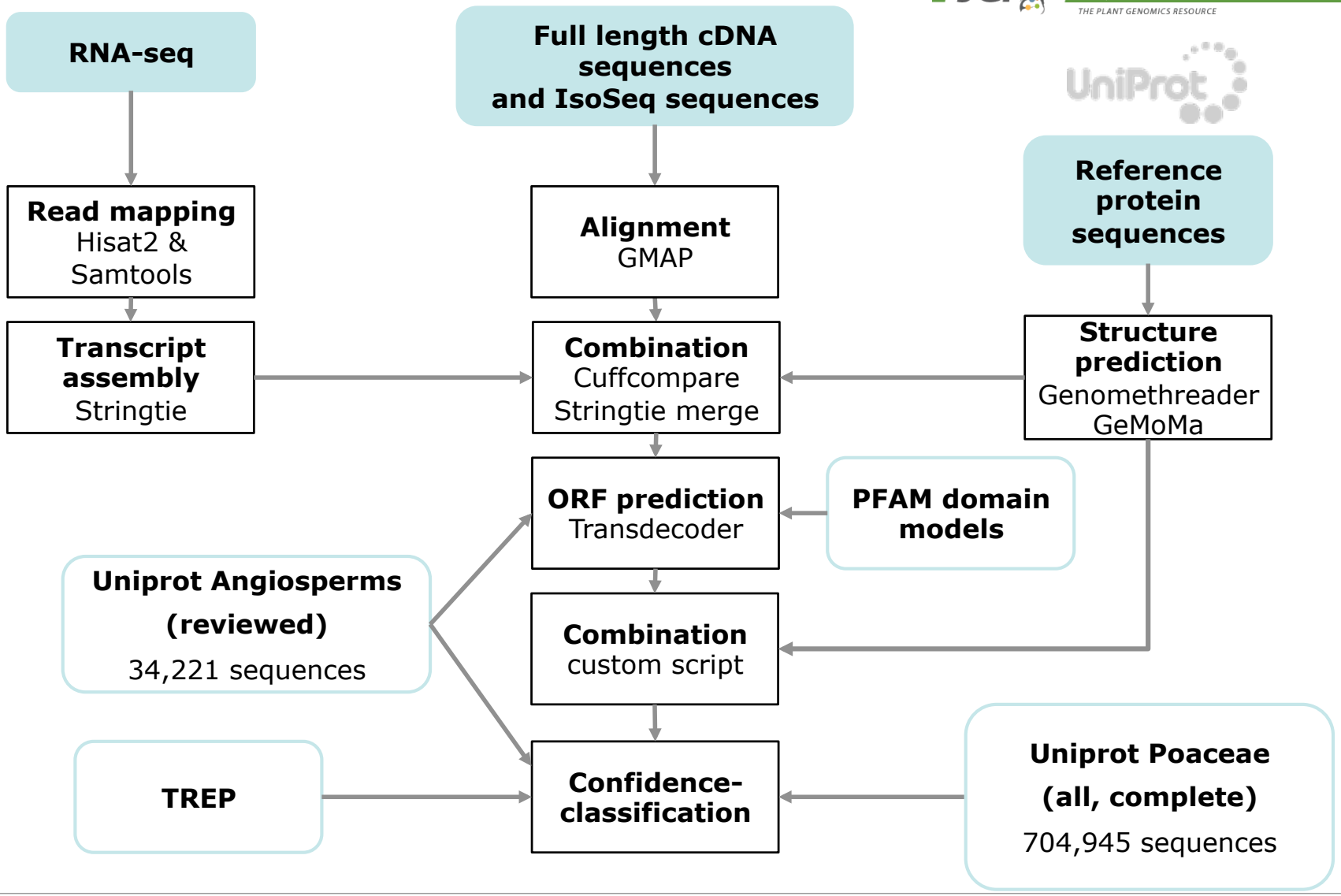
Data for structural gene annotation – PacBio IsoSeq reads

- PacBio isoform sequencing reads from 6 samples (leaf, root, seed, seedling, spike, stem), prov
- overall 817,892 sequences

