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Genetic variability analysis for pseudo black chaff expression and yield traits among wheat (*Triticum aestivum* L.) genotypes

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Abstract

Pseudo black chaff is associated with the presence of the stem rust resistance gene *Sr2* in wheat. This trait is used as morphological marker for stem rust resistance. Genetic variability and correlation studies between PBC and other yield traits are important for assisting selection for stem rust resistance gene. Genetic estimates like heritability and genetic advance revealed that plant height has highest heritability (broad sense) and biomass has lowest. SPAD1 was found significantly negative correlated with PBC whereas Days to heading has positive significant correlation.

Keywords: PBC, SPAD, Days to heading, wheat, heritability

Introduction

Wheat (*Triticum aestivum* L.) is considered as king of cereals and it provides foods to 36% of the global population contributing 20% of the food calories. It attains a unique position as it is used widely for the preparation of a wide range of food stuffs. Stem rust is one of the deadly diseases of wheat crop affecting other host range also and severely reducing yield. *Puccinia graminis* f.sp. *tritici* causes black/stem rust of wheat and the pathogen evolves in due course of time and proves virulent against prevailing resistance genes. Pseudo-black chaff or melanism or false black chaff is morphological trait used for selection of stem rust resistance gene *Sr2* gene as it has been found to be linked with it and has partial dominant nature. It results from a deposition of melanoid pigments and is completely associated with the presence of the stem rust resistance gene *Sr2* (Sheen *et al.*, 1968; Hare and McIntosh, 1979; Kota *et al.*, 2006) [8, 3, 5]. Symptoms include brown to black discolouration of the glume extending from slight longitudinal marks to large black areas covering most of the glume surface. High level of PBC expression (especially on glumes) also thought to be potent enough to reduce crop yield and makes it undesirable for farmers (Hare and McIntosh, 1979; Sheen *et al.*, 1968) [3, 8]. Presence of genetic variability for this trait is therefore favoured for screening stem rust resistance as it reveals about the presence of variation in their genetic constitution and provides the basis of effective selection. Genetic variability can be partitioned into heritable and non-heritable components with the aid of genetic parameters such as variance, genotypic coefficient of variation, heritability and genetic advance, which serve as a basis for selection of some outstanding genotypes from existing ones. Correlation of PBC with other yield attributing traits is important to carry out as it gives information on positive or negative association of yield traits with this morphological marker.

Material and Methods

The present was carried out at the Agricultural Research Farm, Institute of Agricultural Sciences, B.H.U., Varanasi during Rabi season 2016-17. The experiment was conducted in a Randomized Complete Block Design with 30 elite lines (Appendix.1) of wheat in three replications on protected with fungicide (Tebuconazole formulation grade@1g/ liter) and non-protected conditions respectively. Observations were recorded for 13 characters, *viz.*, days to heading, plant height, Number of tillers per meter, glaucousness index, SPAD1, SPAD2, green seeker1, green seeker2, biomass, plot yield, 1000-grain weight, area under disease progress curve (AUDPC) and pseudo-black chaff (PBC). Observations on 3 randomly selected plants from each genotype were collected and average data was taken into consideration.

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Results and Discussion

Variability studies for pseudo-black chaff (PBC) and other yield attributing traits were undertaken with 30 wheat lines

the mean performance and range of all the 30 genotypes for all characters under study have been presented in Table 1 and 2 for protected and inoculated condition.

Table 1: Summary of the observation on 11 traits under protected conditions in 30 wheat genotypes.

	DH	PH	NT	G. I.	Spad1	Spad2	GS1	GS2	Biomass	PY	TGW
Min	63	70	101.33	1.6667	43.5	39	0.45667	0.31	258.33	102.33	35.173
Max	76	108	248.67	4.3333	48.833	45.767	0.64	0.44667	583	242	58.273
Mean	69.45831	83.67716	153.7916	3.437503	46.25938	42.90934	0.525521	0.361563	457.7191	191.6466	48.30303

DH=Days of heading, PH=Plant height, NT=Number of tillers per meter, G. I.=Glaucousness index, Spad=SPAD reading, GS=Green seeker, PY=Plot yield, TGW=1000-grain weight, AUDPC= Area under Disease Progress Curve, PBC= Pseudo black chaff

Table 2: Summary of the observation on 11 traits under non-protected conditions in 30 wheat genotypes.

