



DArT: 2005 & 2006 shipments

Ky L Mathews

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Genotypes

2005 shipment

- 275 lines (151 crosses)
 - 39 (32) C39IBWSN
 - 150 (68) M24SAWSN
 - 60 (37) C17HRWSN
 - 26 (14) ISWSN

2006 shipment

- 135 lines (122 crosses)
 - 72 (72) 40IBWSN
 - 37 (27) 25SAWSN
 - 9 (9) 22SAWSN
 - 1 (1) ASN
 - 16 (16) Australian (primary synthetic controls)

- 410 lines (254 crosses)
- 6 removed for poor data quality
- 80 crosses have > 1 selection

Markers

2005 shipment

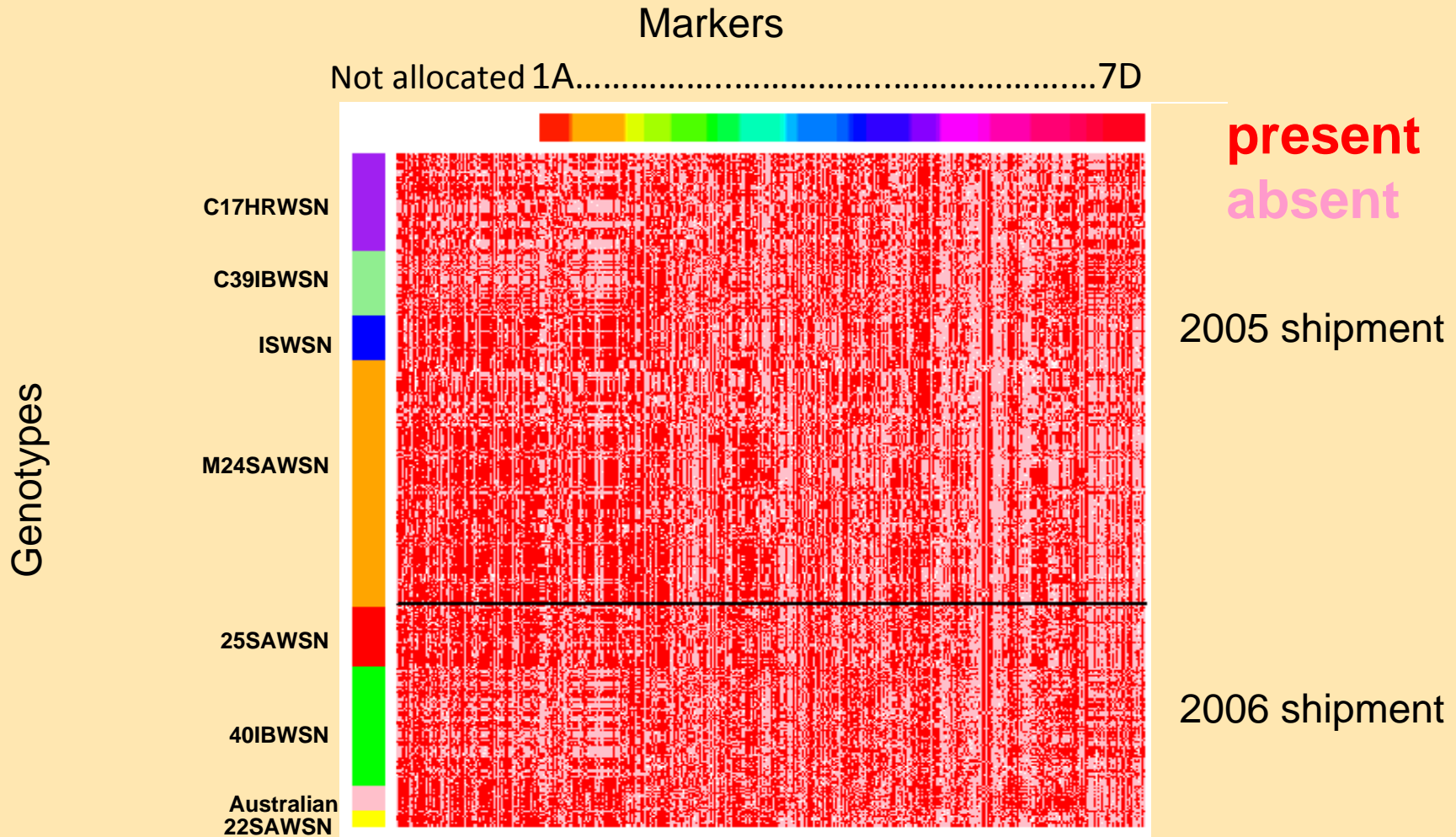
- 1058 markers
 - 981 wheat
 - 23 rye
 - 54 triticale

