Summary of Genotyping Data from the 2009 Regional Performance Nurseries
Final version, Nov. 2009

Hard winter wheat breeding lines from the 2009 Northern and Southern Regional Performance Nurseries were analyzed for 46 traits using 82 markers. The complete data set is included in the attached spreadsheet. A large number of markers was used this year to assess the usefulness and level of interest in these markers. We will reduce the number of markers for next year's data set. If you wish to express an interest in any of these markers (or other markers) for next year's data, please contact Bob Bowden (Robert.Bowden@ARS.USDA.GOV) who is heading a committee to decide which markers will be used next year.

Except where noted, protocols used for all assays are listed on the MASWheat website (http://maswheat.ucdavis.edu/protocols/index.htm).

Abiotic Stress Traits

1. Aluminum Tolerance 4DL

SSR markers WMC331 and ALMT1-SSR3A (Mol Breeding 2006 18:171–183) were used for screening of the 4DL Al-resistance QTL. Ten entries were positive for both SSR markers and most likely have the 4DL Al tolerance QTL (AP06TA4520, HV9W04-1594R, HV9W05-1125R, Jackpot, KS06O3A-57-1, KS06O3A-58-1, OK04111, OK04525, TX01V5134RC-3, & TX05A001828). An additional 7 lines were positive for only the WMC331 SSR marker and might have the 4DL Al tolerance QTL (KS970093-8-9-1-1, NE05426, OK05128, SD05118-1, SD07W053, TX05A001822, & Wesley).

2. Aluminum Tolerance 3BS

SSR marker BAR344 was used to screen for the 3BS Al tolerance QTL. Eighteen entries were positive for BAR344 (CA9W07-818, CA9W07-819, HV9W04-1186W, Jerry, KS020056TM-4-1, KS06O3A-57-1, KS06O3A-58-1, KS970093-8-9-1-1, NE05496, NE06469, OK05212, SD05118-1, SD07126, SD07W053, SD07W084, Trego, TX05A001614, & TX05A001822).

Anatomy and Morphology Related Traits

3. Plant Height (Rht1)

One gene-specific STS marker was used to detect the Rht1 gene (TAG 2002 105:1038-1042). All but 4 lines (Kharkof, KS970093-8-9-1-1, OK04525, Scout66) had the Rht1-B1b-Short allele.

4. Plant Height (Rht2)
One gene-specific STS marker was used to detect the Rht2 gene (TAG 2002 105:1038-1042). Only two lines (KS970093-8-9-1-1, OK04525) had the Rht2-D1b-Short allele.

5. Plant Height (Rht8)
One linked SSR marker (GWM261, TAG 1998 96:1104-1109) was used to detect Rht8. Two lines (NE05549, Wesley) had the 211 bp band linked with Rht8 and may carry the Rht8 gene.

Fungal Disease Resistance Traits

6. Eyespot (Pch1)

One SSR marker (XustSSR2001-7DL) was used to detect linkage to the Pch1 gene. All tested lines appear to be susceptible.

7. FHB Wheat Scab (3BS QTL)
Two SSR markers (GWM533, UMN10) were used to detect the presence of a QTL on chromosome 3BS that confers resistance to wheat scab. Only one line, TX05A001614, was positive for both markers. Four lines were positive for GWM533 (HV9W04-1594R, NI04427, T163, & T166).

8. FHB Wheat Scab (5AS QTL)
Two SSR markers (BAR40, GWM186) were used to detect the presence of a QTL on chromosome 5AS, mapped in Frontana, that confers minor resistance to wheat scab. Four lines were positive for both markers (CO04393, OK05212, SD07165, & TX05A001639).

9. Lr19
One STS primer, Lr19-130, was used to detect Lr19 resistance. Only two entries (AP06T3832, OK04525) were positive.

10. Lr21
Non-published primers for a shorter fragment were used for detecting the Lr21 resistance allele. This set of primers was based on the gene sequence provided by Dr. Li Huang from Dr. B. Gill's lab. Known positive (WGRC07, WGRC27) and negative (WGRC02, Wichita) control lines were tested with the new primers and showed the expected alleles. Entries HV9W05-1125R, KS020056TM-4-1, and LE1911 carry the Lr21 resistance gene.

