



Estimation of genetic variability among peanut genotypes for resistance to leaf spot disease

Q. Bano¹, M. Hassan¹, S.B. Hussain², M. Javed², M.A. Zulfiqar³,
M. Younas⁴, M. Baber⁵, M. Zubair⁶ and S.M. Hussain⁷

¹Department of Plant Breeding and Genetics, PMAS Arid Agriculture University, Rawalpindi, Pakistan

²Department of Plant Breeding & Genetics, Faculty of Agricultural Sciences & Technology, Bahauddin Zakariya University, Multan, Pakistan

³PARC, Research and Training Station, Bahauddin Zakariya University, Multan, Pakistan

⁴Department of Plant Breeding & Genetics, University of Agriculture, Faisalabad, Pakistan

⁵Institute of Molecular Biology & Biotechnology, Bahauddin Zakariya University, Multan, Pakistan

⁶Department of Forestry & Range Management, FAS&T, Bahauddin Zakariya University, Multan, Pakistan

⁷NARC, Islamabad, Pakistan

Corresponding author: S.B. Hussain

E-mail: drsyedbilal@hotmail.com

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ABSTRACT. This study aimed to identify high-yielding peanut genotypes with resistance to leaf spot disease. The experiments

included material from fourteen local and four exotic peanut genotypes that showed highly significant differences among morphological and disease severity parameters in all the genotypes which, in turn, suggested diversity genotypes. Disease severity analysis showed that the highest disease score and damaged leaf area were observed in the genotype Kelincer and the lowest scores and leaf damaged areas were observed in Majalaya super and BARI-2000, respectively. Based on these results, the genotypes BARI-2011, Chakori, Golden, BARI-89, Majalaya Super, BARD-699, BARI-2000, SP-1, and No. 334 can be used by breeders in peanut improvement programs for the development of new cultivars with higher disease resistance and increased yield.

Key words: Genetic variability; Peanut; Resistance; Leaf spot

INTRODUCTION

Peanut (*Arachis hypogaea* L.) belongs to the family Fabaceae and is widely cultivated for its edible seeds and high forage value for livestock. This plant is also known as groundnut or monkey nut (Acquaah, 2007). The crop is genetically drought tolerant and can reach maturity without any irrigation. It is cultivated worldwide on an area of 23.28 million ha, with a production of 39.93 million metric tons and an average yield of 1720 kg/ha. China leads the world producing 16.70 million metric tons of peanuts on an area of 4.70 million ha (USDA, 2013). In Pakistan, this leguminous oil seed crop is cultivated in an area of approximately 81.5 thousand ha, with a production of 91.4 thousand tons, 85% of which is contributed by the Pothohar regions of Punjab, 12% by KPK (Khyber Pakhtonkhwa), and 3% by Sindh, Pakistan (Anonymous, 2013). In Pakistan, the average pod yield of peanut was recorded as 1100 kg/ha, which was considered very low compared to developed countries producing 2500 kg/ha. The constraints in peanut productivity mainly include a narrow genetic base due to its susceptibility to various biotic and abiotic stresses. Among biotic stresses, fungal diseases cause the most plant damage. Early and late leaf spot caused by *Cercospora arachidicola* and *Cercosporidium personatum* are the most common and serious diseases of peanut worldwide. Individually or together they cause losses of approximately 50% in pod yield; in areas where rust disease occurs; a combined attack of foliar diseases cause losses up to 70% in yield (Anonymous, 2013). Although CLS can also be controlled with the use of appropriate fungicides, their use is expensive and not readily available to small-scale farmers (Hossain et al., 2007). The development of disease-resistant cultivars is a robust, cost effective, and environment friendly solution among all the disease management approaches. In addition, disease-free forage of high nutritional value would impact livestock feeding. Therefore, it is useful to identify sources of resistance for the development of disease-resistant varieties of peanut.

The present study aimed to evaluate the genetic diversity of disease and yield-related parameters in peanut germplasm and identify leaf spot-resistant, high-yielding genotypes to be used in subsequent breeding programs.

