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Research Article

Genetic variability of barley germplasm (*Hordeum vulgare*) for spot blotch disease resistance in natural and artificial epiphytotic condition

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Abstract
Spot blotch is having a severe impact on barley *per se* performance; therefore an experiment was conducted during *rabi* season 2016-17 at, Banaras Hindu University, Varanasi (also known as hot spot for spot blotch) in natural and artificial ephiphytotic condition, in order to find out genetic variability existing among released varieties of barley for disease resistance under consideration. The finding of this investigation showed that spot blotch resistant components and all the yield related traits showed a highly significant difference. Therefore efforts have been made to screen these varieties to find out the disease reaction based on the area under disease progress curve (AUDPC) and which will be available to research domain for further utilization in trait specific crop breeding. The study showed that without sacrificing the grain yield, variety HUB 113 was found to be resistant to this hot spot. It has the genetic capability to restrict the pathogen in order to maximize the yield level.

Keywords
Barley, spot blotch, resistance, hot spot

Introduction

Barley is one of the most ancient and world's first domesticated crops and belongs to a very important family *Poaceae*, tribe triticeae and genus *Hordeum*. In India, mainly two types of barley are being cultivated *viz.* six-row and two-row which are evolved from *Hordeum vulgare ssp. agriocrithon* originated in Tibet (Aberg, 1940) and *Hordeum vulgare ssp. spontaneum* originated in south-west Asia, respectively (Harlan, 1976).

The utmost, importance of barley crop can be understood by the fact that during the ancient era, grains of barley were used as currency by Sumerian and Babylonian and it is an unavoidable source for brewing and malting purpose and to a lesser extent, it is an ingredient in the Indian diet. Apart from this, barley is known for its numerous medical properties since it has beta-glucans which is having the capability to lower the risk of cardiovascular disease (Kumar *et al.*, 2014)

However, in the present scenario, this model crop is facing a severe problem of spot blotch disease caused by *Bipolaris sorokiniana* especially in the provenance of hot and humid climate (Dubin and Ginkal, 1991). Many researchers have reported that pathogen is not only responsible for yield loss (Clark, 1979; Dostaler *et al*., 1987; Van Leur, *et al*., 1991) however it is also affecting the germination, seedling emergence and greatly impairing the quality of malt/grain of the crop (Nutter *et al*., 1985). Average yield loss reported from a range of 15.5 % to 100 % in case of severe infection (Dubin and Ginkal, 1991; Duveiller and Gilchristtt, 1994; Srivastava *et al*., 1971; Mehta, 1998).

To meet the demand of an increasing population we must breed for a disease resistance cultivar and for that we have to mine the germplasm to know genetic variability existing in the population which is a pre-requisite for any crop improvement activity. Isolating the resistant genotype which can combat *Bipolaris sorokiniana* will be an effective strategy to exploit existing variability for the trait under consideration (Verma *et al*., 2013). Based on the above facts, the present investigation is employed in such a way that after mining of germplasm, it can undergo screening for disease resistance under natural as well as biotic stress conditions.

Material and Methods

Ninety six varieties of barley were procured from a collection maintained by Banaras Hindu University of All India Co-ordinated Barley improvement project. These varieties were evaluated during the *rabi* season of 2016-17 under the natural and artificial epiphytotic conditions at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi.

Stress condition created by using aggressive isolate of *Bipolaris sorokiniana* obtained from Division of Mycology and Plant Pathology, Banaras Hindu Varanasi in the form of 10^4 spores/ml sporidial suspension maintained as per Duveiller *et al.* (2002). Inoculums of the pathogen were sprayed during evening hours to meet out pathogen favorable hot and humid condition at tillering, flag leaf emergence and anthesis of crop growth period with light irrigation in the evening (Joshi and Chand, 2002)
Data recorded by following standard practices for days to 50% flowering (Hanft and Wych, 1982), days to maturity, plant height in cm (Zadoks *et al*., 1974), spike length with and without awns (cm), number of spikes per plant, grain filling duration in days (Duguid and Brule-Babel, 1994), thousand grain weight (g) and grain yield per plant (g) and area under disease progress curve.

Visual assessment of leaf angle was done immediately after ear emergence (Zadoks growth stage 51-55, see Zadoks *et al*., 1974) in all the experimental material under study and divided into four groups based on flag leaf angle with respect to horizontal plane *i.e.*, 60^o to 90^o for erect leaf, 0^o to 60^o for semi-erect leaf, less than half the length of flag leaf from tip to base was semi-drooping and more than half the length of flag leaf was dropping (Nigam and Srivastava, 1976). Waxiness of leaf sheath was scored at (Zadoks growth stage 69, see Zadoks *et al*., 1974). Each genotype was considered to be waxy, semi-waxy or non-waxy based on the visual appearance of wax on leaf sheath (Prasad *et al.*, 2013).

To assess the infection of spot blotch disease, double-digit scoring (00-99) from Saari and Prescott(1975) and visual scoring made at three Zadok's growth stage 63, 69 and 77, see Zadoks *et al.* (1974) *i.e.*, initiation of anthesis to 50 percent flowering, anthesis complete and late milking respectively. The first digit indicates the vertical progress on the plant and the second digit express disease severity. Double-digit scoring has been converted into disease severity as per formula is given by Duveiller *et al*.(2005)

$$\text{Disease severity (\%)} = \left(\frac{D1}{9}\right) x \left(\frac{D2}{9}\right) x\, 100$$

Where D1 & D2 refers to first and second digit respectively.
Area under disease progress curve (AUDPC) value calculated based on disease severity at GS63, GS69, and GS77 using the percent severity estimations corresponding to the disease ratings (Roelfs *et al*., 1992).

$$AUDPC = \sum_{i=1}^{n} [\{(Yi + Y(i + 1)) / 2\} x (t (i + 1) - ti)]$$

Where, Yi = disease level at time ti t (i + 1) - ti = Time (days) between two disease scores
n = number of dates on which spot blotch was recorded

Based on mean AUDPC values, barley varieties were classified into resistant, moderately resistant, moderately susceptible and susceptible.

