

Marker Assisted Selection for Fusarium Head Blight Resistance in Durum wheat

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Introduction

- *Triticum turgidum* L.var.*durum* is an allotetraploid (genome AABB, $2n=4x=28$)
- 68% of durum produced in United States is from North Dakota (USDA, 2005)
- Heavy economic losses due to Fusarium head blight (scab) caused by *Fusarium graminearum* Schwabe
- Long periods of humidity and Warm temperatures ranging between 28 to 32 °C



Control

- Cultural
- Chemical
- Biological
- Resistance



Resistance

Types

- Type I – Initial infection
- Type II – Spread of infection

Sources

- ‘Sumai3’ (6x), Wangshuibai (6x)



Hypotheses

- MAS is efficient over phenotypic selection
- Resistant lines for FHB can be identified with MAS



Why MAS?

- FHB is quantitative trait
- Low heritability
- Difficulties in phenotyping



Materials and Methods

- Two populations were developed using Sumai3 as the donor parent for MAS:

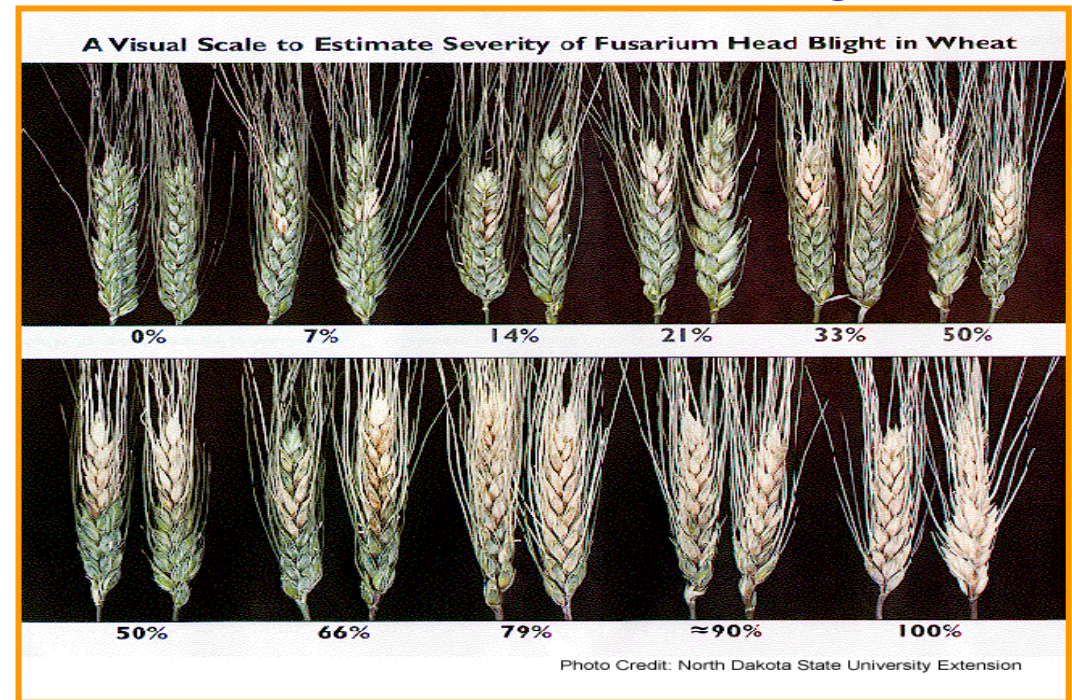
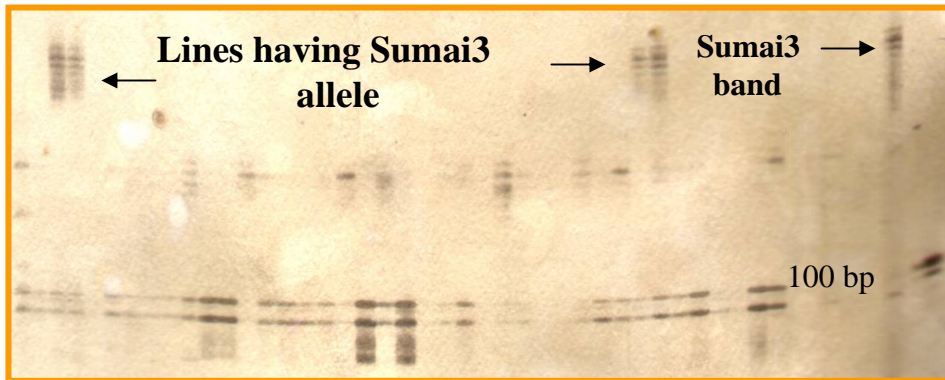
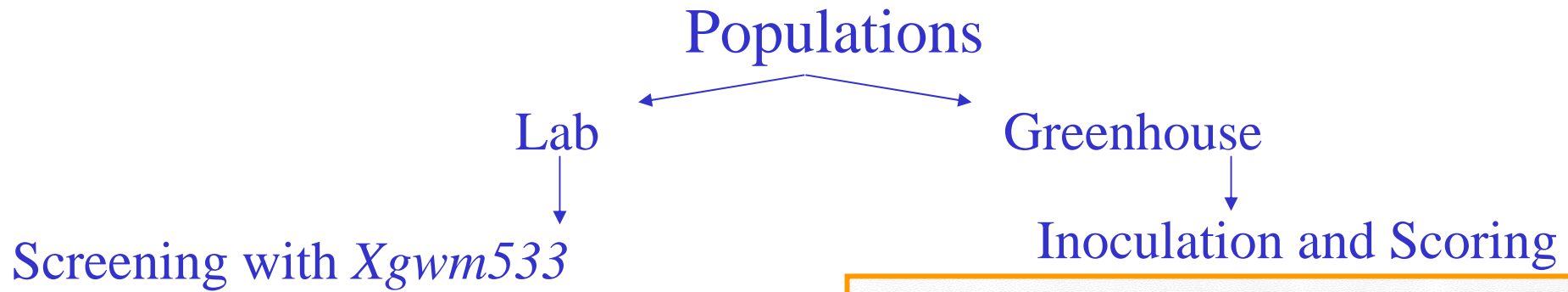
Population I: Ben/3/Sumai3/Sceptre//D88816 (BC₁F_{2:4})

