

# **Genetics and Genealogy of resistance to SBCMV in UK germplasm**

**4th SGC Genetics and Genomics  
Workshop**

**NIAB, 15<sup>th</sup> March 2006**



National Institute  
of Agricultural Botany

# Objectives

- **Develop molecular markers that tag genes for SBCMV resistance in UK germplasm**
- Compare the efficiency of classical versus association-based approaches

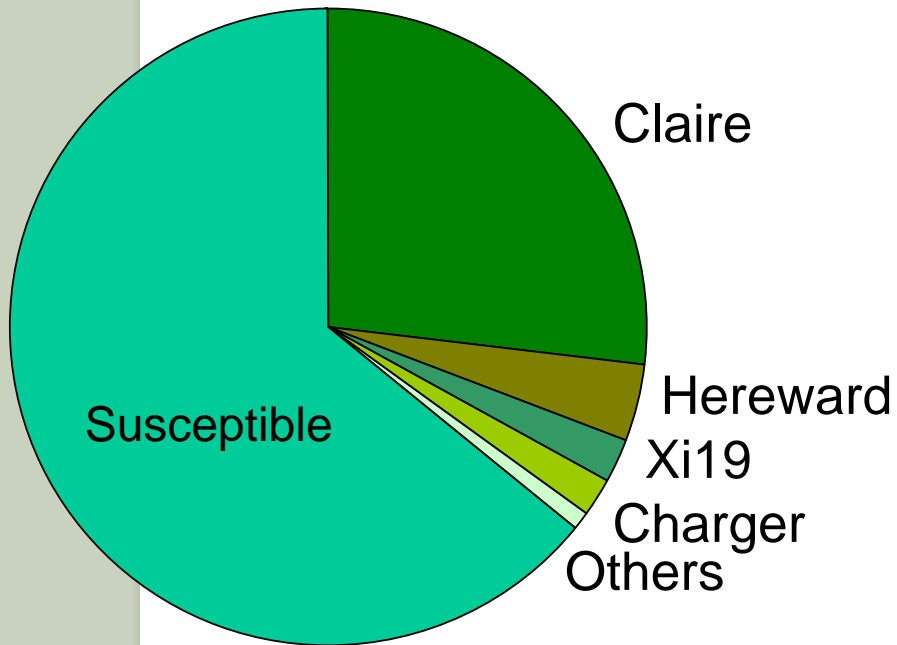
# SBCMV status of 2006

## Recommended List winter wheat varieties

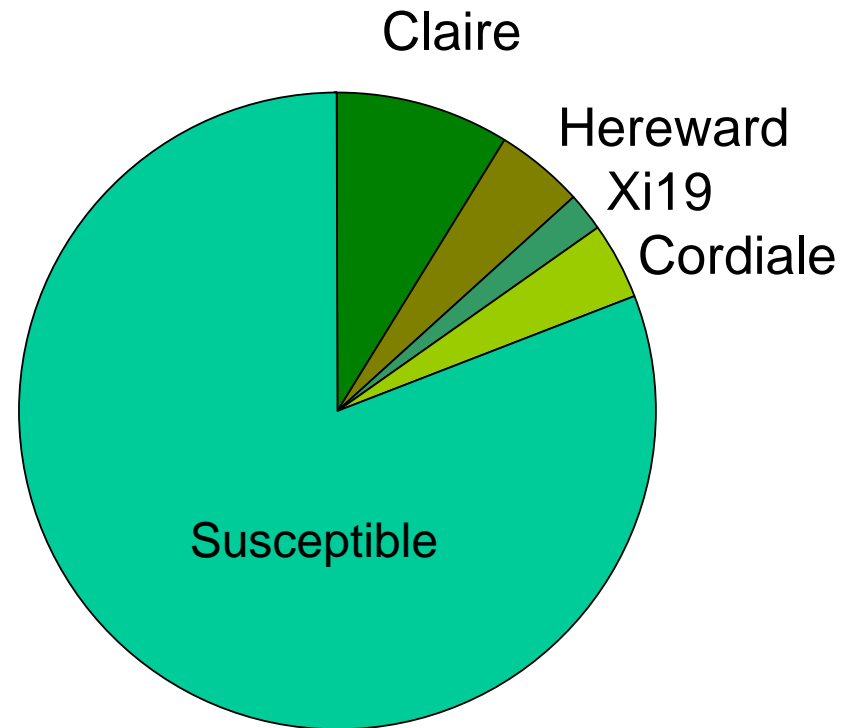


# % UK wheat acreage sown with SBCMV-resistant varieties

2002



2006

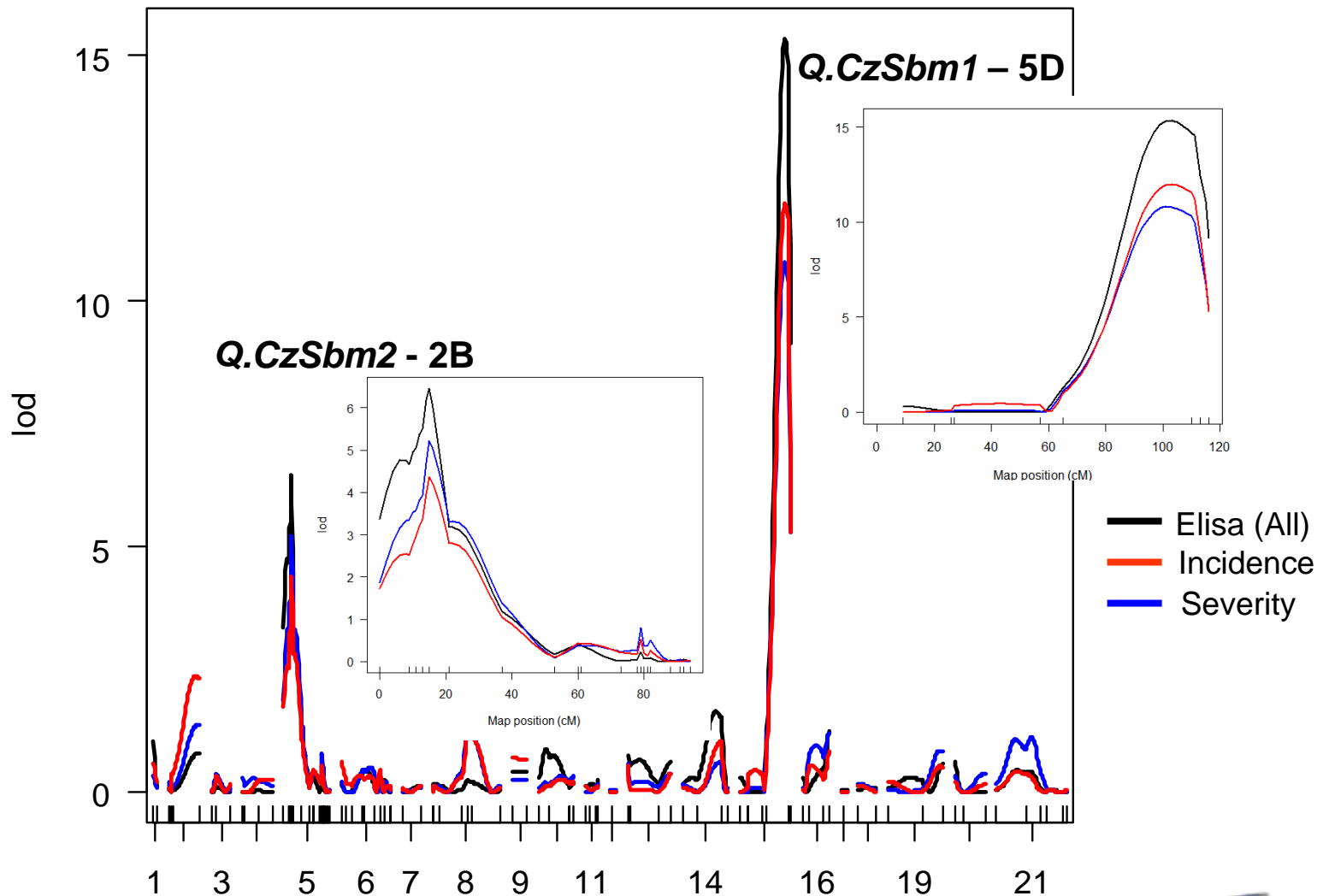




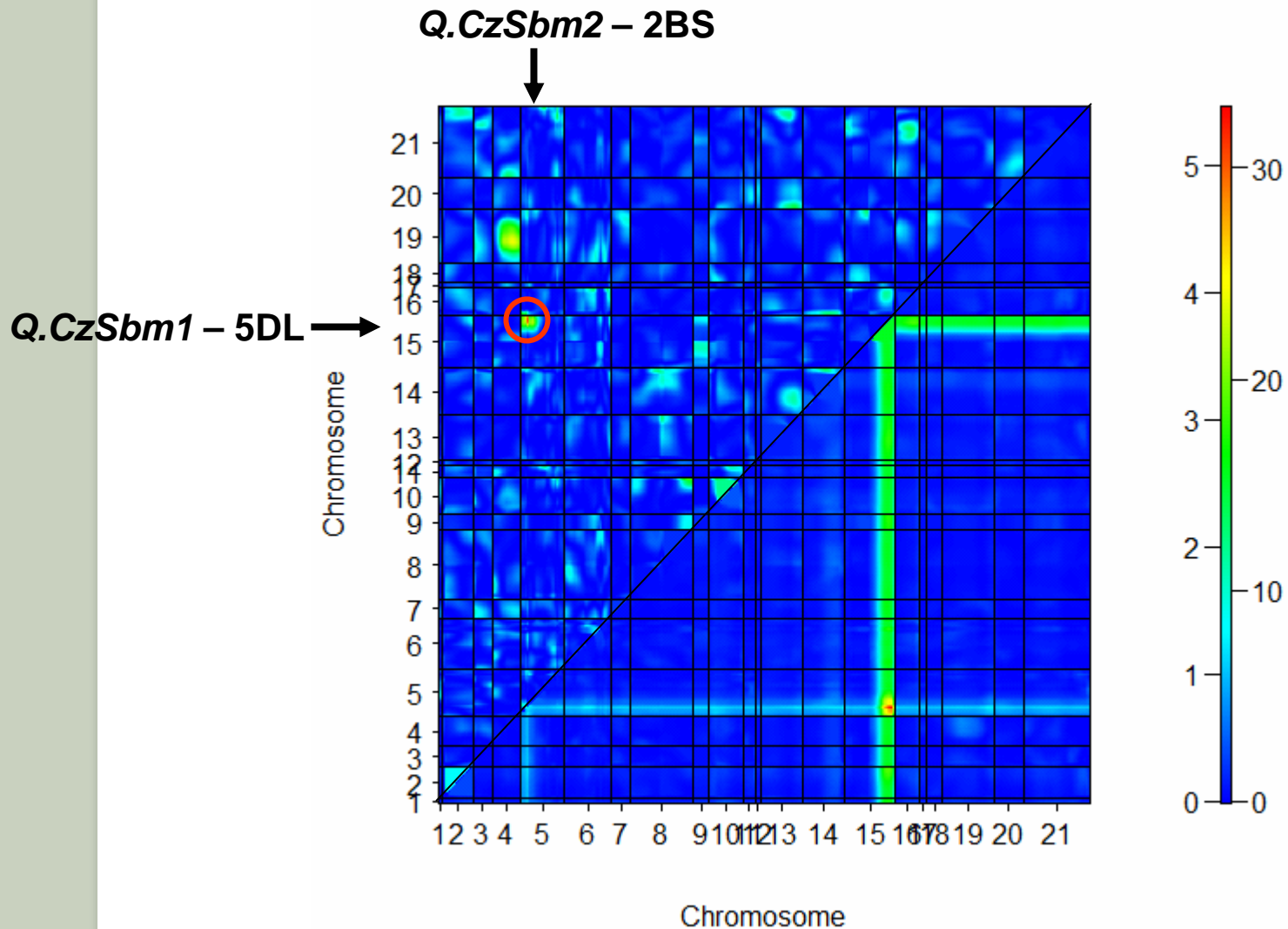