Calculation of disease severity and AUDPC has been done in MS Excel by using appropriate formula and analysis of variance was performed to partition the total variability into sources (Panse and Sukhatme, 1964) by Windostat version 9.3 indostat series.

Result and Discussion

Genetic variability for different traits is a prerequisite and is a basic input for any crop improvement program. Expression of characters like yield and yield associated traits are governed by genes. The variability can be either on positive or negative direction depending on the gene associated with the trait and its effect on the trait expression with respect to its environment. Thus, the study at the level of natural variation, in terms of trait expression, is foremost to start the breeding program by keeping the future needs in mind to enhance and sustain barley production for the welfare of human beings as well as livestock.

Mean values of genotypes (best performing ten based on mean yield, g/plant) for different characters in natural conditions and in biotic stress conditions are presented in Table I and Table II respectively. Analysis of variance showed that all the observed traits exhibited a highly significant difference at $p<0.01$ under natural (Table III) as well as in artificial epiphytotic conditions (Table IV). A large amount of genetic variability existed in this germplasm and breeders can exploit these relevant traits for further crop improvement. The success in crop improvement of barley depends on the ability to define and assemble the required genetic variability and utilize it to identify the genotypes which can combat under biotic stress like spot blotch disease.

Genetic parameters of barley genotypes under natural and biotic stress conditions are presented in Table V and Table VI respectively. Considering the magnitude of the phenotypic coefficient of variation and the genotypic coefficient of variation, the number of spikes per plant, grain yield,

thousand-grain weight, and AUDPC had more variations compared to other traits. Whereas under biotic stress conditions apart from grain yield, spike per plant and AUDPC, PCV and GCV values showed a relatively large amount of genetic variability for grain filling duration, spike length with and without awns. A similar result also reported by Singh *et al.* (2014), Singh *et al.* (2008), Sharma and Maloo (1994), Jalata *et al.* (2011) for grain yield per plant. High heritability (>80 %) was observed for days to 50% flowering, thousand-grain weight, and AUDPC. Therefore, these traits are imparting more genotypic variance towards total phenotypic variation and any selection criteria considering these traits will substantially enhance the yield level. These findings were in accordance with Singh *et al.* (2014), Therrien (2006), Jalata *et al.* (2011). High heritability coupled with high genetic advance estimates were found for plant height, thousand-grain weight and AUDPC.

Limited information is available on the different sources for spot blotch disease resistance in released cultivars. Therefore, it becomes essential to identify the genotypes which can reduce the minacious effect of the disease. Hence, 96 genotypes of barley have been evaluated to classify into different groups based on their disease reaction.

Under natural conditions,96 genotypes of barley have been classified as resistant, moderately resistant, moderately susceptible and susceptible based on their area under disease progress curve (Figure 1). A Total of 23 genotypes were found resistant (Figure III) with mean AUDPC values ranging from 170.8 to 294.11. HUB 113 was found to be resistant to spot blotch since it fetched the lowest AUDPC mean value of 170.8. Sixty genotypes were moderately resistant, six genotypes susceptible and seven genotypes were found moderately susceptible. Under biotic stress conditions, the classification of 96 genotypes of barley is presented in Figure II based on mean AUDPC values. Nineteen genotypes were found resistant (Figure IV) based on their mean AUDPC values and 59 genotypes found moderately resistant whereas nine genotypes were found to be moderately susceptible and nine genotypes were found to be susceptible. The information generated from these findings can provide a research platform to use these varieties in cultivation which are resistant to moderately resistant and hybridization program can be initiated by using most resistant and most susceptible genotype to know their genetic inheritance. Out of ninety-six genotypes, none of the genotypes were found immune, however, variety RD 2503 has been identified with a very high area under disease progress curve value after K-603 and RD 2508. A similar finding reported from Verma *et al*. (2013) with respect to susceptible variety RD 2503, which had the highest digit score at all the four different locations and used as an infector row for their experimental material.

Few genotypes have been identified which can restrict the symptoms and yield loss created by spot blotch disease. The response of genotypes was diverse against pathogenicity of pathogen and significant variability was found with respect to studied traits. Variability in resistance level is a prerequisite for disease resistance breeding (Wink, 1998). To develop tolerance against spot blotch disease, few resistant and moderately resistant genotypes with higher seed yield *per se* under stress conditions were selected as parents in a resistant breeding program. Except for genotypes Alfa 93 (moderately resistant), genotypes HUB-113, DWRUB-52, LSB-2 were resistant with grain yield equal or more than 25 g/plant. Other genotypes Jyoti, BH 902, BHS 400, K24, Lakhan, Vijaya, Bilara 2, Kailash and Rajkiran were also resistant and moderately resistant to spot blotch with yield range 20 to 24.99 g / plant (Figure I & II). The variation observed in natural and biotic stress conditions might be due to host-pathogen interaction with respect to the genetic load of inoculum in case of epiphytotically created field conditions.

The results indicate that only a few numbers of genotypes have been identified with resistant to moderately resistant coupled with good yield. The selection of these genotypes is essential to keep disease below the economic threshold level. Disease symptoms will appear on the genotypes but the extent and magnitude of disease severity can be minimized by providing a higher level of tolerance. Thus the optimum level of yield can be maintained.

