Genetic evaluation of newly synthesized CMS based wheat hybrids for agromorphological traits

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ABSTRACT: A set of thirty national pool hybrids along with six checks were evaluated during *Rabi* 2016-17 at Seed Breeding Farm, JNKVV, Jabalpur to study the genetic variability and association analyses for fifteen traits. Wide range of variation for all the traits was observed, indicating the presence of adequate genetic variability in the material. High phenotypic and genotypic coefficient of variation was observed for harvest index and grain yield/plant, while moderate for ear weight, number of ears/plant, number of tillers/plant, peduncle length, 1000 grain weight, biological yield/plant and number of spikelets/ear. High heritability coupled with high genetic advance as percent of mean was exhibited by harvest index, grain yield/plant, number of ears/plant, number of tillers/plant, peduncle length, ear weight, 1000 grain weight, biological yield/plant, number of spikelets/spike and canopy temperature. Grain yield/plant revealed significant positive association with ear weight, number of ears/plant, number of spikelets/spike, harvest index and 1000 grain weight. Harvest index imposed highest direct positive effect on grain yield/plant, followed by biological yield/plant, days to heading and plant height. Hybrids PHW 16-6, PHW 16-29, PHW 16-1, PHW 16-26 and PHW 16-10 were found superior over the best check HD 2967 on the basis of grain yield/plant. The result of present study could be exploited in planning and execution of future breeding programme in hybrid wheat.

Key words: Genetic variability, heritability, genetic advance, association analyses

Wheat (*Triticum aestivum* L.) is the world's second most important staple food crop next to the rice for more than 35 percent of world's population. It produces about 20% food resources of the world with high productivity and occupying a prominent position. India is the second largest wheat producer in the world with a production level of 107.18 million tonnes. Madhya Pradesh is the second largest producer state of wheat with area, production and productivity of 6.03 million hectare, 18.58 million tonnes and 3083 kg/ha, respectively(Anonymous, 2019-20).

High yield and better quality are the prime object of the breeder. To meet out the demand of wheat by 2020 AD, hybrid development is an innovative alternative approach. Serious interest in hybrid wheat was started in the 1960s accompanied by public research, but these efforts were not crowned with the successful establishment of wheat hybrids in the global wheat market (Longin *et al.*, 2012). The exploitation of heterosis in wheat appears more promising in view of an ever-growing world population and climate change. Consequently, hybrid wheat is again attracting strong attention in the wheat breeding community as it has great potential to boost grain yield.

For improvement of yield, the knowledge of genetic variability and heritability is of great importance for the breeders. However, these traits are influenced by the genotype and environment because of the polygenic nature of the characteristics involved (Gaines *et al.*, 1996;

Novoselovic et al., 2004). For the establishment of breeding programs and formation of selection indexes, heritability is widely used. The most effective condition for selection is high heritability coupled with high estimates of genetic advance. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. Phenotypic and genotypic coefficients of variations, heritability and genetic advance have been used to assess the magnitude of variance in hybrid wheat genotypes. Similarly, an attempt was also made to analyze grain yield and its attributing traits of wheat by correlation and path coefficient analyses. The present study is therefore, aimed at assessing genetic variation, heritability, genetic advance and association of yield attributing traits in recently developed bread wheat hybrids.

MATERIALS AND METHODS

Experimental material comprising 30 cytoplasmic male sterility (CMS) based wheat hybrids (received from Genetics Division, IARI, New Delhi) along with six checks were planted in randomized completely block design with three replications at Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur during *Rabi* season, 2016-17. The recommended agronomic practices were followed to raise the healthy

crop. Five plants were randomly selected from each genotype per replication for recording the agronomic data. Observations were recorded on days to 50%heading, days to maturity, plant height (cm), peduncle length (cm), ear length (cm), ear weight, number of tillers/plant, number of ear/plant, number of spikelet/ear, biological yield/plant (g), harvest index (%), 1000-grain weight (g) chlorophyll content (SPAD Units), canopy temperature (°C) and grain yield/plant (g). The data obtained were subjected to the biometrical analysis. The genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), broad sense heritability (h² (bs) %) and genetic advance in percent mean (GAPM) were estimated by the formula suggested by Singh and Chaudhary (1985). The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973). The heritability was categorized as suggested by Robinson et al. (1949) and genetic advance by adopting the method of Johnson et al. (1955). Correlation coefficient and path coefficient was worked out as method suggested by Milleret al. (1958) and Dewey and Lu (1959), respectively.