# Mapping Study

- Genome-wide QTL scans in **Avalon** x **Cadenza** DH and **Claire** x **Malacca** RIL populations (239, 178 markers resp.)
- Phenotyping in field and glasshouse evaluations – ELISA used to quantify virus
- Comparative mapping of resistance QTL across populations

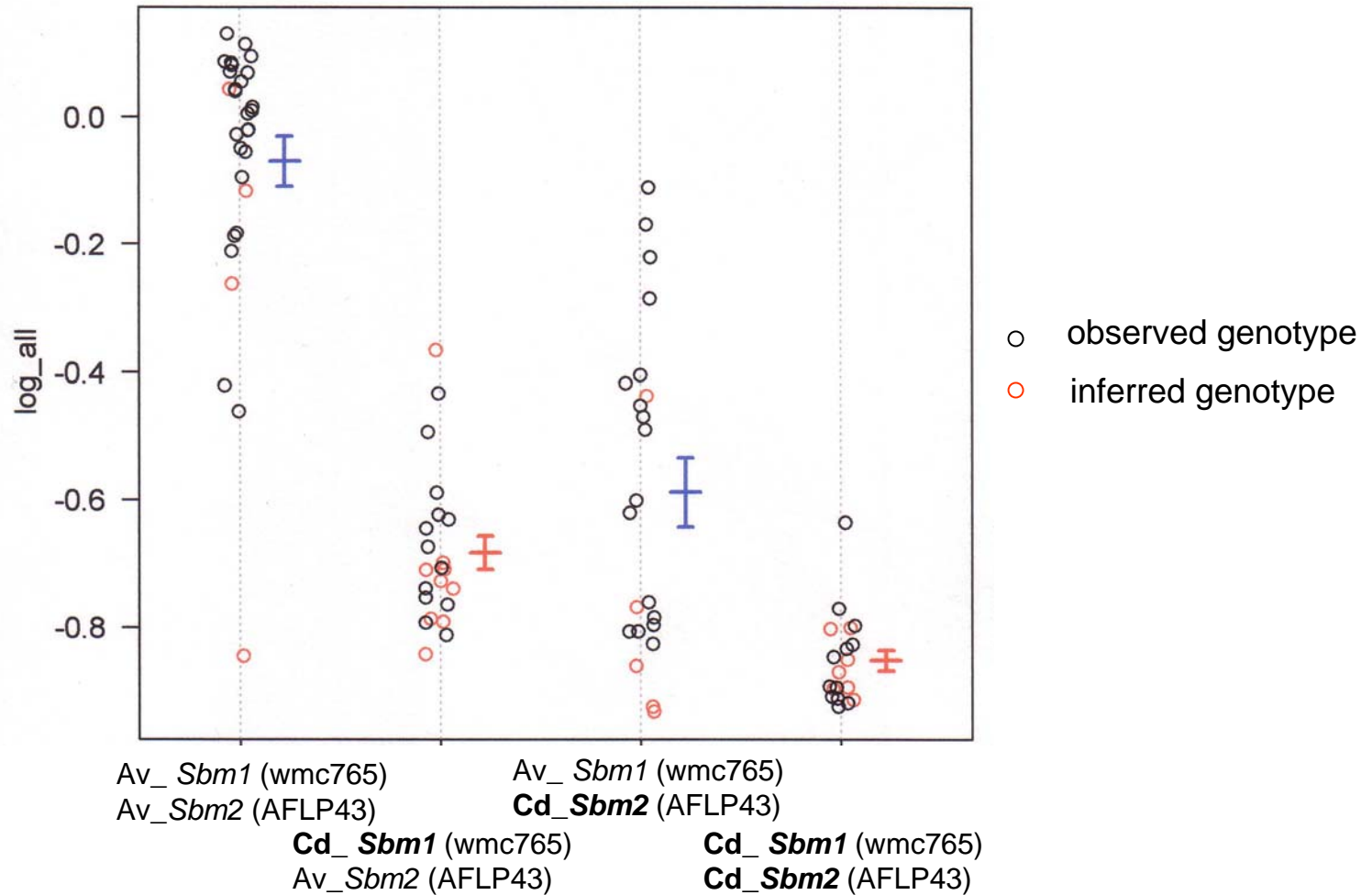
# AxC Interval Mapping (R/QTL)



