Utilization of the IWGSC Resources: Application to Wheat Breeding

UNIVERSITY OF SASKATCHEWAN

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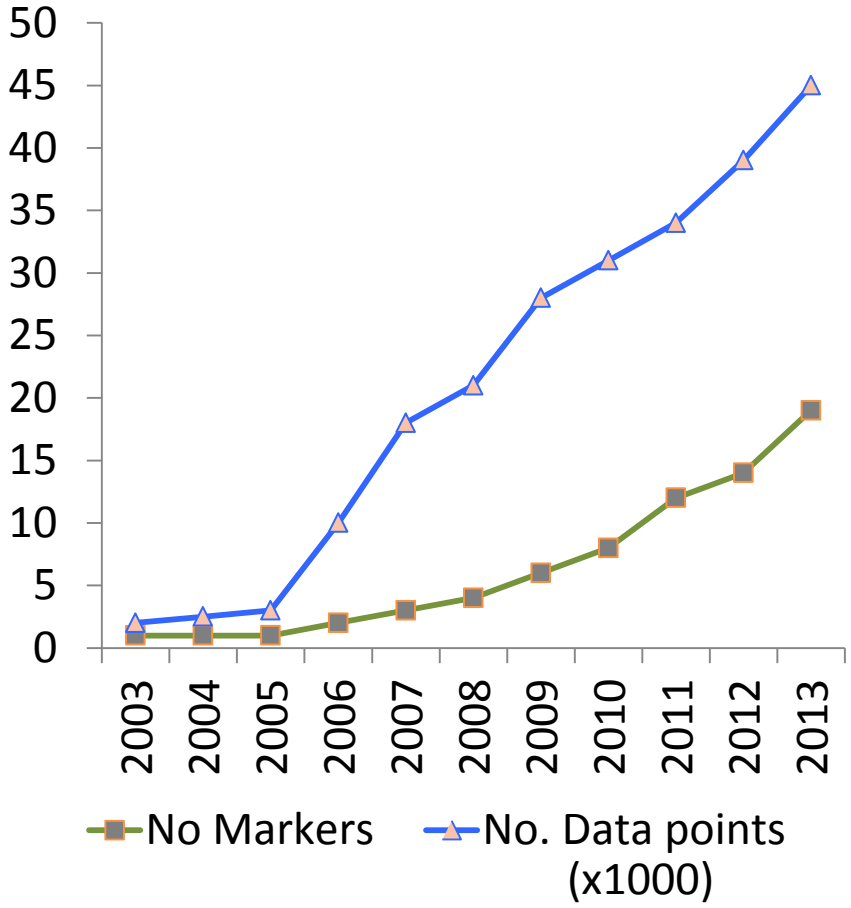
IWGSC Workshop, PAG, Jan 2014

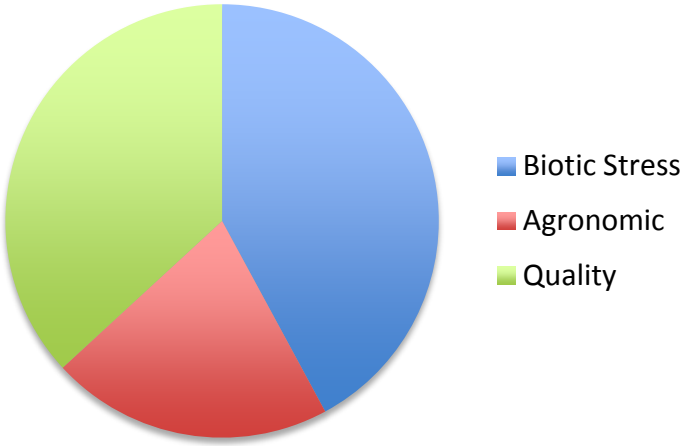
Wheat Breeding at the UofS

- Spring and durum wheat breeding
- Objectives
  - »Yield, maturity
  - »Abiotic stresses (terminal drought, heat)
  - »Biotic stresses (Rusts, FHB, Leaf-spotting diseases, Insect pests)
  - »Quality, Quality, Quality

Marker Assisted Breeding



Focus: Stacking of single genes



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Canadian Triticum Advancement through Genomics