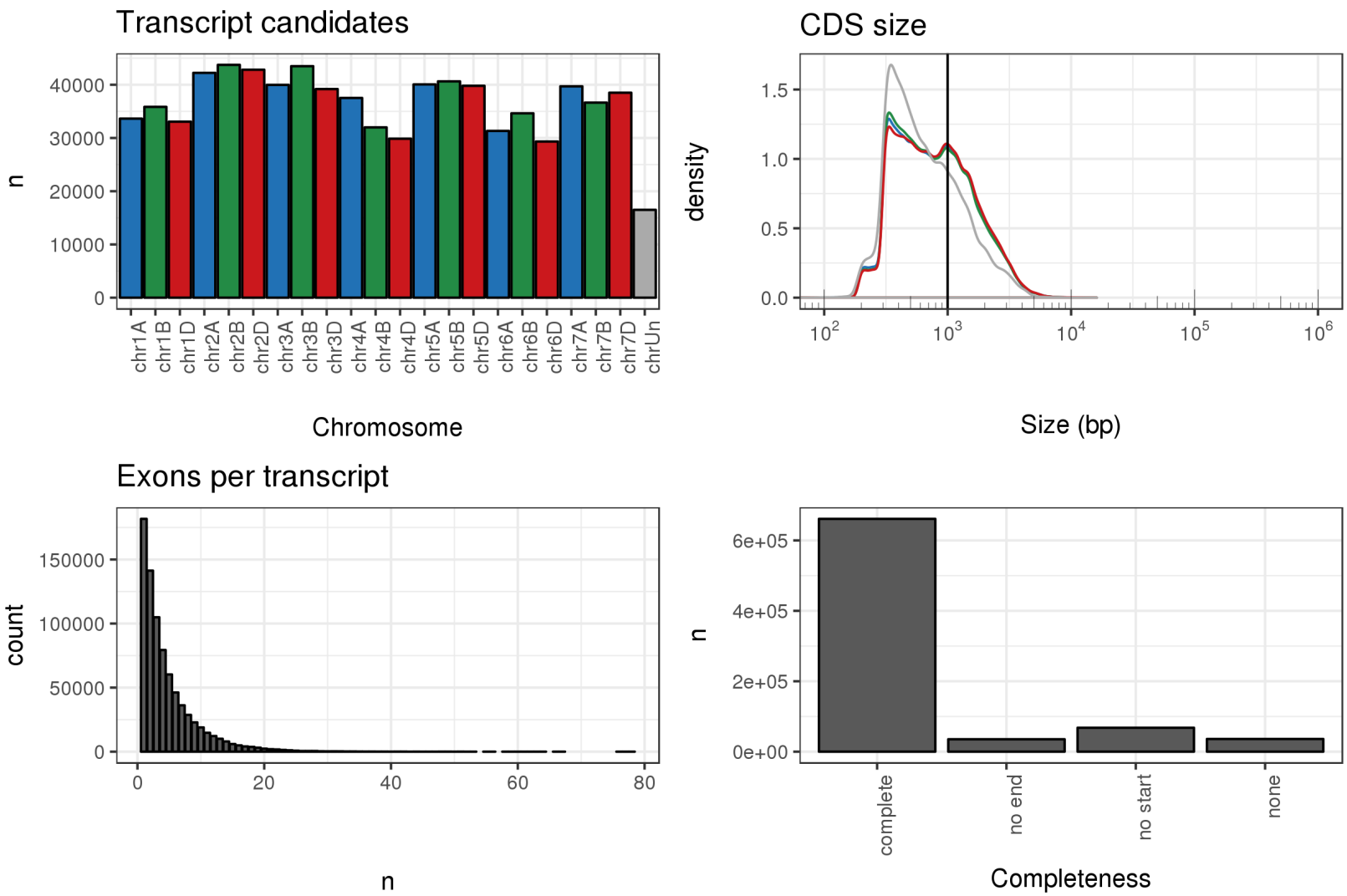
Earlham Institute
Decoding Living Systems

(Tom Barker and Luca Venturini)

PGSB gene annotation pipeline



Gene candidates



800,504 transcripts at 234,588 loci

Confidence classification

TREP: Hypothetical proteins ("PTREP") for the identification of divergent TEs
UniPoa: Uniprot Poaceae protein sequences
UniMag: Uniprot Magnoliophyta protein sequences (validated)

- Protein blast of protein candidates to three databases
- maximal query coverage for TREP
- maximal relative overlap for protein databases

