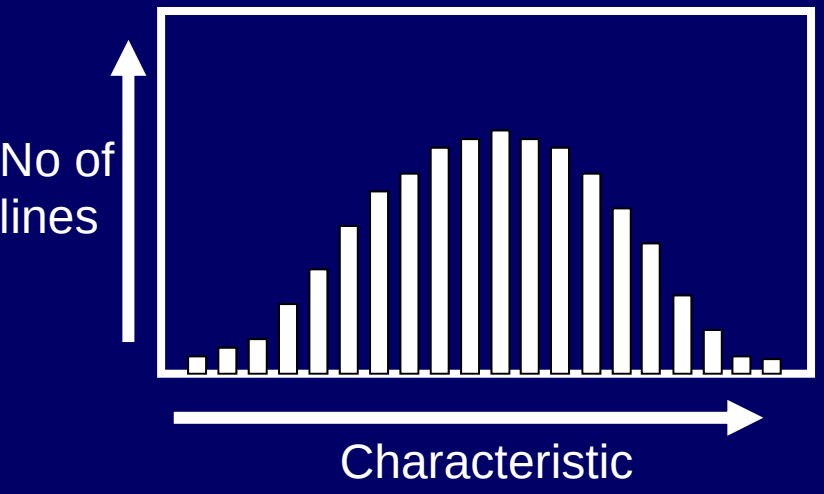
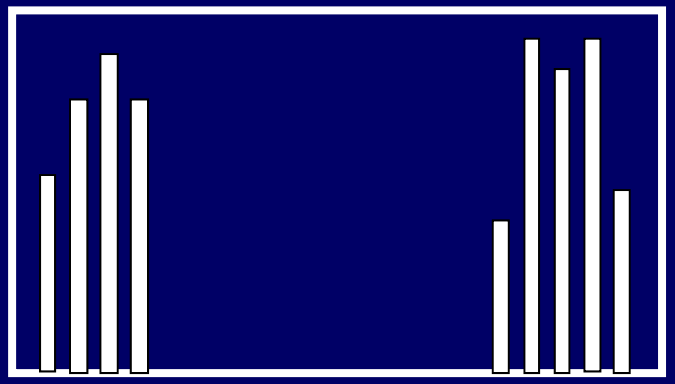
Avalon x Cadenza

Simon Griffiths

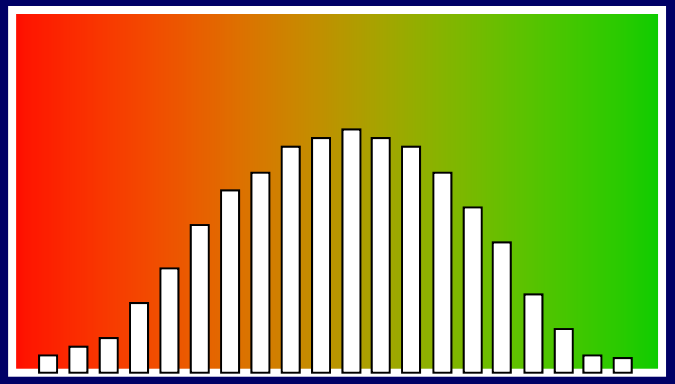
WGIN Stakeholders November 2009

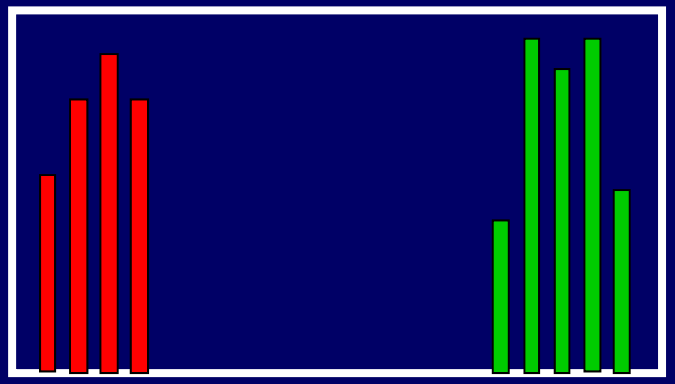
Wheat Genetic Improvement is Quantitative (mostly)





Wheat Genetic Improvement is Quantitative (mostly)





- The genes influencing quantitative traits like grain yield can be identified as Quantitative Trait Loci (QTL).

- The identification of QTL requires precise segregating populations and associated molecular markers, ideally assembled into genetic maps representing the 21 pairs of wheat chromosomes.

- WGIN has developed this set of resources for the Avalon x Cadenza doubled haploid population.

