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## Screening and identification of elite wheat genotype(s) for yield and yield contributing traits under biotic stress conditions

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### Abstract

Thirty-seven advanced segregating wheat populations (provided by BISA- CIMMYT) along with three check varieties were screened for yellow rust resistance and genetics of variability. Yellow rust screening revealed that four genotypes were immune to yellow rust, five were resistant and seventeen genotypes were moderately resistant. However, nine genotypes showed moderate susceptibility and only two genotypes were 100% susceptible to yellow rust. High PCV and GCV were observed for yellow rust resistance and moderate PCV and GCV were observed for the number of spikes per plant and grain yield per plant whereas low values for the rest of the traits. High heritability along with high GA were observed in yellow rust resistance, plant height, no of spikes and biological yield, which indicates these characters were governed by additive gene effect therefore efficient for selection. Correlation analysis revealed that a highly significant positive correlation of grain yield per plant was observed with number of spikes/plants, biological yield, and harvest index at both genotypic and phenotypic levels. Number of spikes per plant had the highest positive direct effect on grain yield per plant, followed by days to maturity, yellow rust scoring and thousand-grain weight.

**Keywords:** Biotic, breeding, stripe rust, resistance, stress, heritability, genetic advance, correlation, path analysis

### Introduction

Bread Wheat is one of the most widely grown cereal crops in the world, and a staple food for more than 2.5 billion people worldwide. Due to the increase in human population and climate change (global warming), there has been a challenge in improving *per se* production and grain quality. In addition, evolution of new races of disease pathogens (rusts, mildews, bunts, smuts etc.) and insect biotypes, crop damage has been increasing day by day. On average, approximately 20% of wheat production is lost due to disease and pests. Thus for sustainable wheat production and food security, we require disease resistant and high yielding wheat varieties. Therefore, the present study entitled “Screening and identification of elite wheat genotype(s) for yield and yield contributing traits under biotic stress conditions” was conducted with objectives to screen wheat genotypes for yellow rust resistance, estimate the genetic variability, correlation and path analysis. The selection of superior pedigree and better agronomy will result in enhancing wheat productivity. The presence of genetic variability in the gene pool provides an easy opportunity for identification of desirable phenotypes. As yield is a polygenic character controlled by several composite characters and their interaction with environment. The nature and degree of interrelationships between grain yield and its contributing components have been determined using correlation analysis. Understanding the link between yield and its component characters, as well as among the component characteristics themselves, can help enhance selection efficiency.

### Materials and Methods

The experiment material consisted of thirty-seven wheat cultivars procured from Borlaug Institute for South Asia, BISA- CIMMYT, Ludhiana. 3 local DBW 222, PBW 667 PBW 824 were also used for monitoring in randomized block design at the experimental area of the Department of Plant breeding and genetics, School of agriculture, Lovely Professional University, Jalandhar, Punjab during Nov 2021 to April 2022. The field was divided into three replications, each replication was divided into 40 plots of 0.6m \* 2m (i.e., 1.2m<sup>2</sup> under one plot), with the spacing of 20cm between the lines and 5cm with in plants. Sowing was done on

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4 lines by leaving 1 line empty. In each replication 37 elite genotypes along with 3 checks were screened. Recommended package of practices was followed for healthy crop raising. Yellow rust spores were sprayed as fine mist by using spray pump. Inoculum was collected from fresh infected leaves having uredia. The spraying was done at evening and morning time, as low temperature and high humidity is favorable for spore germination and disease spread. Rust epidemic was created by repeated spraying. Observations were recorded for days to 50% flowering, days to maturity, plant height, number of spikes, SPAD value, test weight/1000-grain weight, grain yield per plant, biological yield per plant and harvest index. The screening of genotypes for yellow rust resistance was done according to the modified Cobb's scale. The data obtained were subjected to evaluation of Analysis of variance of Randomized Block Design as given by (Panse and Sukhatme, 1962), Heritability in broad sense as given by (Hanson *et al.*, 1956), Genetic advance as given (Johnson *et al.*, 1955), Correlation coefficient analysis as given by (Miller *et al.*, 1958), Path coefficient analysis as given by (Dewey and Lu, (1959).