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GenomePrairie

University of Saskatchewan

Agriculture and Agri-Food Canada

NRC·CNRC Canada

University of Regina

National Agri-Food Biotechnology Institute

K-State Kansas State University

INRA

IWGSC Resources in Breeding

BAC Libraries

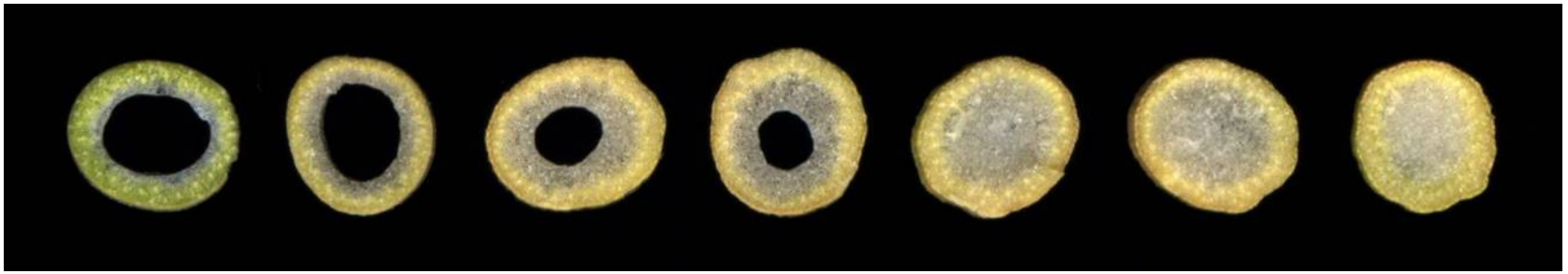
Physical Maps

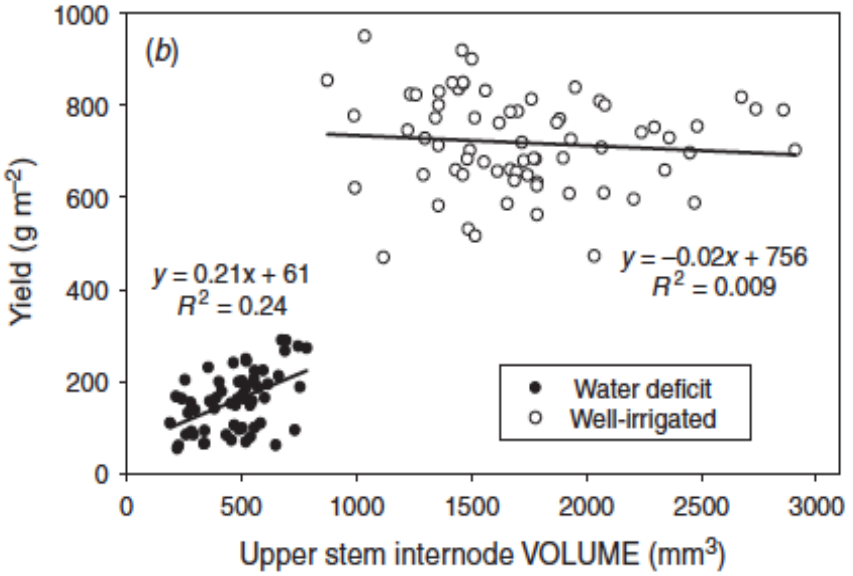
Wheat Survey Sequence

3B Sequence

- Unlimited source of DNA markers for MAS/Genomic Selection
- Candidate genes for traits = perfect markers
- Reduce the time and improve the success of resolving QTL
- Discovery and exploitation of new alleles

Speeding Gene Discovery: Stem Solidness in Wheat

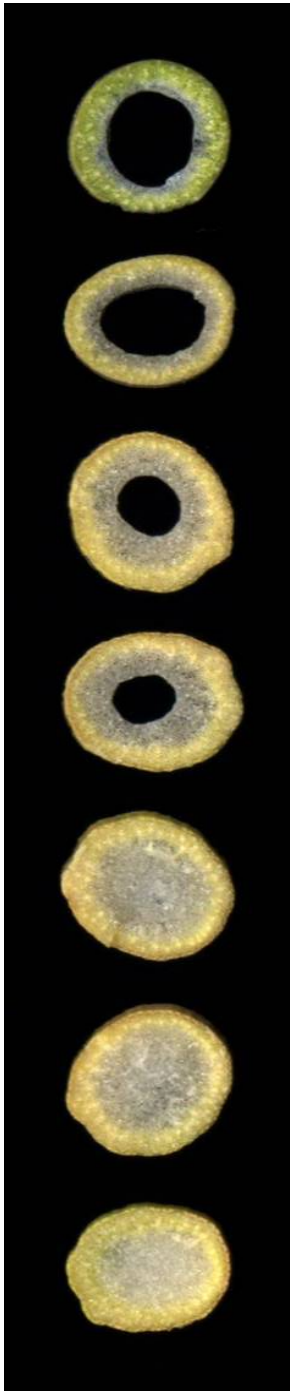




Saint Pierre et al. 2010; Functional Plant Biology, 37, 166.