2006 shipment

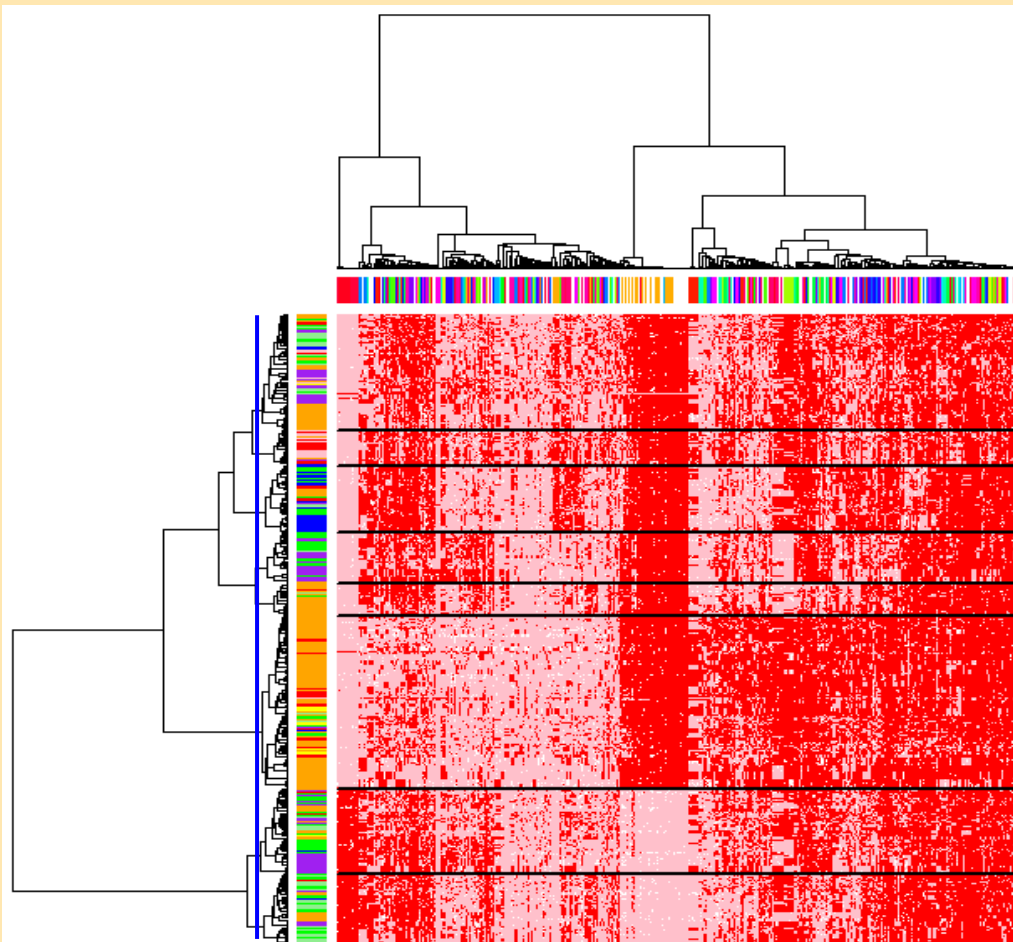
- 2382 markers
 - 2209 wheat
 - 49 rye
 - 124 triticale

