Genetic Mapping of *MlUM15*: an *Aegilops neglecta*-derived Powdery Mildew Resistance Gene in Common Wheat

M. Worthington[1], J. Lyerly[1], S. Petersen[1], G. Brown-Guedira[2], D. Marshall[2], C. Cowger[2], R. Parks[2], and J. P. Murphy[1]

[1]Department of Crop Science, North Carolina State University; [2]USDA-ARS, Raleigh, NC

Introduction

Powdery mildew (*Blumeria graminis* f. sp. *tritici*) is a common and often economically damaging foliar disease of wheat in the Southeastern US. Disease symptoms include loss of grain yield and reduced flour quality.

Race-specific host plant resistance is a reliable, economical, and environmentally benign form of disease prevention. However, widely deployed powdery mildew resistance genes are usually defeated within several years of release (Parks et al., 2008). Molecular markers linked to resistance genes enable breeders to pyramid multiple resistance genes in a single cultivar and disrupt directional selection pressure.

Over 70 genes conferring resistance to powdery mildew have been confirmed at 44 loci (*Pm1* to *Pm50*) (Cowger et al., 2012).Although seven formally designated *Pm* genes originated in *Aegilops* species, none have been introgressed from *Aegilops neglecta*.

The objectives of this study were to characterize the powdery mildew resistance introgressed from *Ae. neglecta* into the wheat germplasm line NC09BGTUM15 (NC-UM15) and identify molecular markers linked to the resistance gene which could be useful for marker assisted selection.

Materials and Methods

Population Development

- The powdery mildew resistant germplasm line NC-UM15 is a BC_2F_8-derived line from the pedigree Saluda*3/TTCC 223. TTCC 223 is an *Ae. neglecta* Req. ex Bertol. accession (2n=4x=28; genomes UUMM) collected in Turkey.
- NC-UM15 was crossed to the susceptible cultivar 'Saluda' to produce 198 $F_{2:3}$ families used in subsequent disease evaluations.