Out of 96 genotypes, nine (9.38 %) were found with drooping leaves, forty-nine (51.04%) with erect, one (1.04%) with semi-drooping and thirty-seven (38.54%) with semi-erect leaves (Figure V). Joshi and Chand (2002) found a positive correlation (0.58) between leaf angle and AUDPC which indicated a positive influence of leaf erectness on severity to spot blotch disease. The present study also showed that the genotypes with either resistance or moderately resistance were having erect or semi-erect leaf except for HBL-391 and VLB 56 (moderately resistant with drooping and semi drooping leaves respectively). Few genotypes were having resistant or moderately resistance with drooping or semi-drooping leaves, and some susceptible genotypes were also found with erect and semi-erect leaves. However, there is

a positive correlation between the progress of the leaf angle towards erectness. The mechanism behind the association of erectness of leaf angle and spot blotch disease resistance is leaf moisture or dew which deposits on the leaf surface. Under erectness, water drop cannot remain on the leaf surface for a long time. Whereas drooping or semi-drooping leaf orientation provides a surface to withstand moisture for a long time, more chance for disease occurrence. Deposited dew or moisture will provide a congenial microenvironment for the germination of *Bipolaris sorokiniana* spores. A similar interpretation has been reported from Sahoo (2000); Joshi and Chand (2002). In support of that, Duvalier *et al.*(1998) also reported that the congenial environment for spot blotch development is continuous exposure of plants at 25° C and 100% relative humidity then incubated at 24℃ and 85% RH for 144 hours. Therefore, this condition may be created by dew or free water adhering to the leaf tip of that leaf whose orientation is progressing towards droopiness. Joshi and Chand (2002) reported that erect leaf is important for increasing photosynthesis and dry matter accumulation by capturing greater sunlight since erect leaf will provide a proper canopy for sunlight to fall directly to the leaves.

Apart from the advantage of having erect to semi-erect leaf in low disease development in contrast to drooping and semi-drooping, greater disease development in spot blotch is also reported by Huber and Gillepsie (1992) that greater leaf canopy may promote disease development in spot blotch by restricting sunlight resulting in a reduction of water loss through evapo-transportation.

Out of 96 genotypes, eighty (83.33 %) were found to be waxy, fourteen (14.58 %) non-waxy and two semi-waxy as per visual scoring of leaf waxiness (Figure VI). Prasad *et al.* (2013) reported that two traits *viz.* waxiness and erect leaf were associated with a higher level of spot blotch disease resistance. This may be due to the presence of wax on leaf or stem which can prevent the spot blotch pathogen spore germination by reducing the retention of moisture on leaves. Compared to these, a very small number *i.e.*, 96 genotypes have been taken for this study and results showed that eighty genotypes have been found with waxy leaves and out of these fifty-four genotypes (80% of genotypes) were found to be resistant to moderately resistant, which shows somewhere that waxiness is an advantage in terms of keeping spot blotch infection at a low level. However, few genotypes also found which have nonwaxy leaf but resistant to moderately resistant and waxy leaf having moderately susceptible to susceptible disease reaction for spot blotch. But, all the non-waxy leaves had less than 20 g/plant yield and higher AUDPC values in general.

The direct relationship can be confirmed by taking a large number of germplasm with multi-location and multiyear data as shown by earlier reporters. Therefore, it may be suggested that keeping the criteria of one trait to minimize the disease level at low severity is not advisable instead of that an integrated approach must be used to minimize the spot blotch infection at a low level.

Research and development always aimed to maximize the yield level by identifying the constraint faced by the crop. As reported from many workers, this study gives the impression that spot blotch is responsible for minimizing the yield level through several factors especially in a hot and humid climate. Therefore apart from mining genetic variability, and screening of barley, we need to include the parameters which are environmentally neutral like molecular markers and storehouse of research findings must be used in order to maximize the yield by reliable contributing factors.

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Table 1. Mean values of ten best performing barley genotypes for grain yield (g/plant) under natural conditions

S.N.	Genotypes	PH	D50%F	GFD	SLWOA	SLWA	SPP	DM	GY	TGW	AUDPC
1	LAKHAN	99.68	75.67	38.33	8.35	17.86	8.11	114.00	32.57	42.39	432.31
2	HUB 113	95.56	81.67	36.67	7.66	11.51	10.11	118.33	30.31	46.05	170.80
3	LSB 2	82.83	75.00	41.00	7.55	11.93	6.44	116.00	27.83	46.23	229.74
4	ALFA 93	98.50	76.33	38.00	9.17	15.70	11.00	114.33	27.67	31.53	378.02
5	DL 70	96.52	74.00	35.00	7.97	16.54	5.22	109.00	27.66	40.79	625.11
6	KAILASH	96.94	74.33	38.33	8.68	16.84	9.56	112.67	26.85	43.29	313.02
7	K 24	101.18	76.67	39.33	10.15	10.06	9.78	116.00	26.58	42.80	296.15
8	DWRUB 52	71.71	73.67	41.00	7.34	11.99	9.67	114.67	26.36	49.12	184.71
9	BH 946	81.84	77.67	35.00	6.52	13.31	8.11	112.67	26.15	43.57	211.43
10	VIJAYA	85.60	74.00	37.33	8.26	15.78	8.56	111.33	25.67	43.45	362.80

Where, PH = Plant height, D50% F= days to 50% flowering, DM= days to maturity, GFD= grain filling duration, SLWOA= spike length without awns, SLWA = spike length with awns, SPP = spike per plant, GY= grain yield, TGW= thousand grain weight, AUDPC= Area under disease progress curve.

