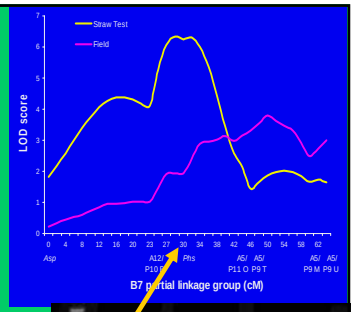
# Marker-Assisted Backcrossing of QTL for resistance to Sclerotinia white mold in pinto bean

Phil Miklas, Karen Bosak, Ken Grafton,
ARS, NDSU

## Objectives

- Backcross existing resistance-linked QTL markers into pinto bean
- Determine utility of MAS for white mold resistance breeding
- Develop pinto bean lines with improved resistance to white mold



## Straw test is scored from 1-9

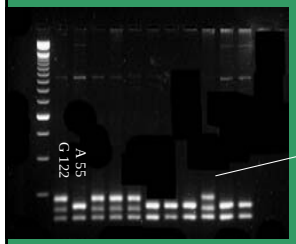
**1=no symptoms**
**3=invasion of the stem to the1st node**
**5=invasion to the middle of the 1st internode**
**7=just past the 2nd node**
**9=total plant collapse**

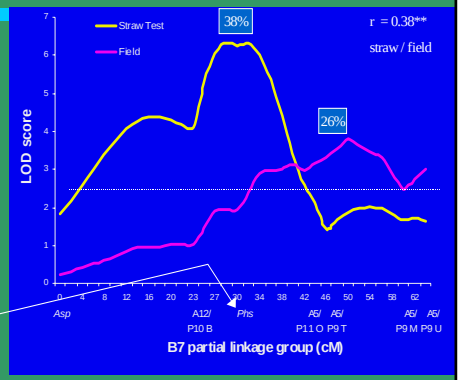
## Disease reaction in field is scored from 1 to 9

**Disease severity: Field**
**1=no diseased plants**
**3=20-30% disease plants**
**5-10% infected tissue**
**5=40-50% diseased plants**
**20-30% infected tissue**
**7=60-70% diseased plants**
**40-50% infected tissue**
**9=80-100% diseased plants**
**60-100% infected tissue**

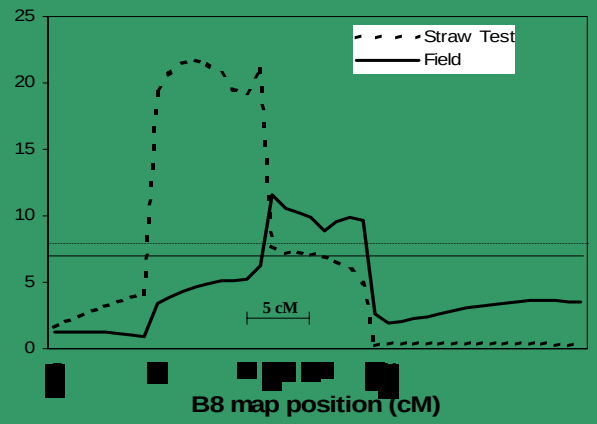
**maturity, height, lodging, canopy porosity, yield, green stem**

## QTL for white mold resistance in A55 x G122 RIL pop.




## Benton x NY6020-4 RIL population




## Pinto*4/G122 – generation advance

Winchester/4/Winchester/3/CO81-12034//G122/Winchester

MAS MAS

BC3F1

MAS

| BC3F2 | BC3F2:3 | BC3F3:4 | BC3F4:5 | BC3F4:6 | |
|---|---|---|---|---|---|
| x | x | x | — | B | |
| x | x | x | — | B | |
| x → | x → | x → | — → | B → | Expts |
| x | x | x | — | B | |

B7 QTL (Phs SCAR marker)

## Pinto*4/G122 – marker segregation

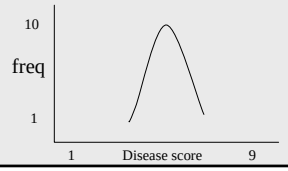
| Population | Lines | Generation | Marker | Ratio |
|---|---|---|---|---|
| 011A | 50 | $BC_3F_{4:6}$ | 32+/18- | 1:1 |
| 011D | 38 | $BC_3F_{4:6}$ | 18+/20- | 1:1 |

