

SHORT COMMUNICATION

High Kernel Weight Genotypes of Indian Bread Wheat (*Triticum aestivum* L.)

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In an experiments on assessment and identification of elite Indian wheat genotypes, IC138896, IC138893, IC28664, IC35069, IC532841, IC534435, IC534777, IC534787, IC82197, and IC82198, showed high kernel weight compared to 'Moti (HD-1949)'. These can be gainfully used as parental lines in breeding for increasing grain weight, both for hybridization and selection.

Key Words: Indian wheat, High kernel weight, Parental lines, Phenological characteristics, *Triticum aestivum*

Wheat (*Triticum* spp. L.) is one of the most important cereal crops that was crucial in the rise of famous civilizations and has been the chief vehicle of green revolution across the world. It has been playing the key role in India's food security and self-sufficiency.

India's rate of gain in wheat production has declined during the last two years due to adverse weather conditions (Singh, 2016). On the other hand, strong selection pressure for yield under high input conditions during and after green revolution has eliminated considerable genetic diversity in the breeding pools of major crops, including wheat, causing erosion of genetic potential for adaptation to emerging challenges of climate change (Voss-Fels *et al.*, 2015). In addition, the bottlenecks of hexaploidisation followed by breeding have considerably narrowed down the bread wheat (*Triticum aestivum* L.) diversity to the extent that yields in many regions appear to be unexpectedly stagnating (Voss-Fels *et al.*, 2015). Genetic diversity analyses and identification of elite genotypes can address this dilemma by providing detailed knowledge to characterize and utilize the available genetic diversity in the germplasm collections.

As compared to modern high yielding varieties, local cultivars and landraces have higher genetic variability and adaptation to the different local stress conditions and, therefore, are valuable tools for identifying genes for achieving high grain yield in arid and semi-arid

areas (Lammerts-van-Bueren *et al.*, 2005). Worldwide efforts are on to assess the phenotypic diversity of local landraces in order to mine useful genes and to assess the exploitable diversity, in wheat and other crops to utilize this untapped diversity: for instance, Dikshit *et al.* (2004) and Routray *et al.* (2007) reported on rice landraces and Uttaranchal wheat landraces, respectively. While genetic diversity can be estimated based on various criteria, agro-morphological characterization is a primary step for conservation and utilization of plant genetic resources (Zarkti *et al.*, 2012).

In order to generate information, useful for wheat crop improvement through breeding and/or biotechnology, six hundred and eighteen Indian wheat collections, supplied with thanks by Late Dr SK Mishra, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, were assessed for morphological and phenological characteristics. These were grown at the experimental farm of ICAR-Indian Agricultural Research Institute, New Delhi (latitude: 80°38'23"N, longitude: 77°09'27"E, and with an elevation of 228.61m above msl) for two consecutive cropping seasons (2011-12 and 2012-13), in two replicates using randomized block (RBD) design, following standard agronomic practices. Data were recorded on five randomly tagged plants in each plot. Recorded value of each trait was averaged over 5 individuals, two replications, and two cropping seasons. Data were analyzed using statistical software SAS, version 9.3 (SAS Institute Inc., USA, 2011).

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Statistical parameters such as standard error mean (SEM), critical difference (CD) and coefficient of variation (CV, %) were estimated for the entire set of 618 genotypes and were used for the comparison. In the present study, as presented in Table 1, performances of these ten genotypes were compared with that of commercial cultivar HD-1949 (IC73210). Selection of superior wheat genotypes regarding high grain yield would be as effective as selection for its components, including thousand seed weight (Peltonen-Saino *et al.*, 2007). The relation of these traits with grain yield and the interrelationships have special importance as the basis for selecting high yielding genotypes (Sabaghnia *et al.*, 2014). In the set of 618 Indian wheat accessions, IC73210 was a commercial cultivar Moti (HD-1949), which is a triple dwarf wheat with grain color amber and medium bold, good for chapati making (www.dacnet.nic.in) and, therefore, ten high kernel weight genotypes identified in the present study were compared with HD-1949.