Avalon x Cadenza Map Summary

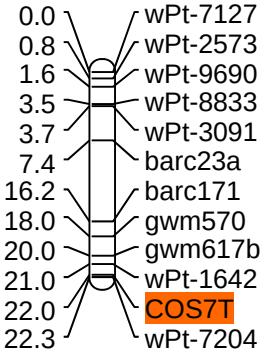
- 28 linkage groups
- 2000cMs
- 355 markers in total
  - 178 SSRs, 97 DaRT, 36 COS markers
  - 23 NIAB AFLP, 13 Perfect markers, 8 STMP
- Use other maps for reference
  - Somers consensus
  - Komugi map
  - ITMI

New and Improved…

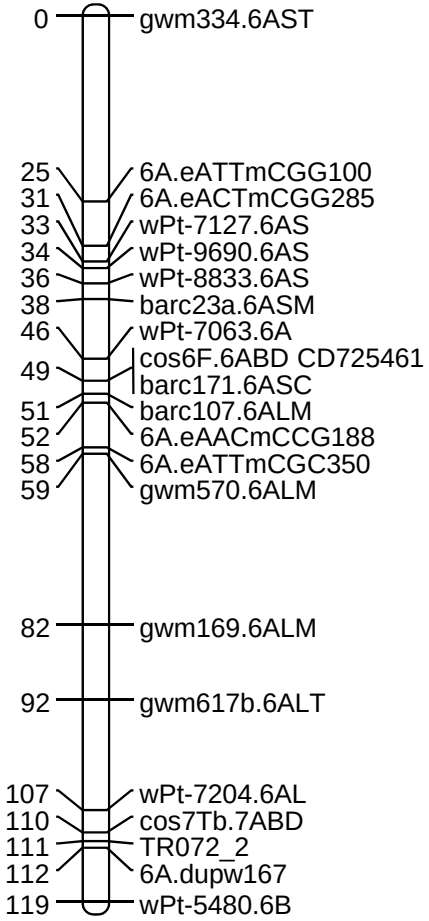
6A before

6A

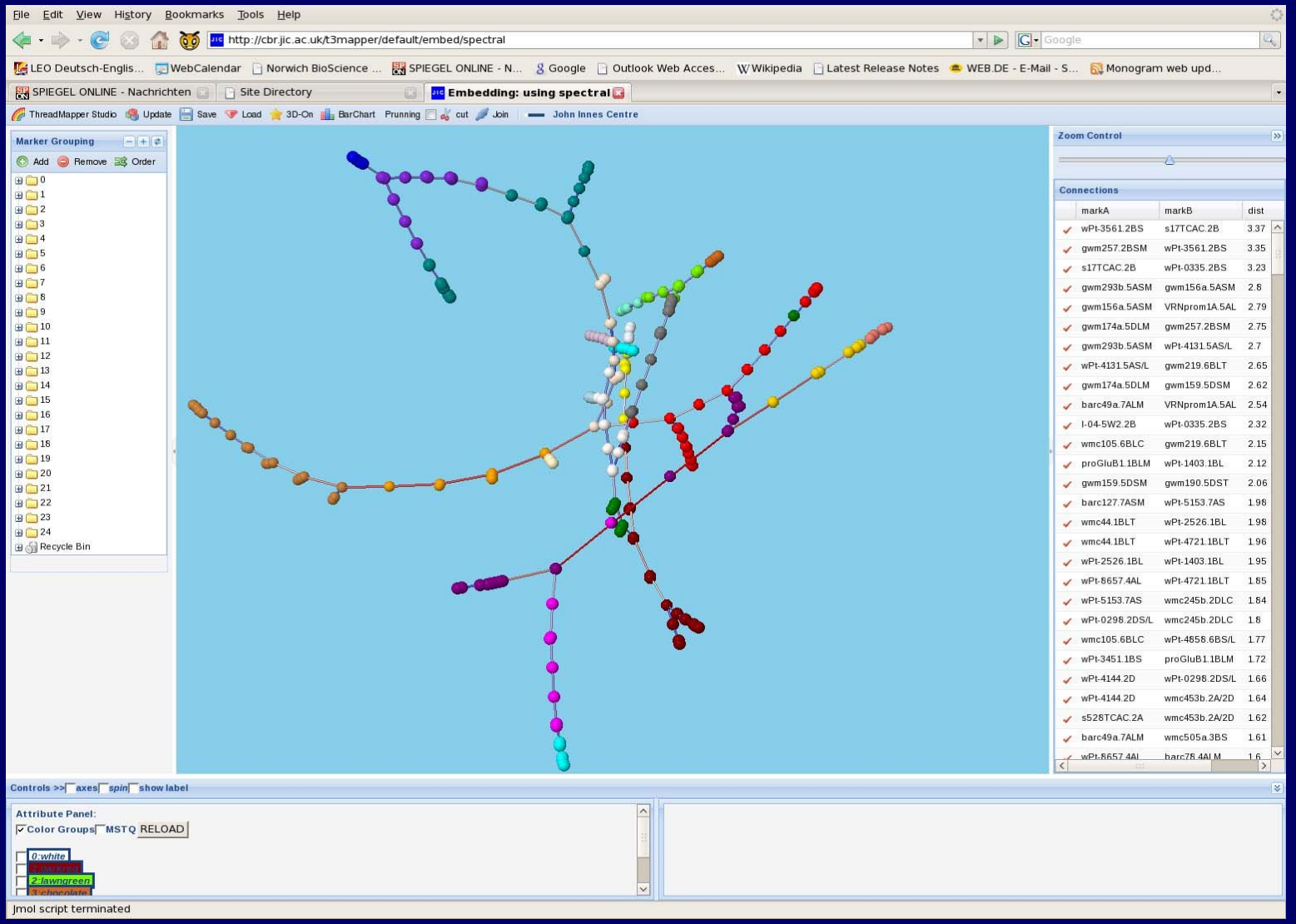
6A



6A after



AxC in Threadmapper



Avalon x Cadenza workshop 3rd November 2009

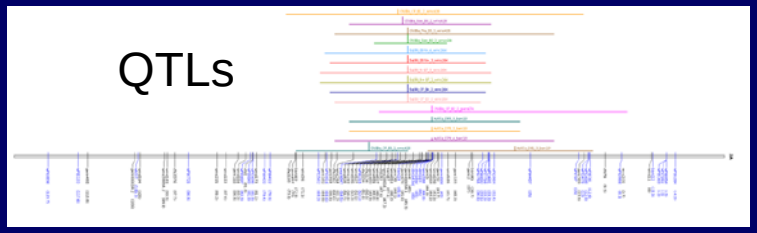
- Over 40 participants academic and industry
- Diseases- Yellow rust, Soil borne mosaic virus, Take All, Septoria
