

Enhanced Fusarium head blight resistance in bread wheat and durum by alien introgressions

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ABSTRACT

After intensive screening Fusarium head blight (FHB) resistance has been identified in a number of wheat wild relatives. The resistance obtained from *T. monococcum* and *Ae. speltoides* has now been incorporated into a stable background and values for most agronomic traits such as yield, hectoliter weight, thousand kernel weight, height and maturity compares favourably with check cultivars. Grain quality parameters such as protein content and flour yield also did not differ from check cultivars. FHB resistance was also identified in *T. timopheevi*, *Ae. cylindrica*, *T. miguschovae* and *Th. elongatum*. The resistance identified in tritordeum and *Th. elongatum* is being introgressed into durum wheat.

INTRODUCTION

Fusarium head blight caused by *Gibberella zea* is a common disease of cereals in all temperate growing regions of the world. With the world's two best sources of resistance (the cultivars Sumai3 and Frontana) being only partially resistant, a search was initiated in the secondary and tertiary gene pools of the Triticeae, with which to enhance these levels of resistance (Fedak et al., 1997; Fedak et al., 2003; Cao et al., 2003). We chose to work on accessions that were not being employed elsewhere. In this report we will present data on the field performance of lines of hexaploid wheat that were selected from progenies of crosses to wild wheat species.

MATERIALS AND METHODS

Details on the origin of the resistance of *Triticum/Aegilop* species were presented elsewhere (Fedak et al. 2003). Very briefly, the *T. monococcum* accession was crossed to the cultivar AC Superb and resistant selections were backcrossed to AC Superb and AC Barrie. Three backcrosses of the *Ae. speltoides* progeny was required to restore fertility. The *T. timopheevi* accession was crossed to the cultivar Crocus; approximately 1500 F2 seeds were used to imitate a cycle of SSD that culminated in the FHB resistant selection TC 67 (Cao et al.) being selected out of the F9 progeny.

Selection for disease resistance was done by point inoculation under greenhouse conditions during the selection and backcrossing phases. For point inoculation, 10ml of a 50,000 spore suspension was injected into a central floret at a stage when 50% of the spike was at anthesis. Symptoms were scored at 21 dap following inoculation. The best lines from the point inoculation experiments were grown in field pots, initially in one meter double rows then in replicated trials. The inoculum source in the field plots was inoculated corn-barley spawn, with twice daily irrigation to maintain humidity levels. Flowering dates were recorded and symptoms (incidence and severity) scored at 21 days following the 50% flowering stage. Standard checks in these trials were Roblin, Sumai 3 and AC Barrie. Advanced lines such as M321 & S184 were evaluated in standard four replicate tests with cultivars Barrie & Hoffman as standard checks. DON analysis was determined by an ELISA technique (Sinha and Savard, 1997) on extracts from 1 gram samples of ground grain. Protein contents and flour yield of grain samples were determined by routine methods.

RESULTS AND DISCUSSION

The lines shown in Table I were selected for lowest DON content combined with reasonable agronomic tests. The lines M321 and S184 were selected out of the *monococcum* and *speltoides* progeny following two years of selection in greenhouse and field trials. Their DON contents were 3.5 and 3.9 ppm compared to Sumai3 and Roblin at 2.9 and 9.1 respectively after those trials.

The two lines were grown in replicated yield trials in 2007 and agronomic data was scored and compared to the standard checks AC Barrie & Hoffman as shown in Table 1. The cultivar Hoffman is exceptionally high yielding with low protein content and relatively low flour yield. AC Barrie on the other hand has good milling and baking quality. As shown in Table 2, the grain yields of M 321 & S184 were quite similar and 1% lower than AC Barrie. The test weights and thousand kernel weights of both lines composed favourably to AC Barrie.

Table 1. Agronomic Performance of Interspecific Derivatives M 321 and S184

Genotypes	Yield (kg/ha)	Days to head (day)	TSTWT (kg/hl)	TKW (g)	HT (cm)	Protein (%)	Flour (%)	DON (ppm)
M 321	3272	64	79.3	34.4	76	13.9	57.5	1.6
S 184	3246	61	80.3	35.0	86	13.3	67.2	0.7
AC Barrie	3304	61	80.5	34.6	79	13.7	66.8	4.5
Hoffman	4597	61	82.0	44.0	89	10.9	61.9	7.8
Suami 3	-	-	-	-	-	-	-	0.7
Roblin	-	-	-	-	-	-	-	10.4

In terms of days to heading, M 321 was three days later than S 184 which was equal to AC Barrie. In terms of plant height, S 184 was 10 cm taller than M 321 but both approximated the height of AC Barrie. It has been our experience that, in transferring FHB resistance from wheat cultivar such as Sumai 3 and Frontana, there was a tendency for resistant progeny to be late and tall. Although these traits are not complex in inheritance, it took some effort to select out lines that approximated the checks for these two parameters. In the present study, excessive lateness and plant height was overcome. Though not shown in the tables, the lodging resistance of the two derived lines was about equal to AC Barrie.

Other parameters that are difficult to restore after crosses to FHB resistant lines are those associated with baking quality. As shown in Table 2, the grain protein of the two experimental lines was nearly equal and not markedly different from that of AC Barrie. In terms of flour yield, S 184 was marginally higher than AC Barrie and both were somewhat higher than M 321. The relatively high flour yield of S 184 is probably the result of three backcrosses to AC Superb.

QTL analysis to assign markers to resistance loci is proceeding to facilitate the pyramiding of these QTL with other known resistance. Preliminary indications are that the FHB resistance in M 321 is controlled by a unique locus on chromosome 5A while in S 184 several introgressions have been detected in the B genome. Thus these unique sources of FHB resistance with minimal linkage drag are now being pyramided with other sources of resistance and are being utilized in wheat breeding programs.

The testing of FHB resistant lines obtained from crosses to *T. timopheevi*, *Ae. cylindrica* and *T. miguschovae* is

not as advanced as that of the lines reported above. Advanced lines from each of these combinations were grown in two-replicate yield trials in 2007. In all cases, lines with DON levels, approximating those of Sumais3 were observed. Studies on development of molecular markers and populations for gene pyramiding have been initiated with all combinations currently being studied. For the improvement of FHB resistance in durum wheat, the resistance detected in tritordeum, *T. carthlicum* and *Th. elongatum* is being introgressed.

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