Population II: Lebsock/3/D901442//Sumai3/D901442
(BC₃F_{2:5})

- Populations were screened with SSR markers *Xgwm533* and *Xsts3b-256* that are tightly linked to *Qfhs.ndsu-3BS*



Phenotypic Selection vs. MAS



Phenotypic Selection vs. MAS

- Initial phenotypic analysis of the populations was based on a **single measurement**. Hence, FHB score >21% is the reliable data.
- Molecular marker data were able to identify lines with or without the Sumai3 allele for *Xgwm533*



Phenotypic Selection vs. MAS

Population I

Type II disease severity	Sumai3 allele present	Sumai3 allele absent	Total
<21%	438	688	1126
>21%	80	591	671
Total	518	1279	1797

← Efficiency of selection = 88%



Phenotypic Selection vs. MAS

Population II

Type II disease severity	Sumai3 allele present	Sumai3 allele absent	Total	
<21%	78	106	184	
>21%	19	63	82	← Efficiency of selection =77%
Total	97	169	266	



Marker Assisted Selection

Populations



Screen with *Xgwm533* and selected homozygous lines



Backcross Population I to 'Ben' and Population II to 'Lebsock'



Self BC₂F₁



Screen BC₂F₂ with marker and self selected lines

Contd -



Marker Assisted Selection

Screen BC₂F₃ with marker

↓
Self BC₂F₄ lines

↓
Evaluated BC₂F₅ lines with and without markers phenotypically and genotypically

The BC₂F₅ lines without the marker were susceptible both under field and greenhouse conditions

↓
Send resistant lines with and without marker to NZ for seed increase and possible preliminary yield trials in 2005

Screen with new marker *Xsts256*



Marker Assisted Selection

Lines selected for field trial

	(+) Score < 21%	(+) Score > 21%	(-) Score < 21%	Total
	-----Number of lines-----			
Population I	114	33	31	178
Population II	28	13	20	61

- Three locations (Prosper, Langdon and scab nursery at Prosper) and 2 replications at each location
- Population I 14 X 14 and Population II 8 X 8 simple lattice
- Two replications in 2005 fall greenhouse RCBD



Field Trials

- Population I significant at both the locations
- Population II significant at Prosper
- $G * E$ not significant
- Broad sense heritability - 0.3 and 0.5 in the two populations respectively