- Resource capture- Yield, Nitrogen use efficiency
- Adaptation- Heading date, height
- Others- Quality, disease.....

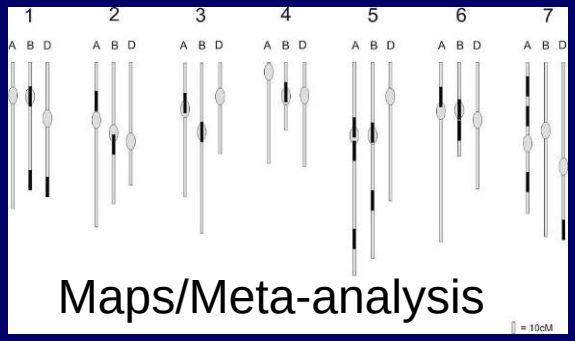
Dissection of genetic gain in UK winter wheat

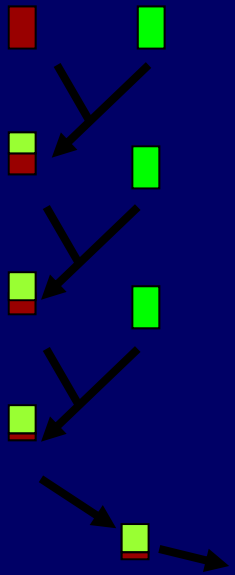
crosses

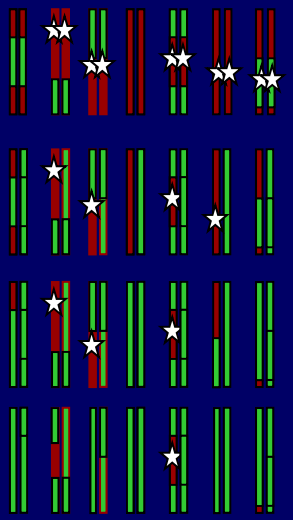
- Spark x Rialto
- Avalon x Cadenza
- Buster x Charger
- Charger x Badger
- Savannah x Rialto
- Shango x Shamrock
- Malacca x Charger
- Savannah x Renesansa
- Lynx x Cadenza
- Beaver x Soissons
- Weebil x Bacanora
- Milan x Catbird

How do these alleles work in combination to make wheat better?