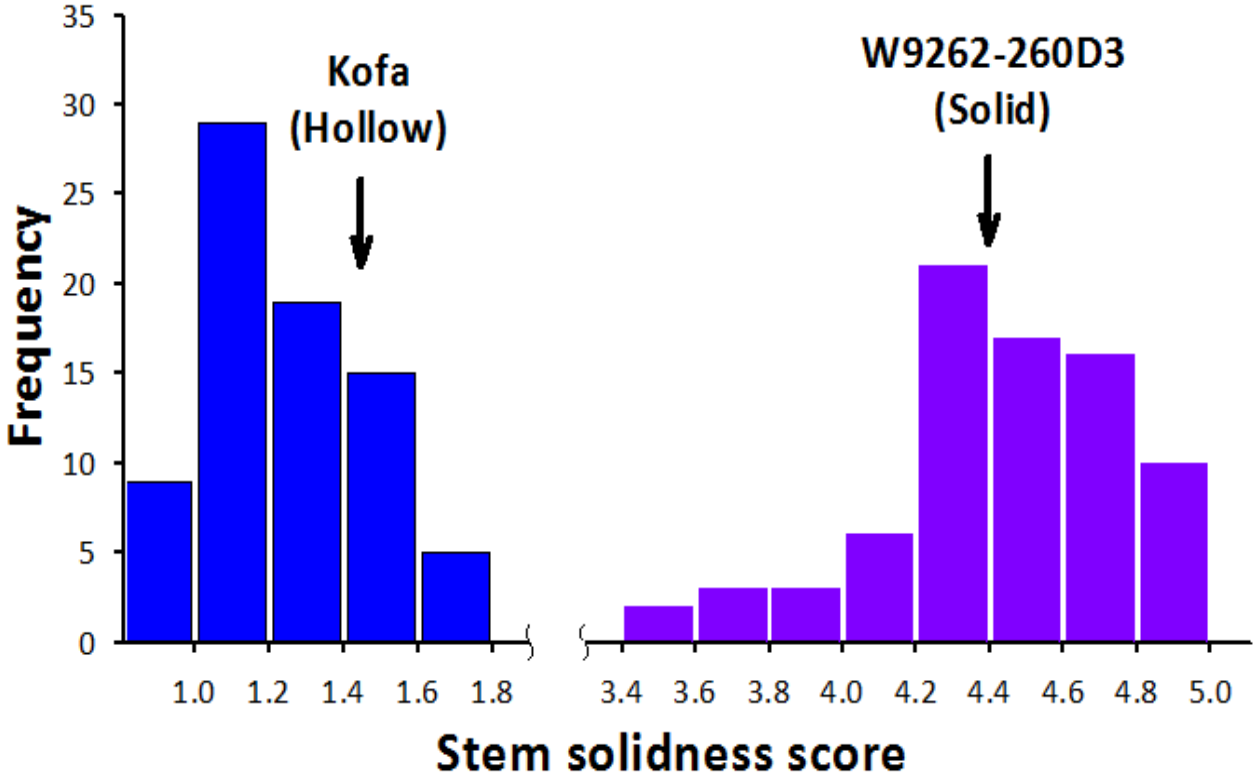
Genetics of Stem Solidness

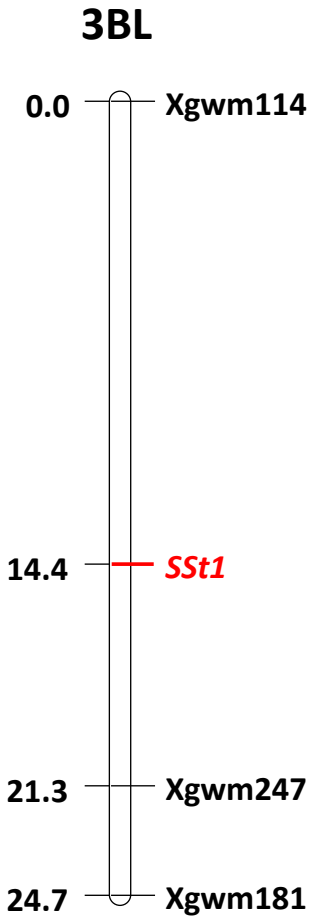
- **Quantitative expression in hexaploid wheat**
  - Expression influenced by environment
  - *Evidence* of suppression in hexaploid wheat
- **Single dominant gene in durum wheat**
  - Little environmental influence on expression
  - “discrete” classification



Stem Solidness in Wheat

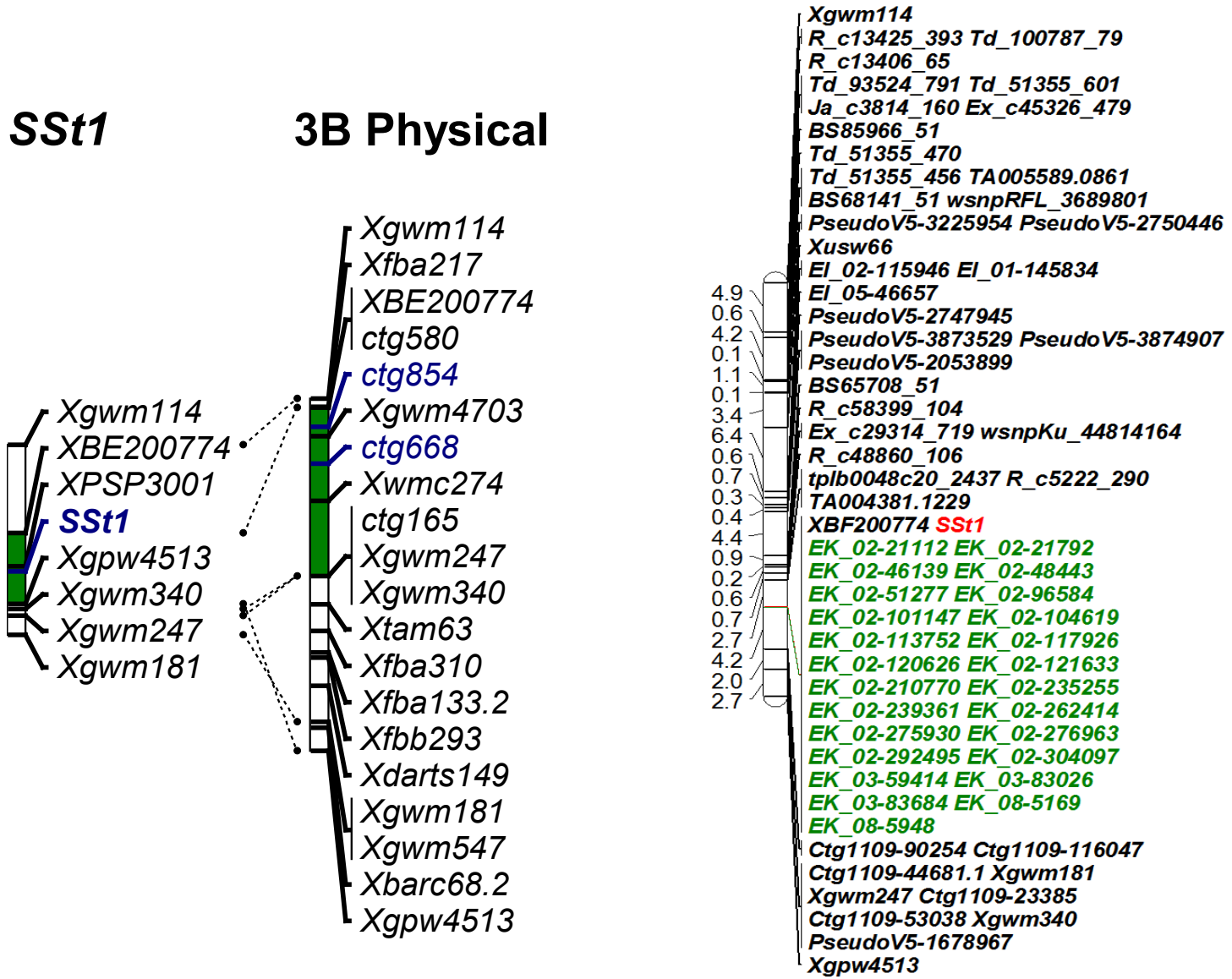
DH population of durum wheat (155 lines)