MATERIAL AND METHODS

The experiment was conducted in the Department of Plant Breeding and Genetics,

at PMAS-Arid Agriculture University, Rawalpindi, during 2013-2014, which is located at 33.6058 N and 73.0437 E of latitude and longitude, respectively. The experiment was conducted using a completely randomized design with five experimental replicates. Eighteen genotypes were grown in sandy loam soils with 45 cm row spacing and 10 cm plant to plant spacing. One month after sowing, the plants were inoculated with *C. arachidicola* and *Phaeoisariopsis personata*. Data on the number of pods per plant, number of seeds per pod, biological yield, pod yield, seed yield, leaf area, number of days to the appearance of 1st leaf spot after inoculation, number of spots per leaf, and leaf spot area were recorded. The data were subjected to simple analysis of variance technique of Steel et al. (1997) to observe whether the research material differences for plant traits are significant.

RESULTS AND DISCUSSION

Number of pods per plant

Increased number of pods per plant contributes towards increased yield in peanut varieties. Analysis of variance for the number of pods per plant showed highly significant differences among all the genotypes (Table 1). The genotype Majalaya Super demonstrated the maximum pods per plant (15.4), followed by SP-1 (14.6), Golden (13.6), Chakori (13.5), and BARD-699 (13.4). The minimum number of pods was observed in genotypes Kelincer, Majalaya, No. 334, and BARI-89, which showed statistically similar results (5.2).

These results contrast with the findings of Naeem-ud-Din et al. (2012) in the case of BARI-2011.

Table 1. Analysis of variance for number of pods per plant.

No. of pods	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	575.764	17	33.868	13.578	0.000
Within groups	174.6	70	2.494		
Total	750.364	87			

Grand mean = 11.13; CV = 14.16%.

Number of seeds per pod

Analysis of variance for number of seeds per pod showed highly significant difference between genotypes (Table 2). The maximum (30.2) seeds per pod were found in genotype BARI-2011 followed by Majalaya Super (26), SP-1 (25.5), No. 334 (25), Chakori (23.5), and BARI-2000 (23). The minimum number of seeds was recorded in genotypes Kelincer (9), 96CG005 (12.8), and 11CG005 (13.2). The increased number of seeds per pod may be a result of disease resistance or other morphological traits in BARI-2011 and the other respective genotypes with greater numbers of seeds per pod.

These results are consistent with the findings of Naeem-ud-Din et al. (2012), who found that BARI-2011 has more seeds per pod as well as being a better plant type when compared to No. 334, Chakori, BARI-2000, Golden, and BARD-479. They also observed resistance against root rot and *Cercospora* leaf spot in BARI-2011.

Table 2. Analysis of variance for number of seeds per pod.

No of seeds	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	2403.791	17	141.399	31.95	0.000
Within groups	309.8	70	4.426		
Total	2713.591	87			

Grand mean = 20.06; CV = 10.47%.

Biological yield per plant

Analysis of variance showed that there is a significant difference among the selected genotypes for biological yield per plant as shown in Table 3. The maximum biological yields were observed in the genotypes Golden (36.2 g), BARI-89 (33.6 g), Chakori (31.5 g), and No. 334 (29.4 g). Majalaya Super and BARI-2011 had the same biological yield (27.2 g), while the biological yield per plant minimums were recorded for 11CG005 (12.2 g), Kelincer (12.2 g), 96CG005 (14.2 g), Bard-479 (15.2 g), and Majalaya (16.2 g), respectively.

These results are consistent with the findings of Saeed and Hassan (2009), who obtained an average biological yield of 2815 kg/ha for genotype Golden, while that for BARI-2000, BARD-479, and No. 334 were 2258, 2398, and 2146 kg/ha, respectively.

Table 3. Analysis of variance for biological yield per plant (grams).

Biological yield	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	4413.33	17	259.608	22.332	0.000
Within groups	813.75	70	11.625		
Total	5227.08	87			

Grand mean = 22.60; CV = 15.08%.

Pod yield per plant

Analysis of variance of yield showed highly significant differences between all the genotypes (Table 4). Chakori and BARI-2011 have maximum pod yields of 13.5 and 12.4 g, respectively; where as the lowest yielding genotypes were 11CG005 (4 g), Bard-479 (4.8 g), and Kelincer (5 g).