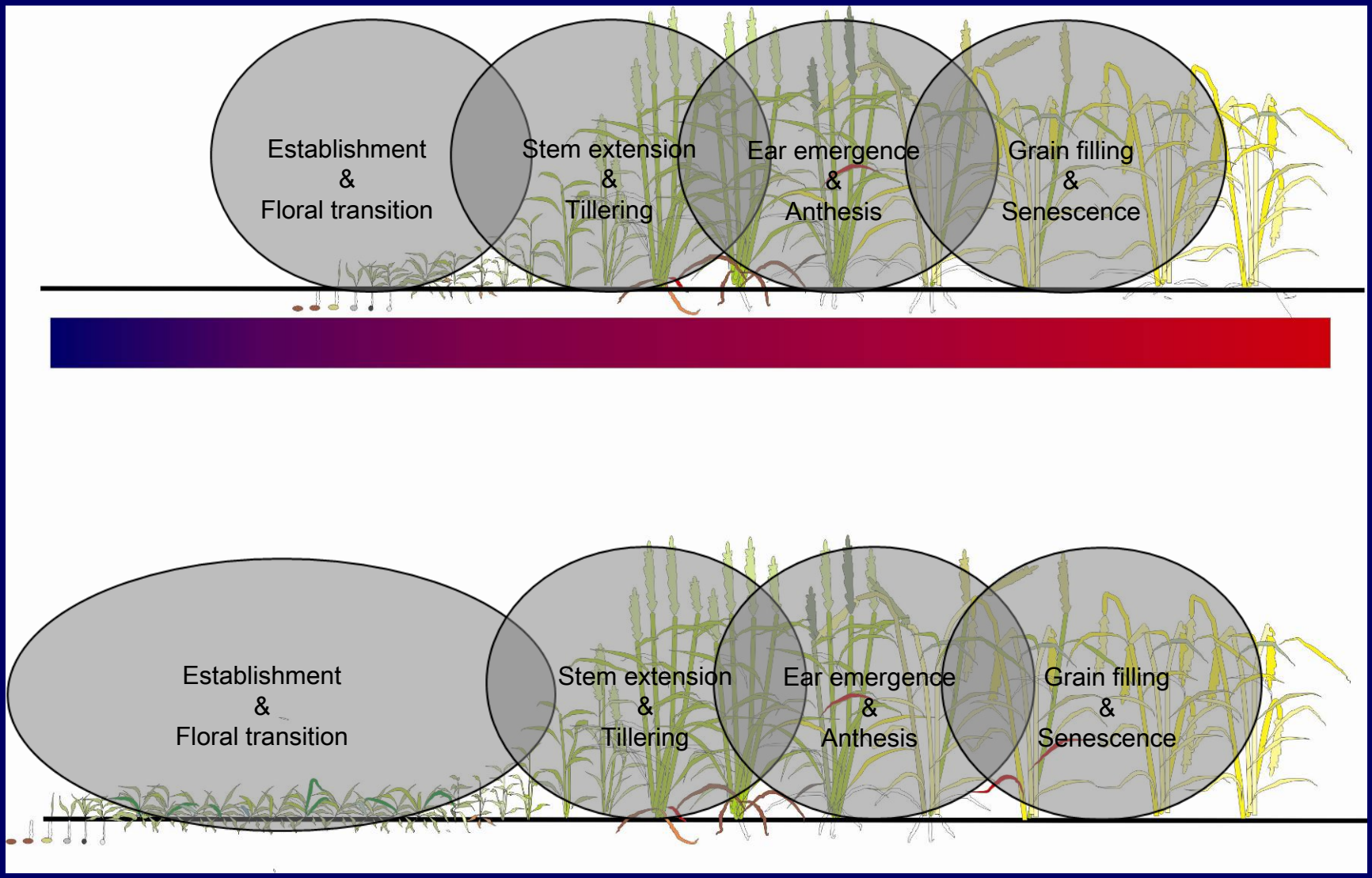


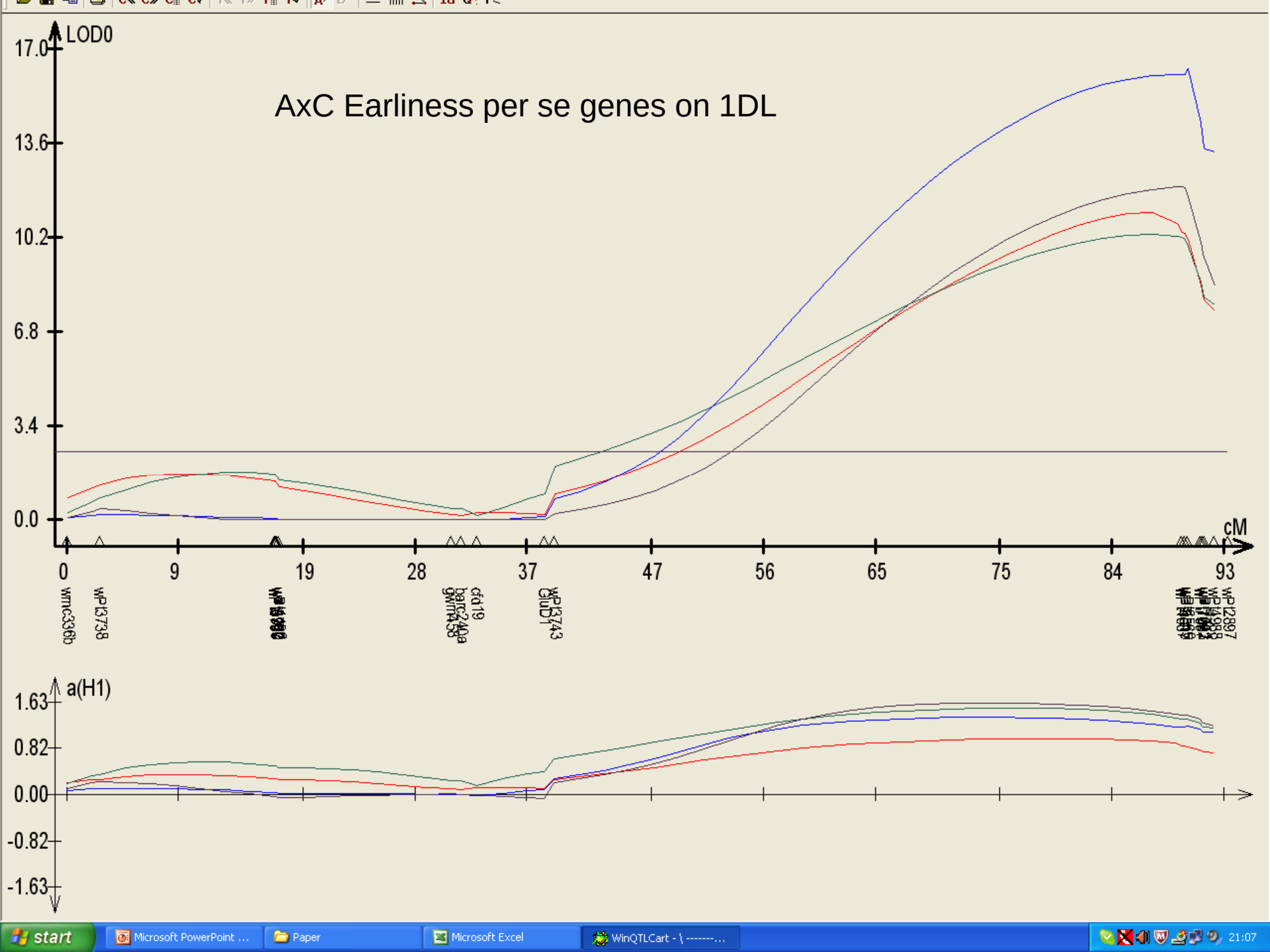


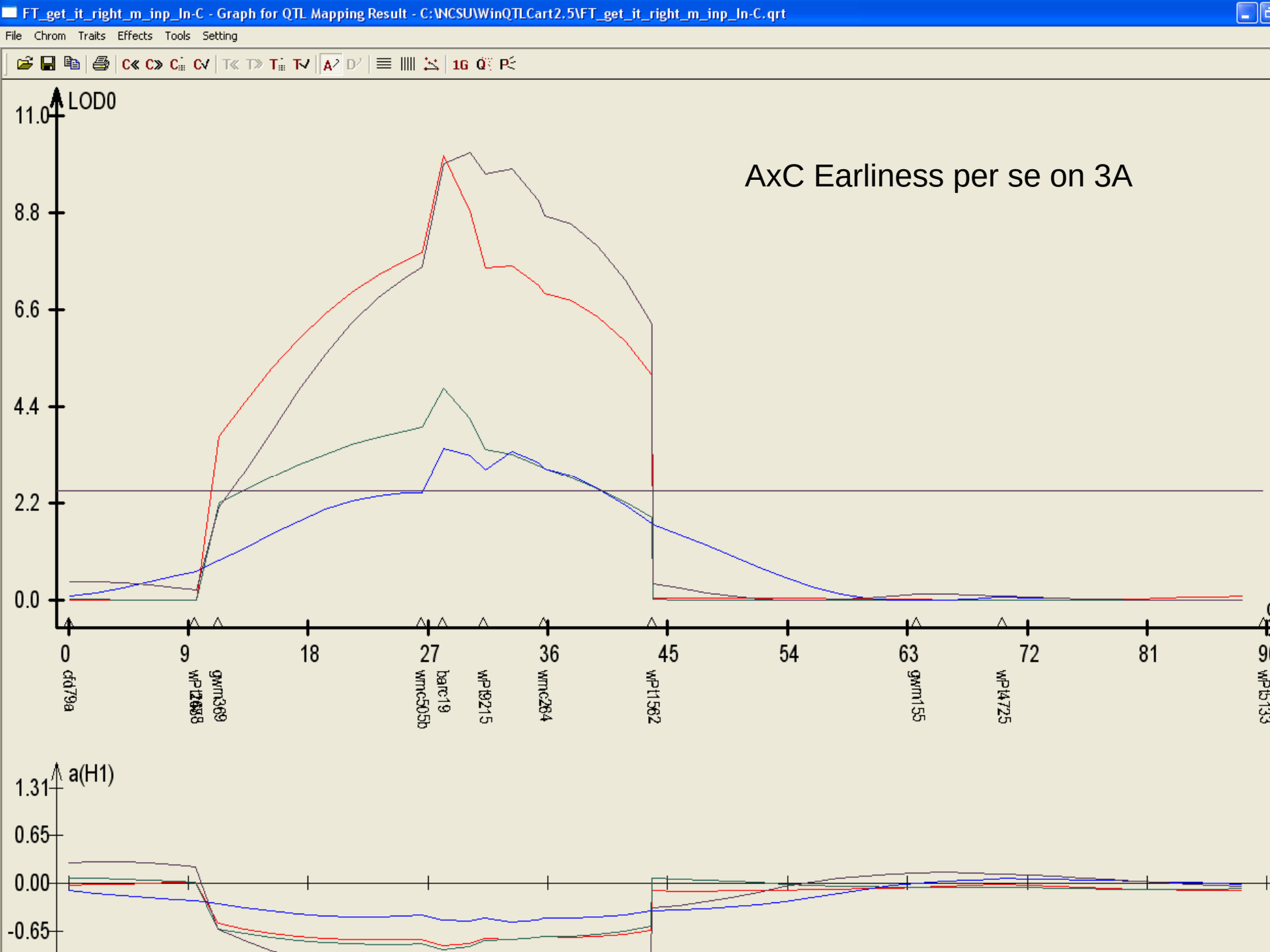
Isogenics

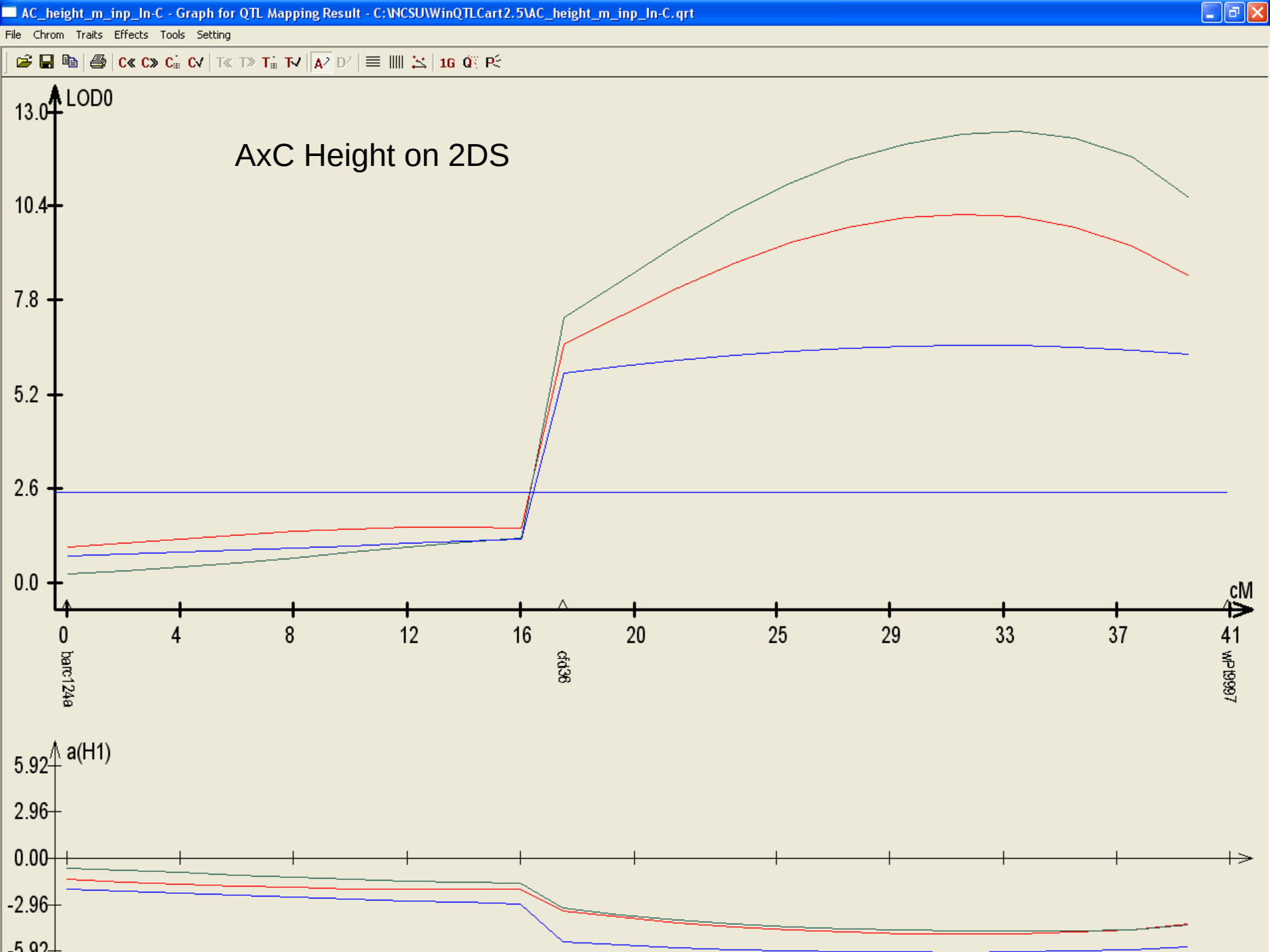
Fitting wheat to it's environment

The genetic fine tuning of adaptation

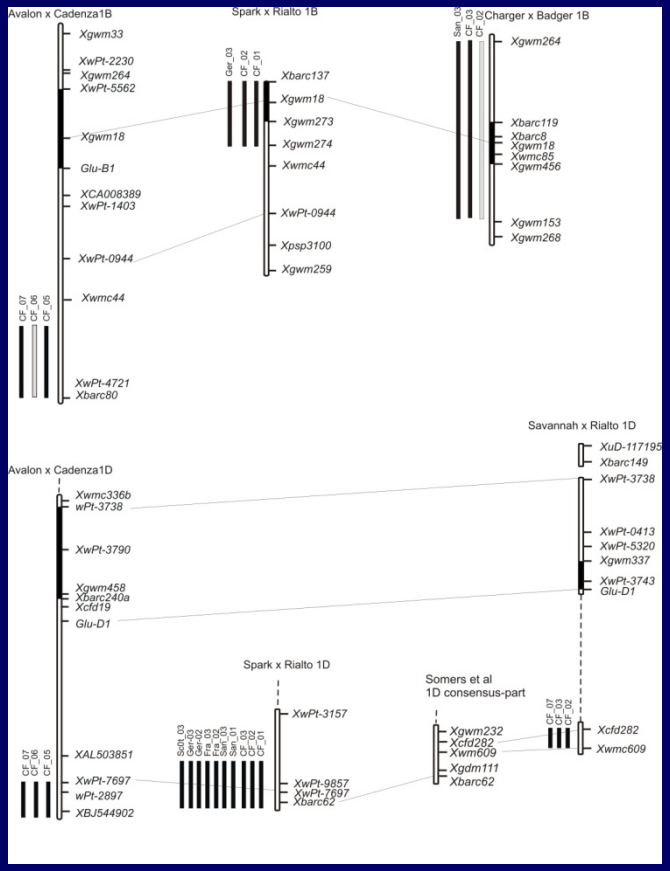