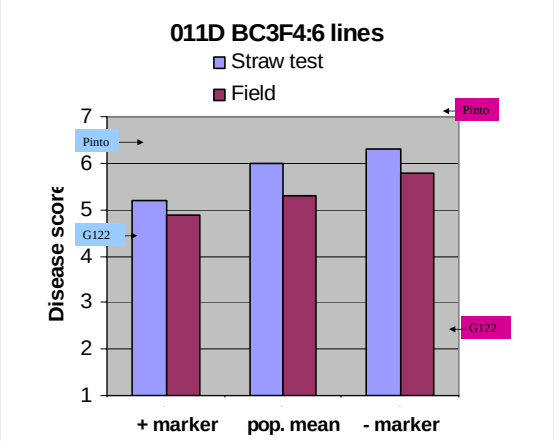
B7 QTL (Phs SCAR marker)

## Pinto*4/G122
## marker/ trait cosegregation (regression)

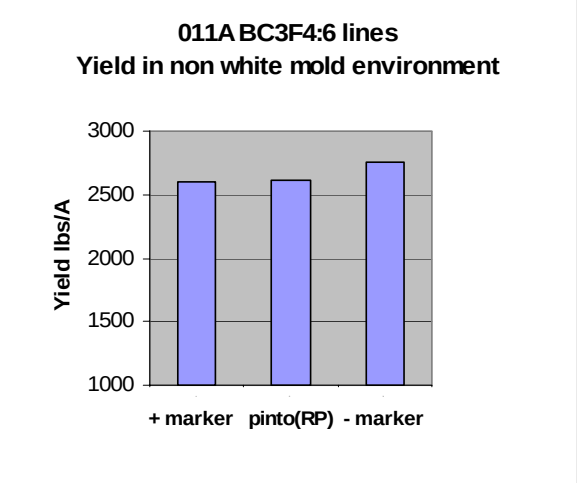
| Population | Generation | Straw test | Field |
|---|---|---|---|
| | | $R^2$ | |
| 011A (50) | $BC_3F_{4:6}$ | 42.3% | NS |
| 011D (38) | $BC_3F_{4:6}$ | 62.4% | 13.1% |

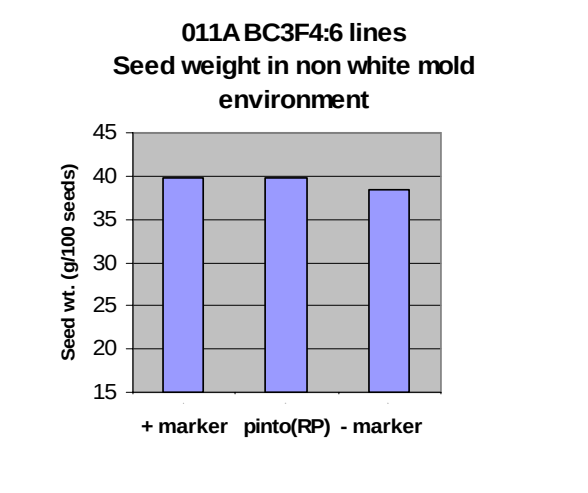
B7 QTL (Phs SCAR marker)

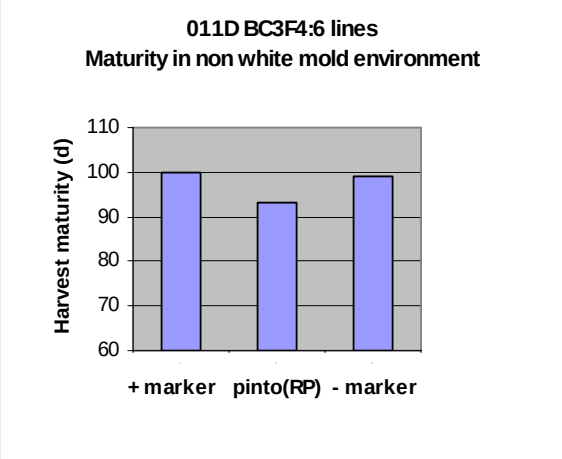



B7 QTL-Phs marker from G 122





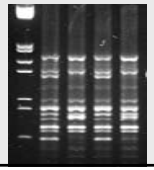

## Pinto*3/NY6020-4 – generation advance

| Population | Lines | Generation |
|---|---|---|
| Maverick/3/Maverick//Maverick/NY6020-4 | | |
| MAS → 005C (MAS) | 52 | $BC_2F_{4:6}$ |
| Maverick/3/OT9630-17-25//OT9630-17-25/NY6020-4 | | |
| MAS → 006D (MAS) | 33 | $BC_2F_{4:6}$ |

B8 QTL (SS18 SCAR marker, and C5 and AW19 RAPDs)

## Pinto*3/NY6020-4 – marker segregation

| Population | Lines | Generation | markers | ratios |
|---|---|---|---|---|
| 005C | 52 | $BC_2F_{4:6}$ | 24+/28- | 1:1 |
| 006D | 33 | $BC_2F_{4:6}$ | 14+/19- | 1:1 |

