Habib R, Shah MM, and Swati ZA. 2006. Assessment of genetic variability in synthetic hexaploid wheat conferring resistance against Fusarium head blight. *In:* Breeding for success: diversity in action. Proc 13th Aus Plant Breed Conf, Christchurch, New Zealand (Mercer CF, Ed). NZ Grassland Association Inc., Dunedin, New Zealand. Pp. 1228-1237.

Hassan SW, Shah MM, Maqbool K, and Pervez A. 2007. Comparisons of DNA marker based genetic diversity with phenotypic estimates using maize genotypes. Genet Mol Res (In review).

Farooq U, Khan A, Ahmad VU, Haq A-U, Khan SS, Farooq R, Pervez A, and Shah MM. 2007. Complete (1)H and (13) C NMR assignments of two new trans-clerodane diterpenoids from Otostegia limbata. Magn Reson Chem 45(9):766.

Maqbool K and Shah MM. 2006. Evaluation of wheat and triticale for morphological traits in sub-tropical regions of Pakistan. Pakistan J Agric Res (submitted).

Maqbool K, Shah MM, and Hussain F. 2007. Genetic analysis of wheat crosses for agronomic traits using diallel mating design. J SUBRAO (Accepted).

Shah MM, Hassan SW, and Swati ZA. 2006. Identifying genetic diversity in a set of Pakistani maize germplasm using RAPD analyses. *In:* Breeding for success: diversity in action. Proc 13th Aus Plant Breed Conf, Christchurch, New Zealand (Mercer CF, Ed). NZ Grassland Association Inc., Dunedin, New Zealand. Pp. 1026-1033.

Shah MM and Gill KS. 2001. High density mapping of gene-rich region present on homoeologous group 5L of wheat and barley. Barley Genet Newslet 31:18.

Shah MM and Hassan A. 2005. Distribution of genes and recombination on wheat homoeologous group 6 chromosomes: A synthesis of available information. Mol Breed 15(1):45-53.

Shah MM and Pervez A. 2007. Comparative genomic analysis of *Ph1* gene for wheat improvement. *In:* Proc 2nd EsDev 2007 Conf, CIIT, Abbottabad, Pakistan (Accepted).

Shah SH, Shah MM, Khan MS, Shaheen M, and Swati ZA. 2005. Capturing salinity tolerance in wheat by directed molecular biological approaches. *In:* Proc 1st Internat Conf Environmentally Sustainable Development (ESDev–2005). COMSATS, Institute of Information Technology, Abbottabad, Pakistan, 28 June, 2005. Paper number WA-40.

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Breeding for semidwarf habit and high grain yield in hexaploid wheat.

Wheat is an excellent crop for Pakistan and serves as staple food crop. To achieve high yield, raising productivity per unit area by adapting modern technologies such as high-yielding cultivars, improved cultural practices, and proper management of crop are needed. In 2006–07, an overall production of 23,520 x 10^6 t was achieved from an area of 8,493.9 x 10^6 ha (Table 1).

Table 1. Wheat area and production in Pakistan for the year 2006–07 (Source: Ministry of Food, Agriculture and Livestock, Islamabad Pakistan).

Province	Area (x 10^3 ha)	Production (x 10^3 tons)	Yield (kg/ha)
Punjab	6,393.1	17,850.0	2,792
Sindh	937.1	3,409.0	3,638
NWFP	754.8	1,390.0	1,842
Balochistan	408.9	871.0	2,130
Total	**8,493.9**	**23,520.0**	**2,769**

Wheat breeding at NIA, Tando Jam. Wheat breeding at the NIA is being pursued with the objectives of developing new cultivars endowed with high yield and good quality characters with tolerance to biotic and abiotic stresses. Currently, our breeding material is at different stages of evolution and is summarized below.

Performance of candidate cultivar 7-03. The candidate cultivar 7-03 has completed two years of National trials. The line tested in farmers' fields in performance trials. The candidate was tested in the Hyderabad, Matyari, Sanghar, and Khairpur districts. The line is resistant to both rusts according to CDRI (Cereal Disease Research Institute), Islamabad, in screening during 2006–07.