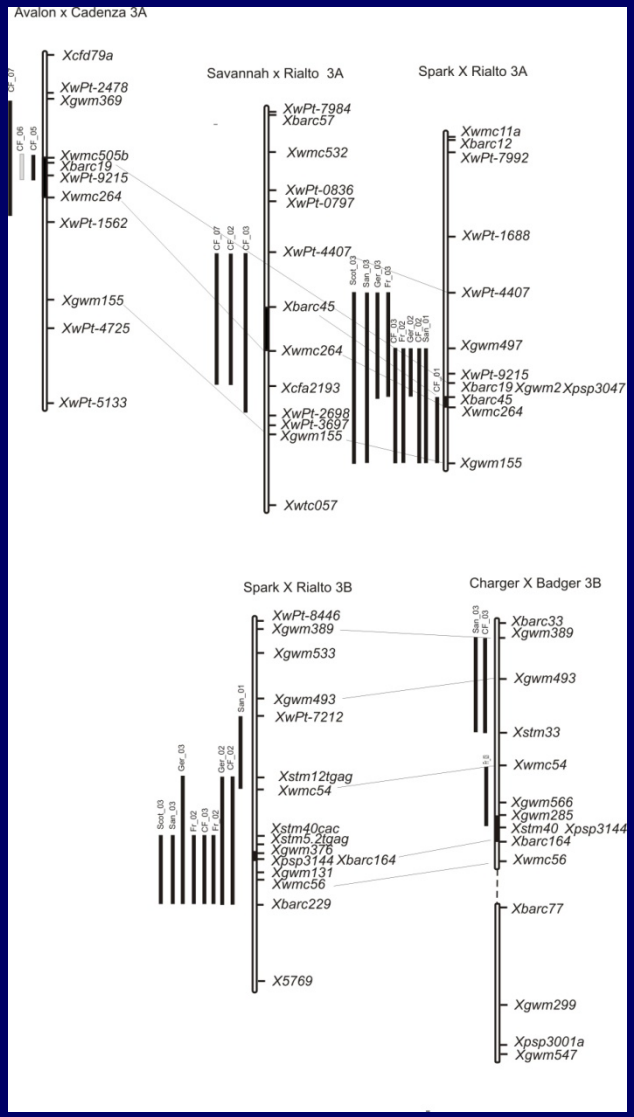

AxC Earliness per se genes on 1DL
LOD0
17.0
13.6
10.2
6.8
3.4
0.0
cM
0
9
19
28
37
47
56
65
75
84
93
wmc336b
wPt3738
cfd19
barc240a
gwm458
wPt3743
GluD1
wPt2897
a(H1)
1.63
0.82
0.00
-0.82
-1.63


FT_get_it_right_m_inp_In-C - Graph for QTL Mapping Result - C:\NCSU\WinQTLCart2.5\FT_get_it_right_m_inp_In-C.qrt
File Chrom Traits Effects Tools Setting
LOD0
11.0
8.8
6.6
4.4
2.2
0.0
AxC Earliness per se on 3A
0 9 18 27 36 45 54 63 72 81
cfa79a
gwm369
wmc505b
barc19
wPt9215
wmc264
wPt1562
gwm155
wPt4725
a(H1)
1.31
0.65
0.00
-0.65


AC_height_m_inp_In-C - Graph for QTL Mapping Result - C:\NCSU\WinQTLCart2.5\AC_height_m_inp_In-C.qrt
File Chrom Traits Effects Tools Setting
LOD0
AxC Height on 2DS
13.0
10.4
7.8
5.2
2.6
0.0
cM
0
4
8
12
16
20
25
29
33
37
41
barc124a
cfd36
wPt9997
a(H1)
5.92
2.96
0.00
-2.96
-5.92

Allelic variation is very common for many of these QTL





Are 1DL and 3AS combinations related to performance?