RESULTS AND DISCUSSION

Highly significant mean squares, due to genotypes for all the traits under study in thirty six wheat hybrids revealed the presence of enough genetic variability in the material was presented in (Table 1). The present result implied that this population of wheat genotypes would respond positively to selection. The wide range of variation observed in all the characters offer scope of selection for development of desirable type of wheat hybrids. The presence of large amount of variability might be due to diverse source of material as well as environmental influence affecting the phenotypes. Similar findings in wheat were also reported by Tiwari et al. (2017), Sharaan et al. (2017), Neeru et al. (2017) and Getachew et al. (2017).

The results pertaining to mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as percent of mean (GAM) for all the traits studied are furnished in (Table 2).

There will be better scope of improvement through selection for traits having high value of genotypic coefficient of variation (GCV). The GCV and PCV provide information about relative amount of variation in different traits. A perusal of coefficient of variation revealed that the higher estimate of GCV and PCV was observed in case of harvest index (24.88% and 24.98%) and grain yield/plant (21.18% and 21.28%). Similar findings have been also reported by Phougat et al. (2017). Moderate estimate of GCV and PCV were recorded for number of ears/plant (18.73% & 18.97%), ear weight (18.27% & 19.25), number of tillers/plant (17.84 % & 18.08 %), peduncle length (17.64% & 17.79), 1000 grain weight (14.85 % & 14.87 %), biological yield/plant (14.23 % & 14.24 %) and number of spikelets/spike (11.08 % & 11.16%). Report of Tiwari et al. (2017) for peduncle length, grain yield/plant, ear weight and Mecha et al. (2016) for test weight support our results for GCV and PCV in wheat population. While, other traits viz., plant height (4.21% and 4.23 %), days to maturity (6.26 % and 6.39%) and days to 50 % heading (6.50 % and 7.02 %) exhibited low phenotypic and genotypic coefficient of variation. This indicated low variability for such traits among genotypes. Kumar et al. (2003) revealed low PCV and GCV for days to 50% heading and days to maturity.

The proportion of genetic variability which is transmitted from parents to

of yield traits from the analysis of variance in wheat hybrids	Mean Sums of Squares
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Source	df						Mea	Mean Sums of Squares	Squares							
ofvariation		DFF	DM	Ηd	PL	EL	EW	NTPP	NEPP	NSPE	TGW	BYPP	IH	GYPP	СС	CT
Replication	2	10.39	10.39 10.03 0.22	0.22	0.74	0.13	0.08	0.35	0.25	0.45	0.29	8.21	4.15	4.71	0.04	0.96
Treatment	35	59.14**	59.14** 159.65** 52.14**	52.14**	2	1.77^{**}	1.13^{**}	4.53**	4.57**	9.46**	143.12**	152.63**	437.44**)4**	26.40**	8.51**
Error	70	3.05	2.26	0.15	0.12	0.04	0.04	0.04	0.03	0.04	0.08	0.09	1.18	0.25	0.05	0.06
C.D5%		2.85	2.45	0.63	0.56	0.36	0.33	0.33	0.32	0.32	0.48	0.51	1.77	0.82	0.36	0.4
C.D1%		3.78	3.25	0.84	0.76	0.49	0.43	0.43	0.43	0.43	0.64	0.68	0.64 0.68 2.35 1.	1.08	0.47	0.53
DH = Days to 50% heading, DM = Days to maturity, PH = Plant height (cm), PL = Peduncle length (cm), EL = Ear length (cm), EW = Ear weight, NTPP = Number of tillers/plant, NTPP = Number of ti	0% head	ing, DM=I	Days to ma $DE = M_{11122}$	turity, PH	= Plant hei	ght(cm),]	PL = Pedu	ncle length	n (cm), EL	= Ear leng	th(cm), E	W = Ear W(sight, NTF	P = Numb	oer of tille	rs/plant, - Groin
yield/plant (g), $CC = Chlorophyll content (SPAD Units), CT = Canopy temperature (°C)$	CC = Ch	lorophyll cc	nuent (SP/	AD Units)	, CT = Can	opy tempe	trature (°C	ן אכוציוו וצ)	- 111 G ()	-DIUIUSIV	ii yiciu/hi	allt (<i>B)</i> , 111			1110(0	

