Characterization of Wheat Lines Derived Through MAS for BYDV **Resistance and High Grain Protein Content**



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RESULTS

Height Pro

Table 3: Least squares means for traits for HGPC

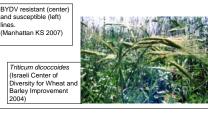
s Yield Test weight Hei

INTRODUCTION AND OBJECTIVES

Wheat (Triticum aestivum L.) is one of the world's most widely grown crops. As such an important crop, wheat is consistently being enhanced for yield and quality traits. Barley yellow dwarf virus (BYDV) is a worldwide problem in wheat and resistance to BYDV is an important objective in many breeding programs. High grain protein content (HGPC), important for its nutritional value and its contribution to bread baking quality, is another common breeding objective though it is often negatively correlated with grain yield. Molecular markers associated with BYDV resistance ('TC14' source from Thinopyrum intermedium) and HGPC ('Glupro' source from Triticum turgidum var. dicoccoides) may be used in marker-assisted selection (MAS) to identify genotypes that carry these introduced segments. For BYDV resistance, the BYAgi sequence characterized amplified region (SCAR) marker was developed as a tool to identify plants that carry the translocation that confers resistance (Stoutjesdijk et al., 2001). For HGPC, the microsatellite marker Xuhw89 was reportedly diagnostic for the Gpc-B1 region that confers the introduced HGPC characteristic (Distelfeld et al., 2006). Few studies have reported on the use of these markers in MAS for these traits.

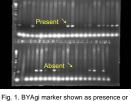
Our objective was to characterize the direct and indirect effects of MAS-based introgression of BYDV and HGPC genes on grain yield, quality, and agronomic traits in hard winter wheat near-isogenic lines.



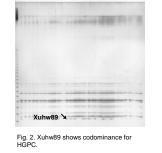


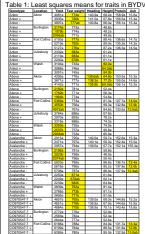
MATERIALS AND METHODS

- Sets of BC5F2-derived near-isogenic lines differing for the presence of BYDV resistance (TC14 source) or HGPC (Glupro source) were developed via backcrossing with marker-assisted selection. For both traits, different genetic backgrounds were used.
- The SCAR marker BYAgi (Fig. 1) was used for marker analysis for the BYDV set using marker protocols as described in Stoutjesdijk et al. (2001). The microsatellite maker Xuhw89 (Fig. 2) was used for the HGPC set using marker protocols as described in Distelfeld et al. (2006). Homozygosity of the NILs for the respective linked marker was confirmed by progeny testing of BC5F2:3 plants.
- Field experiments were conducted in 2007 in a latinized row-column split-plot arrangement with two replications at five locations in eastern Colorado (Fort Collins, Akron, Burlington, Julesburg, and Walsh). Main plots were the different recurrent parent-gene combinations and subplots were the respective homozygous marker positive and marker negative BC5F2:4 lines. Several BC5F2:4 lines for each recurrent parent-gene combination were tested. Recurrent parents were also included as checks.
- A subset of the marker positive and marker negative NILs for BYDV resistance were evaluated in a field BYDV screening nursery in Manhattan, KS in 2006-07. Forty-eight total lines were tested in an RCBD with four replications. BYDV resistance scores were collected on a row basis as the percentage infection.
- Grain vield, vield components, plant height, heading date, and NIR-predicted grain protein content and wheat ash were recorded. Data were analyzed with Proc Mixed of the SAS system (SAS Institute Inc., 2003) as a split-plot design with a nested random entry effect and parents and location as fixed effects

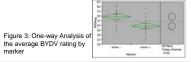


absence for BYDV resistance









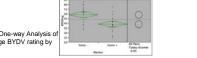
·Significant differences were observed in several instances between the recurrent parent and the BYDV marker-positive and BYDV markernegative groups (Table 1, highlighted in yellow) In several cases, the recurrent parent showed higher values than the marker-positive group. suggesting some negative pleiotropic effect of the BYDV translocation on these traits. This effect was generally not observed, however, in the comparisons between the respective marker negative and marker-positive groups

·Significant differences were observed between the marker-positive and marker-negative groups for BYDV resistance (Table 2). This suggests that the marker was effective in selection of BYDV during backcrossing using MAS.

•For the HGPC group, significant differences in grain protein content were observed in only three of 15 comparisons (Table 3, highlighted in vellow). These differences were only observed at the Fort Collins location, which was an irrigated location. In each of these cases, the markerpositive group had higher grain protein cont than the recurrent parent and the markernegative group.

·Grain vield was significantly lower in the marker-positive group in only two compariso one of these being Fort Collins with the CO970547-7 background (Table 3).

 Significant reductions in test weight were observed in 11 out of 15 comparisons (Table with genetic background apparently not invo as a factor in the reductions (Table 3)



	CO970547-7 Fort Collins	5899a	781a	87.0a	137.0a	13.5a
ent	CO970547-7 +	5146b	766b	89.9a		13.4a
	CO970547-7 -	5895a	777ab	86.6a	135.4a	13.6a
	CO970547-7 Julesburg	2909a	695a	67.0a	156.9a	17.1a
	CO970547-7 +	2659a	689a	71.3a	159.1a	
	CO970547-7 -	2775a	693a	64.7a	157.4a	
	CO970547-7 Walsh	3586a	766a	83.7a	133.1a	14.8a
	CO970547-7 +	3227a	766a	85.1a	130.6a	14.3a
ons.	CO970547-7 -	3332a	775a	79.7a	131.8a	14.5a
e 3),						
lved						

Table 2: Analysis of Variance for the average BYDV

ating by marker										
ource	DF	Sum of Squares	Mean Square	F Ratio	Prob > F					
larker	1	1063.1818	1063.18	14.6985	0.0004					
rror	40	2893.304	72.33							
. Total	41	3956.4858								

SUMMARY

•Marker-assisted selection (MAS) was effective in producing nearly-isogenic lines (NILs) with reduced susceptibility to BYDV, though the overall difference between the marker-positive and marker-negative groups was not great

•For the BYDV NILs, several instances of reduced grain yield and increased test weight were associated with the presence of the BYDV introgression in the NILs. No consistent differences were observed between the groups for heading date, plant height, grain protein content, or wheat ash.

•Marker-assisted selection (MAS) was effective in producing NILs with increased grain protein content, though the differences were only observed in the high yielding, irrigated environment. Reduced yield was observed in these cases, though the differences were significant in only one genetic background. Multiple instances of reduced test weight were observed among the NILs carrying the marker linked with the HGPC gene.

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