Table 2. Mean values of ten best performing barley genotypes for grain yield (g/plant) under biotic stress conditions

S.N	Genotypes	PH	D50%F	GFD	SLWOA	SLWA	SPP	DM	GY	TGW	AUDPC
1	HUB 113	91.49	84.33	25.67	6.58	7.07	6.56	110.00	28.36	42.56	220.09
2	ALFA 93	83.94	84.67	19.00	8.18	13.72	5.55	103.67	24.92	28.30	282.19
3	LSB 2	76.16	78.00	31.33	6.94	8.72	4.11	109.33	24.84	44.33	283.22
4	DWRUB 52	65.24	75.33	32.33	6.03	8.63	5.83	107.67	24.70	44.12	197.57
5	K 24	97.16	76.00	30.33	6.62	7.32	3.00	106.33	23.22	41.78	339.22
6	LAKHAN	83.38	78.00	28.33	7.01	14.03	4.22	106.33	23.19	37.32	423.97
7	BH 946	74.82	74.00	34.33	5.88	10.11	4.22	108.33	23.18	43.30	257.51
8	KAILASH	86.59	78.33	28.33	6.46	11.77	5.89	106.67	22.34	40.35	438.04
9	RAJ KIRAN	73.03	78.33	29.33	6.13	10.26	4.89	107.67	22.05	33.94	322.51
10	BHS 400	78.72	84.00	26.00	5.74	11.82	5.06	110.00	21.70	40.05	333.45

Where, PH = Plant height, D50% F= days to 50% flowering, DM= days to maturity, GFD= grain filling duration, SLWOA= spike length without awns, SLWA = spike length with awns, SPP = spike per plant, GY= grain yield, TGW= thousand grain weight, AUDPC= Area under disease progress curve.

Table 3. Analysis of variance in 96 genotypes of barley under natural conditions

Sources of Variation	PH	D50%F	GFD	SLWOA	SLWA	SPP	DM	GY	TGW	AUDPC
Replication (DF=2)	542.36	29.43	15.55	0.01	0.41	48.74	87.75	40.42	0.06	44493.14
Treatment (DF=95)	242.15**	43.29**	47.18**	2.58**	8.38**	8.59**	33.59**	51.70**	102.28**	129999.88**
Error (DF= 190)	32.92	3.27	10.64	0.90	2.05	1.39	7.86	9.59	4.00	6855.91
Mean	87.93	76.56	35.67	7.91	13.87	7.94	112.23	20.14	35.17	422.07
C.V.	6.52	2.36	9.15	11.99	10.32	14.85	2.50	15.48	5.69	19.62
F ratio	7.36	13.23	4.43	2.87	4.09	6.18	4.27	5.39	25.56	18.96
S.E.	3.31	1.04	1.88	0.55	0.83	0.68	1.62	1.79	1.16	47.80
C.D. 5%	9.24	2.91	5.25	1.53	2.30	1.90	4.52	4.99	3.22	133.36
C.D. 1%	12.19	3.84	6.93	2.01	3.04	2.50	5.96	6.57	4.25	175.91
Range Lowest	65.48	73.67	19.00	6.07	10.06	4.44	103.33	7.96	21.82	170.80
Range Highest	104.01	96.33	41.00	10.15	17.86	12.11	118.33	32.57	46.80	1178.04

Note- ** Significance @ 1% and * Significance @ 5%
Where DF = degree of freedom, PH = Plant height, D50% F= days to 50% flowering, DM= days to maturity, GFD= grain filling duration, SLWOA= spike length without awns, SLWA = spike length with awns, SPP = spike per plant, GY= grain yield, TGW= thousand grain weight, AUDPC= Area under disease progress curve.

Table 4. Analysis of variance in 96genotypes of barley under epiphytically created biotic stress conditions

Sources of Variation	PH	D50%F	GFD	SLWOA	SLWA	SPP	DM	GY	TGW	AUDPC
Replication (DF=2)	499.64	66.17	80.39	0.64	1.60	3.32	29.34	4.75	4.96	24.91
Treatment (DF=95)	222.91**	64.20**	60.56**	2.17**	10.40**	7.84**	28.85**	17..87**	99.96**	173788.71**
Error (DF= 190)	16.76	4.38	7.53	0.98	2.28	0.65	3.98	4.67	1.52	12694.09
Mean	76.91	79.10	26.07	6.26	10.14	4.71	105.18	15.87	38.22	523.03
C.V.	5.32	2.64	10.70	15.85	14.93	17.13	1.90	13.62	3.22	21.54
F ratio	13.30	14.67	8.04	2.20	4.57	12.07	7.25	3.83	65.86	13.69
S.E.	2.36	1.21	1.58	0.57	0.87	0.47	1.15	1.76	0.71	65.05
C.D. 5%	6.59	3.37	4.42	1.60	2.43	1.30	3.21	3.48	1.98	181.46
C.D. 1%	8.70	4.44	5.83	2.11	3.21	1.71	4.24	4.59	2.62	239.36
Range Lowest	55.09	74.00	18.33	4.17	5.69	1.78	100.00	5.03	26.18	197.57
Range Highest	97.23	100.00	34.33	8.57	14.71	11.05	111.00	28.36	53.76	1358.99

Note- ** Significance @ 1% and * Significance @ 5%
Where DF = degree of freedom, PH = Plant height, D50% F= days to 50% flowering, DM= days to maturity, GFD= grain filling duration, SLWOA= spike length without awns, SLWA = spike length with awns, SPP = spike per plant, GY= grain yield, TGW= thousand grain weight, AUDPC= Area under disease progress curve.