11. Lr34/Yr18
The slow leaf rusting gene Lr34 and yellow rust resistance gene Yr18 are flanked by two markers (SSR marker SWM10, TAG 2006 113:1049–1062; STS marker csLV34-LR34, TAG 2006 114:21–30). A new marker (Lr34Exon11Indel) based on the actual gene sequence, was also used to detect the Lr34 gene. Ten lines were positive for all 3 markers (Antelope, AP06T3832, AP06TA4520, HV9W05-1125R, NX05M4499-1, OK04111, OK04315, OK04525, TX01V5134RC-3, & TX05A001828). However, lines OK04525 & TX05A001828 may be segregating for Lr34 resistance. Also, Jagger is known to carry a non-functional (susceptible) allele for Lr34 which tests positive (resistant) using all 3 of these markers. Entries with Lr34 resistance descended from Jagger will be false positives. We hope to have a marker to detect the non-functional Jagger allele by next year.

12. Lr37/SR38/Yr17
The three rust resistance genes are on a chromosome segment that does not appear to recombine with bread wheat chromosomes. The STS marker (VENTRIUP-LN2) should be therefore completely linked with the resistance genes. The following 26 lines were positive for the marker and likely have the alien segment (AP00x0100-51, AP05T2413, AP06T3832, AP06TA4520, HV9W03-1596R, HV9W04-1186W, HV9W04-1594R, HV9W05-1125R, Jackpot, KS020056TM-4-1, KS06HW46-3, KS06O3A-57-1, KS06O3A-58-1, NE05426, NE06545, NX05M4180-6, OK04111, OK04315, OK04525, SD07126, SD07W053, T166, TX01V5134RC-3, TX04V075080, TX05A001822, & TX05A001828).

13. Lr39/Lr41
These two resistance genes appear to be the same or closely linked genes. SSR markers BAR124 & GDM35 are reported to be closely linked to Lr39. No entries carried both markers and only KS05HW136-3 was positive for BAR124.

14. Lr50
Lr50 is moderately close (6.7 cM) to microsatellite marker GWM382 on wheat chromosome arm 2BL. None of the lines were positive for marker GWM382.

15. Sr2
The Sr2 resistance gene has been effective worldwide for more than 50 years. It has recessive inheritance and expresses primarily as adult-plant resistance. It is located on 3BS in the same region as the FHB QTL. The SSR marker, STM559TGAG (TAG 2004 109: 1641–1647), derived from GWM533, was used along with markers X3B028F08 & X3B042G11 (Mol Breeding (2008) 22:15–24) to assay for Sr2 resistance. Thirteen lines were positive for all 3 markers (Antelope, CO03W054-2, CO04393, HV9W03-1596R, KS05HW136-3, OK04111, OK04525, OK05128, Scout66, T164, Trego, TX05A001398, & TX06A001263). The following 24 lines were positive for markers X3B028F08 & X3B042G11 (AP00x0100-51,

AP05T2413, CA9W07-817, CO03064-2, CO04499, HV9W05-1125R, Jerry, Kharkof, NE05403, NE05430, NE05496, NI04420, NI04427, NW04Y2188, NX05M4499-1, OK04315, SD07165, T163, T165, T166, TAM-107, TX05A001614, TX05A001639, & TX05A001828).

16. Lr24/Sr24
Two STS markers were used to screen for Lr24/Sr24. Sr24#12 and Sr24#50 (TAG 2005 111: 496–504) are both STS markers closely linked to Sr24 and typically amplify only one band. Fourteen lines were positive for both markers (SD07165, CA9W07-817, CA9W07-818, CA9W07-819, Jerry, KS05HW136-3, KS06HW46-3, LE1911, NE05549, NE06469, SD05118-1, Trego, TX01V5134RC-3, TX05A001822, & Wesley). Entry SD07165 was positive for marker Sr24#12 only.

17. Sr36/Sr40
One SSR marker (WMC477) was used to screen for Sr36 & Sr40 resistance. No entries were positive for Sr36. Three entries were positive for Sr40 (HV9W03-1596R, Kharkof, & NX05M4180-6).

18. Sr39
One STS marker (Sr39) was used to screen for Sr39 resistance. No entries were positive for Sr39.

19. Yr36
One STS marker (Yr36-WKS1, www.sciencexpress.org, 19 February 2009) was used to screen for Sr39 resistance. No entries were positive for Yr36.