**Table 1:** Yellow rust scoring method

Infection type	Symptoms	Description
0	Leaves free from mycelium	Immune
1-3	Slight flecking of necrotic spot	Highly Resistant
3-5	Slight mycelium; very slight spore production	Resistant
5-7	Moderate development of mycelium: slight spore formation	Moderately resistant
7-9	Development of mycelium and spore formation	Moderately susceptible
>9	Abundant mycelium development and sporulation	Susceptible

## Results and Discussion

Screening for rust resistance, yield and yield attributing characters revealed that four genotypes namely (GS/2020-21/5028, GS/2020-21/1037, GS/2020-21/4020 and GS/2020-21/4021) were immune to yellow rust. Whereas five genotypes (GS/2020-21/8011, 5ELHT/2020-21/408, 5ELHT/2020-21/411, 5ELHT/2020-21/407 and GS/2020-21/4055) were resistant and seventeen genotypes were moderately resistant. However, nine genotypes showed moderate susceptibility and only two genotypes (GS/2020 1057, GS/2020-21/5012) were 100% susceptible for yellow rust. Two check varieties DBW 222, and PBW 667 were observed to be resistant and PBW 824 was moderately susceptible to yellow rust. Thereby it has been proposed to evaluate selected 9 (4 immune +5 resistant) genotypes further in replicated row trials (RRTs) along with checks for further investigation.

Out of nine (immune + resistant) genotypes, 5ELHT/2020-21/411 performed well for number of spikes/plants, biological yield, plant height along with grain yield per plant. The phenotype 5ELHT/2020-21/407 also performed well for thousand grain weight, biological yield, days to 50% flowering along with grain yield per plant. GS/2020-21/1037 performed well for biological yield and grain yield. GS/2020-21/4021 showed superiority for number of spikes along with grain yield. 5ELHT/2020-21/408 performed well for thousand grain weight, days to maturity and plant height. GS/2020-

21/8011 performed well for days to maturity and harvest index. GS/2020-21/5028 performed well for harvest index.

In addition, the genotypes which had high mean performance for various traits might also be used in wheat improvement programs as donor parent for desirable character. The genotypes that have taken less time to 50% flowering are 4ELHT/2020-21/728 (88 days), GS/2020-21/2040, GS/2020-21/9007CWYT/2020-21/608, CWYT/2020-21/607 (89days), 5ELHT/2020-21/407(90days) respectively. Similarly, genotypes (5ELHT/2020-21/408 and CWYT/2020-21/607 takes 120 days for grain maturity and GS/2020-21/2042, GS/2020-21/8011(121 days each). The four-genotype exhibited maximum chlorophyll content are GS/2020-21/1057 (52.43), GS/2020-21/3036 (51.60), 4ELHT/2020-21/706 (51.27), GS/2020-21/9007 (51.17), GS/2020-21/2040 (50.90) respectively. In addition, 5ELHT/2020-21/411 (70.94cm), 4ELHT/2020-21/706 (71.15cm), 5ELHT/2020-21/408 (71.65cm), 5ELHT/2020-21/403 (73.76cm), 4ELHT/2020-21/758 (73.87 cm) had relatively shorter plant height. Higher number of spikes/plant were observed for 5ELHT/2020-21/411 (5.5), GS/2020-21/4021 (5.3) also showed higher grain yield as discussed above. Biological yield per plant was maximum in 5ELHT/2020-21/411 (25.0 g), 4ELHT/2020-21/729(24.4g), GS/2020-21/1037 (24.2g), GS 2020-21/4051(24.2g), 5ELHT/2020-21/407 (24.1g).

Analysis of variance revealed presence of highly significant variability among treatments for days to 50% flowering, days to maturity, plant height, no of spikes, yellow rust resistance and biological yield and non-significant for replications. It indicates the presence of the consisted amount of genetic variability for these traits and selection was efficient for these traits. For grain yield per plant and thousand grain weight data is significant for both replications and treatments.