offspring is reflected by heritability. In this context, the high estimates of heritability were recorded for biological yield per plant (99.8%), 1000 grain weight (99.8%), chlorophyll content (99.4%), harvest index (99.2%), plant height (99.1%), grain yield/plant (99.0%), number of spikelets/spike (98.6%), peduncle length (98.4%), canopy temperature (97.9%), number of tillers/plant, number of ears/plant (97.4%), days to maturity (95.9%), ear length (91.8%), ear weight (90.1%) and days to 50% heading (86.0%). Rahman et al. (2016) and Rajshree and Singh (2018) also reported high heritability values for canopy temperature, spike length, 1000 grain weight, grain yield/plot and harvest index which in fact demonstrated the presence of additive genes effect indicating effectiveness of selection for the improvement of these traits. Selection will be more effective for those traits having high heritability, because these traits are governed predominantly by additive gene action and could be improved through individual plant selection.

High heritability coupled with high genetic advance as percent mean were observed for harvest index, grain yield/plant, number of ears/plant, number of tillers/plant, peduncle length, ear weight, 1000 grain weight, biological yield/plant, number of spikelets/spike and canopy temperature. Similar results were also reported by Ghallab et al. (2016) for 1000 grain weight and Rajshree and Singh (2018) for number of tillers/plant and harvest index. It indicated predominance of additive gene action. Therefore, direct selection for such trait would be effective. The high heritability coupled with moderate genetic advance was recorded for chlorophyll content, ear length, days to maturity and days to 50% heading. Whereas, high heritability coupled with low genetic advance was observed for plant height. High heritability with high or moderate genetic advance indicated

predominance of additive gene action for controlling these characters. Thus, simple selection can be practiced to improve these traits.

Correlation coefficient analysis

Yield is a complex quantitative trait governed by large number of genes and highly influenced by environment. Hence, the selection of superior genotypes based on yield, as such is not effective. For a rational approach towards improvement of yield, selection has to be made for the components of yield. Association of yield components and yield thus assumes special importance on the basis of indirect selection. Correlation coefficient at phenotypic level is presented in the (Table 3). Significant and positive correlations were observed between days to 50% heading and days to maturity. Similar, findings were observed by Dharmendra and Singh (2015) for days to maturity. Days to maturity showed highly significant positive correlation with number of tillers/ plant and plant height and significant positive with ear length.

Plant height showed highly significant positive correlation with days to maturity and significant positive with number of ears/plant, whereas, number of spikelets/spike had negative significant correlation with plant height. Number of tillers/plant showed highly significant positive association with days to maturity and days to 50% heading, while significant negative with 1000 grain weight. Similar findings were found by Chhibber and Jain (2014) and Dharmendra and Singh (2015). Number of spikelets/spike revealed highly significant positive association with grain yield/plant and ear length, whereas, negative significant with plant height. These findings corroborated the earlier findings of Baloch *et al.* (2013) and Dharmendra and Singh (2015). Number of

Table 2: Estimates of genetic parameters for 15 quantitative traits of 36 CMS based wheat hybrids

Traits	Range	Mean	GCV(%)	PCV (%)	h ² (b)(%)	Genetic advance (% of mean)
Days to 50% heading	58.7-75.7	66.45	6.50	7.02	86.00	12.43
Days to Maturity	102.3-129.7	115.65	6.26	6.39	95.9	12.63
Plant height (cm)	92.1-108.6	98.81	4.21	4.23	99.1	8.64
Peduncle length (cm)	9.2-20.6	15.56	17.64	17.79	98.4	36.06
Ear length (cm)	9.0-12.0	10.45	7.25	7.57	91.8	14.32
Ear weight (cm)	2.27-4.27	3.31	18.27	19.25	90.1	35.72
Number of tillers/plant	4.70-9.56	6.85	17.84	18.08	97.4	36.27
Number of ears /plant	4.46-9.33	6.56	18.73	18.97	97.4	38.08
Number of spikelets/ spike	12.93-19.16	15.99	11.08	11.16	98.6	22.66
1000 grain weight	36.72-65.40	46.48	14.85	14.87	99.8	30.57
Biological yield/plant (g)	37.27-63.25	50.11	14.23	14.24	99.8	29.28
Harvest Index (%)	24.76-82.79	48.46	24.88	24.98	99.2	51.05
Grain yield/plant (g)	12.96-32.94	23.89	21.18	21.28	99.0	43.41
Chlorophyll content (SPAD Units)	37.36-47.45	42.02	7.05	7.07	99.4	14.49
Canopy temperature (°C)	16.60-23.13	20.03	8.38	8.47	97.9	17.08