HC1 : UniMag and complete

HC2 : not UniMag and (UniPoa and not TREP) and complete

LC1 : (UniMag or (UniPoa and not TREP)) and not complete

LC2 : not UniMag and not UniPoa and not TREP and complete

REP : not (UniMag and complete) and TREP

none: not UniMag and not UniPoa and not TREP and not complete

Gene prediction results

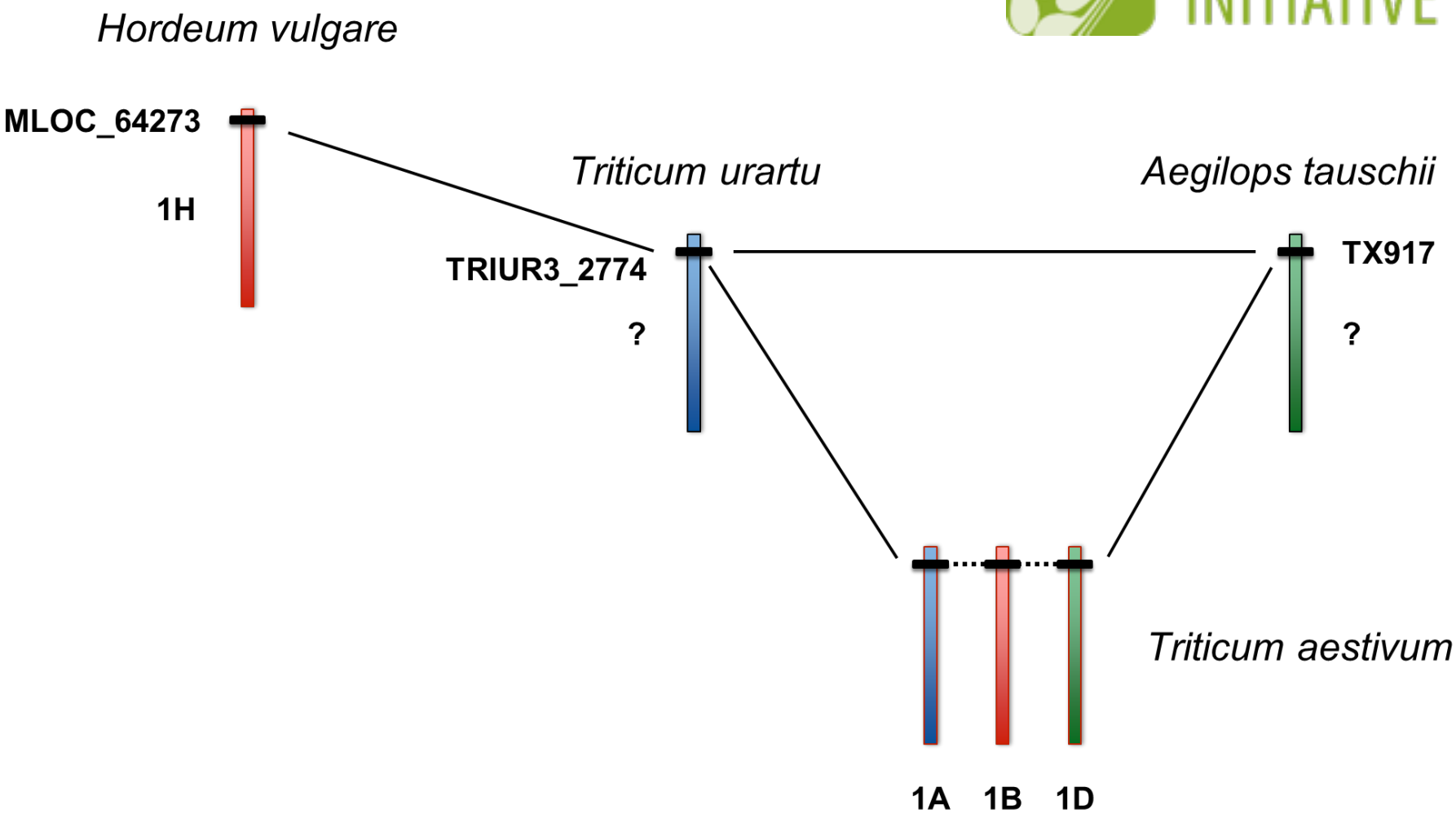
	HC	LC
Number of genes	104,696	100,947
Mean locus size (bp)	4,546	1,825
Median locus size (bp)	2,021	566
Number of single transcript genes	48,526	82,791
Number of multi transcript genes	56,170	18,156
Number of transcripts	297,971	134,126
Mean transcripts per gene	2.8	1.3
Mean transcript size (bp)*	1,258	611
Median transcript size (bp)*	1,071	453
Mean exons per transcript*	4.5	1.7
Median exons per transcript*	3	1
Number of single exon transcripts*	29,939	66,828
Number of multi exon transcripts*	74,757	34,119