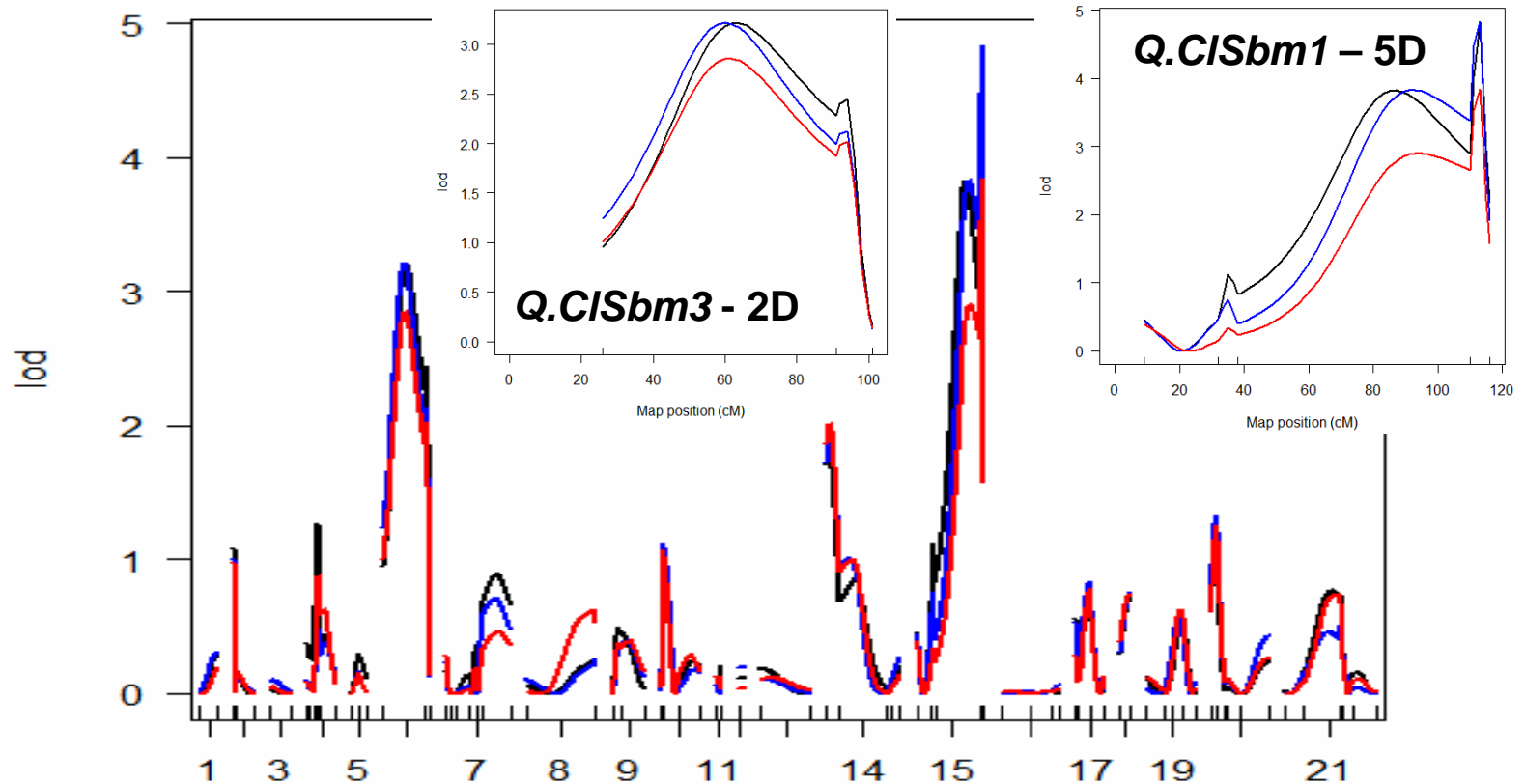
# Interactions between QTL



# *Sbm1* and *Sbm2* are additive



# CxM Interval Mapping (R/QTL)



— Elisa (All)  
— Incidence  
— Severity



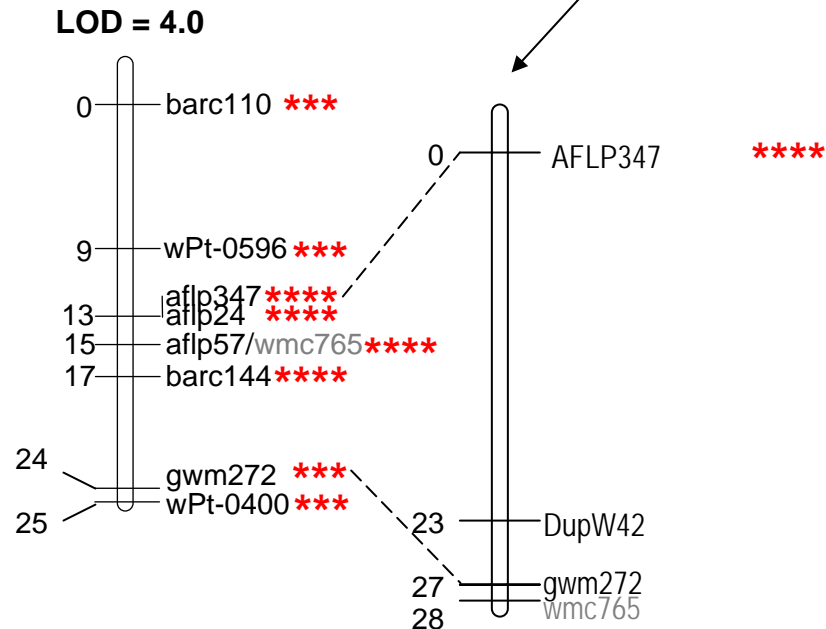
# *Sbm1* region comparative linkage mapping