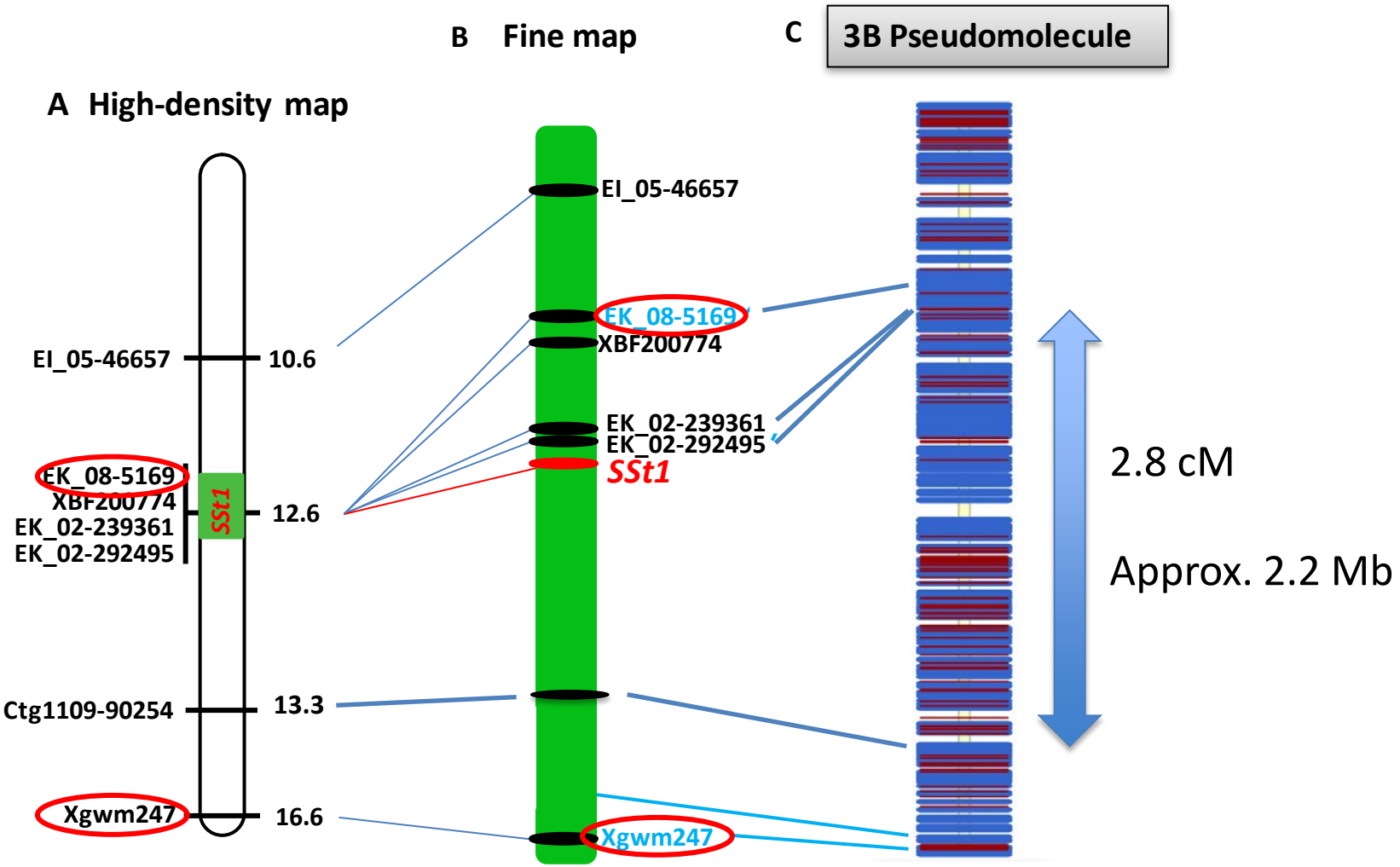


Houshmand et al. (2007)
Mol Breeding 20:261

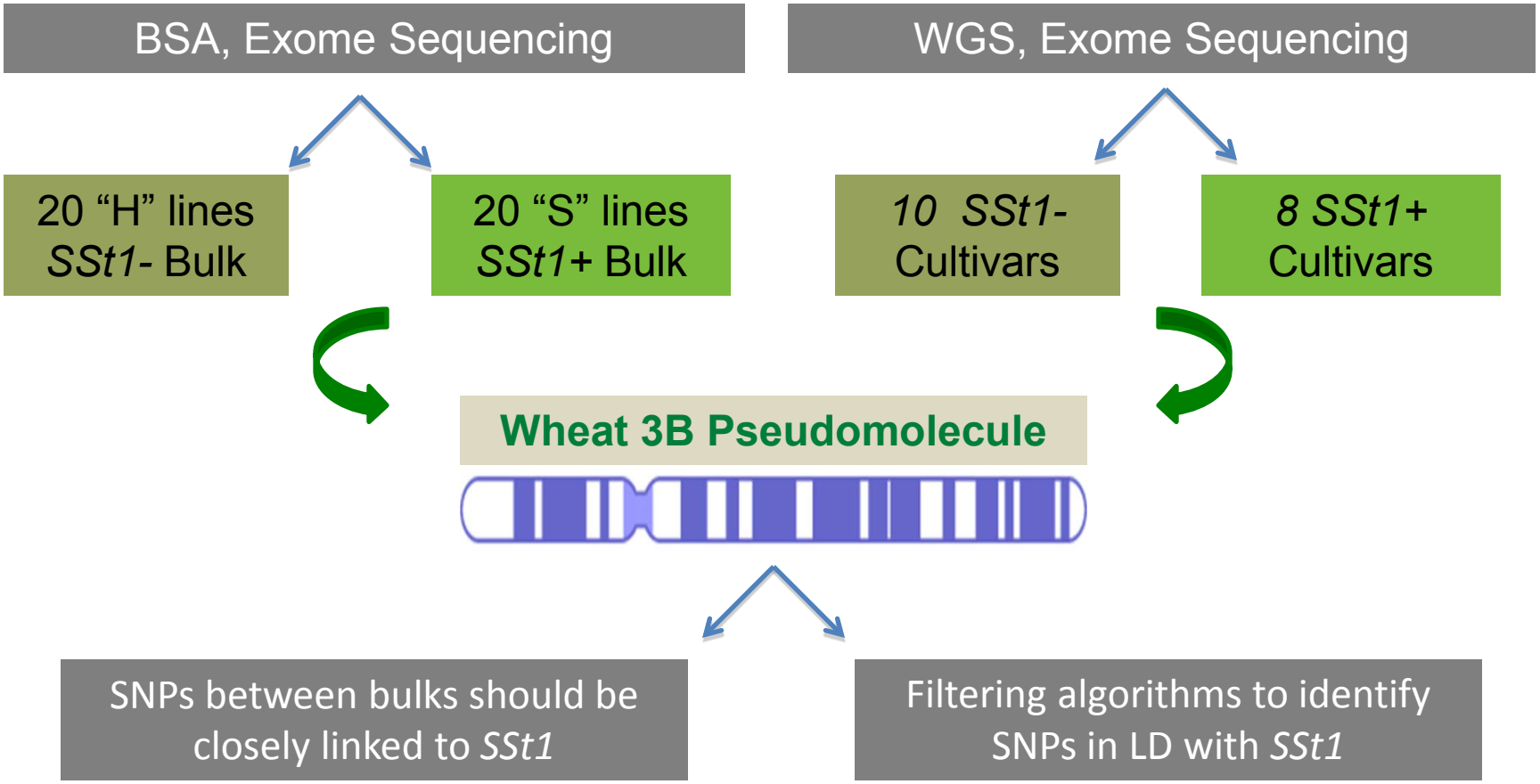
Physical Map -- High Density Map



Speed Gene Discovery:
Towards Cloning SSt1