- 956 markers overlapped
 - 880 wheat
 - 22 rye
 - 54 triticale
- 24% not allocated to a chromosome
- 6% allocated to more than one chromosome

Pre-analysis



Genotype groupings



Jaccard's distance and
Ward's clustering
ng = 8 groups

1:mix of all nurseries

2:Australian and Australian backgrounds

3:predominantly ISWSN

4:C17HRWSN and 40IBWSN

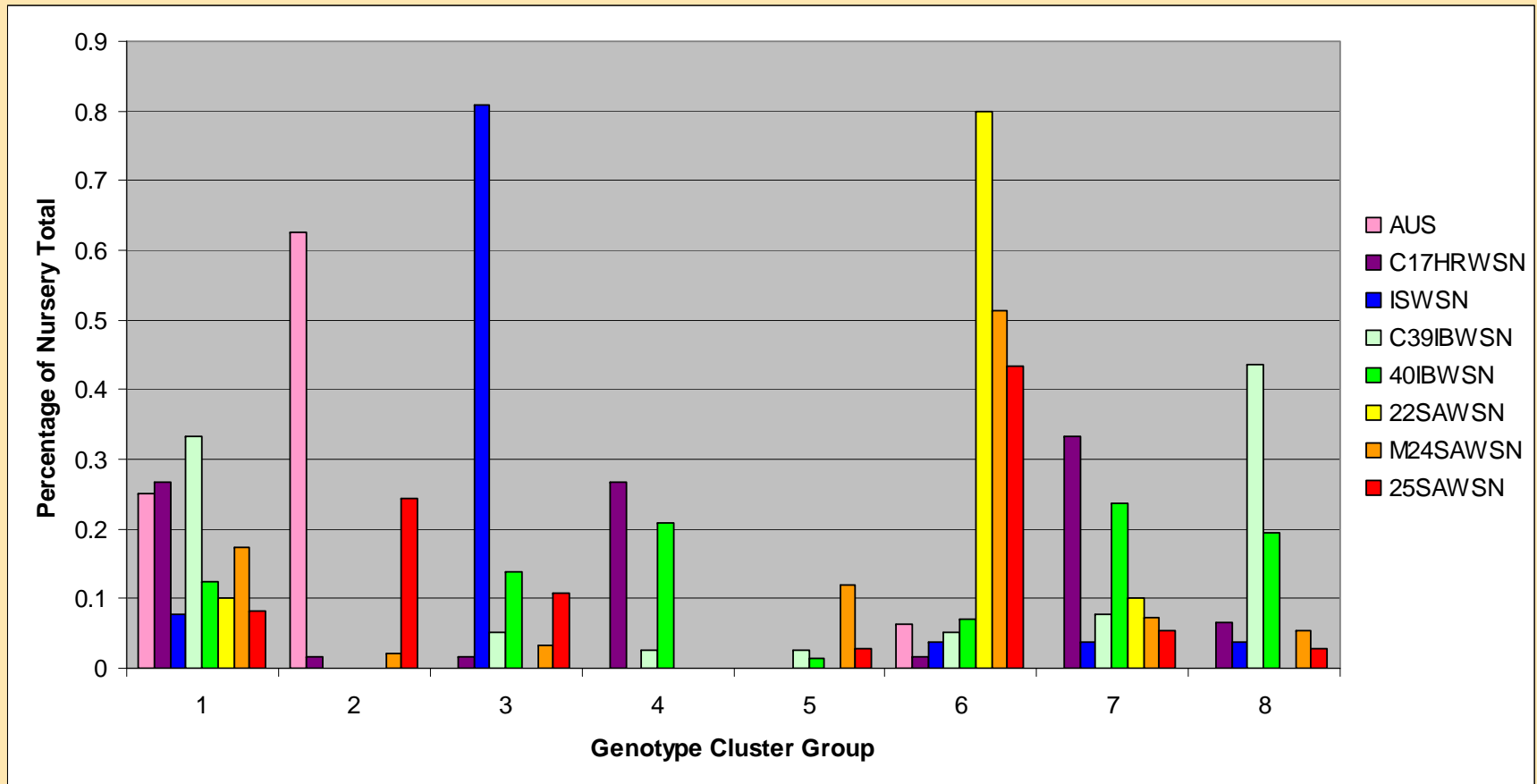
5:55% of all lines containing MILAN/KAUZ in pedigree
in this group