Table 5. Genetic parameters of barley genotypes under natural conditions

S.N	Parameter	PH	D50%F	GFD	SLWOA	SLWA	SPP	DM	GY	TGW	AUDPC
1	Environmental Variance	32.92	3.27	10.64	0.90	2.05	1.39	7.86	9.59	4.00	6855.91
2	ECV	6.53	2.36	9.15	11.99	10.32	14.85	2.50	15.38	5.69	19.62
3	Genotypical variance	69.75	13.34	12.18	0.56	2.11	2.40	8.58	14.03	32.76	41047.99
4	GCV	9.50	4.77	9.78	9.47	10.47	19.52	2.61	18.60	16.27	48.00
5	Phenotypical variance	102.66	16.61	22.82	1.46	4.16	3.79	16.44	32.46	36.76	47903.90
6	PCV	11.52	5.32	13.39	15.28	14.70	24.53	3.61	28.29	17.24	51.86
7	h² (Broad Sense)	0.68	0.80	0.53	0.38	0.51	0.63	0.52	0.43	0.89	0.86
8	GA as % of Mean 5%	16.13	8.81	14.72	12.09	15.37	32.00	3.88	25.09	31.65	91.54
9	General Mean	87.93	76.56	35.67	7.91	13.87	7.94	112.23	20.14	35.17	422.07

Where, PH = Plant height, D50% F= days to 50% flowering, DM= days to maturity, GFD= grain filling duration, SLWOA= spike length without awns, SLWA = spike length with awns, SPP = spike per plant, GY= grain yield, TGW= thousand grain weight, AUDPC= Area under disease progress curve.
ECV = Environmental coefficient of variation, GCV =Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation,
h^2 =Heritability, GA = Genetic advance

Table 6. Genetic parameters of barley genotypes under biotic stress conditions

S.N	Parameter	PH	D50%F	GFD	SLWOA	SLWA	SPP	DM	GY	TGW	AUDPC
1	Environmental Variance	16.76	4.38	7.53	0.98	2.28	0.65	3.98	4.67	1.52	12694.09
2	ECV	5.32	2.65	10.70	15.85	14.93	17.13	1.91	13.62	3.22	21.54
3	Genotypical variance	68.72	19.94	17.68	0.40	2.71	2.40	8.29	4.40	32.81	53698.20
4	GCV	10.78	5.65	16.39	10.04	16.28	32.90	2.75	13.22	14.99	44.31
5	Phenotypical variance	85.48	24.32	25.21	1.38	4.99	3.05	12.27	9.07	34.33	66392.30
6	PCV	12.02	6.23	19.57	18.76	22.09	37.09	3.34	18.98	15.33	49.27
7	h² (Broad Sense)	0.80	0.82	0.70	0.29	0.54	0.79	0.68	0.485	0.96	0.81
8	GA as % of Mean 5%	19.91	10.53	28.27	11.07	24.72	60.11	4.65	27.01	30.19	82.08
9	General Mean	76.91	79.10	26.07	6.26	10.14	4.71	105.18	15.87	38.22	523.03

Where, PH = Plant height, D50% F= days to 50% flowering, DM= days to maturity, GFD= grain filling duration, SLWOA= spike length without awns, SLWA = spike length with awns, SPP = spike per plant, GY= grain yield, TGW= thousand grain weight, AUDPC= Area under disease progress curve.
ECV = Environmental coefficient of variation, GCV =Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation,
h^2 =Heritability, GA = Genetic advance

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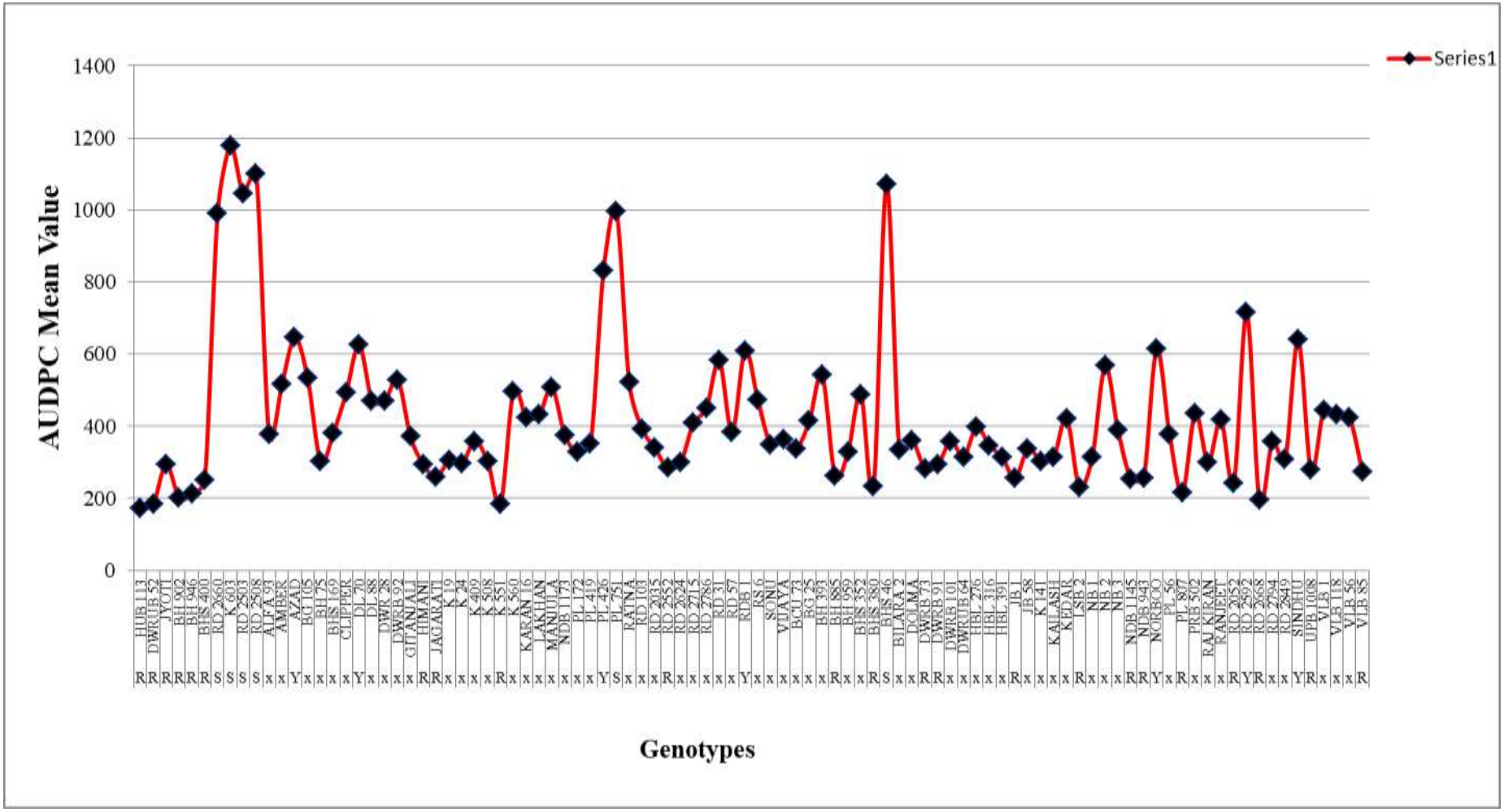

