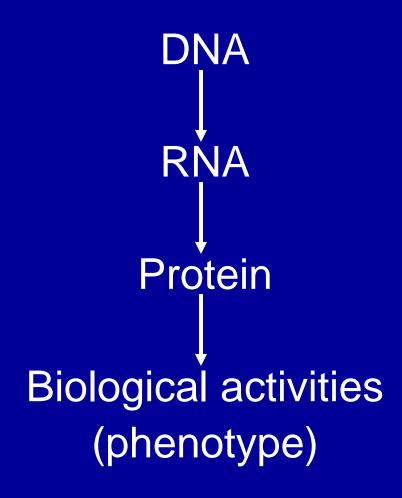
Development & Evaluation of FHB Resistant Near-isogenic Lines Using Marker-Assisted Selection

Jianli Chen

Outlines of This Lecture

- Markers used and being used in plant breeding
- Rationale for using DNA markers in plant breeding
- Benefits by using DNA markers on selection of Fusarium head blight resistance and development of near-isogenic lines

Information flow



Markers used in selection

Morphological markers

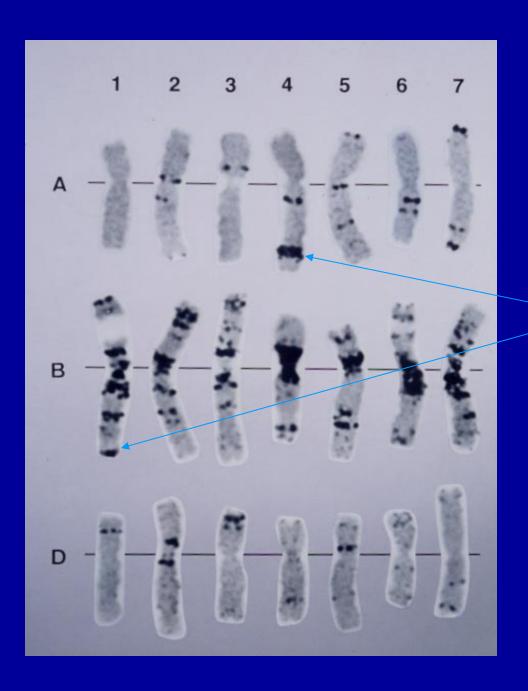
- Association between seed size and a seed coat color marker in beans (Sax, 1923)
- Association between flowering time and flower color in peas (Rasmusson, 1935)

Chromosome markers

C-banding

Isozyme markers

DNA markers



Chromosome Markers

Chromosome Markers



Limitations of previous marker system

- Limited number of markers available
- Undesirable effects on phenotype of many of morphological markers

Advantages for using DNA markers

- No phenotype effect
- Well developed markers systems, such as RFLP, RAPD, SSR, AFLP, SNP, etc
- PCR-based marker systems have potential to automation and applied in conventional breeding

