



Original Paper

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Genetic variability and correlation among traits explaining resistance to *Cercospora* leaf spots in groundnut (*Arachis hypogaea* L.)

Aboubakar HAMASSELBE^{1*}, Ismael SADOU¹ and Celestin KLASSOU²

¹Institute of Agricultural Research for Development (IRAD) PO Box 33 Maroua, Cameroon.

²Institute of Agricultural Research for Development (IRAD) PO Box 415 Garoua, Cameroon.

*Corresponding author, E-mail: ahamasselbe@yahoo.com, Tel: (00237) 77 38 99 90

ABSTRACT

A field experiment was carried out to study genetic variability and correlation between percent defoliation, *Cercospora* severity, yield and yield components in groundnut, in North Cameroon. Genotypic coefficient of variability, broad sense heritability, genetic gain and correlation coefficients between all the characters studied were estimated by the variance components procedure. Results show that *Cercospora* severity and fodder yield at harvest had high and significant genotypic correlation coefficients of +0.74** and -0.61*, respectively with percent defoliation. This indicates that these characters are governed by the same genes (pleiotropism). Thus, selection could be carried out on disease severity and fodder yield at harvest to improve resistance to *Cercospora* leaf spots in groundnut.

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INTRODUCTION

Prior to the introduction of cotton in 1951, groundnut was the major export crop in North Cameroon (Roupsard, 1987). Since 1976, groundnut is no longer exported due to high local consumption, strong competition of cotton for production land and decrease in groundnut production (Seignobos, 2000). Nevertheless, groundnut remains a staple food crop throughout the region (Magrin, 2003). Groundnut pod yield in farmers' fields is low (400-800 kg/ha) due to biotic (foliar diseases and pests), abiotic (low soil fertility and erratic rainfall) and socio-economic (lack of improved seed system facilities and extension services) factors (Seignobos, 2000).

Among the biotic constraints, *Cercospora* leaf spots caused by *Cercospora*

arachidicola Hori (early leaf spot) and *Cercosporidium personatum* (Berk. & Curt.) Deighton (late leaf spot) are the most destructive foliar fungal disease (Monfort et al., 2004). Groundnut yield losses due to *Cercospora* leaf spots are estimated at 50% of pods and 70% of fodder (Ntare, 2001).

Many authors (Anderson et al., 1991; Wynne et al., 1991) have demonstrated that the genetic nature of resistance to *Cercospora* leaf spots in groundnut is quantitative, horizontal, controlled predominantly by additive gene effect. Furthermore, they reported that it is determined by recessive alleles at five loci and independently inherited. This suggests that a cultivar with resistance to both leaf spots could be developed (Wynne et al., 1991).

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The genetic variability and parameters have been calculated for many crops (Maniee et al., 2009; Kahrizi et al., 2010a, 2010b; Garavandi et al., 2011; Safavi et al., 2011). However, from North Cameroon, no information exists on the genetic variability and relationships among quantitative characters explaining resistance to *Cercospora* leaf spots in groundnut (Hamasselbe, 2006). Such information could help breeders to understand the genetic nature of resistance to *Cercospora* leaf spots and develop an appropriate breeding strategy based on host/plant genetic resistance (Medan et al., 2004). The objectives of the study were to (i) assess the extent of genotypic variability, heritability and expected genetic gain of percent defoliation, *Cercospora* severity, yield and yield components, (ii) determine interrelationships between these characters.

MATERIALS AND METHODS

Field experiment was carried out in 2001 and 2002 at the Institute of Agricultural Research for Development (IRAD) Farm, Maroua (10° 35' N 14° 18' E), 421 m above sea level, located in the sudano-sahelian region of North Cameroon.

Twenty groundnut genotypes were evaluated in the study. The checks included were 55-437 and GP-NC 343 a susceptible and a resistant genotype to both leaf spots, respectively (Ntare, 2001). The description of these genotypes is presented in Table 1.

The experiment was laid out in a Randomised Complete Block Design with three replications in both years. The experimental field was ploughed and groundnut seeds were sown on flat seed bed at one kernel per hill (60 kg ha⁻¹ of kernels). Plot size was a single row of 10 m length with spacing between and within rows of 60 cm and 10 cm, respectively. The corresponding plant population was 166.667 plants/ha.

Prior to sowing, groundnut seeds were dressed with Marshall (Carbosulfan FMC 10%) at the rate of 40 g 5 kg⁻¹ of kernel to

control soil borne insects and millipede damage. Compound fertilizer NPK (10-30-10) was applied at the rate of 100 kg ha⁻¹ two weeks after sowing. Weeds were controlled manually and when necessary throughout the growing period of the crop. The first weeding was done at two weeks after sowing to insure better air circulation, rain water penetration in the soil and fertilizer application.

Data were collected on the following parameters:

- Plant height (cm): the height of the main stem from ground level to the tip of 10 randomly chosen and labeled plants per plot at 60 days after sowing (DAS).