Fig. 1. Graphical representation of 96 genotypes of barley with respect to their AUDPC mean values and corresponding disease reaction under natural conditions (where R-Resistant, S- Susceptible, X- Moderately Resistance and Y- Moderately Susceptible)

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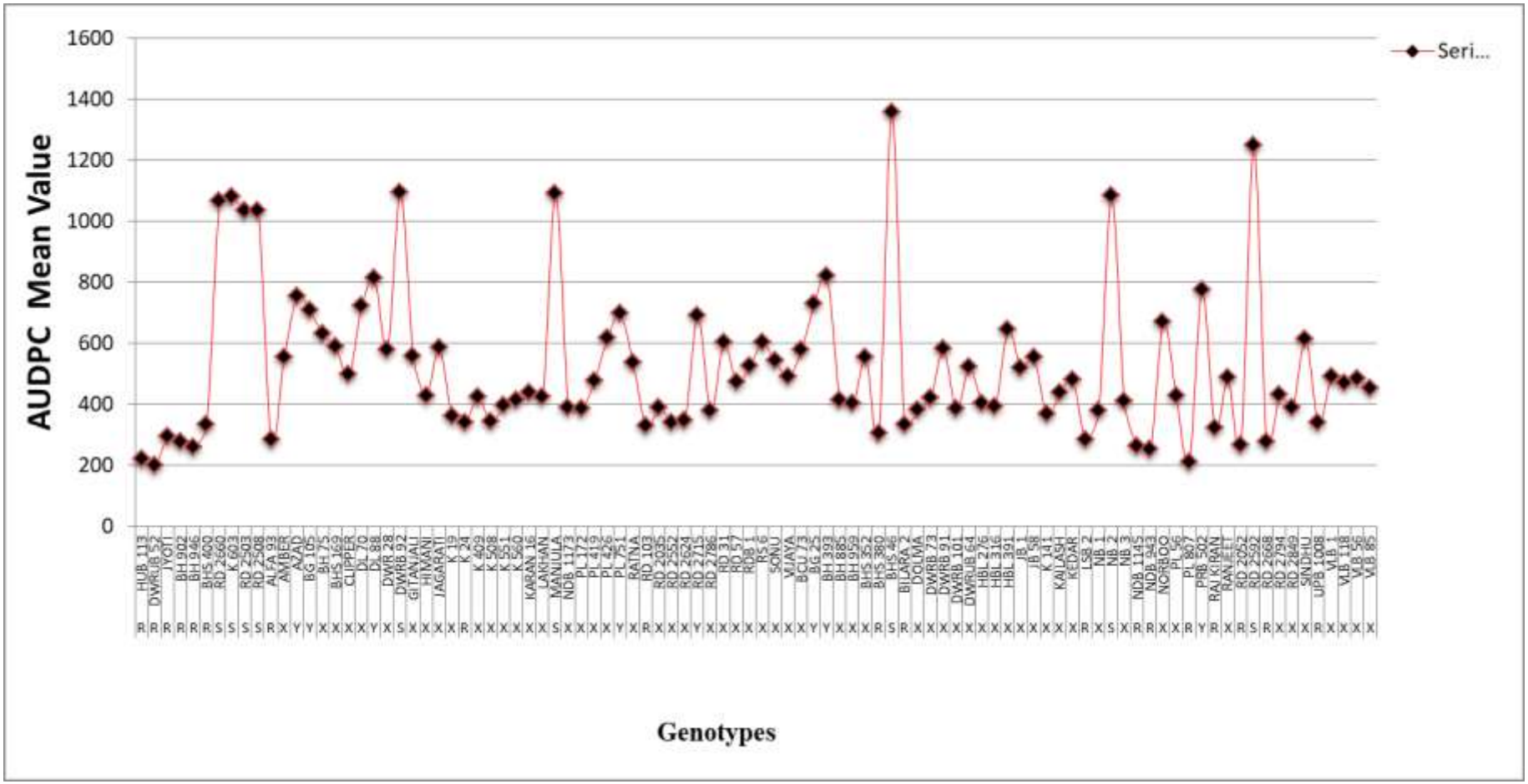