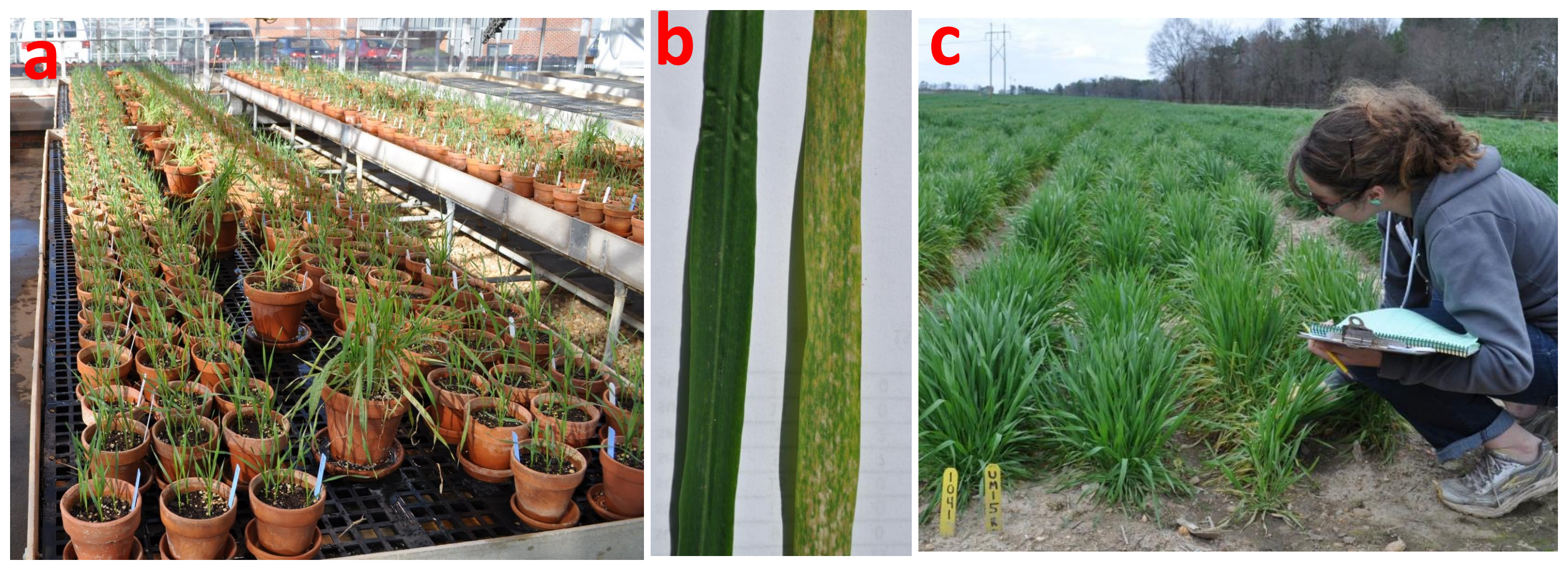

Fig. 1. a) NC-UM15 x Saluda population evaluated for powdery mildew resistance in the greenhouse, (b) resistant and susceptible disease reactions of NC-UM15 and Saluda in the field, (c) scoring $F_{2:3}$ families for disease resistance at Lake Wheeler

Greenhouse Disease Evaluations

- Population was screened for resistance to *B. g tritici* isolate 'Arapahoe'.
- Each experimental unit consisted of 15 seeds of a given $F_{2:3}$ family. with two replicates per family.
- Seedlings were inoculated 22 days after planting by gently shaking conidia from leaves of infected plants.
- $F_{2:3}$ families were classified as resistant, susceptible, or segregating 10 days after inoculation.

Field Disease Evaluations

- $F_{2:3}$ families were evaluated for resistance to natural powdery mildew populations in two replicates at Raleigh and Kinston, NC.
- Experimental units were comprised of single 1.2-m row plots planted with 40-60 seeds.
- Disease ratings were made in March 2012

Table 1. Disease reactions of $F_{2:3}$ families from the NC-UM15 x Saluda population fit expected segregation ratios for a single dominant resistance gene in greenhouse and field evaluations

	Number of $F_{2:3}$ families					
Location	Res.	Seg.	Susc.	Total	χ^2 (1:2:1)	*P* value
Greenhouse	52	87	59	198	3.40	0.18
Raleigh	50	89	59	198	2.84	0.24
Kinston	42	70	45	157	1.96	0.38

Linkage Mapping

- DNA from twenty F_2 plants was pooled into resistant and susceptible bulks and screened with SSR and SNP markers following Miranda et al. (2006) and LGC Genomics protocols.
- SSR and SNP markers polymorphic between resistant and susceptible bulks were used to screen the entire population
- Linkage analysis was conducted in MAPMAKER/EXP (v. 3.0b).

Detached Leaf Testing

- NC-UM15 and 12 other lines with *Pm* genes mapped to chromosome 7AL were tested for differential response to 21 powdery mildew isolates
- Disease reactions were scored as R (resistant), I (intermediate), or S (susceptible) 10 days after inoculation.