6:73% of all lines containing PASTOR in this group

7:mixture but predom C17HRWSN and 40IBWSN

8:mixture but predom C39IBWSN

Genotype Group by Nursery



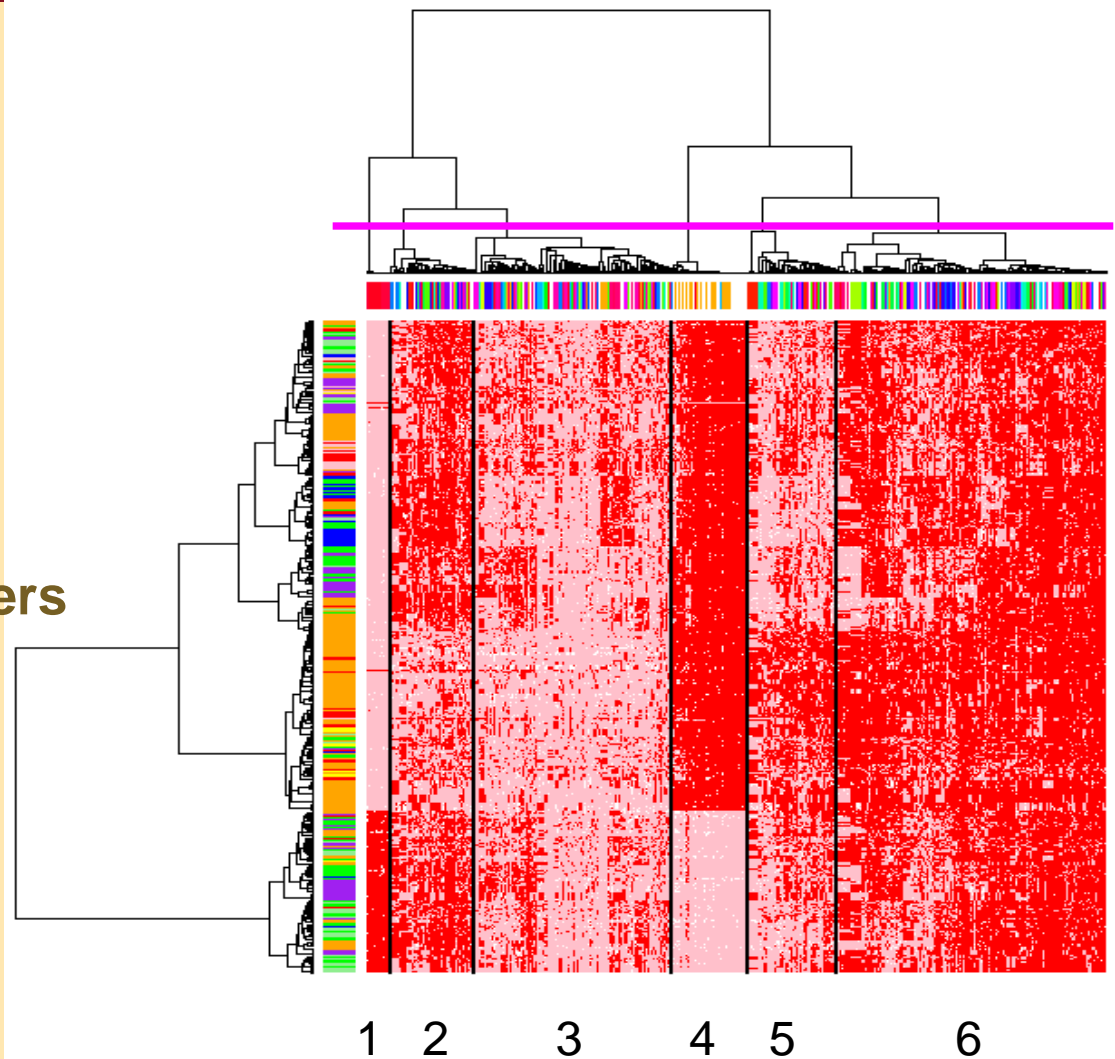
Summary of findings

- IBWSN nurseries are more genetically diverse – less selections from the same cross
- C17HRWSN & 40IBWSN have more lines genetically similar than say 39IBWSB & 40IBWSN
- ISWSN, Australian and SAWSN nurseries are mostly distinct from each other
- C39IBWSN split between non-rye (gp1) and rye (gp8) containing groups