	DH	PH	NT	G. I.	Spad1	Spad2	GS1	GS2	Biomass	PY	TGW
Min	63.333	71	88.67	2	41.8	35.533	0.43667	0.29333	336.3	150	39.43
Max	75.667	109.667	241.33	4.6667	49.567	44.167	0.66	0.48667	1102.7	288.33	64.157
Mean	68.83338	84.80209	153.7281	3.395841	45.20213	40.69372	0.539375	0.380209	561.2313	213.8125	48.67163

DH=Days of heading, PH=Plant height, NT=Number of tillers per meter, G. I.=Glaucousness index, Spad=SPAD reading, GS=Green seeker, PY=Plot yield, TGW=1000-grain weight, AUDPC= Area Under Disease Progress Curve, PBC= Pseudo black chaff

Variability

The analysis of variance (as presented in Table 3) showed significant differences for all 13 observed traits among 30 genotypes. It indicates that there is a considerable inherent genetic difference among these traits of the genotypes. The experiment was conducted in 2 conditions *viz.*, protected with fungicide and non-protected. Conditions were found

significantly varied for only 8 traits *i.e.*, SPAD1, SPAD2, GS2, biomass, plot yield, 1000-grain weight, AUDPC and pseudo-black chaff (PBC). Entry \times Condition was also showed significant variation for only 6 traits *viz.*, plant height, biomass, plot yield, 1000-grain weight, AUDPC and pseudo black chaff (PBC). These reports were supported by findings of Verma *et al.*, (2013)^[6], Kumar *et al.*, (2014)^[6].

Table 3: Analysis of variance for 13 traits among 30 genotypes planted in 2 conditions in wheat.

SoV	Dof	DH	PH	NT	G. I.	Spad1	Spad2	GS1	GS2	Biomass	PY	TGW	AUDPC	PBC
Entry	29	74.58**	529.34**	5312.14**	1.93**	13.58**	13.59**	0.012**	0.0077**	41851.4*	5566.9**	146.09**	26418.4**	23.69**
Cond	1	20	55.55	16.2	0.8	54.01**	216.7**	0.0098	0.0164*	368471**	18931.8**	0.136**	5137976**	43.02**
Rep	2	20.35	10.42	2192.03*	1.4*	60.7**	8.87	0.00052	0.011*	108598	6905.21*	7.55	38093.7**	0.21
Ent*Cond	29	5.48	51.01**	607.22	0.52	6.33	5.43	0.0037	0.0029	41702.8*	2513.29*	47.73*	26418.4**	4.78**
Error	118	8.02	22.93	501.8	0.337	5.32	5.59	0.0027	0.0027	38942	2026.87	65.18	5659.95	2.29
CV		4.09	5.7	14.67	16.76	5.04	5.65	9.81	14.16	9.04	12.15	6.66	14.52	16.71
Mean		69.12	83.87	152.67	3.46	45.71	41.84	0.53	0.37	505.43	203.2	48.43	168.95	1.56

DH=Days of heading, PH=Plant height, NT=Number of tillers per meter, G. I.=Glaucousness Index, Spad=SPAD reading, GS=Green seek er, PY=Plot yield, TGW=1000-grain weight, AUDPC=Area under Disease Progress Curve, PBC=Pseudo black chaff

Heritability and genetic advance

The estimates of heritability (broad sense) and genetic advance (as presented in Table 4) revealed that the estimates of heritability (broad sense) possessed a very high range among different traits under study. Highest heritability was observed for plant height (0.90) whereas the lowest for biomass (0.05), SPAD1 (0.50), SPAD2 (0.52). The higher estimates of broad sense heritability were also found for days to heading (0.89) and number of tillers per meter (0.86), whereas, the relatively higher magnitude of heritability was observed for green seeker1 (0.66) (Table 4 and fig 1). The highest estimate of genetic advance was calculated for number of tillers per meter (93.76) and plot yield (62.86), in the contrast, a lowest estimates were found for green seeker2 (0.08), green seeker1 (0.11), SPAD1 (2.97) and SPAD2

(2.98). A relatively higher magnitude of genetic advance was also observed for plant height (31.03) and a relatively lower magnitude was found for 1000-kernel weight (9.61). The moderate estimates of genetic advance were found in case of days to heading (11.2) and biomass (17.66). Kabir *et al.*, (2015) reported high broad sense heritability and genetic advance for most of the traits. Abinasa and Bultosa (2011)^[1] revealed high genetic advance coupled with high heritability for plant height, whereas, the minimum for number of spikelets/spike. Singh *et al.*, (2013)^[9] reported that high estimates (more than 80%) of broad sense heritability were recorded for tillers per plant, plant height, spike length, grains per spike, grain yield and 1000-grain weight (Table 4 and fig 2).