20. Tan Spot
Two STS markers (Xfcp1 & Xfcp393) flanking the Tsn1 gene in an interval of 0.4 cm were used to screen for ToxA sensitivity. No entries were positive (insensitive to ToxA) for both markers. NE06545 and NX05M4180-6 were positive for Xfcp1. Ten entries were positive for Xfcp393 (CO04499, HV9W04-1186W, KS020056TM-4-1, KS05HW136-3, NE05426, NE05548, NW04Y2188, NX05M4499-1, TAM-107, & Trego).

Growth and Development Traits

21. Pre-harvest sprouting tolerance (3A QTL)
Three SSR markers (BAR57, BAR321 and BAR12) were used to screen for a pre-harvest sprouting tolerance QTL that we have recently mapped on 3A in Rio Blanco. Five lines were positive for all 3 SSR markers (KS06HW46-3, NI04420, OK04111, SD07W084, & T164).

22. Pre-harvest sprouting tolerance 3BL

One STS (Vp1B3, TAG 2007 115:971–980) was used for the Viviparous-1 allelic variant related to PHS tolerance on 3BL. Twenty lines were positive for the marker (Antelope, AP00x0100-51, AP05T2413, CA9W07-817, CA9W07-818, CO03W054-2, HV9W03-1596R, KS05HW136-3, KS06HW46-3, LE1911, NE05403, NE05430, NE06545, NI04420, OK04111, OK04315, OK05128, SD07165, TX05A001398, & TX05A001828). An additional 11 lines appeared to be heterozygous or heterogeneous for the marker (Jerry, KS020056TM-4-1, NW04Y2188, NX05M4499-1, SD07126, SD07W053, SD07W084, T164, TAM-107, Trego, & TX01V5134RC-3).

23. Pre-harvest sprouting tolerance 1BS

One SSR (BAR55) was used to assay for the PHS tolerance QTL on 1BS. Twenty seven lines were positive for the marker (AP00x0100-51, CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, HV9W03-1596R, HV9W04-1594R, HV9W05-1125R, Jerry, Kharkof, KS020056TM-4-1, KS970093-8-9-1-1, NE05403, NE05426, NE05430, NE06545, NI04427, NW04Y2188, NX05M4180-6, NX05M4499-1, OK04111, OK04525, T165, TX05A001398, TX05A001614, TX05A001639, & TX05A001828).

24. Pre-harvest sprouting tolerance 4AL

Two SSR markers (BAR170, GWM397) were used to assay for a PHS tolerance QTL on 4AL. No line was positive for both markers.

25. Vernalization QTL 5AL

One STS (CDO708, Chen and Carver, pre-print) was used to detect a QTL near the Vrn-A1 gene which affects heading date and physiological maturity. Most entries were classified as "Weak" winter types similar to 'Jagger'. Six entries were classified as "Intermediate" winter types similar to cultivar '2174' (AP05T2413, HV9W04-1186W, NX05M4180-6, OK04111, OK04315, & OK05212). Three entries appeared to be segregating for this QTL:, NE06545, NX05M4499-1, & OK04525).

26. Vernalization Vrn-A1

One SNP marker (Vrn-A1-SNPF, TAG 2009 118:881–889) was used to detect winter wheat alleles vrn-A1a and vrn-A1b which affect early season stem elongation. Most entries had the vrn-A1b allele which confers later stem elongation similar to '2174'. Nine entries had the vrn-A1a allele which confers earlier stem elongation similar to 'Jagger' (AP06T3832, AP06TA4520, KS020056TM-4-1, KS05HW136-3, KS06O3A-57-1, KS06O3A-58-1, NW04Y2188, TX05A001822, & TX05A001828). Five entries appeared to be segregating for vrn-A1a and vrn-A1b (AP05T2413, CO03W054-2, CO04393, OK04525, & TX05A001614).