- C17HRWSN is split in 3, non-rye and rye, and ???
- Gp 5 is predominantly Milan/Kauz, 55% of lines with Milan/Kauz in their pedigree are in this group.
- Gp 6 is predominantly SAWSN and 75% of these contain Pastor in the pedigree; 73% of all Pastor containing lines in this group
- 8 crosses appear to segregate for 1BL.1RS

Marker groupings

Jaccard's distance and
Ward's clustering
nm = 6 groups

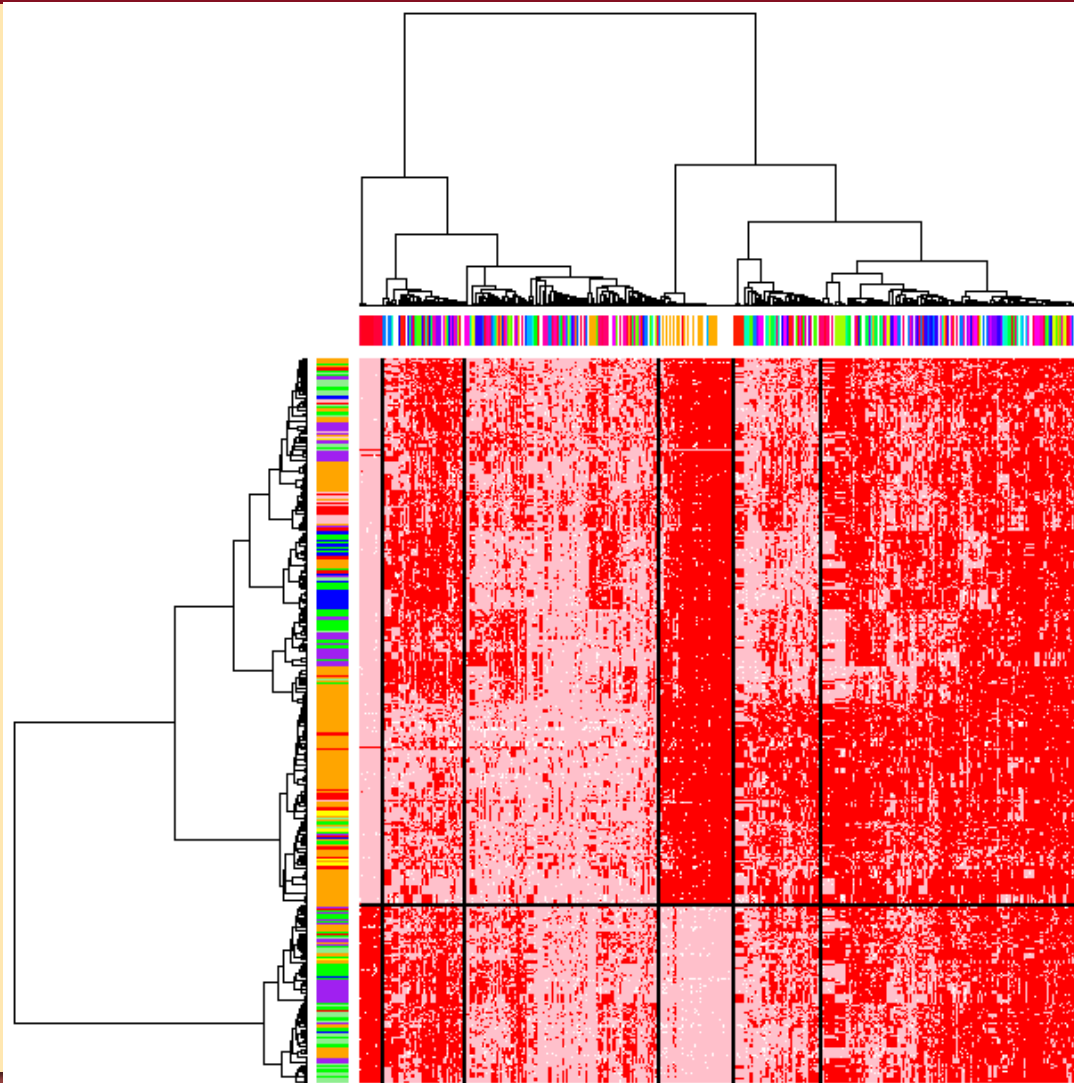
- 1: rye or triticale markers
- 2: 4A, 6A, 2B
- 3: 6B|7A, 1D, 5B, 7A, 4A
- 4: 1B & unassigned markers
- 5: 1A, 3B, 6B
- 6: 7B, 2A, mix