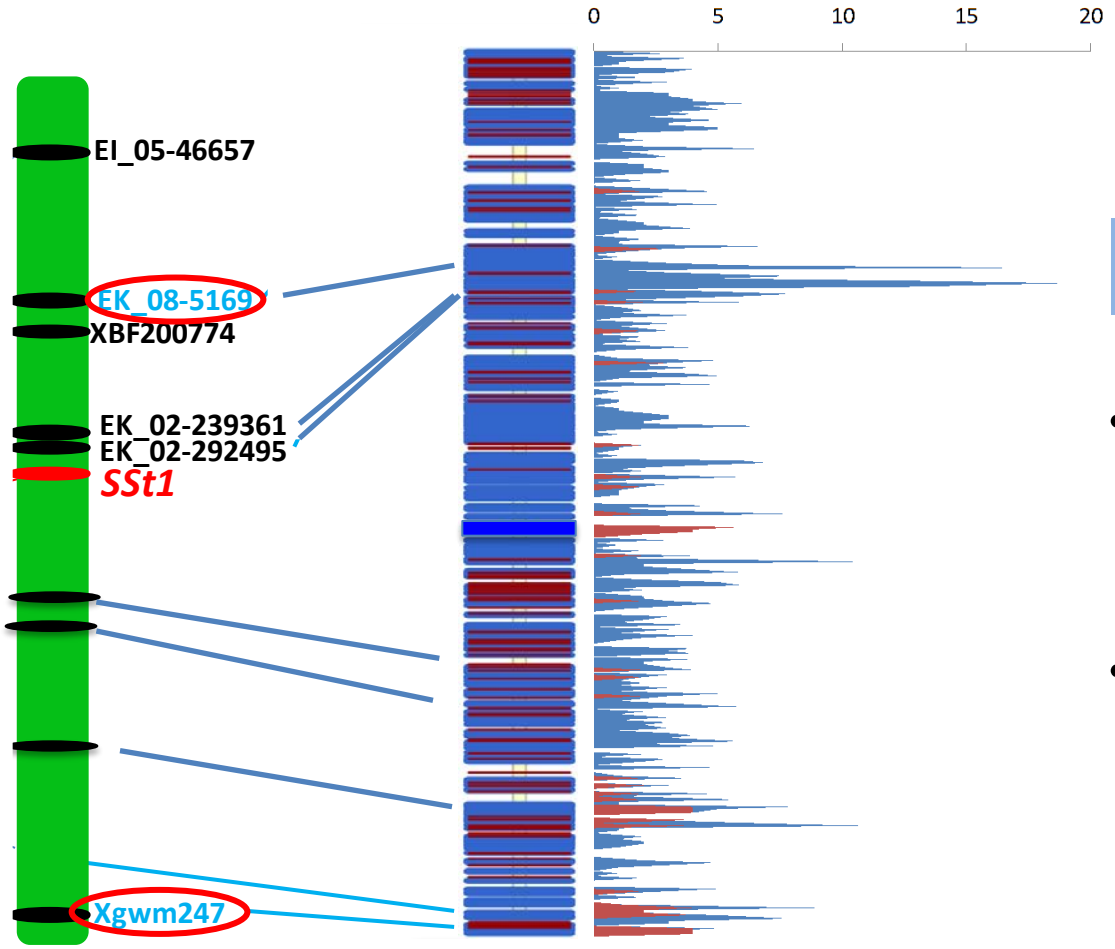


Additional Marker Discovery



Fine Map

No. SNPs



[a]*Includes INDELS*
20 kb sliding window

Candidate Genes?

- Three genes association with cell wall biosynthesis