Performance of candidate cultivar 15-10. Another candidate line, 15-10, has completed one year of testing in national trials. Seed for the second year was sent to national trial; the results are still awaited. The candidate line has the best quality characters as analyzed by NARC (National Agriculture Research Council), Islamabad. The line has the highest grain ash (2.02%) with the exception of line V-022668 (2.112%). Line 15-10 also has the highest grain protein (15.81% d.b) of all lines and check cultivars in the national trial (20 genotypes). The line has the higher wet gluten (40.04%) and the dry gluten (12.34%) than all the check cultivars and lines in National trials in 2005–06. Line 15-10 has a comparatively higher combined grain yield (normal and late sowing) over ten locations of national trials than do the various check cultivars of the respective area. Line 15-10 was resistant to leaf rust during 2006–07 according to CDRI screening.

Zonal Trial Studies. Two candidate lines, 54-03 and 22-03, have completed two years of zonal trials in the Sindh province. Both lines are resistant to leaf rust according to CDRI, Islamabad, screening during the year 2006-07.

Advance Station Trials. Six trials were conducted for yield and yield components studies. Trial I, Trial II, Trial III, and Trial V all have 16 genotypes, including two check cultivars Sarsabz and Kiran-95. Trial IV consisted of 36 genotypes and two check cultivars (Sarsabaz and Anmol), and Trial VI consisted of 11 genotypes with two checks (Sarsabz and Kiran). All the trials consisted of three replicates of six, 4-m rows, except for Trial VI, which was 4.7-m long.

Trial I. In this yield comparison, line 11 (1.850 kg/plot) had the highest grain yield, more than any other line or cultivar. Subsequent lines that had high grain yields were 14 (1.383 kg), 10 (1.367 kg), and 13 (1.350 kg). Possible reasons for the higher grain yield in line 11 could be due to its tall, dwarf plant height and a higher number of grains/spikelet. The higher gain yield in line 14 could be due to its late heading and high number of spikelets/spike. The higher grain yield in line 10 could be due to a very early heading date, even earlier than the check cultivar Sarsabz, a tall, dwarf plant height, and a higher number of spikelets/spike. The higher grain yield in line 13 could be due to the tall, dwarf plant height. Line 06 had the lowest grain yield/plot.

Trial II. In this yield comparison, line 14 (1.083 kg/plot) had the highest grain yield per plot. The high grain yield in line 14 could be due to late heading date; it also had the highest number of spikelets/spike. Subsequent lines that had high grain yields were 10 (1.017 kg), 8 (0.867 kg), and 9 (0.850 kg). Line 7 had the lowest grain yield per plot. In this comparison, the check cultivar Kiran-95 (0.817 kg) had a higher grain yield than Sarsabz (0.783 kg).

Trial III. In this yield comparison, line 04 (1.317 kg/plot) had the highest grain yield/plot when compared to all other genotypes. Subsequent lines with higher grain yields were 8 (1.100 kg), 1 and 10 (1.083 kg), and 11 (0.933 kg). Line 7 (0.667 kg) had the lowest grain yield per plot. The check cultivars had comparatively lower grain yields compared to most of the lines. Kiran-95 (0.817 kg) had higher grain yield than Sarsabz (0.737 kg/plot).

Trial IV (isoline studies). In this trial, line 32 (1.567 kg) had the highest grain yield/plot. Subsequent lines with higher grain yields were 1 (1.350 kg/plot), 29 (1.300 kg), and lines 3, 23, and 33 (1.233 kg). Possible reasons for the high grain yield in line 32 include its early maturity, increased plant height, higher main spike grain yield, and increased number of grains/spikelet. The higher grain yield in line 1 could be due to a mid-maturity date, a higher number of spikelets, an increased number of grains, and a better main spike grain yield. The grain yield in line 29 could be due to a double dwarf plant height. Earliness in days-to-heading and an increased number of grains/spikelet could contribute to the high grain yield in line 3. The higher yield in line 23 could be due to a medium length in days-to-heading and an increased number of grains/spikelet. Line 33 is early in days-to-heading, has a higher number of spikelets, and an increased number of grains/spike and grains/spikelet. The check cultivar Anmol (1.300 kg) had comparatively higher grain yield/plot than Sarsabz (0.750 kg).