- *Cercospora* severity: percent diseased leaves on the main stem of the 10 previous labeled plants at 60 DAS and at harvest using a nine-point field scale for disease rating.

- Percent defoliation: the ratio of leaflets lost to the total leaflets on the main stem of the 10 previous plants at one week before harvest. It was computed as follows:

$$\text{Percent Defoliation} = [(\text{leaflets lost}) / (\text{total leaflets})^{-1}] \times 100$$

- Pod weight (g): the weight of mature pods per plot after two weeks of sun drying in the field.

- Fodder weight (g): the weight of above and under ground biomass after hand picking of dried mature pods per plot.

Components of variance were estimated using the method described by Bliss et al. (1973). They were obtained by equating the mean square of a source of variance to its expectation and solving for the unknown using the form of the general analysis of variance for the two years combined as presented in Table 2. Thus: $\sigma_e^2 = M_e$ (1)

$$\sigma_{gy}^2 = \frac{M_{gy} - M_e}{r} \quad (2)$$

$$\sigma_g^2 = \frac{M_g - M_{gy}}{ry} \quad (3)$$

where, σ_e^2 , σ_{gy}^2 and σ_g^2 are components of variance for error, genotype by environment interaction and genotype, respectively. M_e , M_{gy} and M_g are the observed values of the mean squares for the error, interaction and genotype, respectively.

Genotypic coefficient of variability, was calculated using the formula indicated by Burton and Devane (1963) as follows:

$$GCV \quad (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \quad (4)$$

where, GCV, $\sqrt{\sigma_g^2}$ and \bar{X} are genotypic coefficient of variability, genotypic standard deviation and mean, respectively of a given character.

Heritability estimates were calculated in broad sense as suggested by Fehr (1987):

$$H_b^2 = \frac{\sigma_g^2}{\sigma_{ph}^2} \quad (5) \text{ or}$$

$$H_b^2 = \frac{\sigma_g^2}{\sigma_e^2 + \frac{\sigma_{gy}^2}{y} + \sigma_g^2} \quad (6)$$

Where, r and y are the number of replication and year, respectively.

Genetic gain was computed as indicated by Burton and Devane (1963):

$$\Delta G \quad (\%) = \frac{\Delta G}{\bar{X}} \times 100 \quad (7)$$

where, ΔG (%), ΔG and \bar{X} are genetic gain, genetic advance and mean of a given character.

The phenotypic, genotypic and environment correlation coefficients were estimated using the formulae suggested by Mode and Robinson (1959).

RESULTS

Estimates of genotypic coefficient of variability (GCV), broad sense heritability (H_b^2), genetic advance (ΔG) and expected genetic gain (ΔG %) of the characters studied are presented in Table 3.

- Plant height: This character showed low genotypic coefficient of variability, 18.70%, high heritability, 93.86% and moderate genetic gain, 46.96%.

- *Cercospora* severity at 60 DAS: All the genetic estimates of this trait were low, 3.55, 15.38 and 4.02% for genotypic coefficient of variability, heritability and genetic gain, respectively.

- *Cercospora* severity at harvest exhibited low genotypic coefficient of variability, 9.23%, high heritability, 62.50% and low genetic gain, 22.88%.

- Percent defoliation: Genotypic coefficient of variability for this character was low, 11.96%, heritability estimate was moderate, 43.45% and genetic gain was low, 24.47%.

- Pod yield: Low genotypic coefficient of variability, 17.71%, high heritability, 84.54% along with high genetic gain, 51.33% were recorded.

- Fodder yield: Genotypic coefficient of variability was low, 7.98%, heritability moderate, 32.33% and genetic gain low, 14.09%.

The results indicated that genotypic coefficients of variability for all the characters studied were low, while broad sense heritability estimates varied from low to high. Genetic gain values were low, except for plant height and pod yield.

Phenotypic (p), genotypic (g) and environmental (e) correlation coefficients between plant height, *Cercospora* severity at 60 DAS and at harvest, pod and fodder yield with percent defoliation are given in Table 4.

- Plant height had highly significant negative (-0.46) phenotypic correlation with percent defoliation

- *Cercospora* severity at 60 DAS showed highly significant positive (+0.64) phenotypic and significant positive (+0.58) environmental associations.

- *Cercospora* severity at harvest exhibited highly significant positive phenotypic, genotypic and environmental correlations, +0.88, +0.75 and +0.44, respectively.

- Pod yield had highly significant positive (+0.41) phenotypic relationship with percent defoliation.

- Fodder yield: Significant negative genotypic and environmental correlations, -0.61 and -0.19 respectively, were recorded.

The results showed that phenotypic correlation coefficients were highly

significant and higher than genotypic and environmental correlations except for fodder yield. *Cercospora* severity and fodder yield at harvest had significant genotypic associations with percent defoliation.