- Duplicated lignin biosynthesis regulatory genes

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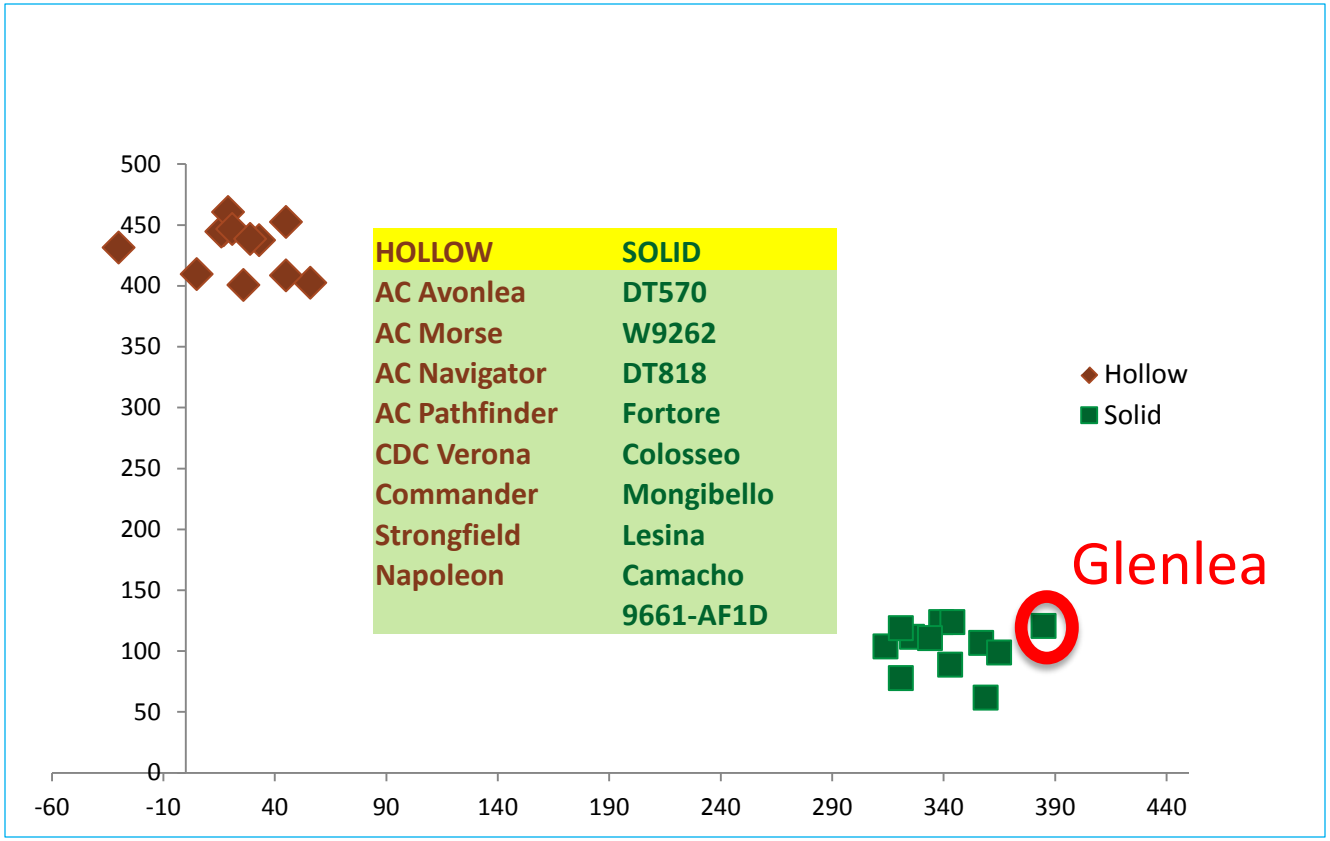
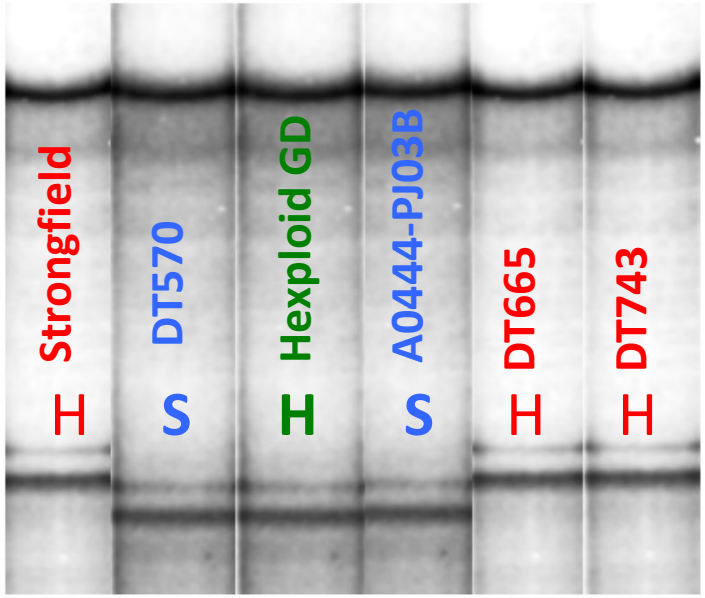
Marker Assisted Selection