## A x C 5DL partial map of *Sbm1* region

239 markers, 92 lines  
SBCMV incidence  
Bonferroni correction

## C x M 5DL partial map (*Sbm1*)

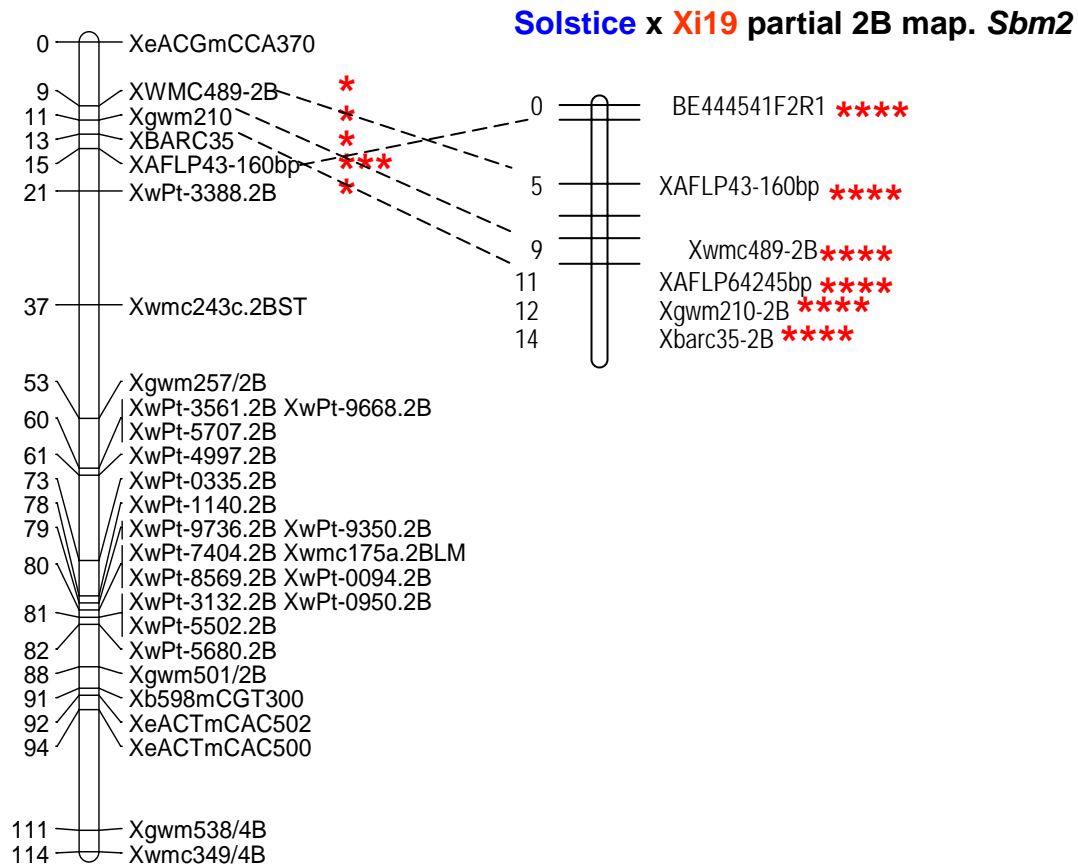
178 markers, 92 lines  
SBCMV incidence  
Bonferroni correction



\* Significance of Single Marker Analysis in QTL Cartographer (\*\*\*\* = sig at 0.01 %)