Crossing

50% DH1 P1 and P2

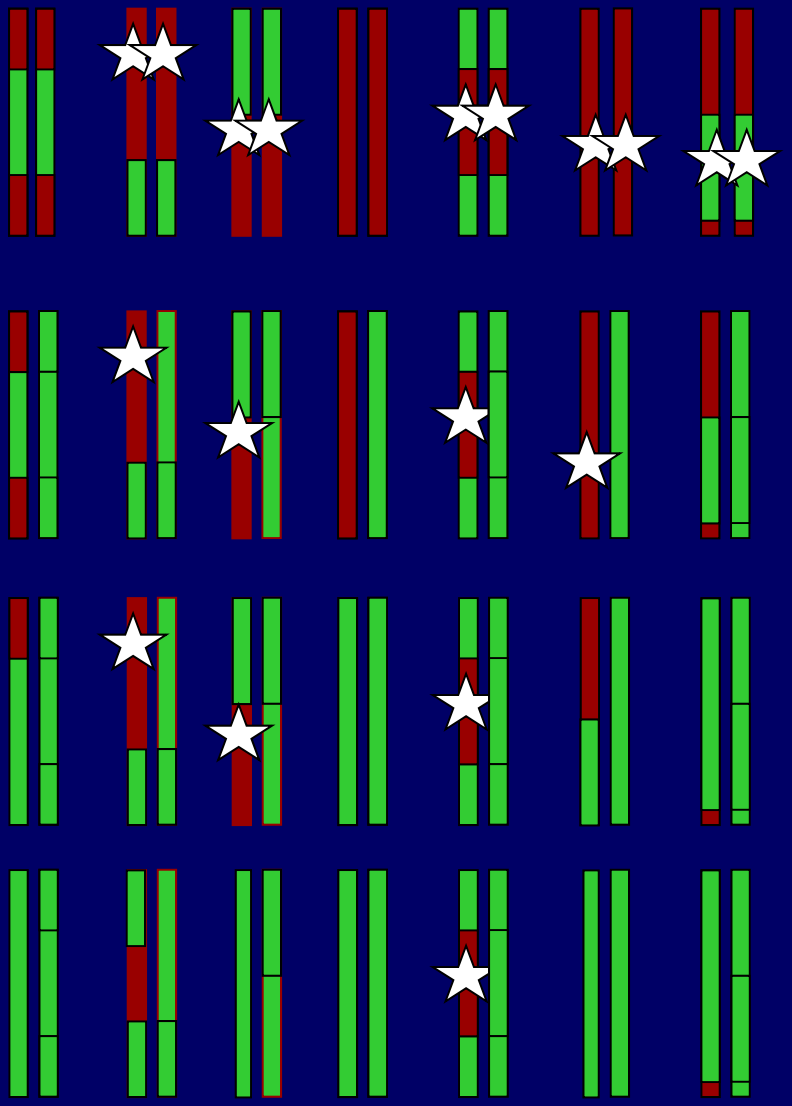
F_1 P1

75% BC_1 P1

87.5% BC_2

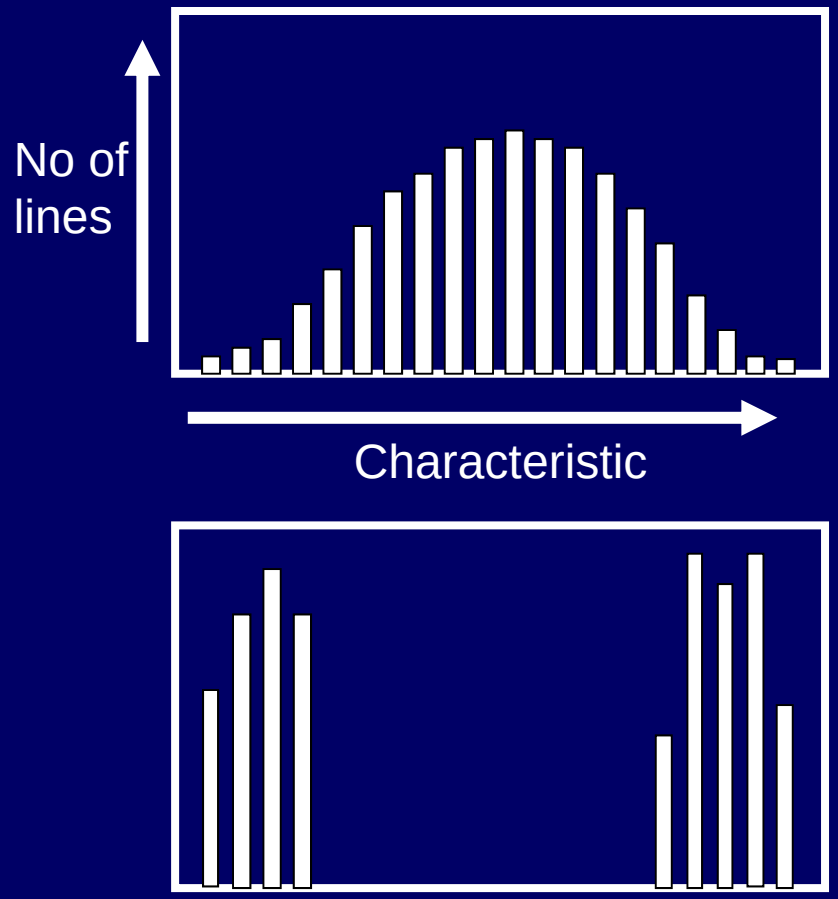
BC_2F_2

Marker Assisted Backcrossing



Population representing both homozygous classes

WGIN2 aim: From QTL to major gene



Acknowledgements

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