D-Genome Suppression of *SSt1*



Crossing of Glenlea derivative (AABBDD) to HOLLOW durum wheat (AABB) = SOLID

Identification of *SSt1* will allow us to design strategies to “unsuppress” SSt1 in hexaploid wheat

WSS and Gene Discovery – Resistance to the OWBM

- Resistance to the OWBM (*Sm1*) - Localized to 2BS
- Current DNA markers are problematic
- Phenotyping is difficult/time consuming

Marker Discovery

BSA + Exome Capture

- 14 “S” lines Sm1- Bulk
- 14 “R” lines Sm1+ Bulk

Cultivar Sequencing (Exome, WGS)

- 15 *Sm1-* Cultivars
- 6 *Sm1+* Cultivars

Wheat 2Bs Wheat Survey

SNPs between bulks should be closely linked to *Sm1*

Filtering algorithms to identify SNPs in LD with *Sm1*

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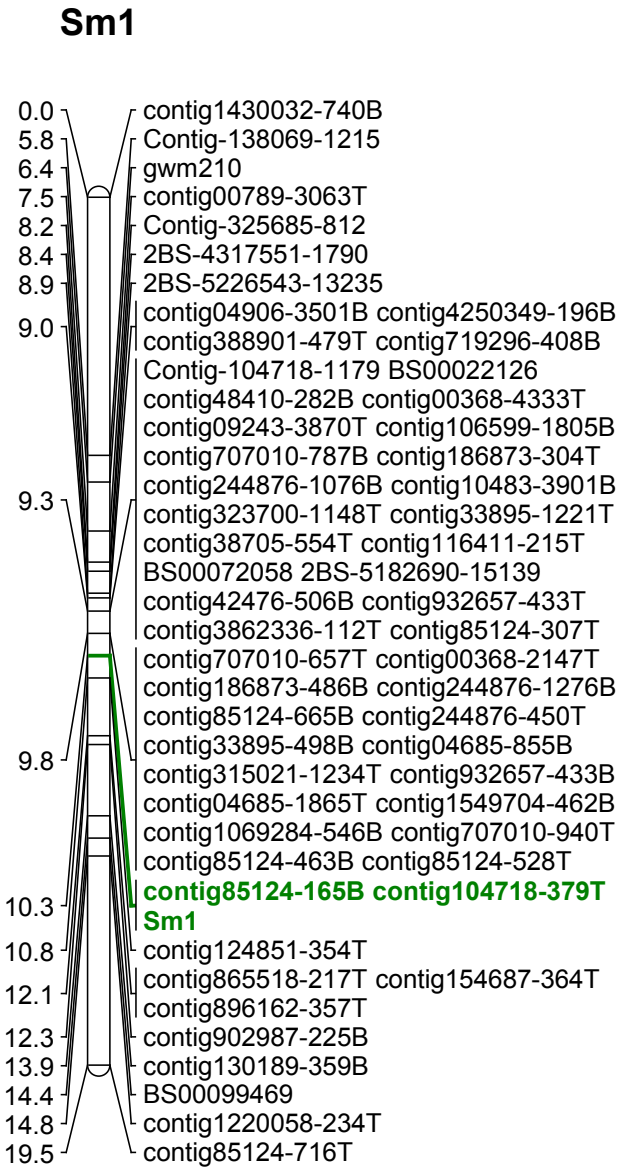
Summary of SNPs

- 3157 SNP calls in 1857 WSS contigs (0.1% Contigs)
- 100 SNPs converted to KASPar
- 67 Mapped to chromosome 2BS
- 59 Mapped with 1 cM of *Sm1*