## Avalon x Cadenza 2B map. *Sbm2*

incidence single marker analysis scores with Bonferroni correction



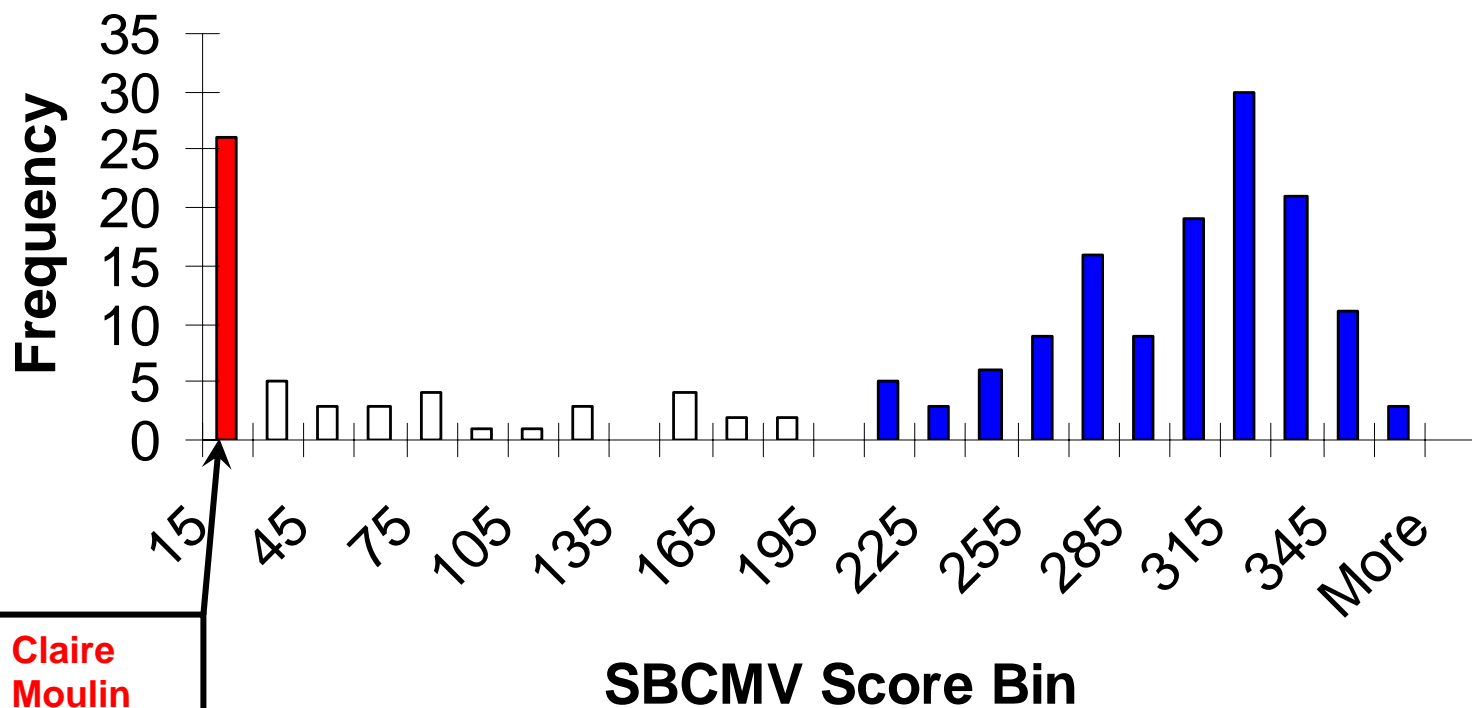
# Association study

1. Can previously known *Sbm1* and *Sbm2* be detected?
2. Are additional loci detected, and if so, are these significant?
3. Does level of recombination/LD in adapted germplasm permit refinement of QTL interval?

## Association study - *design*

- 186 EU winter wheat varieties grown in replicate plots at Hilperton SBCMV trial site in 05/06 and visual assessments of symptoms made
- 188 markers used to control population structure and genome-wide LD patterns - 42 SSRs, 72 SSAPs, 72 NBS-LRR
- SSRs spanning *Sbm1* and *Sbm2* regions scored on panel of 186 varieties
- Balanced representation of 8 major sub-groups found in overall GEDIFLUX project (500+ varieties)

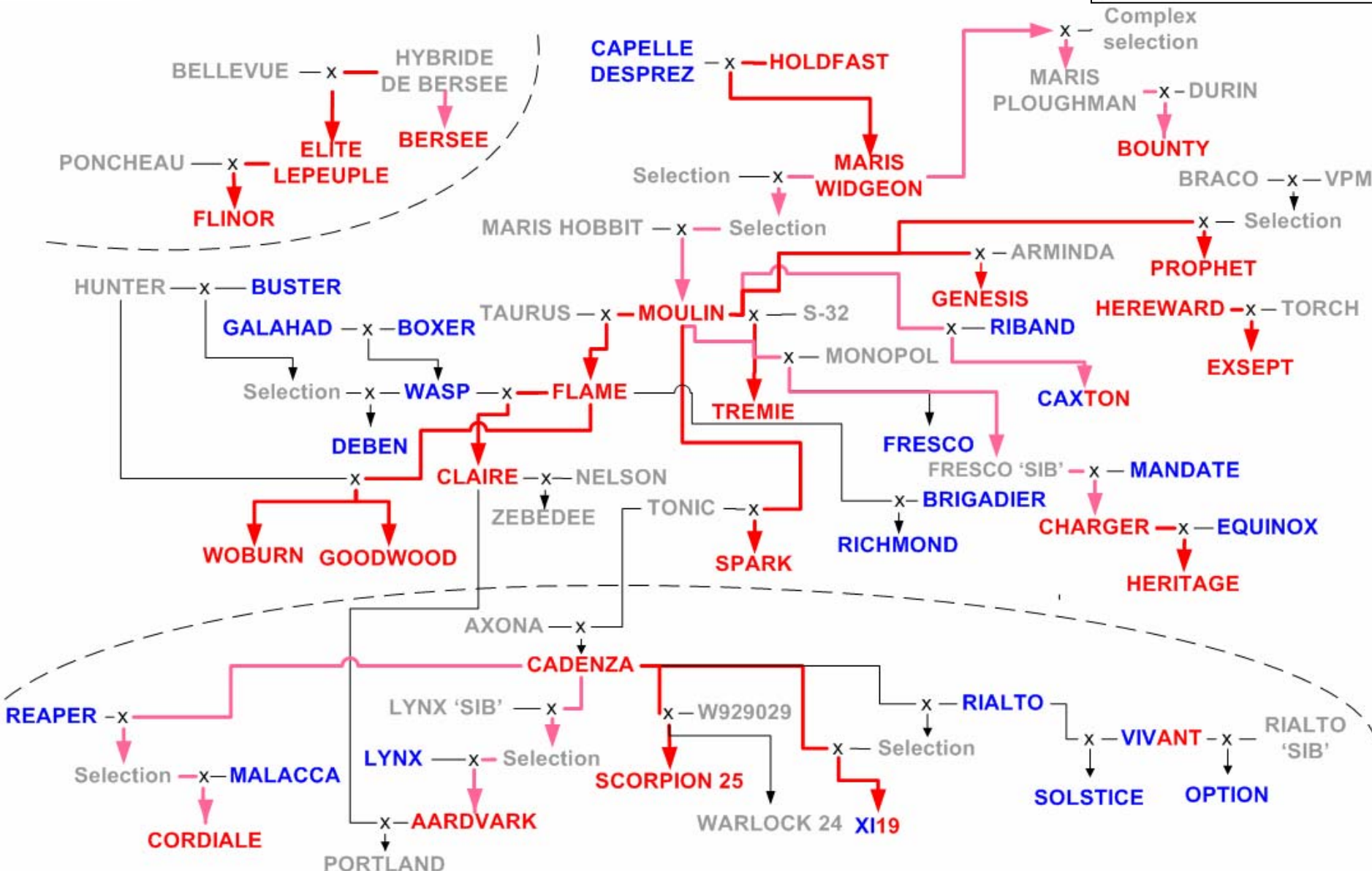
# SBCMV score class frequency for 200 Gediflux variety Wiltshire trial 2006