**Table 2:** Analysis of variance for various yield attributing characters

Characters	Mean sum of square		
	Replication	Treatment	Error
Days to 50% flowering	2.158	27.02**	0.7908
Days to maturity	1.6083	60.44**	0.967
Plant height (cm)	3.2823	118.98**	1.5375
SPAD value	165.176**	23.55	15.39
No. of spikes per plant	0.1510	0.9133**	0.590
Biological yield	1.0396	12.53**	0.970
Thousand grain weight	17.9164**	48.42**	2.658
Yellow rust scaling	0.2615	8.866**	0.753
Harvest index	0.2417**	0.001	0.002
Grain yield per plant (g)	109.65**	2.578**	1.04

High PCV and GCV were observed for yellow rust resistance and moderate PCV and GCV were observed for number of spikes per plant similar results was observed by Prasad *et al.*, 2021, Patilal *et al.*, 2021. In case of grain yield/plant moderate PCV value was observed indicating moderate phenotypic variance similar results was observed by Kumar *et al.*, 2018, Tsegaye *et al.*, 2012. However, low magnitude GCV and PCV was observed for days to 50% flowering, days to maturity, plant height, SPAD value, biological yield, thousand-grain weight and harvest index indicating low variation for these characters in material used for this experiment similar results was observed by Kumar *et al.*, 2018, Prasad *et al.*, 2021, Tsegaye *et al.*, 2012, Yadav *et al.*, 2014, Patilal *et al.*, 2021, Sharma *et al.*, 2018, Gerema *et al.*, 2020, Bankapur *et al.*, 2018, Wlodeet *et al.*, 2016.

**Table 3:** Genetic parameters of variation for seed yield and its components

Characters	Range			Coefficient of variation		Heritability	Genetic advance	Genetic advance as 1% of mean
	Min	Max	Mean	PCV	GCV			
Days to 50% flowering	17.4	25	20.8267	3.222	3.174	0.971	7.692	8.257
Days to maturity	54.4	71.8	65.2419	3.563	3.534	0.984	11.660	9.255
Plant height (cm)	70.94	93.48	81.1790	7.758	7.707	0.987	16.41	20.216
SPAD value	41.27	52.43	46.7883	5.988	3.525	0.346	2.563	5.477
No. of spikes per plant	5.1	5.5	4.3400	12.714	12.29%	0.935	1.363	31.395
Biological yield	17.4	25	20.82	9.816	9.428	0.923	4.979	23.907
Thousand grain weight	54.6	71.8	65.24	6.158	5.987	0.945	10.025	15.366
Yellow rust scaling	0	7.22	0.4109	44.683	42.743	0.915	4.153	107.941
Harvest index	0.36	0.46	0.56	6.106	2.841	-0.217	-0.014	-3.490
Grain yield per plant (g)	7	10.5	9.57	10.829	8.354	0.595	1.457	17.014

Correlation analysis revealed that highly significant positive correlation of grain yield per plant was observed with number of spikes/plants, biological yield and harvest index at both genotypic and phenotypic levels similar results was observed by Mandeep Kumar *et al.*, 2019, Dutamo *et al.*, 2015, S. Anubhav *et al.*, 2020, Gerema *et al.*, 2020. The 1000 grain weight had positive highly significant correlation with grain

yield/plant at the genotypic level but non-significant at the phenotypic level. The traits that showed a highly significant positive correlation between yield and its components should be prioritized during selection to generate high-yielding varieties thereby selection for above mentioned traits will be beneficial.

**Table 4:** Phenotypic and Genotypic (below diagonal bold values) correlation coefficient among characters

TRAITS	DFE	DM	PH	SPAD	NS	BY	TGW	YR	HI	GYPP
DFE	1.0000	0.6173"	0.0073	-0.1858	0.0578	0.0425	-0.0813	-0.2011	-0.0765	-0.0303
DM	0.6339"	1.0000	0.1444	-0.0154	-0.1033	-0.1129	-0.1633	-0.0643	-0.1005	-0.1876
PH	0.0076	0.1456	1.0000	0.0879	-0.1155	-0.1208	-0.0438	-0.1241	0.2405	0.0143
SPAD	-0.3188'	-0.0289	-0.1581	1.0000	0.0962	0.0718	-0.0488	-0.0030	0.767	0.1000
NS	0.0655	-0.1055	-0.1183	0.1417	1.0000	0.9829"	0.2490	-0.2114	-0.0708	0.8440"
BY	0.0460	-0.1120	-0.1211	0.1257	0.9981"	1.0000	0.2333	-0.2049	-0.1140	0.8389"
TGW	-0.0866	-0.1701	-0.548"	-0.0599	0.2668	0.2600	1.0000	0.1227	-0.3158'	0.0369
YR	-0.2171	-0.0690	-0.1349	-0.0439	-0.2325	-0.2201	0.1095	1.0000	-0.2082	-0.2829
HI	0.1948	0.1929	-0.4575"	-0.3372'	0.2056	0.1372	0.7041"	0.4181"	1.0000	0.4417"