Trial V (CIMMYT Coordinated Trial). In this trial, line 6 (2.183 kg) had the highest grain yield/plot, followed by lines 4 (2.167 kg), 1 (2.00 kg), 13 (1.933 kg), and 2 (1.916 kg). The high grain yield in line 6 could be due to its tall, dwarf plant height, longer spikes, higher number of spikelets, and higher number of grains/main spike. The high grain yield in line 4 could be due to its mid-maturity. The high yield in line 1 could be due to its tall, dwarf plant height, higher number of grains/spike, and increased main spike grain yield. A medium maturity and tall, dwarf plant height may contribute to the high grain yield in line 13. Line 2 has long spikes, a higher main spike grain yield, and a larger number of grains/spikelet. The check cultivars Sarsabz and Kiran-95 had grain yields of 1.233 and 1.083 kg/plot, respectively.

Trial VI (double dwarf trial). In this yield comparison, line 08 (1.267 kg) had the highest grain yield/plot. Subsequent lines with high grain yields/plot were 06 (1.167 kg), 01 (1.067 kg), 02 (1.017 kg), and 03 (1.017 kg). The check cultivars Sarsabz (0. 983 kg) and Kiran-95 (0.833 kg) had comparatively lower grain yields than all other lines.

Coleoptile length studies.

Eleven genotypes (seven cultivars and four lines) were studied for coleoptile length in three replicates. Genotypes with Rht_1, Rht_2, Rht_1Rht_2, Rht_8Rht_9, and *rht* were compared for their coleoptile length under controlled environmental conditions. The results suggested that the traditionally tall cultivar C-591 (*rht*) had a longer coleoptile than all other cultivars and genotypes. Subsequent genotypes with long coleoptile lengths were Chinese Spring (*rht*) and Rht8-01 (Rht_8). The cultivars Mara (Rht_8Rht_9), Sarsabz (Rht_1), and Soghat-90 (Rht_2) were not significantly different. Line Rht8-02 has the Rht_8 dwarfing genes but was not significantly different than the double-dwarf cultivar Yeccora (Rht_1Rht_2). These results suggest that dwarfing genes probably do not affect the coleoptile length. The genetic background may affect the coleoptile length of individual cultivars.

Participation in an international meeting.

K.D. Jamali participated in an international project planning meeting and presented country report of the IAEA project No. RAS/05/045 held from 25–30 June, 2007, in Kuala Lumpur, Malaysia.

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Allelic variation of polyphenol oxidase genes located on chromosomes 2A and 2D and development of functional markers for the PPO genes in common wheat.

Polyphenol oxidase (PPO) activity is highly related to the undesirable browning of wheat-based end products, especially Asian noodles. Characterization of PPO genes and the development of their functional markers are of great importance for marker-assisted selection in wheat breeding. In the present study, complete genomic DNA sequences of two PPO genes, one each located on chromosomes 2A and 2D and their allelic variants were characterized by means of *in silico* cloning and experimental validation. Sequences were aligned at both DNA and protein levels. Two haplotypes on chromosome 2D showed 95.2% sequence identity at the DNA level, indicating much more sequence diversity than those on chromosome 2A with 99.6% sequence identity. Both of the PPO genes on chromosomes 2A and 2D contain an ORF of 1,731 bp, encoding a PPO precursor peptide of 577 amino acids with a predicted molecular mass of ~64 kD. Two complementary dominant STS markers, *PPO16* and *PPO29*, were developed based on the PPO gene haplotypes located on chromosome 2D; they amplify a 713-bp fragment in cultivars with low PPO activity and a 490-bp fragment in those with high PPO activity, respectively. The two markers were mapped on chromosome 2DL using a DH population derived from the cross 'Zhongyou 9507/CA9632', and a set of NT and Dt lines 2DS of Chinese Spring. QTL analysis indicated that the PPO gene cosegregated with the two STS markers and was closely linked to SSR marker *Xwmc41* on chromosome 2DL, explaining from 9.6% to 24.4% of the phenotypic variance for PPO activity across three environments. In order to simultaneously detect PPO loci on chromosomes 2A and 2D, a multiplexed marker combination *PPO33*/*PPO16* was developed and yielded distinguishable DNA patterns in a number of cultivars. The STS marker *PPO33* for the PPO gene on chromosome 2A is homologous with *PPO18* that we reported previously, and can amplify a 481-bp and a