27. Vernalization Vrn-D3

One STS marker (Vrn-D3-F6R8, Chen and Carver, pre-print) was used to detect alleles vrn-D3a and vrn-D3b which affect maturity in winter wheat. Thirty six entries had the vrn-D3a allele which is linked to earlier maturing winter wheat similar to 'Jagger' (Antelope, AP05T2413, AP06T3832, CA9W07-818, CO03W054-2, CO04393, CO04499, HV9W04-1186W, HV9W04-1594R, HV9W05-1125R, Jackpot, KS05HW136-3, LE1911, NE05426, NE05496, NE06469, NE06545, NE06607, NI04427, OK04315, OK05128, Scout66, SD05118-1, SD07W053, SD07W084, T163, T164, T165, T166, TAM-107, Trego, TX01V5134RC-3, TX04V075080, TX05A001828, TX06A001263, & Wesley). Twenty seven entries had the vrn-D3b allele which is linked to later maturing winter wheat similar to '2174' (AP00x0100-51, AP06TA4520, CA9W07-817, CA9W07-819, HV9W03-1596R, Jerry, Kharkof, KS020056TM-4-1, KS06HW46-3, KS06O3A-57-1, KS06O3A-58-1, KS970093-8-9-1-1, NE05403, NE05430, NE05548, NE05549, NI04420, NW04Y2188, NX05M4180-6, OK04111, OK04525, OK05212, SD07126, SD07165, TX05A001614, TX05A001639, & TX05A001822). Three entries appeared to be segregating for vrn-D3a and vrn-D3b (CO03064-2, NX05M4499-1, & TX05A001398).

28. Photoperiod Ppd-D1

One STS marker (PPD-D1-R1-R2, Chen and Carver, pre-print) was used to detect photoperiod alleles ppd-D1a and ppd-D1b. Seventeen entries had the ppd-D1a allele which confers long-day insensitivity to winter wheat similar to '2174' (HV9W03-1596R, KS020056TM-4-1, KS970093-8-9-1-1, NE05403, NE05430, NI04420, NW04Y2188, NX05M4180-6, NX05M4499-1, OK04111, OK04315, OK04525, OK05128, OK05212, TX05A001398, TX05A001614, & TX05A001639). Forty five entries had the ppd-D1b allele which confers long-day sensitivity to winter wheat similar to 'Jagger' (Antelope, AP00x0100-51, AP05T2413, AP06TA4520, CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, CO03W054-2, CO04393, CO04499, HV9W04-1186W, HV9W04-1594R, HV9W05-1125R, Jackpot, Jerry, Kharkof, KS05HW136-3, KS06HW46-3, KS06O3A-57-1, LE1911, NE05426, NE05496, NE05548, NE05549, NE06469, NE06545, NE06607, NI04427, Scout66, SD05118-1, SD07126, SD07165, SD07W053, SD07W084, T163, T164, T165, T166, TX01V5134RC-3, TX04V075080, TX05A001822, TX05A001828, TX06A001263, & Wesley). Two entries appeared to be segregating for ppd-D1a and ppd-D1b (TAM-107 & Trego).

Insect Resistance Traits

29. Hessian Fly (H9)

One STS marker (SOPO05) and one SSR marker (CFA2153) were used to detect the presence of H9 resistance to Hessian fly biotype L. No line was positive for both markers. Eight lines were positive for SOPO05 (Kharkof, KS06O3A-58-1, NE05426, SD07W084, T163, T164, T165, & TX05A001828).

30. Hessian Fly (H13)
Two SSR markers (GDM36, and CFD132) were used to test lines for the presence of H13 resistance to Hessian fly biotype L. No line was positive for either marker.

31. Hessian Fly (Hdic)
One SSR marker (CFA2153) was used to detect the presence of Hdic resistance to Hessian fly. Eleven lines were positive for CFA2153 (CO04393, Kharkof, KS020056TM-4-1, NE06607, OK04525, OK05212, SD05118-1, T166, TX05A001614, TX05A001828, & Wesley).

Quality Traits

32. 1RS Translocation
One rye SSR marker (SCM9) was used to detect the presence of the 1RS rye translocation. Most entries were NON-1RS. Eight entries have the 1AL.1RS translocation (AP05T2413, NX05M4180-6, T164, T165, T166, TAM-107, TX01V5134RC-3, TX06A001263). Six entries have the 1BL.1RS translocation:, HV9W04-1594R, KS06O3A-58-1, NI04420, NI04427, SD07W053, & TX05A001614).