**Note:** Significant at 5% and 1% respectively

The value of heritability ranged between 0.987 to -0.217. High heritability (above 60%) was observed for plant height (0.987) followed by days to maturity (0.984), days to 50% flowering (0.971), thousand grain weight (0.945), no of spikes (0.935), biological yield (0.923), yellow rust (0.915). Moderate heritability between 31 to 60% was observed for grain yield per plant (0.595) and SPAD value (0.346). Heritability was observed negative for harvest index (-0.217).

Genetic advance ranged in between 11.660 to -3.490. High genetic advance was observed in plant height (16.41) followed by days to flowering (11.660), thousand grain weight (10.025), days to 50% flowering (7.692), biological yield (4.979) SPAD value (2.563), grain yield per plant (1.457), no of spikes (1.363), genetic advance was observed

negative in harvest index (-3.490).

Heritability and genetic advance together will be better tools for effective selection of specific traits. High heritability along with high GA was observed in yellow rust resistance, plant height, no of spikes and biological yield, which indicates these characters are efficient for selection similar results was observed by Lone *et al.*, 2017, Dutamo *et al.*, 2015, Kalimullah *et al.*, 2012, Patilale *et al.*, 2021, whereas moderate heritability was observed for SPAD value and grain yield per plant and low for the harvest index. High or moderate heritability along with high or moderate genetic advance indicates the presence of additive gene effects in the inheritance of yellow rust resistance, plant height, no of spikes and biological yield thereby selection may be effective in this case.

**Table 5:** Path analysis

TRAITS	DFE	DM	PH	SPAD	145	BY	TOW	YR	HI
DFE	-0.44967	-0.3148	0.0038	0.1583	-0.0326	-0.0228	0.0430	0.1078	-0.0967
DM	0.2162	0.3411	0.0497	-0.0009	44360	-0.0382	-0.5110	-0.0235	0.0658
PH	-0.0020	-0.389	-0.2674	0.0423	0.316	0.0324	0.0146	0.0361	0.1223
SPAD	0.1549	0.0140	0.0768	-0.4860	-0.0689	-0.0611	0.0291	0.0213	0.1639
NS	0.6260	-1.0071	-1.1295	1.3533	95501	9.5320	2.5484	-2.2200	1.9634
BY	-0.3793	0.9242	0.9993	-1.0370	-8.2364	-8.2521	-2.1454	1.8161	-1.1319
TOW	-0.0061	-0.0120	-0.0039	-0.0042	0.0188	0.0183	0.0704	0.0077	0.0495
YR	-0.0343	-0.0109	-0.213	0.0069	-0.0368	-0.0348	0.0173	0.1581	0.0661
HI	-0.1286	-0.1274	0.3022	0.2227	-0.1358	-0.0906	-0.4651	4.2762	4.6605
GYPP	-0.0499	-0.0235	0.0020	0.2326	1.0542	1.0831	0.9544	-0.3726	0.5419

**Note:** Bold figure indicate direct effect

Out of 10 characters, four characters had a positive direct effect on grain yield per plant *viz.* Number of spikes had the highest positive direct effect on grain yield per plant (9.5501), followed by days to maturity (0.3411), yellow rust scoring (0.1581) and thousand-grain weight (0.0704). The characters contributed negative direct effect are biological yield (-8.2521), harvest index (-0.6605), days to 50% flowering (-0.4967), SPAD value (-0.4860), plant height (-0.2674). The highest positive indirect effect on grain yield was exerted by number of spikes per plant via biological yield.

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