Claire  
Moulin  
Cadenza  
etc

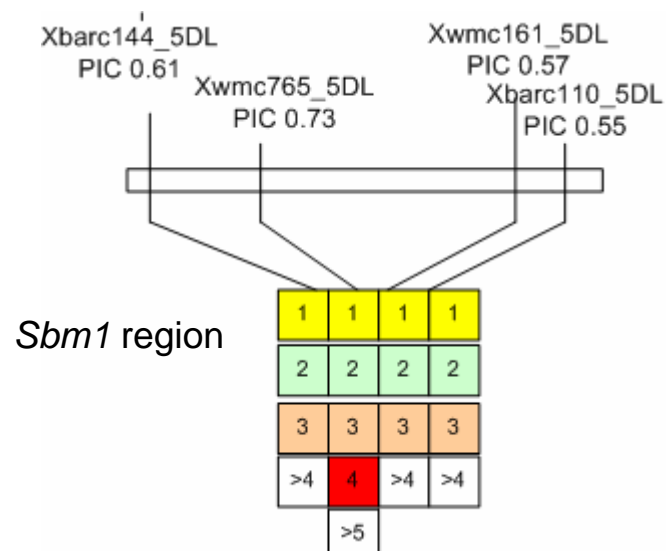
# Pedigree relationships between SBCMV resistant varieties

Red = Tested R  
 Blue = Tested S  
 Grey = Untested



# Clump/ GC results (part 2)

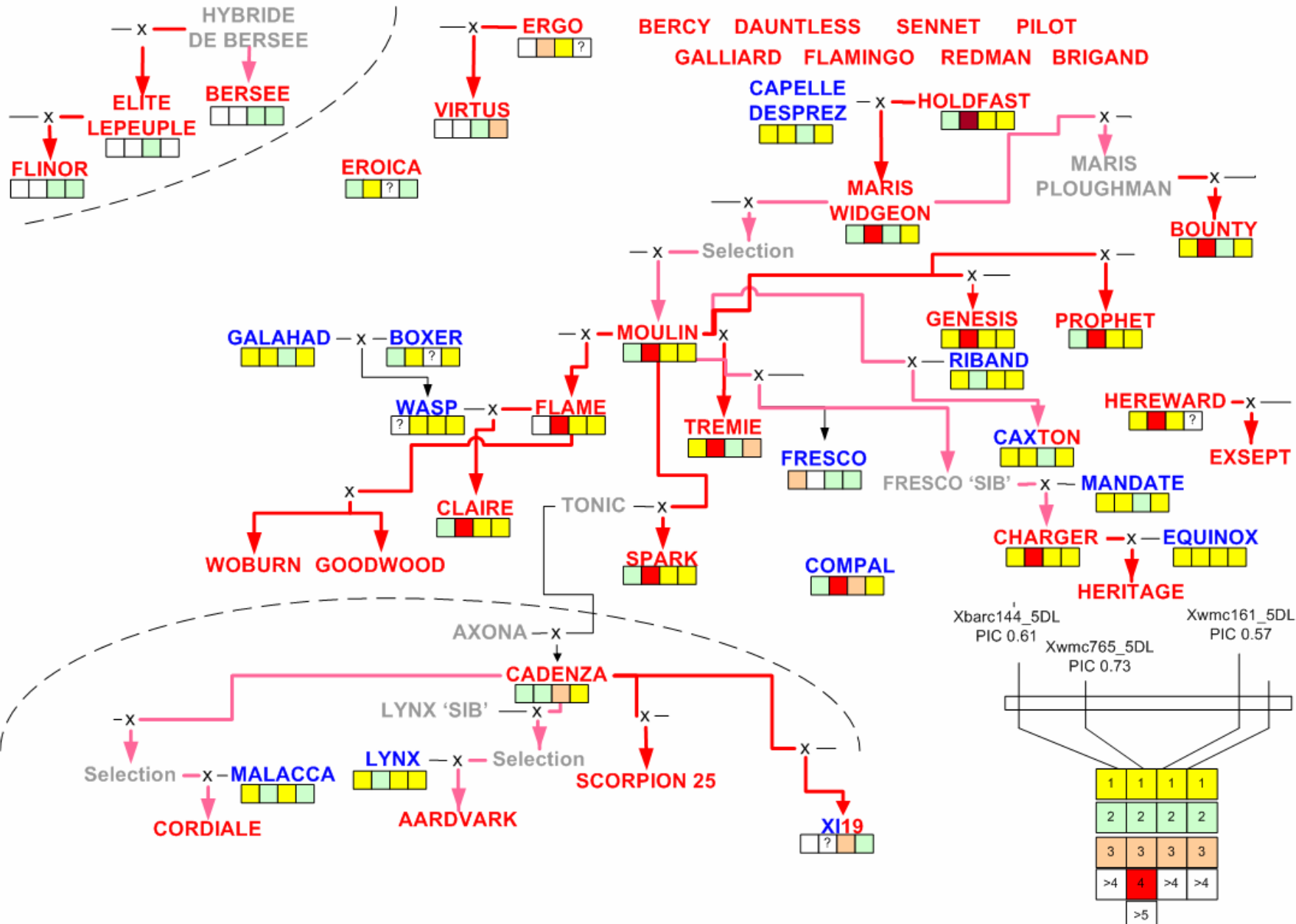
Marker	Raw				Adjusted (GC/DC)			
	p (T1)	p (T2)	p (T3)	p(T4)	p (T1)	p (T2)	p (T3)	p(T4)
cSSR1_ <i>Sbm1</i>	0.000	0.078	0.089	0.001	0.008	0.155	0.208	0.013
cSSR2_ <i>Sbm1</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
cSSR3_ <i>Sbm1</i>	0.747	0.229	0.258	0.639	0.890	0.342	0.419	0.803
cSSR4_ <i>Sbm1</i>	0.013	0.087	1.000	0.025	0.121	0.168	1.000	0.136
cSSR5_ <i>Sbm2</i>	0.273	0.080	0.527	0.215	0.593	0.158	0.660	0.469
cSSR6_ <i>Sbm2</i>	0.876	0.946	0.959	0.935	0.947	0.958	0.972	0.966
average	0.318	0.237	0.472	0.302	0.427	0.297	0.543	0.398
prop (<0.05)	0.500	0.167	0.167	0.500	0.333	0.167	0.167	0.333
prop (<0.01)	0.333	0.167	0.167	0.333	0.333	0.167	0.167	0.167
prop (<0.001)	0.333	0.167	0.167	0.333	0.167	0.167	0.167	0.167