Fig. 2. Graphical representation of 96 genotypes of barley with respect to their AUDPC mean values and corresponding disease reaction under epiphytotically created biotic stress conditions (Where, R-Resistant, S- Susceptible, X- Moderately Resistance and Y- Moderately Susceptible

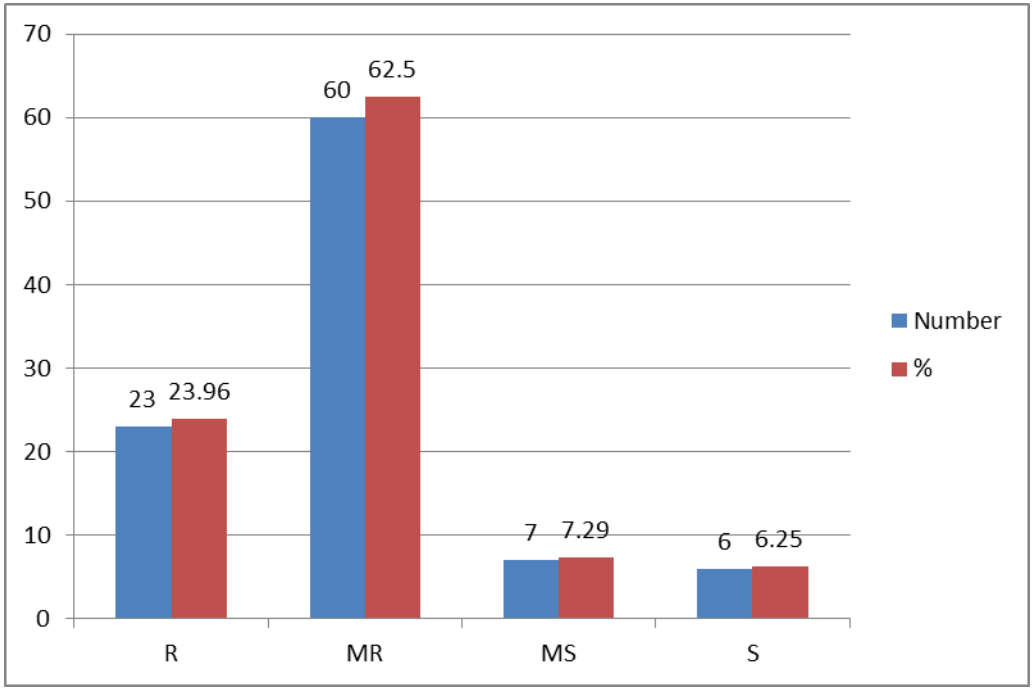

Fig. 3. Frequency distribution of barley genotypes based on AUDPC values into their disease reaction under natural condition

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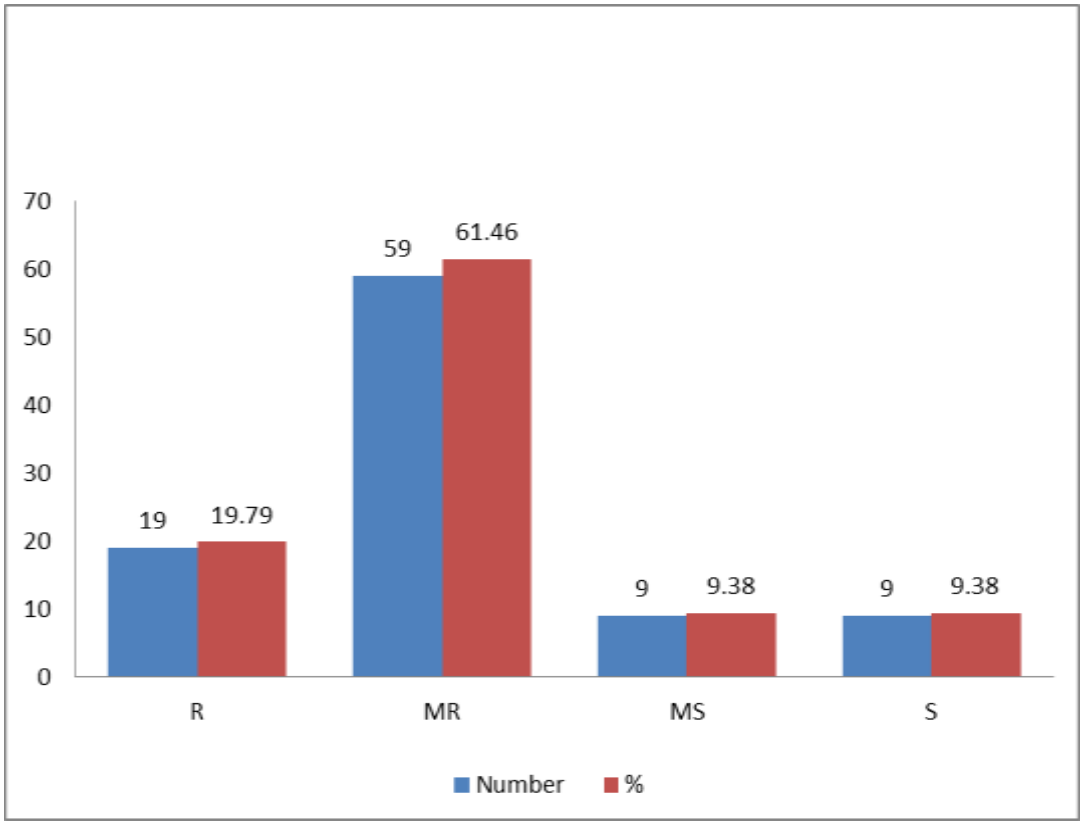