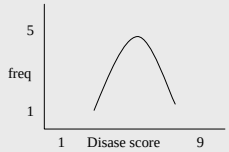


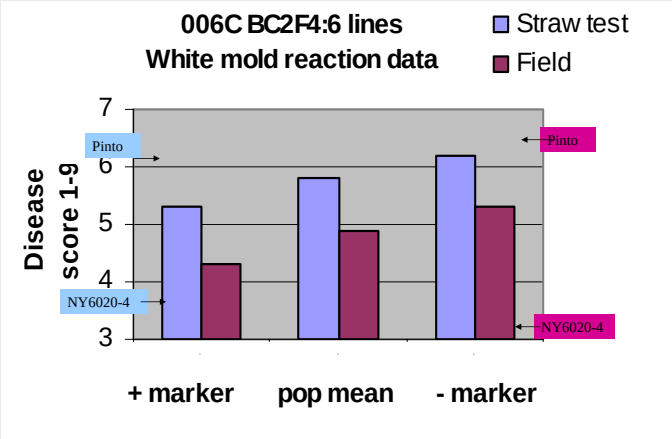
B8 QTL (C5 and AW19 RAPDs)

## Pinto*3/NY6020-4 marker/resistance trait cosegregation (regression)

| Population | Generation | Straw test $R^2$ | Field |
|---|---|---|---|
| 005C | $BC_2F_{4:6}$ | 47.4% | missing |
| 006D | $BC_2F_{4:6}$ | 34.8% | 17.3% |

B8 QTL (AW19 and C5 RAPDs)



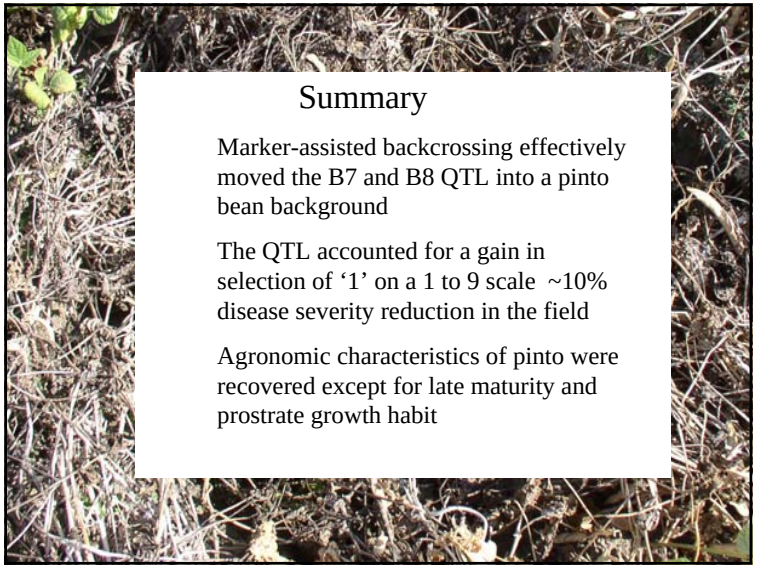



## Pinto*3/NY6020-4
## Agronomic data (pinto bean recovery)

| Trait | + marker | RP Pinto mean | - marker |
|---|---|---|---|
| Yield (lbs/A) | 3390 | 3158 | 2925 |
| Seed size (g $100^{-1}$ seed) | 41 | 43 | 42 |
| Harvest maturity (DAP) | 110 | 92 | 112 |

006D $BC_2F_{4:6}$ population

| Selected pinto lines with white mold resistance from BC-MAS | | | | | |
|---|---|---|---|---|---|
| | Straw | Field | Maturity | Seed wt | Yield |
| | 1 to 9 | 1 to 9 | d | g 100 seeds | lbs/A |
| 011D-3 | 3.9 | 2.8 | 101 | 44.4 | 3695 |
| 011D-39 | 4.2 | 1.8 | 103 | 40.3 | 3319 |
| Winchester | 6.5 | 7.25 | 93 | 40.0 | 2609 |
| | | | | | |
| 006C-30 | 4.7 | 3.5 | 108 | 39.2 | 3695 |
| 006C-33 | 4.8 | 3.5 | 109 | 42.5 | 3319 |
| Maverick | 6.1 | 7.2 | 92 | 43 | 3158 |



## Summary

Marker-assisted backcrossing effectively moved the B7 and B8 QTL into a pinto bean background

The QTL accounted for a gain in selection of ‘1’ on a 1 to 9 scale ~10% disease severity reduction in the field