* for one representative transcript per gene

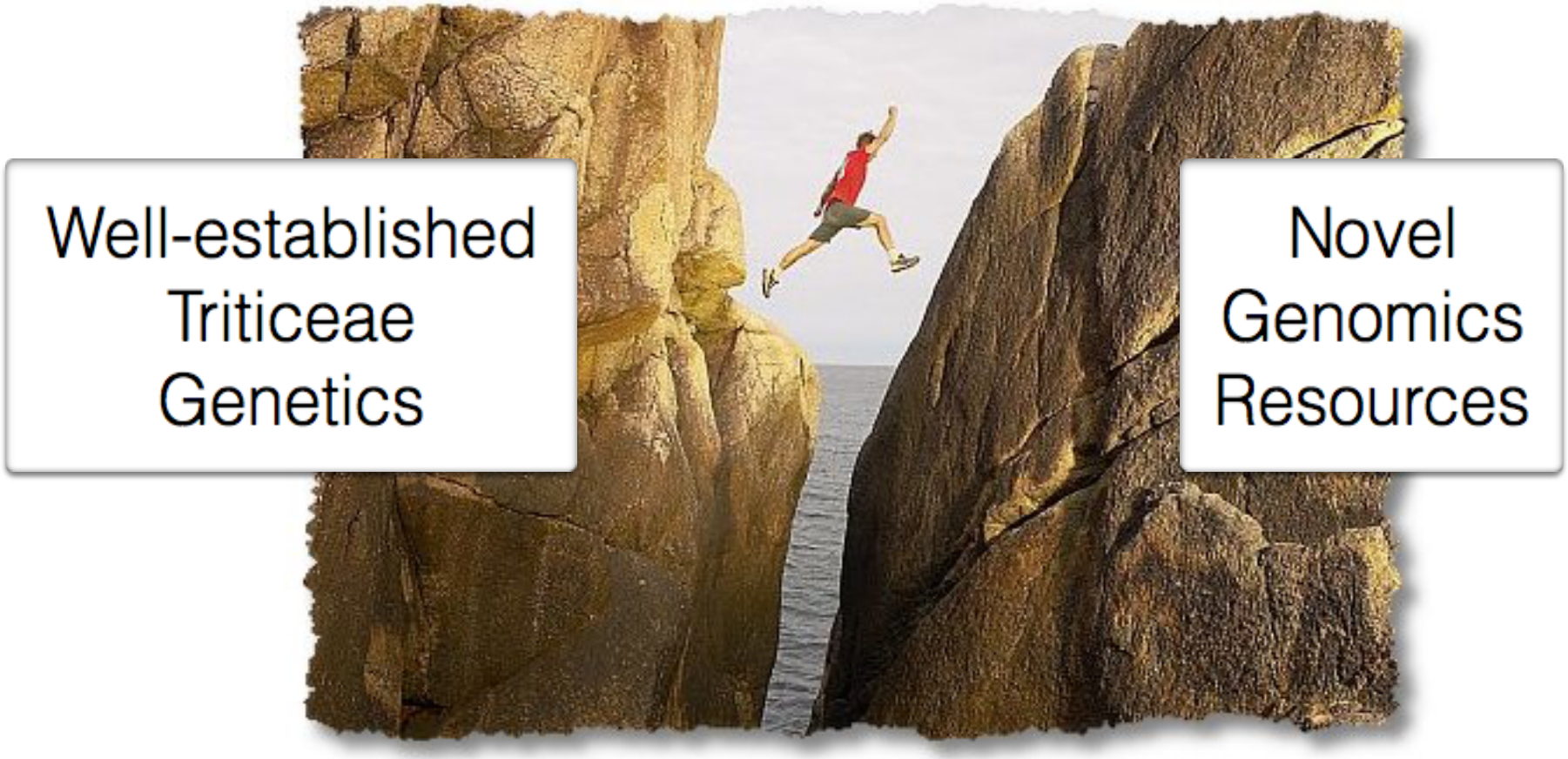
Gene names - *T. aestivum*

Slides from Mario Caccamo (NIAB)