Table 4. Analysis of variance for pod yield per plant (grams).

Pod yield	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	548.773	17	32.281	34.433	0.000
Within groups	63.75	68	0.938		
Total	612.523	85			

Grand mean = 8.31; CV = 11.59%.

Seed yield per plant

The analysis of variance for seed yield per plant showed highly significant differences among all the genotypes (Table 5). The maximum seed yield per plant was observed in

genotype BARI-2011 (6.858 g), which forms a homogeneous group with Chakori (6.365 g), Golden (6.322 g), BARD-699 (5.992 g), and Majalaya Super (5.864 g). The minimum seed yields were observed in Kelincer (1.344 g) and BARD-479 (2.096 g).

Table 5. Analysis of variance for seed yield per plant (grams).

Seed yield	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	201.094	17	11.829	20.301	0.000
Within groups	40.787	70	0.583		
Total	241.882	87			

Grand mean = 4.31; CV = 17.64%.

Disease scoring for fungal pathogen resistance

Scoring of disease was based on visually observing disease severity on a 9-point scale, where 0 is for no disease or no visual symptoms of disease incidence, and 9 is for complete defoliation of the plant. Variation in the development and severity of disease among different genotypes can be scored at different times during the entire cropping period.

Analysis of variance showed that there is a significant difference among genotypes of peanut in the severity of leaf spot disease (Table 6). The maximum scores were observed in genotypes Kelincer (8.6), 11CG005 (8.2), and 02CG002 (7.2). These data suggest that these genotypes are highly susceptible to leaf spot disease. In contrast, the minimum scores were measured in the genotypes Majalaya Super (2.3) and BARI-2000 (3). The genotypes BARD-699 (3.4), Golden (3.6), BARI-2011 (3.8), No. 334 (3.8), and BARI-89 (4) also had reasonable scores and can be considered as moderately resistant genotypes of peanut.

Table 6. Analysis of variance for scoring of leaf spot disease on a scale of 1-9.

Scoring	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	290.773	17	17.104	29.26	0.000
Within groups	39.75	68	0.585		
Total	330.523	85			

Grand mean = 5.31; CV = 14.39%.

Percentage of damaged leaf area by fungal infection

Damaged leaf area is a key parameter used to estimate the infected area of the leaf and has a direct relationship with disease severity, as the diameter of spots and damaged area are both influenced by environment and plant genotype. Analysis of variance showed that there was a significant difference among the genotypes in terms of damaged leaf area after fungal infection (Table 7). The maximum leaf damage was observed in Kelincer (36.12%), BARD-479 (23.031%), 02CG002 (13.286%), and 10CG003 (11.7875%). These varieties may be more susceptible to leaf spot disease than the other genotypes tested. The genotypes that had the minimum mean of damaged leaf area were BARI-2000 (3.508%), SP-1 (4.1), Majalaya Super (4.865%), Golden (5.292%), and Bari-2011 (5.425). These genotypes reflect a better tolerance to leaf spot disease compared to the genotypes with greater damaged leaf areas.

Table 7. Analysis of variance for the percent of damaged leaf area.

Biological yield	Sum of squares	d.f.	Mean square	F-statistics	P value
Between groups	5185.71	17	305.042	273	0.000
Within groups	75.91	68	1.116		
Total	5261.62	85			

Grand mean = 10.832; CV = 9.75%.

DISCUSSION

Based on correlation between morphological and disease severity parameters studied in peanut genotypes for resistance to *Cercospora* leaf spot disease, it can be suggested that genotypes BARI-2011, BARI-2000, BARI-89, Golden, Chakori, Majalaya Super, and SP-1 showed better results in field conditions against *Cercospora* leaf spot disease in terms of better biological yield and lowest score and leaf damaged area with no limitations. These selected genotypes can be expected to show better performance in disease infected areas of Pakistan and to be used by the breeders in peanut improvement programmes, which would help in developing new cultivars with higher disease resistance and increased yield.

Conflicts of interest

The authors declare no conflict of interest.

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