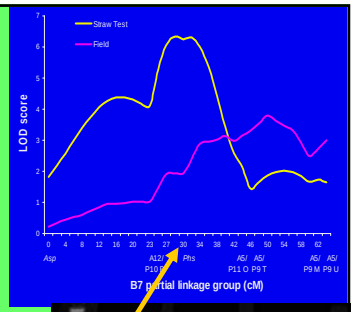
Agronomic characteristics of pinto were recovered except for late maturity and prostrate growth habit

# Identify and Introgress Molecular Markers for White Mold Resistance in Dry Bean

Phil Miklas, Karen Bosak, Ken Grafton,
Marcio Ender, James Kelly
ARS, NDSU, MSU

## Objectives

- ✓ Determine inheritance of Bunsi-derived resistance in pinto bean
- ✓ Perform QTL analysis and develop MAS
- ✓ Release pinto bean lines with improved resistance to white mold



## Objectives for the 2002 work plan: (1st year)

Characterize disease reaction for 85 $F_{5:8}$ RILs
(Aztec pinto-S / ND88-106-04-R)

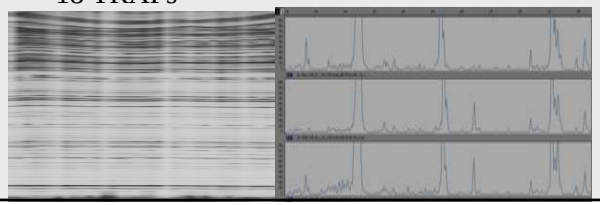
- ✓ One greenhouse straw test – completed
- ✓ Four field trials – 2 in ND and 2 in WA - completed

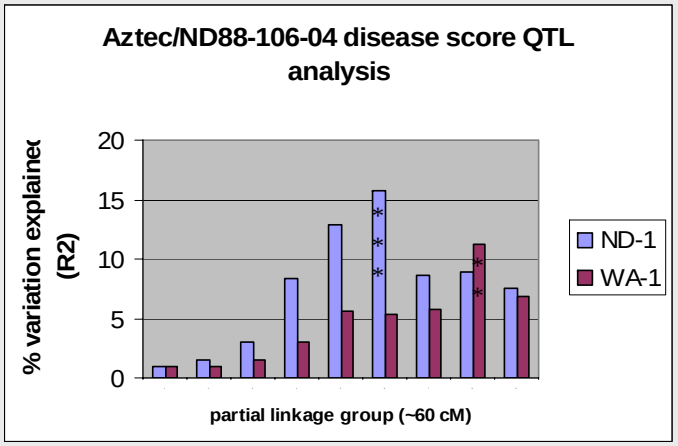
Miklas, P. N., D. Hauf, R.A. Henson, and K. F. Grafton. 2004. Inheritance of ICA-Bunsi-derived resistance to white mold in a navy x pinto bean cross. Crop Sci. 44:1484-1588.

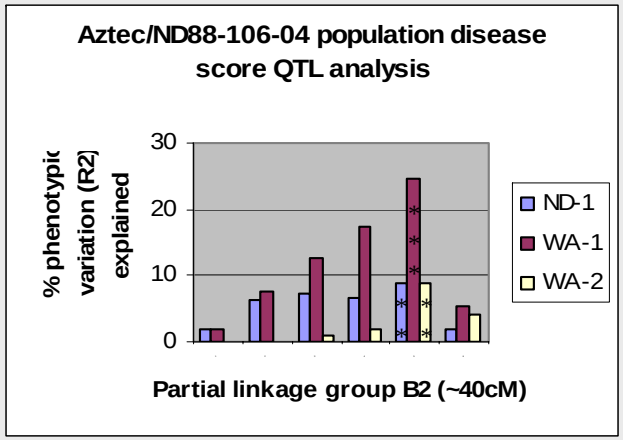
## Molecular marker data (130 markers)