32. Gluten strength, Glu-A1 alleles
Two STS markers (UMN19 & HMWAx*) were used to detect Glu-A1 alleles. Both markers agreed completely. Marker UMN19 also provides co-dominant information. We will no longer use marker HMWAx*. Forty two entries have the Glu-A1-Ax2* allele (Antelope, AP05T2413, CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, CO03W054-2, HV9W03-1596R, HV9W04-1186W, HV9W05-1125R, Jerry, Kharkof, KS05HW136-3, KS06HW46-3, NE05403, NE05426, NE05430, NE05496, NE05549, NE06469, NE06545, NE06607, NI04420, OK04111, OK04315, OK05128, Scout66, SD05118-1, SD07126, SD07165, SD07W084, T163, T164, T165, T166, TAM-107, Trego, TX04V075080, TX05A001398, TX05A001828, TX06A001263, & Wesley). Sixteen entries do not have the Glu-A1-Ax2* allele and could be either Glu-A1-Ax1 or Glu-A1-Ax-null (AP00x0100-51, AP06T3832, AP06TA4520, HV9W04-1594R, Jackpot, KS06O3A-57-1, KS06O3A-58-1, KS970093-8-9-1-1, LE1911, NE05548, NW04Y2188, NX05M4180-6, OK05212, TX05A001614, TX05A001639, & TX05A001822). Eight entries appeared to be segregating for Glu-A1 alleles (CO04393, CO04499, KS020056TM-4-1, NI04427, NX05M4499-1, OK04525, SD07W053, & TX01V5134RC-3).

33. Gluten strength, Glu-A3 alleles
Seven STS markers (GluA3a, GluA3abc, GluA3ac, GluA3d, GluA3e, GluA3f, & GluA3g; TAG 2004 108:1409–1419) were used to detect Glu-A3 alleles. These markers seem to work well with the possible exception of Glu-A3f, which may be producing false positive alleles. Entries HV9W04-1594R & SD07126 have the Glu-

A3b allele. Entries NE05548 & NE06545 have the Glu-A3b & Glu-A3f alleles. Thirty nine entries have the Glu-A3c allele (AP06T3832, AP06TA4520, CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, CO03W054-2, CO04499, HV9W05-1125R, Jackpot, Jerry, KS020056TM-4-1, KS05HW136-3, KS06HW46-3, KS06O3A-57-1, KS970093-8-9-1-1, LE1911, NE05403, NE05430, NE05496, NE05549, NE06607, NI04420, NI04427, NX05M4499-1, OK04111, OK04315, OK05128, OK05212, Scout66, SD05118-1, SD07W053, TX01V5134RC-3, TX04V075080, TX05A001398, TX05A001614, TX05A001639, TX05A001822, & Wesley). Entry CO04393 has the Glu-A3c & Glu-A3d alleles. Three entries have the Glu-A3c & Glu-A3f alleles (Antelope, OK04525, & Trego). Entry SD07W084 has the Glu-A3c & Glu-A3g alleles. Three entries have the Glu-A3d allele (AP00x0100-51, NW04Y2188, & SD07165). Seven entries have the Glu-A3e allele (Kharkof, KS06O3A-58-1, NE05426, T163, T164, T165, & TX05A001828). Three entries have the Glu-A3f allele (HV9W03-1596R, NE06469, & TX06A001263). Finally, seven entries (AP05T2413, HV9W04-1186W, NE04490, NE06436, NX05M4180-6, T166, & TAM-107) produced no allele information with these markers.