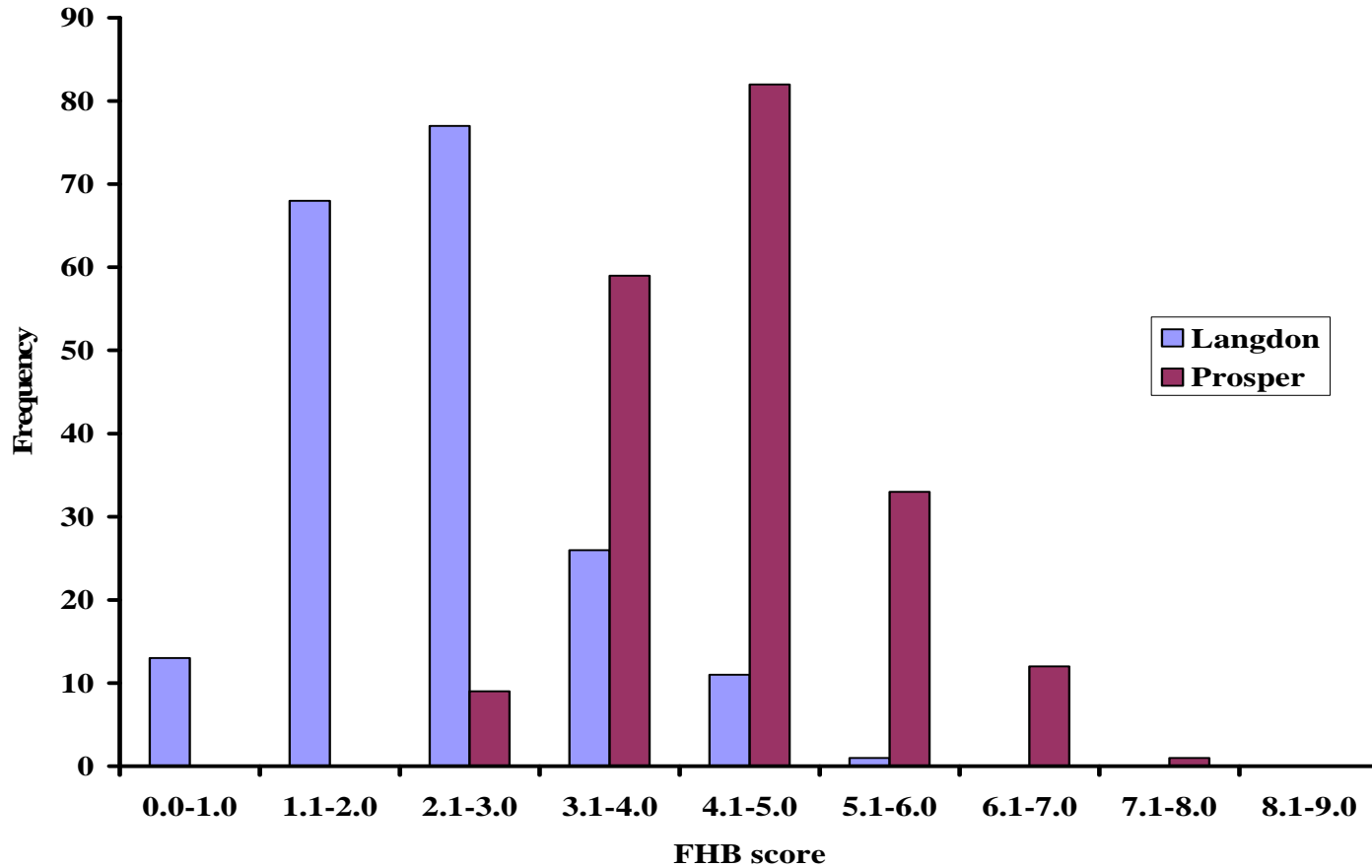


Means of the Checks at Various Locations

	Prosper	Langdon	Scab Nursery	Greenhouse
	----- disease reading (1 - 10) -----			%
Belzer	4.7	1.5	2.8	16.4
Divide	4.7	1.7	2.7	20.7
D91103	5.5	1.7	5.1	92.2
Grenora	6.0	2.7	6.2	13.2
Ben	6.0	2.7	6.0	58.3
Lebsock	5.0	2.5	5.7	83.0
Maier	5.7	3.0	3.5	14.3
Mountrail	6.7	2.2	6.0	72.0
Pierce	6.2	1.7	5.5	37.8