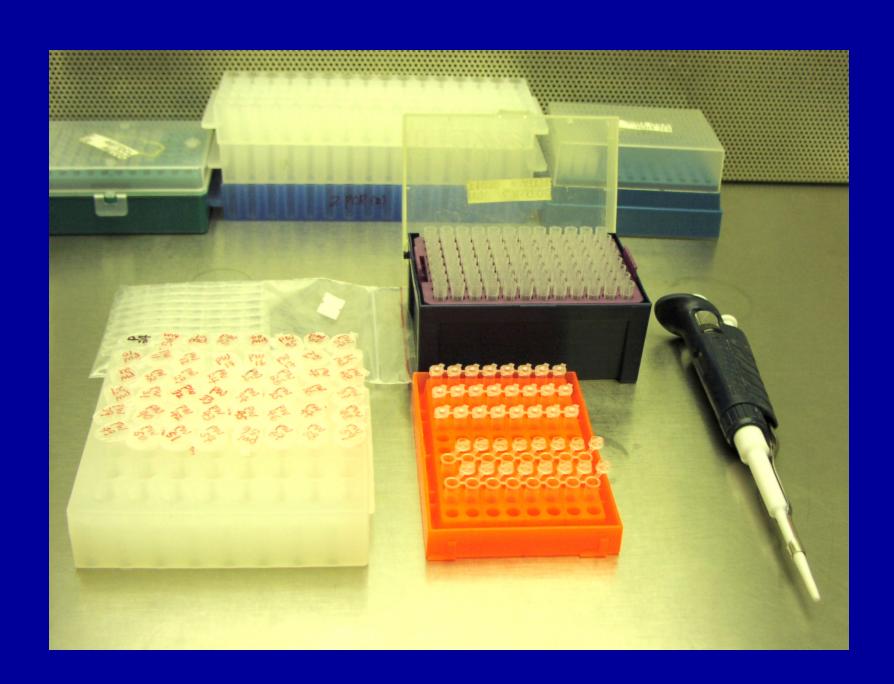
What does PCR-based Marker

- Less DNA needed
- Easy to assess and automation



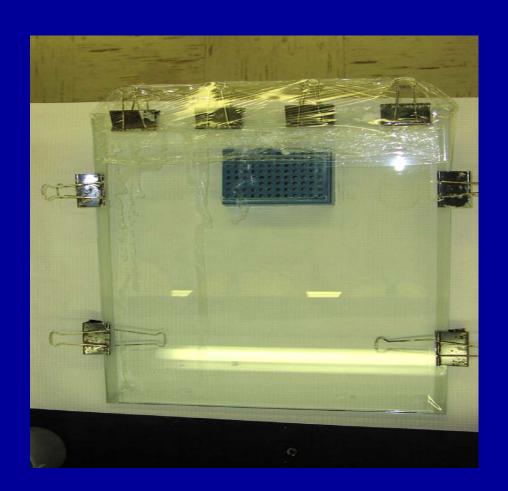
PCR Automation

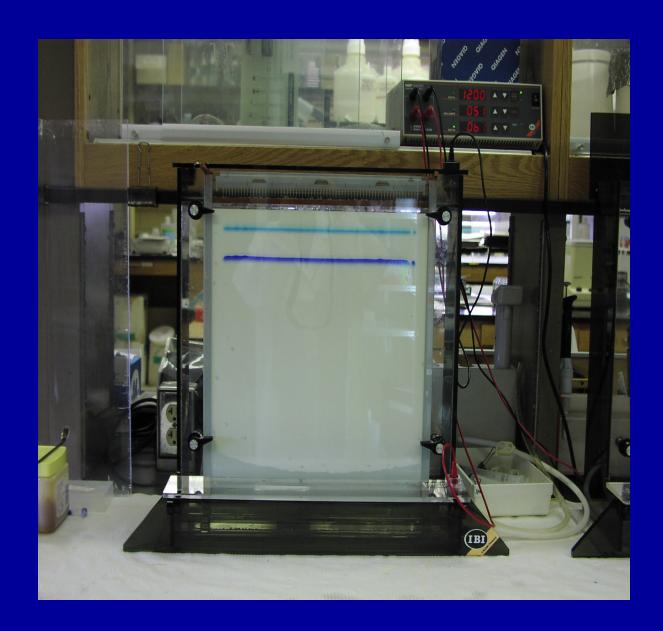






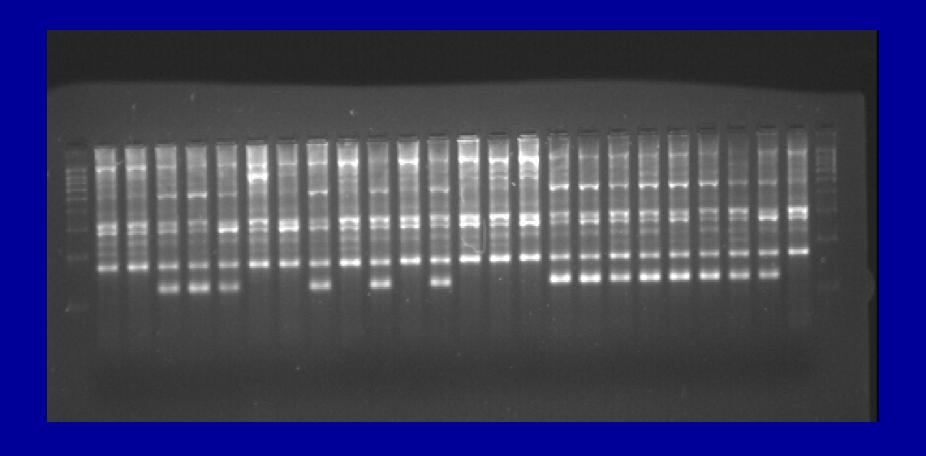






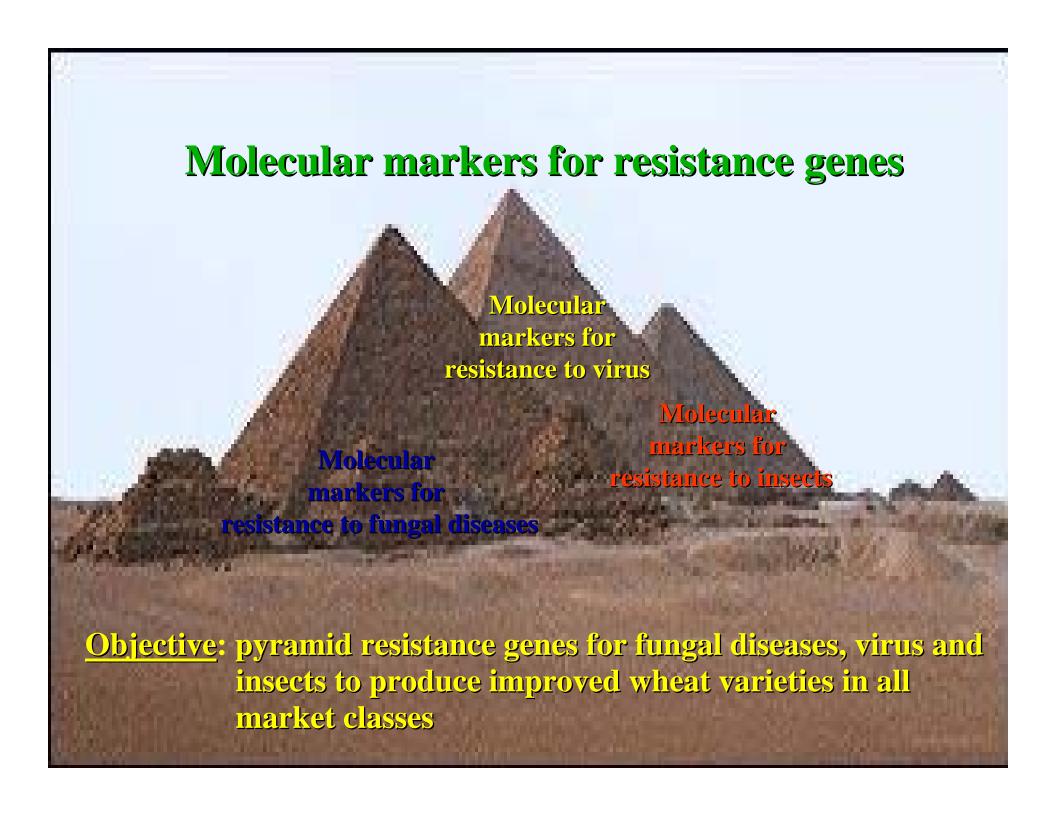


SSR Markers: BARC 55



Applications of DNA Markers in Plant Breeding

- Measure genetic diversity among lines
- Fingerprint lines for legal purposes
- Control genetic purity in the seed production process
- Marker-assisted selection



Molecular markers for breadmaking quality

<u>Objective</u>: provide an integrated manipulation of breadmaking characteristics using molecular markers

Molecular markers for gluten strength

Molecular markers for hardness

Molecular markers for grain protein content

Selected genes

Quality

- Grain protein content OTL.ndsu.6BS
- Starch quality
 Waxy mutants
- Gluten strength Glu-B3, GluA1,B1, D1
- Pentosan content
- Hardness

 Pinb-D1b, Pinb
 A^m1
- Pre-harvest sprouting QTL.1, 2, 3, 4
- Semolina color*Yp*

Resistance

- O Leaf rust Lr37, Lr47, Lr21, Lr39
- Stripe RustYr15, Yr17, Yr5, YrHTAP
- Fusarium head blight QTLfhs.ndsu.3B, QTL3A
- Eyespot Pch1, Pch2
- BYD Virus
 Bdv2
- WSM Virus
 Wsm1
- WSSM Virus Wss1
- Hessian Fly
 H9, H13
- Russian Wheat Aphid Dn2, Dn4