34. Gluten strength, Glu-B1 alleles

Two STS markers (BxMAR & HMWBx) were used to detect Glu-B1 alleles. Twelve entries had Glu-B1-Bx7 & Glu-B1-Bx17 (AP05T2413, AP06T3832, AP06TA4520, HV9W05-1125R, Jackpot, KS06O3A-57-1, NE05548, SD07126, SD07W053, SD07W084, TX01V5134RC-3, & TX04V075080). Two entries had Glu-B1-Bx7 & appeared to be segregating for Glu-B1-Bx17 & NON-Glu-B1-Bx17 (KS020056TM-4-1 & TX05A001828). Trego appeared to be segregating for Glu-B1-Bx7 & Glu-B1-Bx20. OK04315 had Glu-B1-Bx20. Only one line, CO03W054-2, had Glu-B1-Bx7^{oe}. Based on these markers, all that is known about NX05M4499-1 is that it is NON-Glu-B1-Bx17. Forty one entries had only Glu-B1-Bx7 (Antelope, AP00x0100-51, CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, CO04393, HV9W04-1186W, HV9W04-1594R, Jerry, Kharkof, KS05HW136-3, KS06HW46-3, KS06O3A-58-1, KS970093-8-9-1-1, LE1911, NE05403, NE05426, NE05430, NE05496, NE05549, NE06545, NE06607, NI04420, NI04427, NW04Y2188, NX05M4180-6, OK04525, OK05212, Scout66, SD05118-1, SD07165, T163, T164, T165, TAM-107, TX05A001398, TX05A001614, TX05A001639, TX06A001263, & Wesley).

35. Gluten strength, Glu-B3 alleles

Ten STS markers (GluB3a, GluB3b, GluB3c, GluB3d, GluB3e, GluB3fg, GluB3g, GluB3h, GluB3i, & GluB3bef, TAG 2009 118:525–539) were used to evaluate Glu-B3 alleles. Some markers produced no bands, other produced band sizes that were very different from the published size, and several produced conflicting information. Poor marker information plus the lack of controls for all of the Glu-B3 alleles indicates that this data should not be used. The allele calls have been left in the 2009 spreadsheet for those interested in them; however, data produced

from these markers is not reliable at this time. If there is interest, will get the needed positive controls and attempt to optimize the markers for the 2010 data set.

36. Gluten strength, Glu-D1 alleles

Glu-D1 alleles were genotyped using 3 STS markers. HMWDx5 & UMN25 (TAG 2008 118:177–183) were used for Glu-D1-Dx5. Marker UMN25 also detects Glu-D1-Dx2. Marker UMN26 (TAG 2008 118:177–183) was used to detect alleles Glu-D1-Dy10 & Glu-D1-Dy12.

Eight entries had alleles Glu-D1-Dx2 & Glu-D1-Dy12 (AP05T2413, HV9W05-1125R, KS970093-8-9-1-1, LE1911, NX05M4180-6, OK05212, T166, & TAM-107).

Fifty entries had alleles Glu-D1-Dx5 & Glu-D1-Dy10 (Antelope, AP00x0100-51, AP06T3832, AP06TA4520, CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, CO03W054-2, CO04499, HV9W03-1596R, HV9W04-1186W, HV9W04-1594R, Jackpot, Jerry, Kharkof, KS020056TM-4-1, KS05HW136-3, KS06HW46-3, KS06O3A-57-1, KS06O3A-58-1, NE05403, NE05426, NE05430, NE05496, NE05548, NE05549, NE06469, NE06545, NE06607, NI04427, OK04111, OK04315, OK05128, SD05118-1, SD07126, SD07165, SD07W053, SD07W084, T163, T164, TX01V5134RC-3, TX04V075080, TX05A001398, TX05A001614, TX05A001639, TX05A001822, TX05A001828, TX06A001263, & Wesley). Scout66 had alleles Glu-D1-Dx2, Glu-D1-Dx5, & Glu-D1-Dy12.

Seven entries (CO04393, NI04420, NW04Y2188, NX05M4499-1, OK04525, T165, & Trego) appeared to have alleles Glu-D1-Dx2, Glu-D1-Dx5, Glu-D1-Dy10, & Glu-D1-Dy12.

37. High Grain Protein Content, HGPC

One STS marker (UCW89) very closely (0.1 cM) linked with the Gpc-B1 gene was used to identify the gene for HGPC. No line was positive for the HGPC marker.

38. Grain Texture, Pina-D1

One dominant STS marker (Pina-D1) was used to screen for the presence of wild-type Pina-D1a, soft alleles. Most entries carry the Pina-D1a wild, soft allele. Ten entries were positive for the Pina-D1b, hard allele (AP00x0100-51, AP06TA4520, HV9W04-1594R, Jackpot, KS06HW46-3, KS06O3A-58-1, OK04111, OK04315, OK04525, & TX05A001639).