SSR1 - gwm415 (5AS)		0.691	0.829	0.797	1.000		0.864	0.868	0.860	1.000	
SSR9 - gwm291 (5AL)		0.107	0.520	0.569	0.718		0.384	0.618	0.693	0.849	
SSR19 - gwm213 (5BS)		0.309	0.591	0.569	0.733		0.626	0.677	0.693	0.857	
SSR2 - gwm408 (5BL)		0.065	0.695	0.712	0.064		0.298	0.762	0.799	0.240	
SSR14 - gwm190 (5DS)	8.9	0.131	0.006	0.003	0.037		0.424	0.021	0.016	0.174	
BARC110 (5DL)	100.0	0.013	0.087	1.000	0.025		0.121	0.168	1.000	0.136	
wmc161 (5DL)	106.5	0.747	0.229	0.258	0.639		0.890	0.342	0.419	0.803	
wmc765 (5DL)	109.7	0.000	0.000	0.000	0.000		0.000	0.000	0.001	0.000	
BARC144 (5DL)	112.7	0.000	0.078	0.089	0.001		0.008	0.155	0.208	0.013	
SSR10 - gwm272 (5DL)	119.0	0.347	0.135	0.134	0.365		0.657	0.233	0.273	0.613	
SSR5 - gwm334 (6AS)		0.015	1.000	0.195	0.022		0.131	1.000	0.350	0.126	
SSR32 - gwm570 (6AL)		0.025	0.205	0.208	0.023		0.176	0.316	0.365	0.129	
SSR28 - gwm680 (6BS)		0.151	1.000	0.720	0.120		0.453	1.000	0.805	0.343	
SSR12 - gwm219 (6BL)		0.001	0.101	0.042	0.005		0.021	0.189	0.123	0.050	
SSR6 - gwm325 (6DS)		1.000	0.808	0.922	0.782		1.000	0.851	0.947	0.885	
SSR40 - gwm1749 (6DL)		0.011	0.158	0.917	0.013		0.109	0.261	0.943	0.090	
SSR36 - gwm834 (7AS)		0.013	0.134	0.135	0.009		0.122	0.232	0.275	0.068	
SSR29 - gwm631 (7AL)		0.800	0.398	0.537	0.946		0.914	0.509	0.668	0.972	
SSR17 - gwm46 (7BS)		0.105	0.177	0.099	0.373		0.380	0.284	0.223	0.620	
SSR33 - gwm577 (7BL)		0.184	0.743	1.000	0.299		0.497	0.800	1.000	0.555	
SSR39 - WMS1619 (7DS)		0.004	0.002	0.002	0.003		0.057	0.008	0.013	0.030	*
SSR42 - gwm437 (7DL)		0.088	0.141	0.124	0.231		0.348	0.240	0.260	0.487	

# Pedigree vs graphical genotypes



# Association study - *questions*

1. Can previously known *Sbm1* and *Sbm2* be detected?

*Sbm1* – yes. *Sbm2* – no, allele is rare and/or we used insufficiently linked markers?

2. Are additional loci detected, and if so, are these significant?

Yes, but significance remains to be seen.

3. Does level of recombination/LD in adapted germplasm permit refinement of QTL interval?

Apparent resolution for *Sbm1* as good as or better than classical mapping

# Acknowledgements

**NIAB** – Vince Lea, Susan Freeman, James Cockram, Silvia Doveri, Ian Mackay, Vicky Fanstone, Rosemary Bayles

**CSL** - Christine Henry, Giles Budge

**JIC** – John Snape

**Nickerson Advanta Ltd**

Simon Berry, Chris Chapman

**Lochow – Petkus GmbH**

Viktor Korzun

**GEDIFLUX collaborators**

Simon Orford

Robert Koebner

Martin Ganal

LINK funding – Defra and HGCA