Genotype groupings, $ng = 2$

1BL.1RS

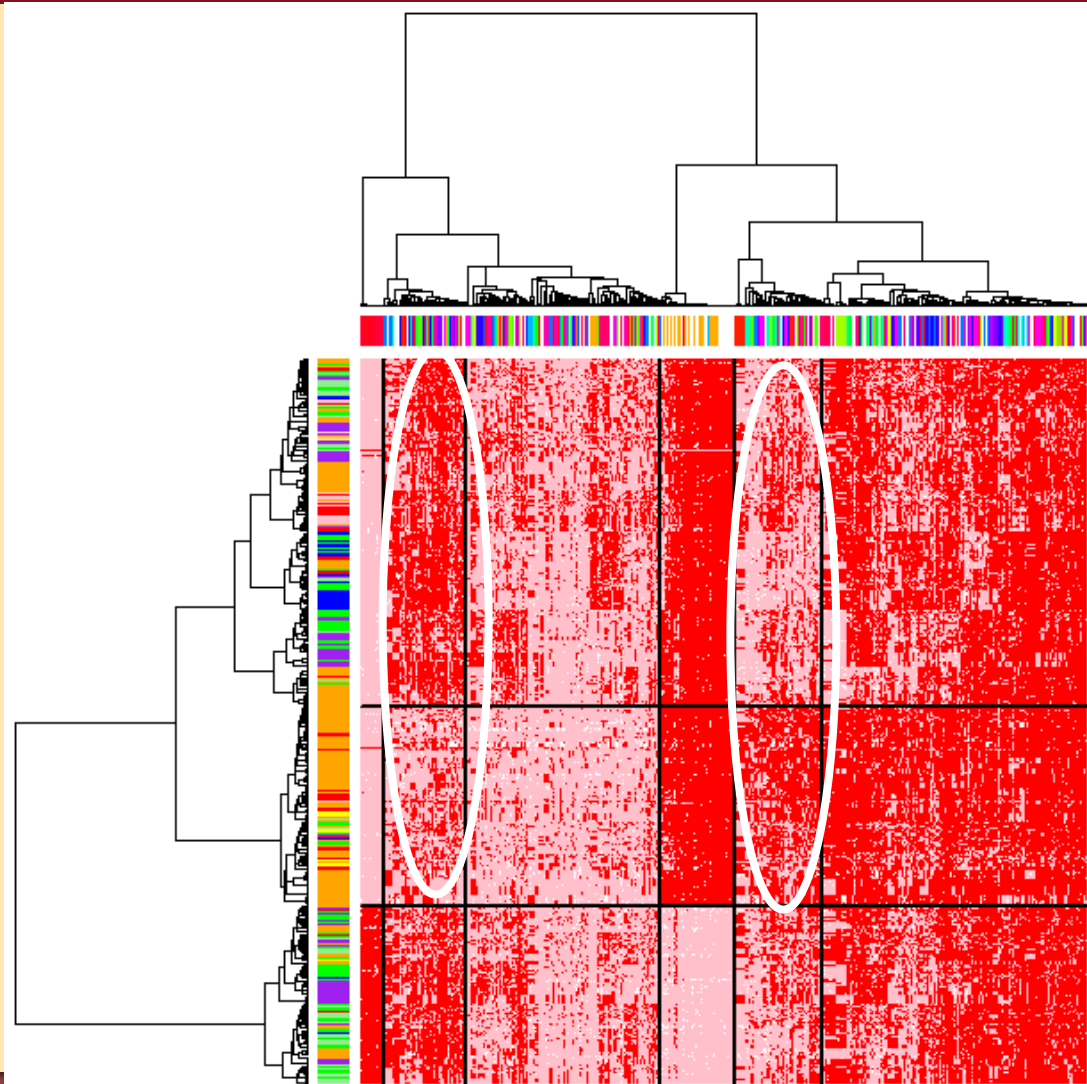
data from Vivi
Arief (UQ) on