Results

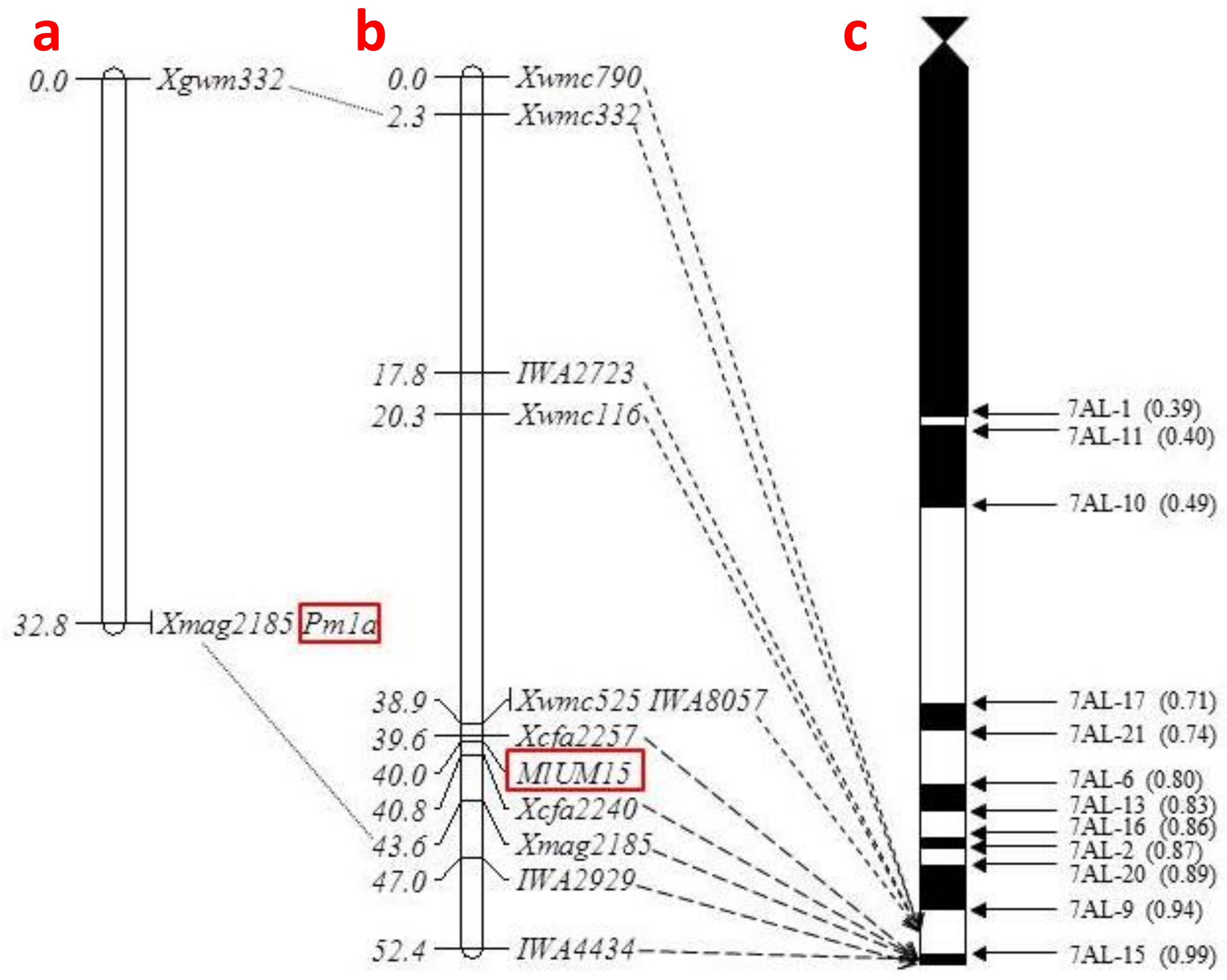

Fig. 2. (a) Map position of *Pm1a* according to Neu et al. (2002) (b) Genetic map of *MlUM15.* Marker names are at the *right* and map distances (cM) are on the *left*. Common markers are connected with *dotted lines*. (c) Physical map of chromosome 7AL. Molecular markers from the genetic map of *MlUM15* are connected to their appropriate physical deletion bins with *dashed lines*. Markers in the 0.94-0.99 bin are connected with *short dashes* and markers in the terminal bin (0.99-1.00) are connected with *long dashes*.