DH DM	СС	CT	ΡΗ	PL	EL	EW	NTPP	NEPP	NSPE	BYPP	IH	TGW	GYPP
1.000 0.869 **	0.019	-0.136	0.087		0.144	0.084	0.291^{**}	0.159	-0.012	0.185	-0.072	-0.068	-0.022
1.000	0.059	-0.108	0.267 **		0.192 *	-0.139	0.353 * *	0.165	-0.042	0.144	-0.067	0.032	0.015
	1.000	-0.045	-0.132		0.013	-0.170	-0.101	0.005	0.089	-0.028	0.061	-0.004	0.060
		1.000	0.177	-0.071	0.019	0.233 *	0.048	-0.066	-0.029	0.294 * *	0.066	-0.161	-0.262*
			1.000		0.172	0.083	0.180	0.227 *	-0.287 * *	- 0.106	0.133	0.068	0.084
					-0.313 * *	0.079	0.043	0.209 *	-0.180	-0.195 *	0.096	-0.178	-0.018
					1.000	0.222 *	-0.104	0.148	0.033	0.081	-0.119	-0.006	0.099
						1.000	-0.385 * *	0.085	-0.109	0.170 *	0.095	-0.023	0.214*
							1.000	0.096	0.078	-0.003	-0.055	-0.192*	0.109
								1.000	0.101	0.352 * *	0.001	0.0067	0.231^{*}
									1.000	0.089	-0.059	-0.102	0.217^{**}
										1.000	-0.472* *	-0.045	0.123
											1.000	-0.271 **	0.807^{**}
												1.000	0.340 **
													1.000
,** Indicates level of significance at 5% and 1% respectively ML - Durate 5000 kinedia: DM - Durate and the respectively	ce at 5% a: - Dans 40	nd 1% rest	pectively CC - Chi	too Ilvelace		I Inite?	- E		(J0) cm.4	tuola – Ila	42.24	1	DI – D
*, ** Indicates level of significance at 5% and 1% r DH = Davs to 50% heading. DM = Davs to matur	ce at 5% a: = Davs to	nd 1% resp maturity.	pectively CC = Chlo	prophyll con	ntent (S	[A	PAD Units).	PAD Units). CT = Canor	PAD Units). CT = Canony tempera	$PADIInits) CT = Canony temperature (^{0}C)$	PA D I Jnits) $CT = Canony temperature (^{0}C)$ PH = Plant	PAD1Inits) CT = Canony temperature (°C) PH = Plant height (cm	espectively iiv. CC = Chloronhvll content (SPA D I Inits). CT = Canony temperature (°C). PH = Plant height (cm). PI = Peduncle lenoth

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DT – Days to 20% nearing, DM – Days to maturity, CC – Critorophryn content (SFAD Onlis), CI – Cattopy temperature (C), FT – Frant neigin (cm), FL – Feduricie rengut (cm), EL = Ear length (cm), EW = Ear weight, NTPP = Number of tillers/plant, NEPP = Number of ear/plant, NSPE = Number of spikelet/ear, BYPP=Biological yield/plant(g), HI = Harvest index (%), TGW = 1000-grain weight (g), GYPP = Grain yield/plant (g)