website



Genotype groupings, $ng = 3$

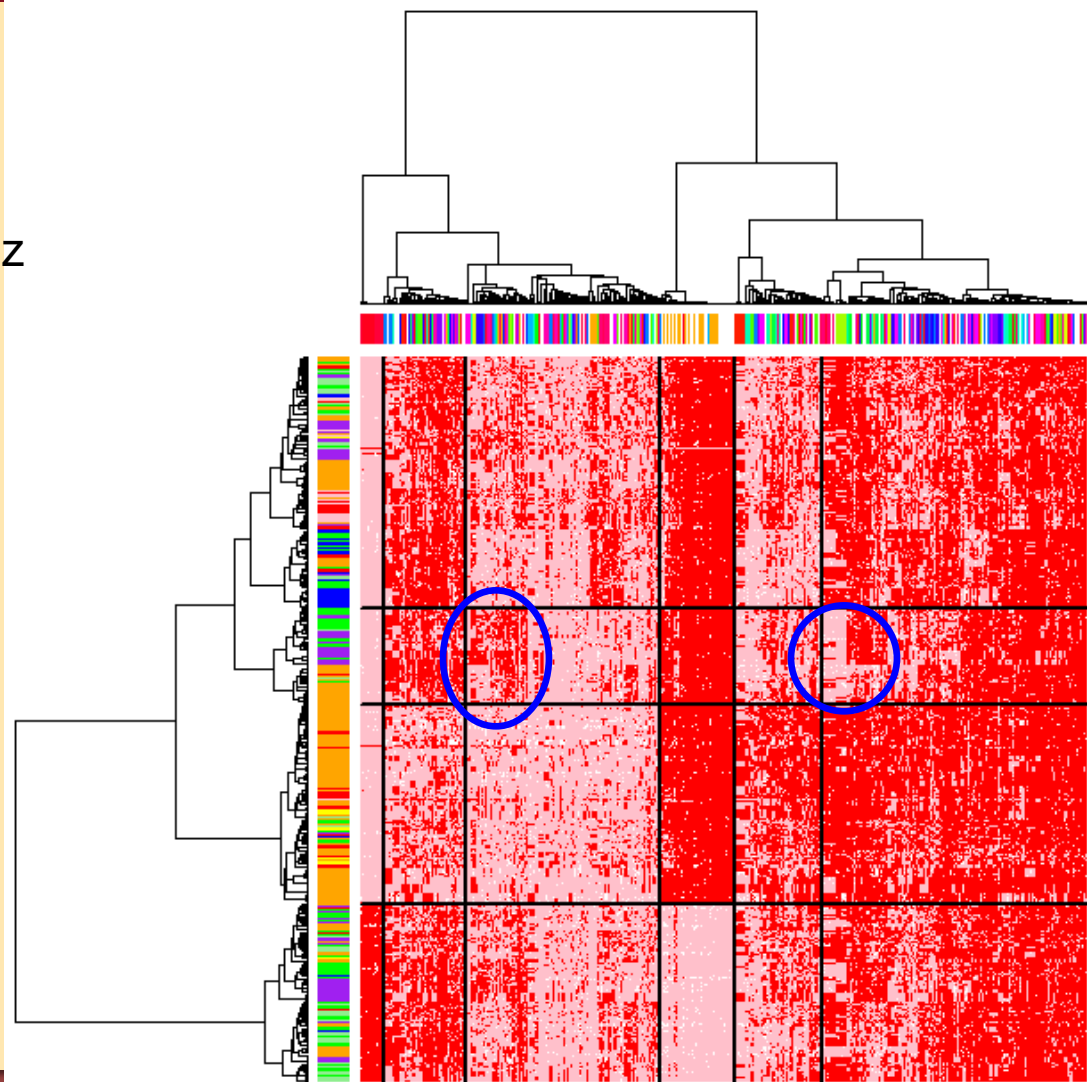
within non-rye:

- Pastor (SAWSN) vs rest
- absence 4A, 6A, 2B and presence 1A, 3B, 6B



Genotype groupings, $ng = 4$

- within non Pastor:
- HRWSN, IBWSN, Milan/Kauz
 - presence 6B|7A, 1D and absence 7B, 2A



Summary of Findings

- IBWSN most diverse
- ISWSN, SAWSN & Australian lines are less diverse
- C17HRWSN and 40IBWSN contain genetically similar material
- 1BL.1RS is most distinct molecular discriminator (CAGE projects >> DArT Projects **1B1R presence by V.Arief (UQ)**)
- molecular differences between SAWSN and other nurseries are based on Pastor in pedigree

Collaboration with Triticarte

- list of SSR markers linked to traits of interest given to Triticarte for linking to their consensus map
- ideal marker list to screen across all incoming material
 - based on list from CIMMYT
 - 70 markers for disease, soil borne pathogens, viruses and insects, quality, phenology, morphology

Mapping wheat DArT markers

- Assigned >4,000 markers from the WHEAT 2.6 array to chromosomes by evaluating segregation patterns in a total of 100 mapping populations
- Tested consensus-mapping strategy on chr. 3B data: built a 'synthetic map' derived from 20 component maps:
 - 798 DArT markers, 162 other markers
 - However, strategy is inefficient and error-prone; alternative approach & software tools required
- Next 3 months: refine assignment to chromosome arms by genotyping a panel of flow-sorted chromosome arms derived from ditelosomic lines
- In parallel, developed a 15,000-clone DArT array using flow-sorted D genome chromosomes from a mixture of cultivars (including CIMMYT synthetics):
 - Next 3 months: isolate polymorphic clones (markers) and assemble them into a genotyping array
 - Subsequently, genotype new markers across a sufficient number of mapping populations
- Build consensus maps for the other 20 chromosomes as soon as:
 - Mapping data from D genome-enriched array available
 - Software tools for alternative consensus-mapping strategy ready
- Consensus map to contain a list of trait-linked SSR markers, assembled by Ky Mathews and genotyped by Ken Chalmers in 2 mapping populations

Future work

- Linkage analysis with phenotypic data
- Future DArT work – ESWYT, SAWYT and ICARDA material
- Data and summaries available online
- Analysis with DArT consensus map when it comes online