Fig. 4. Frequency distribution of barley genotypes based on AUDPC values into their disease reaction under biotic stress condition

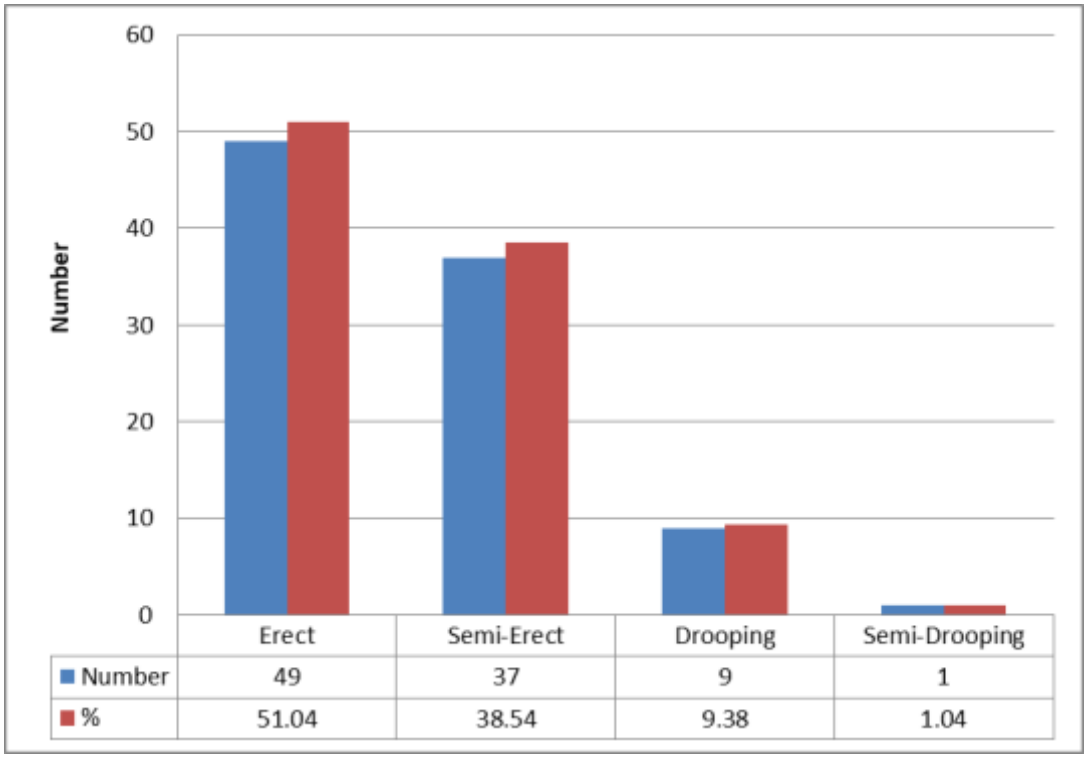

Fig. 5. Leaf angle frequency distribution among ninety six genotypes of barley

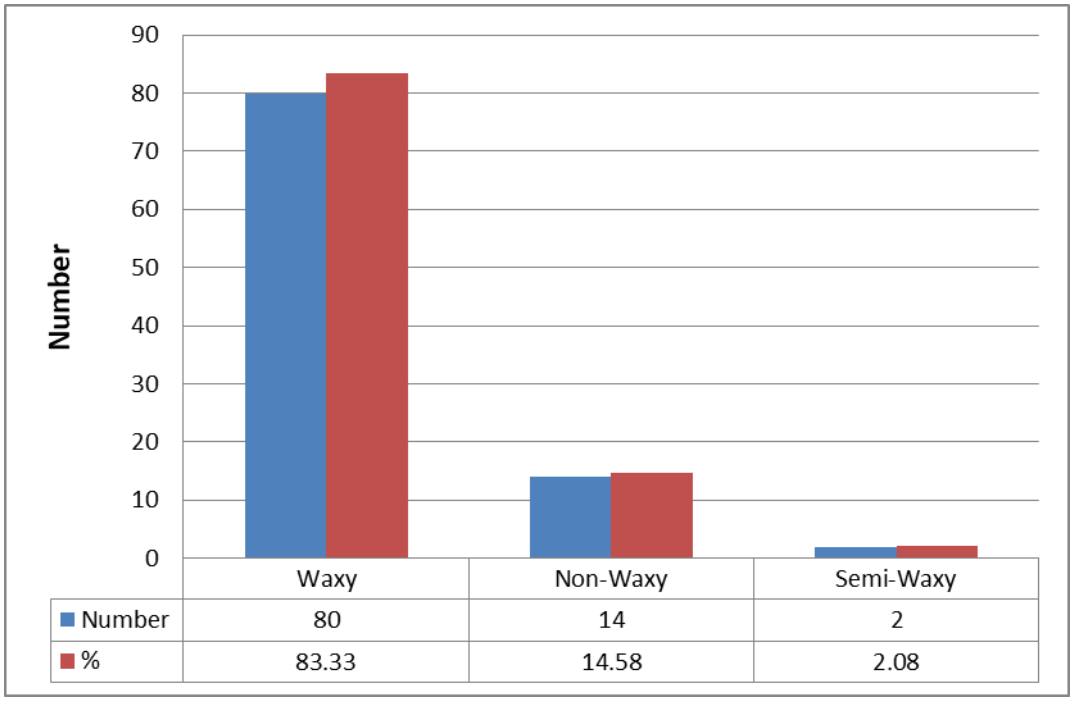

Fig. 6. Leaf waxiness frequency distribution among ninety-Six genotypes of barley

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