The genotype IC5344777, as shown in Table 1, registered the highest thousand kernel weight (65.5 g in 2011-12, and 69.99 g in 2012-13) amounting to more than the double of the commercial cultivar HD-1949 (32.5 g in 2011-12, and 30.5 g in 2012-13) during both the years followed by genotypes IC534787 (58.6 g in 2011-12, and 56.37 g in 2012-13), IC82197 (48.2 g in 2011-12, and 46.54 g in 2012-13), IC35069 (45.8 g in 2011-12, and 44.6 g in 2012-13), IC138893 (45.05 g in 2011-12, and 44.52 g in 2012-13), IC532841 (43.3 g in 2011-12, and 41.84 g in 2012-13), IC82198 (41.5 g in 2011-12, and 41.88 g in 2012-13), IC138896 (41.23 g in 2011-12, and 42.84 g in 2012-13), IC534435 (40.25 g in 2011-12, and 42.05 g in 2012-13), and IC28664 (40 g in 2011-12, and 41.08 g in 2012-13). Our result showed higher values than those of previous reports for bread wheat (Sabaghnia *et al.*, 2014). In terms of days to head emergence, days to 50% flowering, and days to physiological maturity; most of these genotypes were comparable to the HD-1949, except IC534787 that showed the longest duration for physiological maturity (155 days in 2011-12 and 150 days in 2012-13) followed by IC534777 (140 days in 2011-12, and 145 days in 2012-13), and IC82198 (100 days in both the years). IC28664, IC534435, IC82197, and IC82198 produced 50% flowers in 5 days after head emergence, while the other genotypes took 10 to 15 days. Our results were congruent with the report of Zarkti *et al.* (2012). In case of average spike length, as depicted in Fig. 1,

Table 1. Comparative performance of twelve high-kernel-weight genotypes of Indian bread wheat (*Triticum aestivum* L.)

Genotypes	Thousand kernel weight (g)		Days to physiological maturity		Days to 50% flowering		Days to head emergence		Plant height (cm)		Spike length (cm)		Number of seeds per spike	
	2011-12	2012-13	2011-12	2012-13	2011-12	2012-13	2011-12	2012-13	2011-12	2012-13	2011-12	2012-13	2011-12	2012-13
IC_73210 (Moti/HD-1949)	32.5	30.5	90	90	70	70	55	60	53.25	55.6	8.3	8.5	35	33
IC_138896	41.23	42.84	90	90	70	70	60	65	92.5	90.3	10.7	9.5	39	37
IC_138893	45.05	44.52	100	95	75	70	60	60	95.25	95.55	9.8	9.5	44	43
IC_28664	40	41.08	90	90	70	70	65	65	80	82.1	12	12.5	49	47
IC_35069	45.8	44.6	95	90	75	70	60	65	110.4	109.1	12.5	12	45	43
IC_532841	43.5	41.84	95	90	70	70	60	60	91.5	89.05	8	8.5	25	27
IC_534435	40.25	42.05	95	95	70	70	65	65	106	106.05	10.5	10	56	57
IC_534777	65.5	69.99	140	145	110	120	110	110	102.6	103.6	10.5	10.5	42	38
IC_534787	58.6	56.37	155	150	115	120	110	110	98.07	99.85	12.8	12.5	30	42
IC_82197	48.2	46.54	100	95	75	70	65	65	91.5	91.85	11.2	11.5	55	53
IC_82198	41.5	41.88	100	100	75	70	65	65	80.04	78.95	10.3	9.5	58	61
SE(m)	0.13	0.12	0.38	0.35	0.06	0.05	0.04	0.04	0.03	0.03	0.04	0.05	0.9	0.87
CD (0.05%)	0.36	0.33	1.05	0.97	0.17	0.14	0.11	0.11	0.08	0.08	0.11	0.14	2.49	2.41
CD (0.01%)	0.47	0.44	1.38	1.27	0.22	0.18	0.15	0.15	0.11	0.11	0.15	0.18	3.28	3.17
CV (%)	25.92	28.37	19.21	19.36	23.01	24.67	25.61	27.28	8.56	9.02	16.95	18.58	37.94	39.27