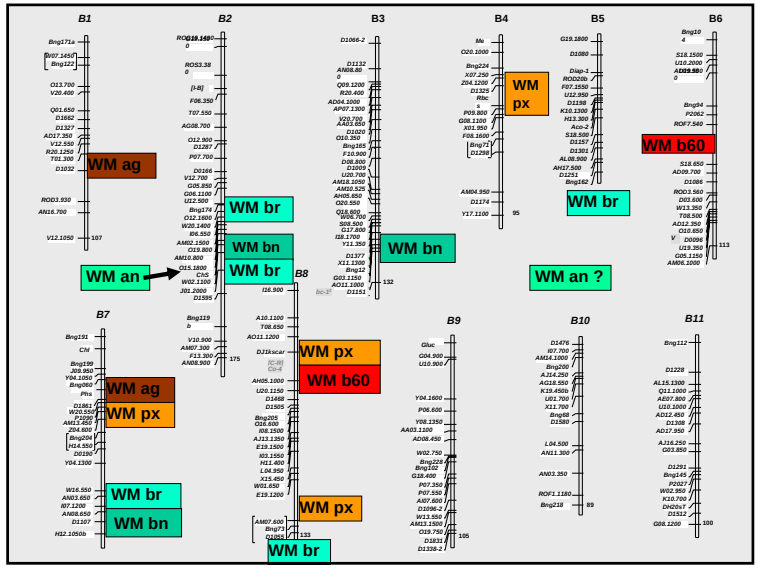
Aztec/ND 88-106-04 RIL population

- 5 genes: Ur-3, I, P, C, Znd
- 3 SCARS: SW13, SK14, SAP6
- 99 RAPDs, 5 AFLPs
- 18 TRAPs





WA: Bean White Mold Nursery 2003 - partial

| Line | Type | Disease score (1-9) Field | Straw test |
|---|---|---|---|
| AN37 | Pinto | 2.8 | 5.5 |
| AN69 | Pinto | 5.2 | 4.9 |
| Bunsi | Navy | 4.7 | 7.7 |
| CO75944 | Pinto | 6.7 | 7.2 |
| Beryl | GN | 7.1 | 7.7 |
| G122 | Cranberry | 2.2 | 5.3 |

## Promising pintos 2003 tests

| Line | WM (1-9) | Lodging (1-9) | Maturity d | Yield kg ha-1 |
|---|---|---|---|---|
| AN-37 | 4.2 | 6.3 | 106 | 2201 |
| AN-69 | 4.1 | 5.2 | 103 | 3313 |
| Aztec | 7.1 | 6.5 | 95 | 2786 |

## Promising pintos 2004 tests - Michigan

| Line | WM % | Maturity d | Seed wt. g 100 sds | Yield kg ha-1 |
|---|---|---|---|---|
| AN-37 | 41 | 93 | 34.6 | 4370 (2) |
| AN-69* | 30 | 96 | 37.5 | 4250 (3) |
| Buster | 56 | 92 | 34.4 | 3600 (15) |
| LSD | 13 | 9 | 2.5 | 580 |

*highest desirability score of 64 entries

26 to 81% was the range for white mold severity

## Summary: (Aztec / ND88-106-04) RIL Pop.

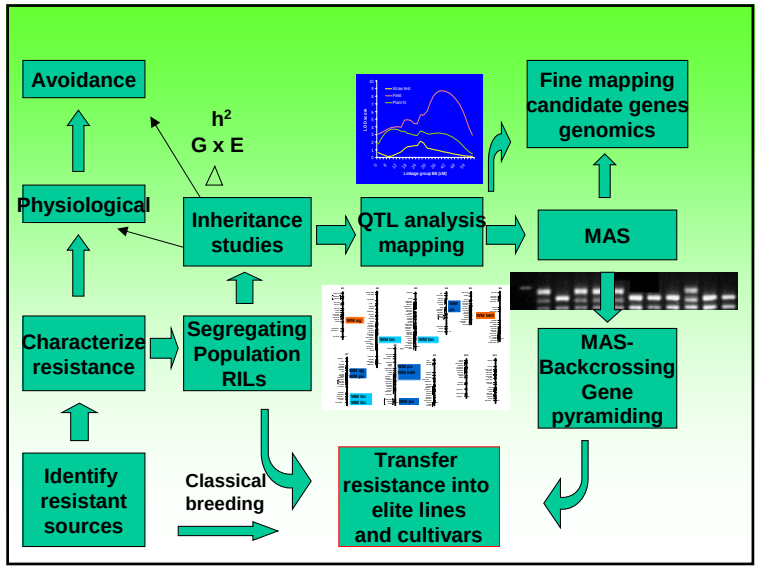
Molecular map is complete, but still need to integrate our linkage groups with the core map

QTL identified for canopy porosity, plant height, stay-green stem trait, late maturity (select against)

2-QTL for partial disease resistance separate from avoidance and stay-green stem traits (also associated with high yield

1-QTL is the same as in Bunsi/Navy and Bunsi/Black populations (MSU)

Promising pintos with partial resistance to white mold slated for release


Avoidance
Physiological
Characterize resistance
Identify resistant sources
h²
G x E
Inheritance studies
Segregating Population RILs
Classical breeding
Transfer resistance into elite lines and cultivars
QTL analysis mapping
Fine mapping candidate genes genomics
MAS
MAS-Backcrossing Gene pyramiding