Backcrossing Marker Assisted Selection

% of adapted **Procedure** genotype 0% + • Adapted Parent **Gene Donor** Gene No selection Gene • 50% + Adapted Parent F1 hybrid Gene No selection Gene Adapted Parent 75% + • Gene Select • Adapted Parent 87% + Gene •• Select •• **Adapted Parent** 94% + Gene Select •• Adapted Parent X 97% + • Gene •• Select •• **Adapted Parent** 98%+ Gene •• Select •• 99%+ Gene Select • • 99%+

Practical Considerations in MAS

- Choice of molecular markers
 - DNA quality and quantity required
 - Degree of polymorphism
 - Reliability
 - Difficulty of assay
- The value, ease and the cost of measurement, and nature of genetic control of your gene determine the way in which molecular markers may be the most effectively used in a breeding program
- Availability of genes fine-mapped (minimized C.O. BTW marker alleles and YFG)

QTL Mapping of FHB Resistance

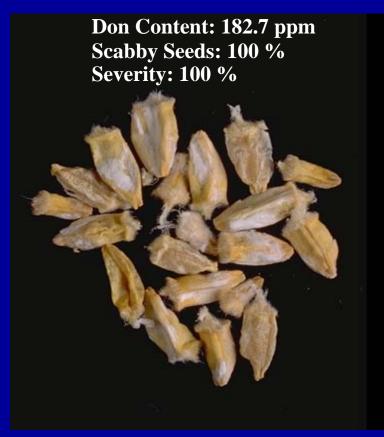
Backcrossing Marker Assisted Selection

Infection Occurred in Field Nursery



Individuals Susceptible to Type II, III and IV Resistance





Moderately Resistant to Susceptible Individuals with Varied Scabby Seeds and Varied DON Content





Field Inoculums Production: Mason Jar Method



Scab Research in Field Nurseries



Coniadial Production: Petridish Method



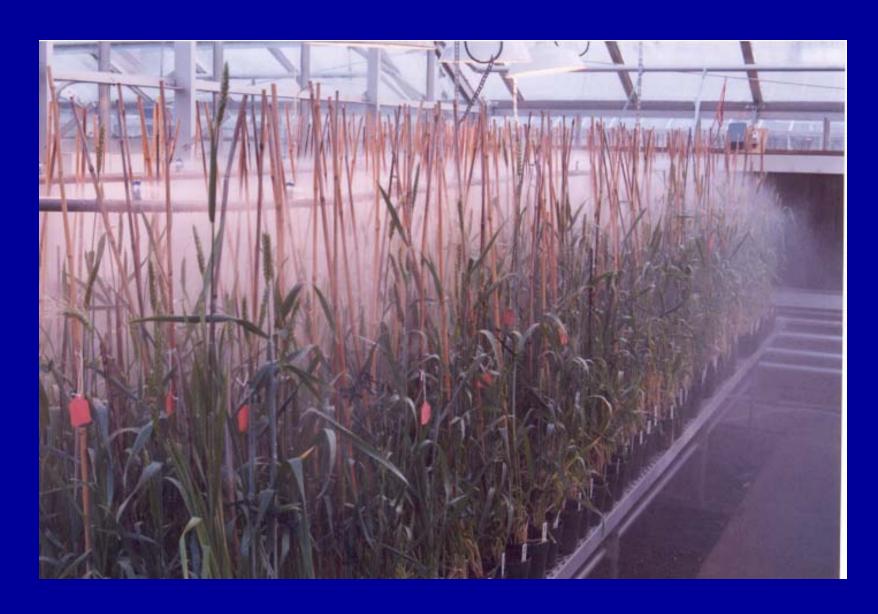




Tools for Greenhouse Inoculation



Screening for Type II Scab Resistance



Chromosome Locations

Aneuploid Analysis		Marker Analysis	
Sumai 3	Other	Sumai 3	Other
1B(2),	1B(3), 1D(2)		
2A(2), 2B(1)	2A(1), 2B(3)	2AL	2AS
3B(1), 3D(1)	3A(2), 3B(2), 3D(3)	3AL, 3BS	3AL, 3BS
	4A(1), 4B(2), 4D(2)	4BS	
5A(2)	5A(4), 5B(3), 5D(3)		5AL
6B(1), 6D(2)	6A(1), 6B(5), 6D(1)	6AS	6BS
7A(1), 7D(2)	7A(5), 7B(2), 7D(1)		7BS

Update on Scab QTL mapping

- QTL on 3BS is available.
- QTL on 5AL is being saturated.
- Other minor QTLs are being identified.
- Does interactions exist among these QTLs???