Table 4: Estimates of heritability (broad sense) and genetic advance expressed as percent of mean for 12 characters in wheat

	DH	PH	NT	Spad1	Spad2	GS1	GS2	Biomass	PY	TGW	AUDPC	PBC
Heritability	0.89	0.90	0.86	0.50	0.52	0.66	0.57	0.05	0.53	0.54	0.42	0.79
Genetic Advance under Selection	11.22	31.03	93.76	2.97	2.98	0.11	0.08	17.66	62.86	9.61	136.51	6.01

DH=Days of heading, PH=Plant height, NT=Number of tillers per meter, G. I.=Glaucousness index, Spad=SPAD reading, GS=Green seeker, PY=Plot yield, TGW=1000-grain weight, AUDPC= Area under Disease Progress Curve, PBC=Pseudo black chaff

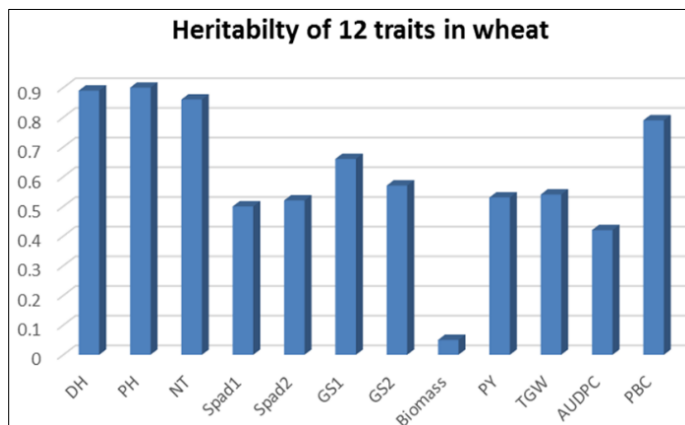


Fig 1: Study of heritability of 12 characters in wheat

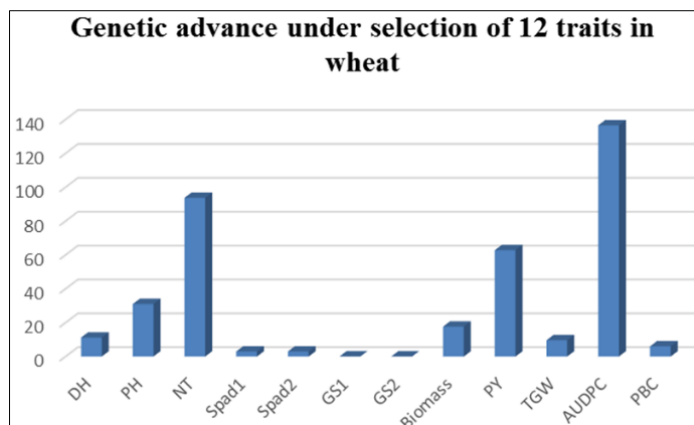


Fig 2: Study of genetic advance under selection of 12 characters in wheat

Correlation analysis

The phenotypic correlation coefficients were worked out among all 12 characters. Table 5 revealed that the days to heading was found significantly and positively correlated with green seeker (0.397), plot yield (0.389), pseudo-black chaff (0.389) and a highly significant negative correlation was found with 1000-grain weight (-0.487). The number of tillers per meter possessed a positive significant correlation with green seeker1 (0.438), green seeker2 (0.393) and a highly positive significant correlation with plot yield (0.477). The

green seeker1 value was highly significantly and positively correlated with green seeker 2 (0.691), plot yield (0.608) and a significant and positive correlation with AUDPC (0.438), in contrary, was significantly and negatively correlated with 1000-grain weight (-0.319). The green seeker2 also possessed a highly positive significant correlation with plot yield (0.746). Tsegaye *et al.*, (2012) ^[10], Cifci (2012) ^[2], Abderrahmane *et al.*, (2013) ^[1], Pandey *et al.*, (2013) ^[7] and Zeeshan *et al.*, (2014) ^[13] observed similar correlations between morphological traits

Table 5: Phenotypic correlation coefficients among 12 characters

	PH	NT	G. I.	Spad1	Spad2	GS1	GS2	Biomass	PY	TGW	AUDPC	PBC
DH	0.037	0.285	-0.206	-0.135	0.004	0.297	0.397*	0.151	0.389*	-0.487**	0.273	0.389*
PH		-0.066	-0.386*	0.062	-0.031	-0.184	0.075	0.203	0.045	0.242	-0.028	0.161
NT			0.136	0.150	0.120	0.438*	0.393*	-0.097	0.477**	-0.319	0.005	0.018
G. I.				0.085	-0.0185	-0.17271	-0.429**	-0.343	-0.231	0.031	-0.126	-0.237
Spad1					0.908**	0.247	0.254	0.095	0.115	-0.118	0.056	-0.433*
Spad2						0.347	0.337	0.068	0.179	-0.167	0.143	-0.302
GS1							0.691**	0.120	0.608**	-0.319*	0.438*	-0.363
GS2								0.254	0.746**	-0.357	0.139	-0.129
Biomass									0.293	0.055	0.197	-0.129
PY										-0.201	-0.366*	0.003
TGW											-0.345*	-0.152
AUDPC												-0.067
PBC												0.723

DH=Days of heading, PH=Plant height, NT=Number of tillers per meter, G. I.=Glaucousness index, Spad=SPAD reading, GS=Green seeker, PY=Plot yield, TGW=1000-grain weight, AUDPC=Area under Disease Progress Curve, PBC=Pseudo black chaff

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