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	ΡH	DM	сc	CT	Ηd	PL	EL	EW	NTPP	NEPP	NSPE	BYPP	IH	TGW	GYPP
ΗΠ	0.2132	0.2019	0.0059	-0.0299	0.0201	0.0324	0.0352	-0.0216	0.0691	0.0362	-0.0054	0.0429	-0.0165	-0.0152	0.0251
DM	-0.2291	-0.2420	-0.0154	0.0269	-0.0666	-0.0084	-0.0505	0.0357	-0.0895	-0.0431	0.0095	-0.0354	0.0164	-0.0077	-0.0148
CC	0.0007	0.0016	0.0247	-0.0011	-0.0033	-0.0089	0.0002	-0.0044	-0.0025	0.0001	0.0022	-0.0007	0.0015	-0.0001	0.0596
CT	-0.0011	-0.0009	-0.0004	0.0080	0.0014	-0.0006	0.0002	0.0020	0.0004	-0.0005	-0.0003	0.0024	0.0005	-0.0013	0.2664
Ηd	0.0064	0.0187	-0.0090	0.0122	0.0680	0.0056	0.0125	0.0060	0.0123	0.0158	-0.0196	-0.0072	0.0091	0.0047	0.0842
PL	0.0040	0.0009	-0.0094	-0.0019	0.0021	0.0261	-0.0086	0.0021	0.0011	-0.0054	-0.0048	-0.0051	0.0026	-0.0047	0.0191
EL	-0.0013	-0.0016	0.0000	-0.0002	-0.0014	0.0025	-0.0077	-0.0017	0.0008	-0.0011	-0.0003	-0.0006	0.0010	0.0000	-0.1061
EW	0.0045	0.0065	0.0078	-0.0109	-0.0039	-0.0036	-0.0100	-0.0440	0.0182	-0.0037	0.0051	-0.0079	-0.0045	0.0010	0.2287
NTPP	-0.0193	-0.0221	0.0061	-0.0029	-0.0108	-0.0026	0.0065	0.0247	-0.0596	-0.0060	-0.0047	0.0002	0.0035	0.0116	-0.1138
NEPP	0.0016	0.0017	0.0000	-0.0006	0.0022	-0.0019	0.0014	0.0008	0.0009	0.0093	0.0010	0.0033	0.0000	0.0001	0.2331
NSPE	-0.0002	-0.0003	0.0007	-0.0003	-0.0023	-0.0015	0.0003	-0.0009	0.0006	0.0008	0.0080	0.0007	-0.0005	-0.0008	-0.0198
вүрр	0.1310	0.0953	-0.0185	0.1943	-0.0691	-0.1282	0.0548	0.1176	-0.0019	0.2325	0.0592	0.6507	-0.3075	-0.0291	0.1235
IH	-0.0852	-0.0744	0.0670	0.0725	0.1478	0.1081	-0.1405	0.1125	-0.0639	-0.0018	-0.0698	-0.5196	1.0996	-0.2988	0.8055
TGW	0.0001	0.0000	0.0000	0.0002	-0.0001	0.0002	0.0000	0.0000	0.0002	0.0000	0.0001	0.0000	0.0003	-0.0010	0.3413
DH = Days (cm), EL = _ HI = Harve	DH = Days to 50% heading, DM = Days to maturit (cm), EL = Ear length (cm), EW = Ear weight, NTP HI = Harvest index (%), TGW = 1000-grain weight	nding, DM cm), EW = , TGW = 1(= Days to 1 Ear weigh 000-grain v	maturity, CC t, NTPP=N weight (g), C	Vum VyP	Chlorophyll content ber of tillers/plant, N P = Grain yield/plan	ent (SPAD tt, NEPP=] lant (g)	Units), CT Number of	[= Canopy ?ear/plant, l	/ temperature NSPE = Num	(°C), ber of	PH = Plant he spikelet/ear, l	ieight (cm), BYPP=Biα	, PL = Pedu ological yie	PL = Peduncle length logical yield/plant(g),

Table 4: Path coefficient analysis (genotypic) for yield and its component traits in 36 wheat hybrids

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Trait	Selection criteria	Number of superior accession	Name of the superior accession
Days to maturity	<105 days	3	PHW 16-30, PHW 16-7,
	-		PHW 16-29
Plant height (cm)	<95 cm	6	HD 3086, PHW16-26,
			PHW 16-23, PHW 16-29,
			PHW 16-12, PHW 16-6
Number of tillers/plant	>8	5	PHW 16-30, GW 366,
			PHW 16-18, PHW 16-28,
			HD 2932
Number of spikelets/spike	>18	5	PHW 16-13, PHW 16-23,
			PHW 16-4, PHW 16-10,
			PHW 16-6
Ear length (cm)	>11.5 cm	4	PHW 16-8, HD 2967,
			PHW 16-22, PHW 16-13
Ear weight (cm)	>4 g	5	PHW 16-26, PHW 16-13,
			PHW 16-7, PHW 16-15,
			PHW 16-1
Number of ears/plant	>8	5	HD 2967, PHW 16-15,
			PHW 16-18, PHW 16-9,
			HD 2932
1000-grain weight (g)	>55 g	4	PHW 16-21, PHW 16-23,
			PHW 16-25, PHW 16-9
Biological yield/plant (g)	>60 g	5	HD 2932, GW 366, PHW
			16-16, PHW 16-8, PHW
			16-26
Harvest index (%)	>60 %	6	PHW 16-29, PHW 16-18,
			PHW 16-1, PHW 16-17,
			PHW 16-6, PHW 16-10
Grain yield/plant (g)	>30 g	5	PHW 16-26, PHW 16-29,
			PHW 16-1, PHW 16-6,
			PHW 16-10

Table 5: Promising accessions for various traits in 36 hybrid wheat

ears/plant showed significant positive association with biological yield/plant, plant height and grain yield/plant.