Steps in MAS

- Identify associations between marker alleles and your favor gene
- Use these associations to develop improved lines or populations

Mapping Populations

- Segregation populations, such as F2 & F2:3
- Recombination inbred lines
- Doubled haploid lines
- Near-isogenic Lines

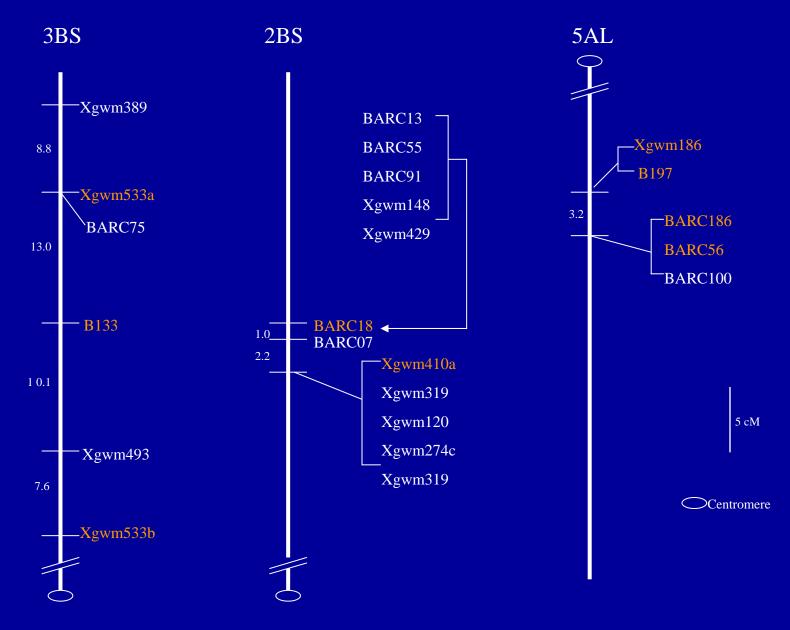
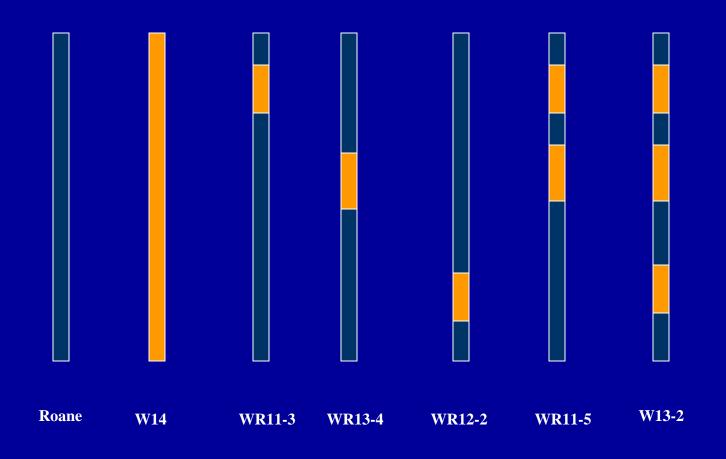


Fig. 1. Genetic map made by MAPMAKER in DH population of Pion2684 x W14

Development of Near Isogenic Lines for 3BS QTL in W14



Backcrossing marker assisted selection

Traits controlled by small numbers of QTL

- MAS can be used to monitor the incorporation of the desirable alleles from the donor source,
- MAS of the recurrent parent can speed the recovery of the recurrent parent genotype

Traits controlled by large numbers of QTL, some with small effect, the probability of identifying marker loci linked to all the QTL is low. When selection with marker loci will be effective? Is selection index helpful?

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Roane 3007-8-5-4 W14







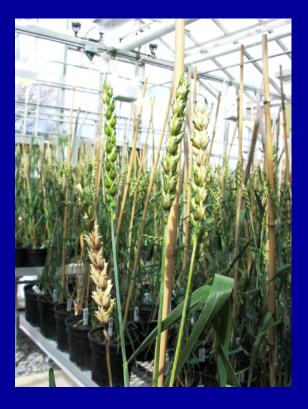
Roane 3008-8-5-5 W14







Ernie 5012-10-2-3 W14







Ernie 5011-8-5-3 W14







Thank You!!!