39. Grain Texture, Pinb-D1

A codominant PCR-CAPs marker (Pinb-D1) was used to screen for Pinb-D1 alleles. Most entries had the Pinb-D1b mutant, hard allele. Fifteen entries had the PinB-D1a wild, soft allele (AP00x0100-51, AP06TA4520, CO03W054-2, HV9W04-1594R, Jackpot, Kharkof, KS020056TM-4-1, KS06HW46-3, KS06O3A-58-1, NX05M4180-6, OK04111, OK04315, OK04525, TX01V5134RC-3, & TX05A001639).

Two entries appeared to be heterozygous for Pinb-D1 alleles (NX05M4499-1, & TX05A001828).

40. Polyphenol Oxidase Activity, PPO-A1
One codominant STS marker (PPO18, Molecular Breeding 2005 16: 209–218) linked to a PPO QTL on 2AL was used to screen for PPO activity. Most entries had the undesirable high PPO activity allele. Only four entries (HV9W04-1594R, KS05HW136-3, NX05M4499-1, & OK05128) had the low PPO activity allele. Entry OK04525 appeared to be heterozygous for PPO-A1 QTL alleles.

41. Polyphenol Oxidase Activity, PPO-D1
Two complementary dominant STS markers (PPO16 & PPO29, TAG 2007 115:47–58) linked to PPO-D1 alleles were used for this assay. Thirty nine entries had the PPO-D1a low PPO allele (CA9W07-817, CA9W07-818, CA9W07-819, CO03064-2, HV9W03-1596R, HV9W04-1186W, Jackpot, Jerry, Kharkof, KS020056TM-4-1, KS05HW136-3, KS06O3A-58-1, KS970093-8-9-1-1, LE1911, NE05496, NE05549, NE06469, NE06545, NE06607, NI04420, NI04427, NW04Y2188, OK04111, OK04315, OK05128, OK05212, Scout66, SD05118-1, SD07165, T163, T165, T166, TAM-107, TX01V5134RC-3, TX04V075080, TX05A001398, TX05A001614, TX06A001263, & Wesley). Nine entries had the PPO-D1b high PPO allele (AP06T3832, CO03W054-2, HV9W04-1594R, HV9W05-1125R, KS06HW46-3, NX05M4180-6, NX05M4499-1, SD07W084, & TX05A001639). Three entries (CO04393, SD07W053, & Trego) appeared to be heterozygous for PPO-D1 alleles. Other entries produced no bands at all and are undetermined.

42. Waxy Mutants, Wx-A1
One codominant STS marker (Waxy-A1-AFC-AR2, Genome 45: 1150–1156 2002) was used to detect Waxy-A1 alleles. Most entries had the Wx-A1a wild allele. Six entries had the Wx-A1b null allele (NE05403, NE05430, NE06607, OK04111, NX05M4180-6, & TX04V075080). Entry NX05M4499-1 appeared to be heterozygous for Wx-A1 alleles.

43. Waxy Mutants, Wx-B1
Two dominant STS markers (Waxy4 & Waxy-B1-BDFL-BRD, Genome 45: 1150–1156, 2002) were used to detect Waxy-B1 alleles. Most entries had the Wx-B1a wild allele. Nine entries had the Wx-B1b null allele (NE05403, NE05430, NE06607, OK04111, NX05M4180-6, & TX04V075080).

44. Waxy Mutants, Wx-D1
One codominant STS marker (Waxy-D1-BDFL-DRSL, Genome 45: 1150–1156 2002) was used to detect Waxy-D1 alleles. Most entries had the Wx-D1a wild allele. Only two entries (NX05M4180-6 & NX05M4499-1) had the Wx-D1b null allele.

Viral Resistance Traits

45. Barley Yellow Dwarf Virus (Bydv2)
One SCAR marker (BYAgi) was used to detect the presence of the Bydv2 gene. No entry had the expected band as found in P961341. The data suggest that none of the lines have Bydv2.

46. Wheat Streak Mosaic Virus (Wsm1)
STS marker (BG263898, Chromosome Research 2007 15:3–19) was used to detect the chromosome segment containing the Wsm1 gene transferred from *Agropyron intermedium*. Nearly all entries lack the Wsm1 gene. The TAM-107 entry was positive for the marker, even though other control sources of TAM-107 were negative for the marker. Entry NW04Y2188 appeared to be positive for the marker.