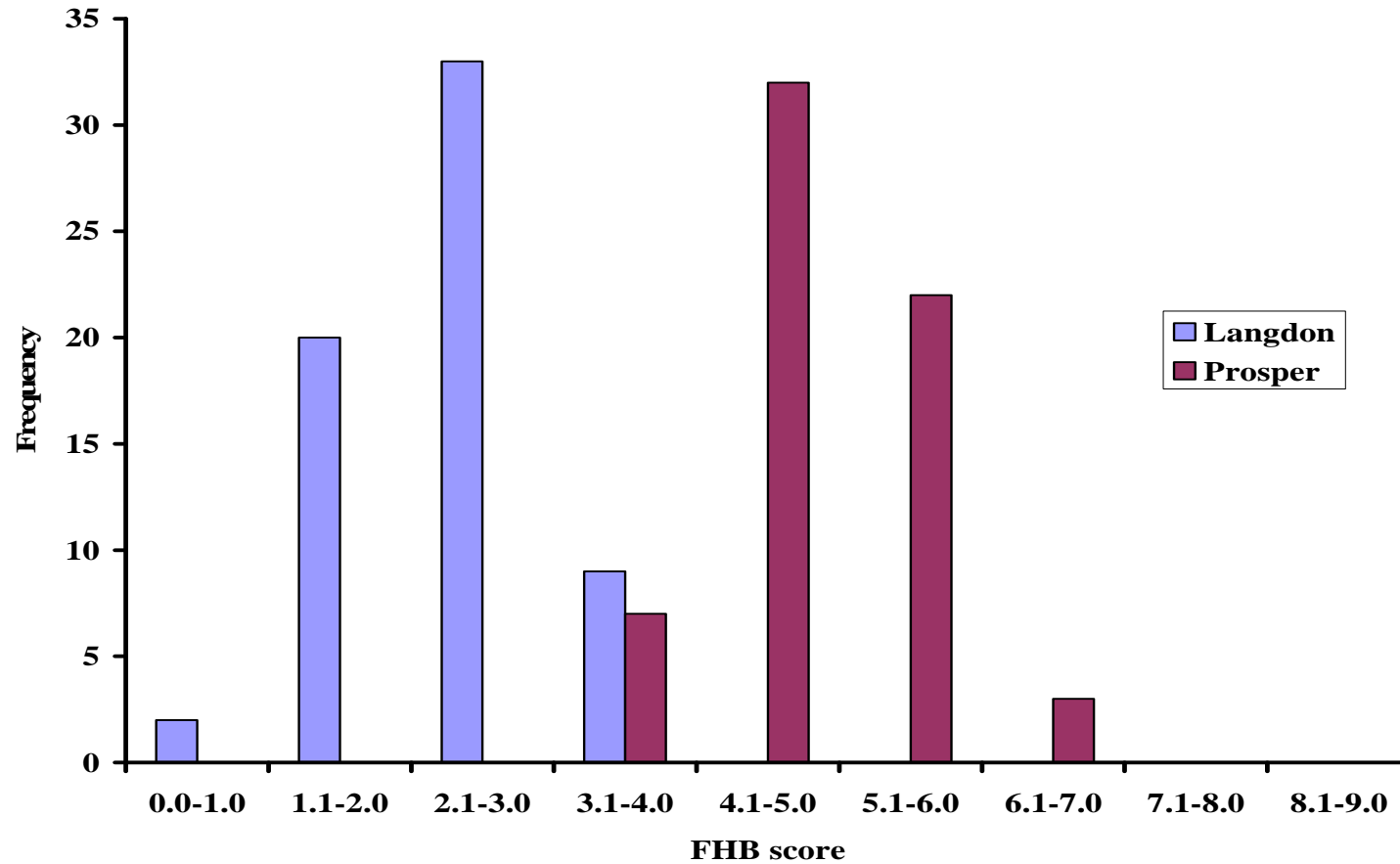
Results



Frequency distribution of FHB of population I at Langdon and Prosper



Results



Frequency distribution of FHB of population II at Langdon and Prosper



Results

Population I

<i>Xgwm533</i>	FHB nursery	Greenhouse
<21% (+ Sumai3)	32	84
<21% (- Sumai3)	4	19
>21% (- Sumai3)	27	12

<i>Xsts256</i>	FHB nursery	Greenhouse
<21% (+ Sumai3)	28	62
<21% (- Sumai3)	8	41
>21% (- Sumai3)	59	29



Results

Population II

<i>Xgwm533</i>	FHB nursery	Greenhouse
<21% (+ Sumai3)	-	15
<21% (- Sumai3)	-	5
>21% (- Sumai3)	20	16

<i>Xsts256</i>	FHB nursery	Greenhouse
<21% (+ Sumai3)	-	4
<21% (- Sumai3)	-	9
>21% (- Sumai3)	48	36



Conclusions

- *Xgwm533* and *Xsts256* are closely associated with Sumai3 allele
- Markers were able to identify lines with or without the Sumai3 allele
- Selection for the QTL significantly increased the level of scab resistance
- Recombinants between marker and QTL were identified indicating the need for more tightly linked loci
- Marker assisted selection can be an effective tool to increase the accuracy and efficiency of selection



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