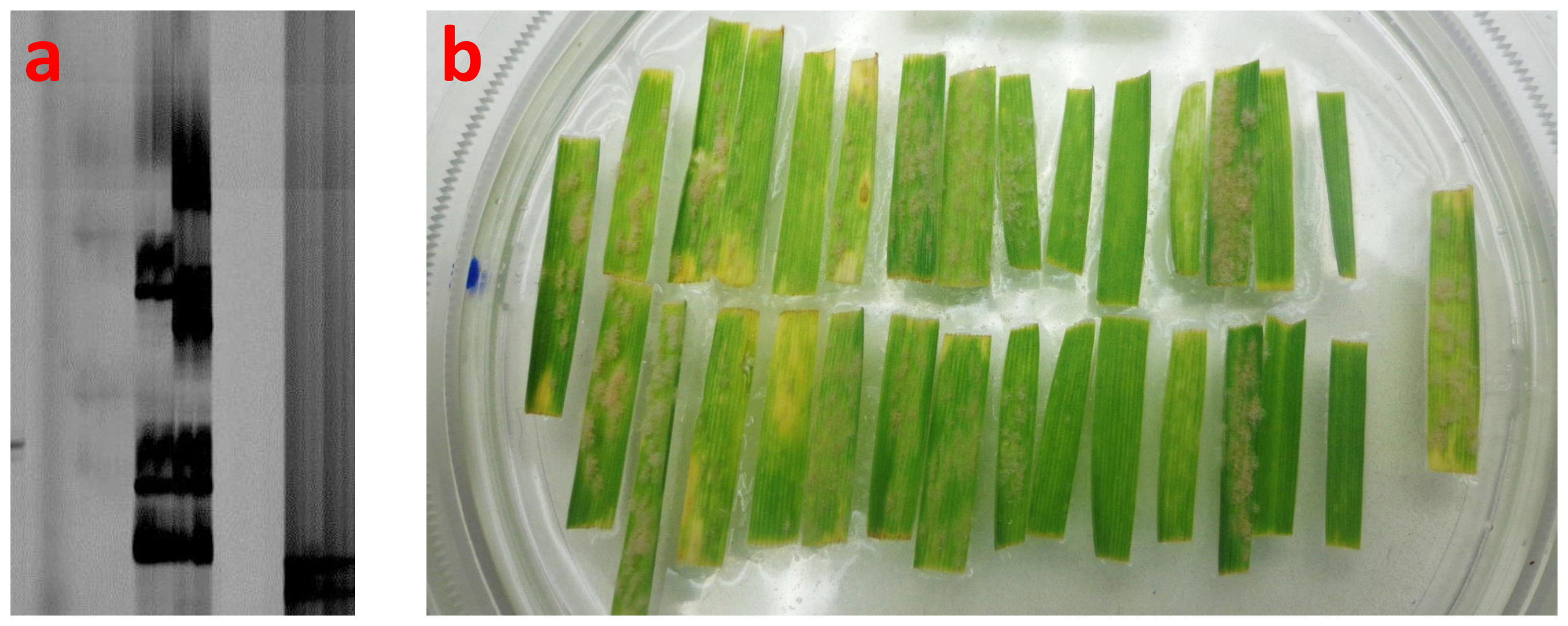

Fig. 3. a) *Xcfa2240* tentatively linked to *MlUM15* in Bulked Segregant Analysis (b) Differential reactions of NC-UM15 (second from left) and wheat lines bearing 12 other *Pm* genes to *B.g. tritici* isolate ABK

Table 2. Disease reactions of NC-UM15, Saluda, 12 genotypes possessing *Pm* genes previously mapped on chromosome 7AL, and susceptible check Chancellor to select *B.g. tritici* isolates evaluated in detached leaf tests.

		B. g. tritici Isolate			
Genotype	*Pm* gene	101a2	127	ABK	Kin-mix
NC-UM15	*MlUM15*	R	R	S	R
Axminster	*Pm1a*	S	R	S	R
MocZlatka	*Pm1b*	R	R	I	R
M1N	*Pm1c*	I	I	I	I
T. spelta	*Pm1d*	S	R	S	R
Virest	*Pm1e*	I	R	S	R
NC96BGTA4	*NCA4*	R	S	S	S
NC96BGTA6	*NCA6*	R	I	I	I
NC-AG11	*Pm37*	R	R	R	R
NC-AG12	*MlAG12*	R	R	R	R
TA2033	*Mlm2033*	R	R	R	R
TA391	*PmTb7A*	R	R	R	R
Saluda	*Pm3a*	R	S	S	S
Chancellor	*Pm10, 15*	S	S	S	S

Discussion

- Greenhouse and field evaluations indicated that a single dominant gene, *MlUM15*, conferred powdery mildew resistance to the wheat germplasm line NC-UM15.
- *MlUM15* mapped to the terminal deletion bin of chromosome 7AL. The multiallelic *Pm1* locus and several temporarily designated *Pm* genes also map to this region.
- Detached leaf tests revealed that NC-UM15 had a different disease response pattern from genotypes carrying alleles of the *Pm1* complex and several temporarily designed genes .
- Alelism tests with *Pm1* will be required to elucidate the relationship between *MlUM15* and other *Pm* loci in the distal region of 7AL.
- The introgression of a new dominant resistance gene from *Ae. neglecta* to soft red winter wheat and identification of useful SSR and SNP markers closely linked to the resistance gene should provide breeders with an effective new source of resistance to powdery mildew

References

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NC STATE UNIVERSITY