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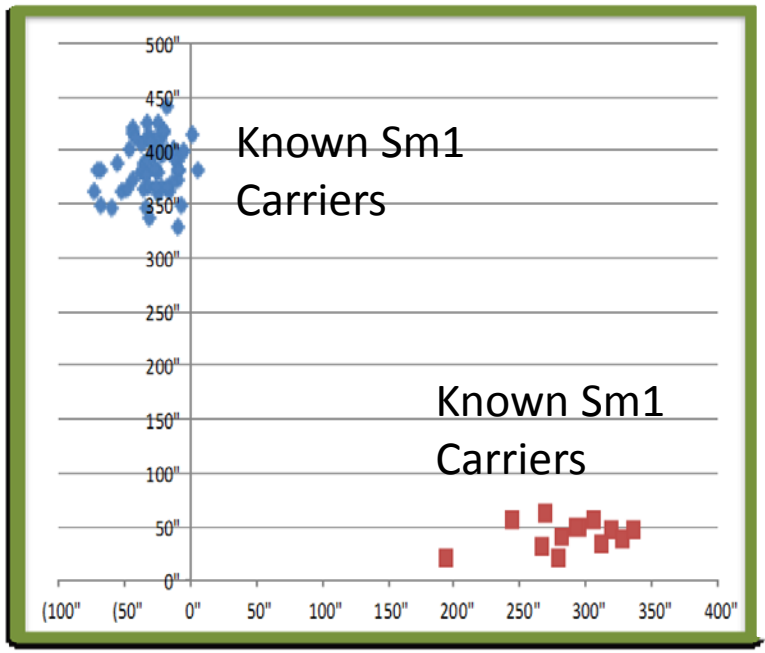
Sm1 Associated SNPs

Locus	Putative Function (Rice proteome)
2BS-1176771	Protein – Unknown function
2BS-5218038	NBS-LRR RGA
2BS-5230237	DNA replication initiation protein
2BS-5239924	C3HC4 zinc-finger protein
2BS-5242325	Protein – Unknown function
2BS-5241927	SAM dependent carboxyl methyltransferase
2BS-5244653	Protein – Unknown function

Ascertainment BIAS



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The WSS as a Resource: Integration of marker types

"Public" Markers

DArT® Markers -- 4,904

Bristol SNP Markers – 5,057

Illumina iSelect Assay – 87,218

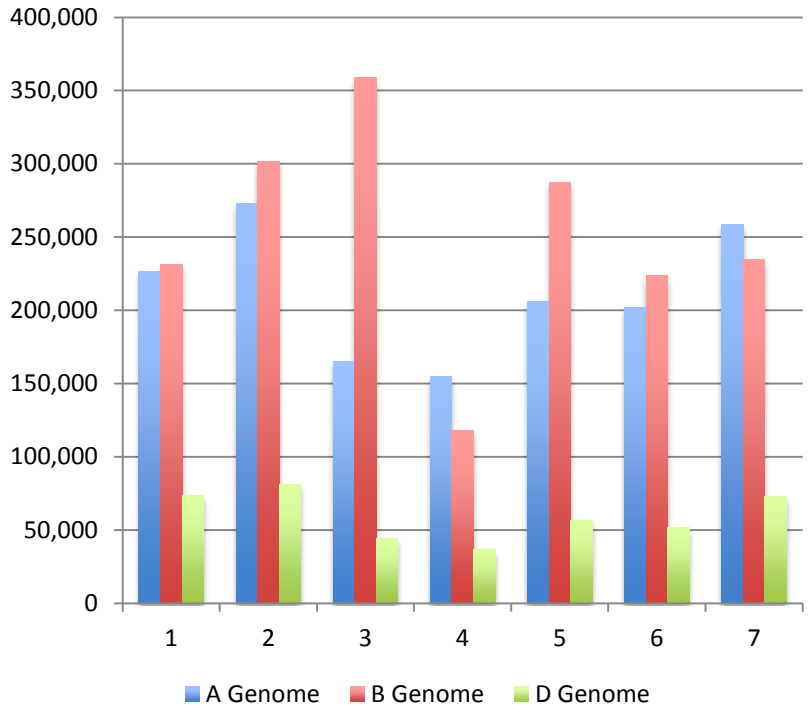
Bin-Mapped ESTs – 16,091

SSR Markers – 290

Wheat "MAS" – 70

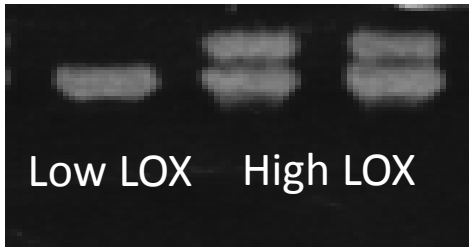
WGS/GBS – 3.3 MILLION

Anchoring of >3.6 Million Markers



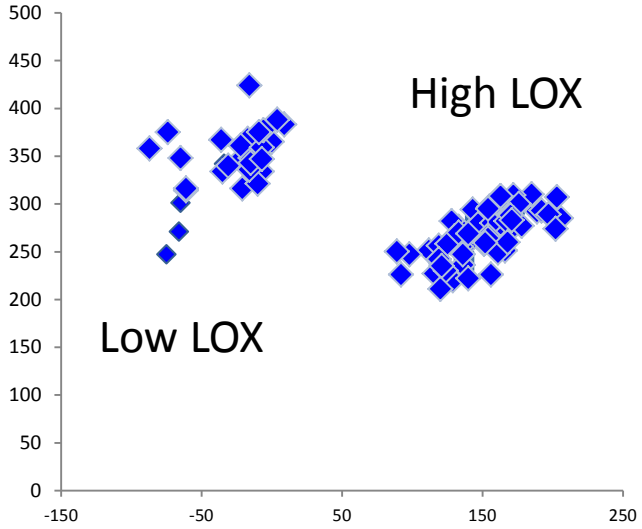
WSS for Marker Improvement: Conversion to HT Genotyping Platforms

Existing Markers → Position in the WSS → Identification of co-localized SNPs



- Dominant marker

CON-495956
3 SNPs



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