Biological yield showed significant positive association with number of ears/plant, canopy temperature, ear weight, whereas, significant negative with harvest index and peduncle length. Similar findings were found by Chhibber and Jain (2014) and Khan et al. (2015) for biological yield. Harvest index reported highly significant negative association with number of grains/plant, biological yield/plant and 1000 grain weight. Grain yield/plant revealed significant positive association with ear weight, number of ears/plant, number of spikelets/spike, harvest index and 1000 grain weight. Significant positive correlation of different traits with grain yield/plant have also been reported by Dharmendra and Singh (2015) and Khan et al.(2015). Selection for these characters can directly be followed for immediate vield improvement.

Path coefficient analysis is also known as standardized partial regression coefficient which is unit less. The

correlation coefficient between traits exhibits the relationship existing between pairs of traits. But, a dependent character is an interaction of product of many mutually associated component characters and change in any one component will disturb whole network of cause and effect system. Path coefficient analysis was carried out using coefficient of all the traits with grain yield per plant and represented in (Table 4).

Maximum positive direct effect on grain yield/-plant was contributed by harvest index (1.0996), followed by biological yield/plant (0.6507), days to 50% heading (0.2132) and plant height (0.0680). This means that a slight increase in one of the above traits may directly contribute to grain yield. Similar results were observed by Phougat *et al.* (2017), Singh *et al.* (2012) for harvest index and biological yield/plant; Majumder *et al.* (2008) for harvest index; Ali and Abdulla (2016) for biological yield/plant and Zare *et al.* (2017) for harvest index.

On the other hand, the maximum negative direct effect was exhibited by days to maturity (-0.2420), followed by

number of tillers/plant (-0.0596) and ear weight (-0.0440) The rest of the traits showed moderate to low positive or negative direct effect on grain yield per plant. Majority of indirect effects of various independent traits *via*. other traits were extremely low of either signs. There were only few characters had higher to moderate positive indirect effects. Harvest index exerted high indirect effect on grain yield/plant *via*. plant height, peduncle length, ear weight and biological yield/plant *via*. number of ear/plant; ear weight, plant height, canopy temperature. Hence these indirect effects should also be kept in the mind while selection for better yield.

On the basis of per se performance promising wheat hybrids were identified for phenological and yield attributing traits and are presented in (Table 5). The selection criterion was made in such a way that minimum numbers of genotypes were identified/ selected for each of the studied traits.

For days to maturity (<105 days) three hybrids were identified (PHW 16- 30, PHW 16-7, PHW 16-29); for plant height (< 95 cm) six hybrids (HD 3086, PHW 16-26, PHW 16-23, PHW 16-29, PHW 16-12, PHW 16-6); for number of tillers/plant (> 8) five hybrids (PHW 16-30, GW 366, PHW 16-18, PHW 16-28, HD 2932); for number of spikelets/ear (>18) five hybrids (PHW 16-13, PHW 16-23, PHW 16-4, PHW 16-10, PHW 16-6); for ear length (>11.5 cm) four hybrids (PHW 16-8, HD 2967, PHW 16-22, PHW 16-13); for ear weight (>4) five hybrids (PHW 16-26, PHW 16-13, PHW 16-7, PHW 16-15, PHW 16-1); for number of ears/ plant (>8) five hybrids (HD 2967, PHW 16-15, PHW 16-18, PHW 16-9, HD 2932); for 1000-grain weight (>55 g) four hybrids (PHW 16-21, PHW 16-23, PHW 16-25, PHW 16-9); for biological yield/ plant (>60) five hybrids (HD 2932, GW 366, PHW 16-16, PHW 16-8, PHW 16-26); for harvest index (>60%) six hybrids (PHW 16-29, PHW 16-18, PHW 16-1, PHW 16-17, PHW 16-6, PHW 16-10) and for grain yield/ plant (>30 g) five hybrids were identified (PHW 16-26, PHW 16-29, PHW 16-1, PHW 16-6, PHW 16-10). These hybrids may be utilized further in wheat breeding programmes to achieve better hybrids. Out of six checks, hybrids PHW 16-6, PHW 16-29, PHW 16-1, PHW 16-26 and PHW 16-10 were found as most promising over best check HD 2967 (29.0g) in terms of grain yield/ plant. The promising hybrids from this investigation may be used as a donor in hybrid wheat programme for the transfer of genes.

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