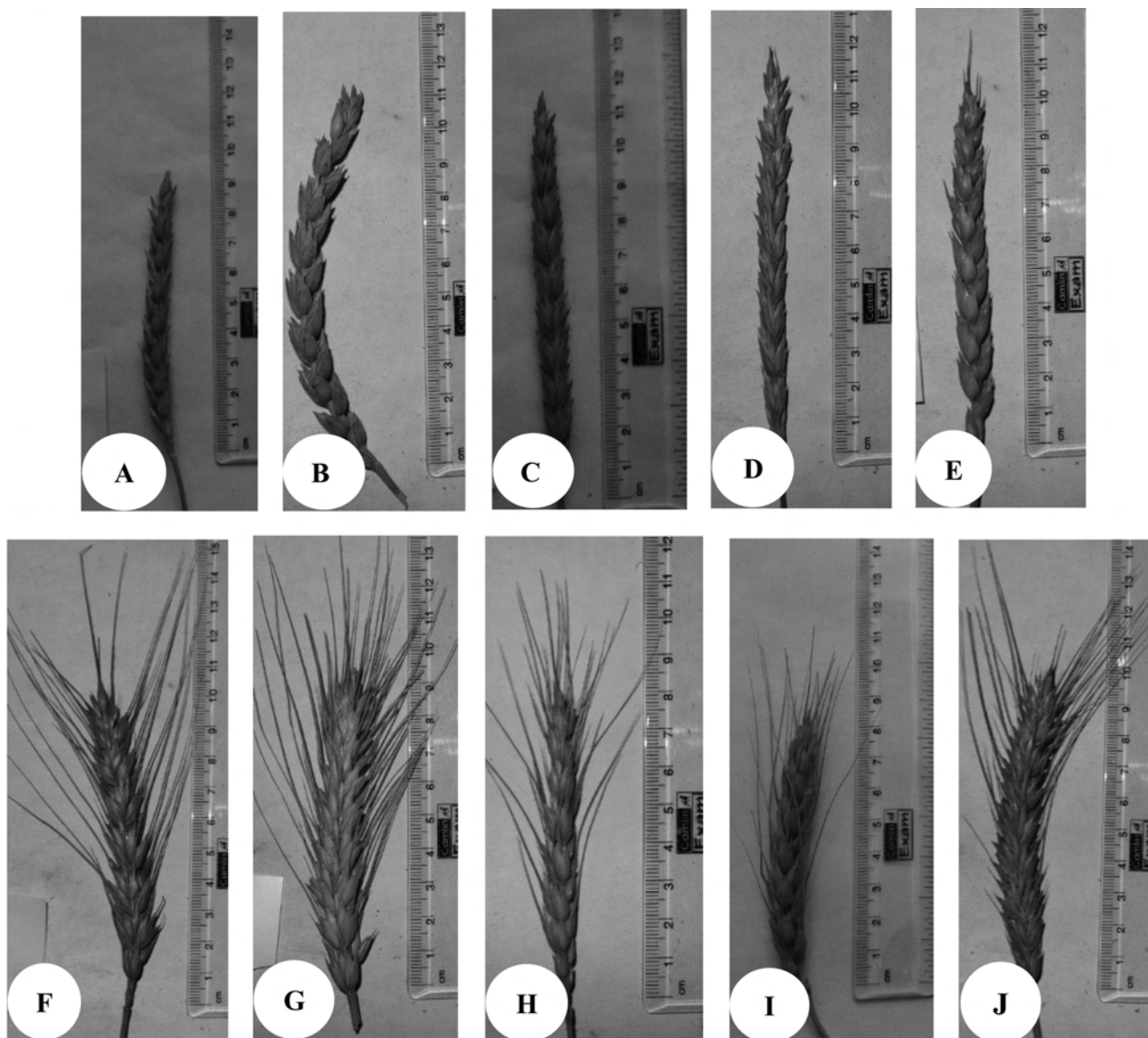


Fig. 1. Spike characteristics of high kernel weight genotypes of Indian bread wheat: A, IC82198; B, IC534787; C, IC82197; D, IC28664; E, IC534777; F, IC534435; G, IC138893; H, IC138896; I, IC532841; and J, IC35069.

and presented in Table 1, longer spikes ranging from 12 to 12.8 cm were recorded in genotypes IC28664, IC35069, and IC534787; whereas, the shorter spikes were observed in genotype IC532841 (8 cm in 2011-12, and 8.5 cm in 2012-13) similar to those of commercial cultivar HD-1949 (8.3 cm in 2011-12 and 8.5 cm in 2012-13). Number of seeds per spike is another important component of grain yield. As shown in Table 1, the highest number of seeds per spike was registered in IC82198 (58 in 2011-12 and 61 in 2012-13) and the lowest (25 in 2011-12 and 27 in 2012-13) values that were below those of commercial cultivar HD-1949

(35 in 2011-12 and 33 in 2012-13) were registered in IC532841. According to Subedi *et al.* (2000), when wheat is stressed during reproductive development, the grain number in fertile florets is reduced. This explains the reason for variation in number of seeds per spike within each genotype between the two cropping seasons (2011-12 and 2012-13).

Figure 1 illustrates, further, visual/qualitative characteristics of spikes of these high kernel weight genotypes. Five genotypes were awnless and the other five were awned; spike density was compact in most of the genotypes except IC534787 which exhibited lax

type; most of them were yellow in glume color except IC534787 which was brown; and, five (IC82198, IC534787, IC82197, IC534777, IC532847, and 35069) were pubescent and the other five lacked glume hairiness. Glume hairiness is another important trait of breeding value as it influences reaction of plant, particularly spike portion, to fungal infection such as powdery mildew.

In wheat breeding, thousand seed weight is one of the important parameters in that it increases seed germination percent, seedling emergence, tillering capacity, spike and yield (Sabaghnia *et al.*, 2014). The results of this study will support efforts of conservation and utilization of Indian wheat landraces in wheat genetic improvement programmes as these high kernel weight genotypes of Indian bread wheat, which are already adapted to local condition due to continuous cultivation and selection for long time by farmers, can be gainfully used by breeders and biotechnologists as parental lines in breeding for increasing grain weight, both for hybridization and selection, as well as in developing mapping population to tag genomic regions for high seed weight.

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