Names in Context



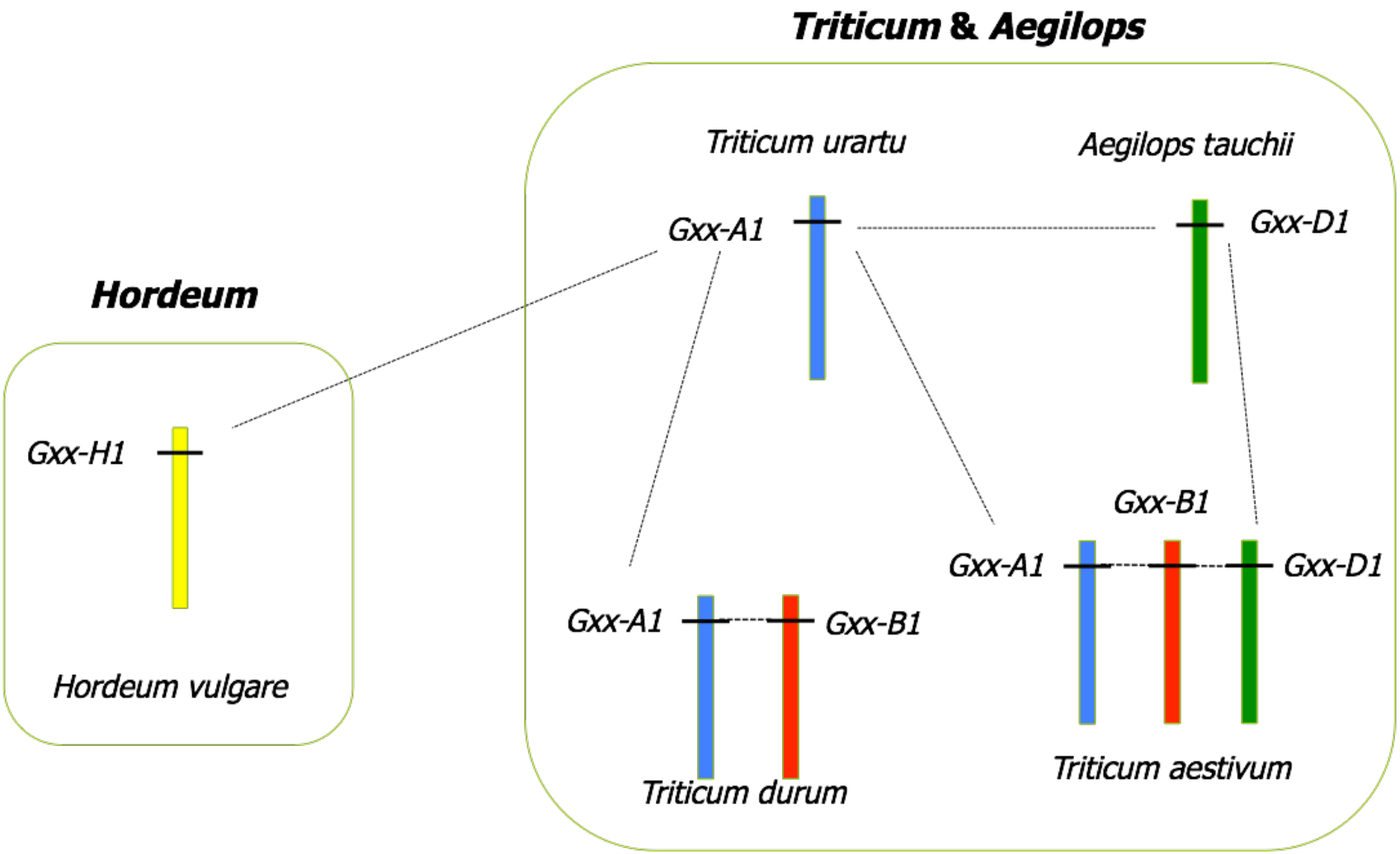
Bridging the Gap



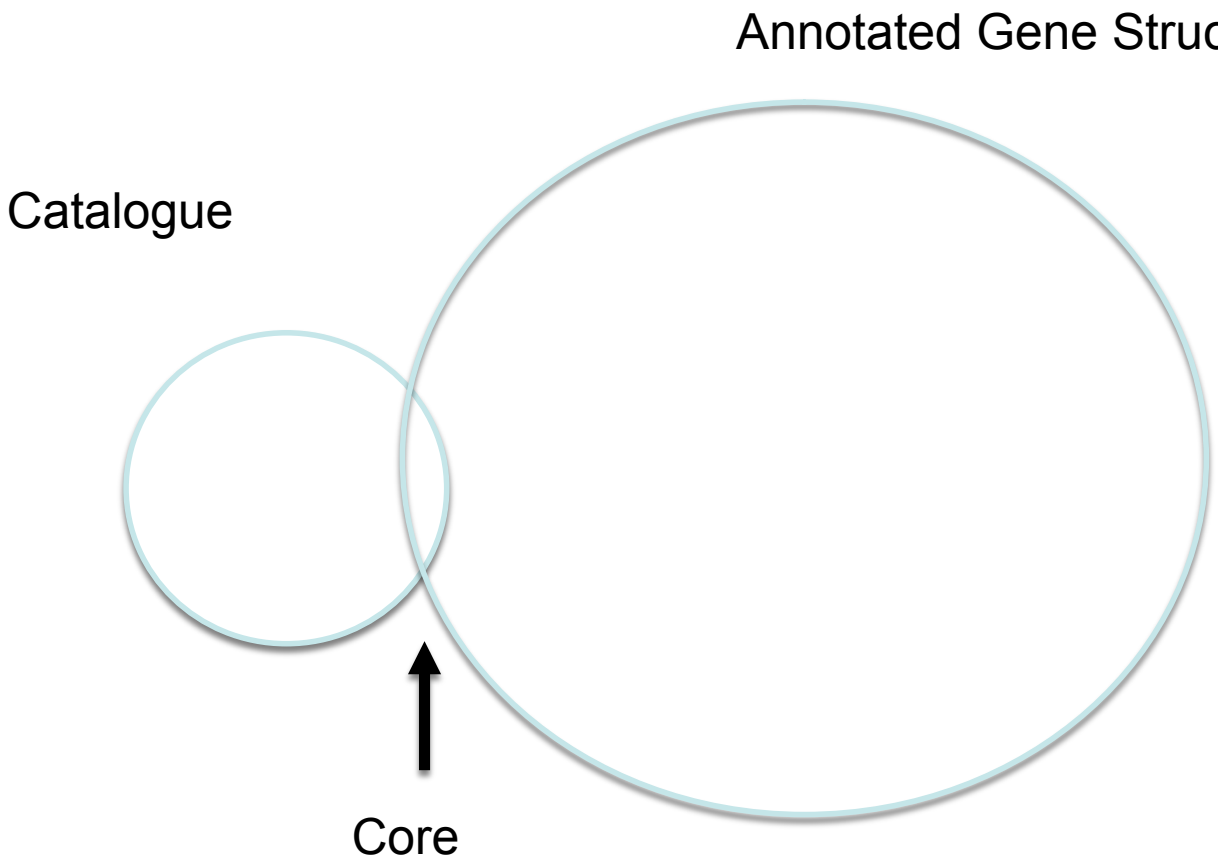
Workshop Objectives
Munich, October 2016

- How can the wheat gene catalog support the provision of gene symbols across the Triticeae tribe.
- Propose guidelines, criteria and schema for the annotation of gene symbols across the Triticeae species.
- Identify gaps in the current datasets to inform and guide projects for Triticeae species in the generation of genomics resources.

Scheme - Gene Symbol Gxx*



Genes vs Genes



Category I. The Catalogue provides sequences (either DNA or peptide) that could be used to **unambiguously** identify a gene structure in a sequence reference. This the priority category for the work on the nomenclature.

Moving forward

Submitted abstracts to several meetings

PAG poster - **P0350**

Group meets regularly over conference call

Funding for meeting in 2017

Look for opportunities to fund more work!

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KWS
KeyGene
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Thank you for your attention!