Table 1: Description of the groundnut genotypes tested for the study.

Genotype	Origin	Taxonomic status
SAMNUT 10	Nigerian improved variety	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)
SAMNUT 11	Nigerian improved variety	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)
SAMNUT 18	Nigerian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> Early maturing (90-100 days)
SAMNUT 21	Nigerian improved variety	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Medium maturing (110-120 days)
SAMNUT 22	Nigerian improved variety	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Medium maturing (110-120 days)
ISAMNUT 23	Nigerian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> . Early maturing (90-100 days)
CGS 269	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> . Early maturing (90-100 days)
CGS 1272	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> . Early maturing (90-100 days)
K3237-80	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> (bunch). Early maturing (90-100 days)
55-437*	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> . Early maturing (90-100 days)
JL 24	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> . Early maturing (90-100 days)
ICGV 86003	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>fastigiata</i> var. <i>vulgaris</i> . Early maturing (90-100 days)
28-206	Cameroonian improved variety	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Medium maturing (110-120 days)
ICG 6902	ICRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)
ICGV 91225	ICRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)
ICGV 92087	ICRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> (bunch). Late maturing (130-140 days)
ICGV 92099	ICRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)
# 3-94	ICRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Medium maturing (110-120 days)
GP-NC 343*	ICRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)
ICGMS 42	IRISAT/genotype	<i>A. hypogaea</i> ssp <i>hypogaea</i> var. <i>hypogaea</i> . Late maturing (130-140 days)

*Check genotypes

Table 2: Form of the general analysis of variance for the two years combined.

Source of variation	df	MS	EMS
Year	y-1		
Replication in year	y(r-1)		
Genotype	(g-1)	M_g	$\sigma_e^2 + r\sigma_{gy}^2 + ry\sigma_g^2$
Genotype x year	(g-1)(y-1)	M_{gy}	$\sigma_e^2 + r\sigma_{gy}^2$
Error	y(g-1)(r-1)	M_e	σ_e^2
Total	ygr-1		

Where, y = number of year; r = number of replication; g = number of genotype; df = degree of freedom; MS = observed mean squares; EMS = expected mean squares; σ_{gy}^2 = genotype by year interaction variance; σ_g^2 = total genetic variance among genotypes; σ_e^2 = error variance.

Table 3: Estimates of genotypic coefficient of variability (GCV.), broad sense heritability (H_b^2), genetic advance (ΔG) and expected genetic gain ($\Delta G\%$) of the characters studied.

Character	G.C.V. (%)	H_b^2 (%)	ΔG	ΔG (%)
Plant height	18.70	93.86	17.59	46.96
C. severity at 60 DAS	3.55	15.38	0.16	4.02
C. severity at harvest	9.23	62.50	1.24	22.88
Percent defoliation	11.96	43.45	8.73	24.47
Fodder yield	7.98	32.33	660.84	14.09
Pod yield	17.71	84.54	867.51	51.33

Table 4: Phenotypic (p), genotypic (g) and environmental (e) correlation coefficients between plant height, *Cercospora* severity at 60 DAS and at harvest, percent defoliation, pod and fodder yield for the characters studied.

Character		<i>Cercospora</i> severity at 60 DAS	<i>Cercospora</i> severity at harvest	Percent defoliation	Pod yield	Fodder yield
Plant height	(p)	-0.186*	-0.250*	-0.461**	0.173	-0.062
	(g)	0.564*	0.833**	0.434	0.629*	0.005
	(e)	-0.012	-0.081	-0.065	0.322*	0.157
<i>Cercospora</i> severity at 60 DAS	(p)		0.712**	0.641**	0.463**	0.165
	(g)		0.687*	0.356	0.560*	-0.016
	(e)		0.529**	0.579*	0.093	-0.077
<i>Cercospora</i> severity at harvest	(p)			0.875**	0.508**	0.052
	(g)			0.749**	0.554*	-0.352
	(e)			0.438**	0.009	-0.057
Percent defoliation	(p)				0.414**	0.085
	(g)				0.312	-0.613*
	(e)				-0.116	-0.188*
Pod yield	(p)					0.109
	(g)					-0.140
	(e)					0.127

*, ** Significantly different at 0.05 and 0.01 level of probability, respectively.

DISCUSSION

All the characters studied showed low estimates of genotypic coefficient of variability, indicating similar genetic potential of the genotypes tested (Shalini et al., 2000). Generally, low genotypic coefficient of variability may be caused by large means relative to small error terms, or vis versa (Omoigui et al., 2006). A low genotypic coefficient of variability may limit the gain that could be made to improve resistance to *Cercospora* in the plant materials tested (Linhart and Gehring, 2003). These results are in accordance with those of Arshall et al. (2002) who reported low genotypic coefficient of variability for yield and yield components in chickpea.

Most of the characters were highly heritable as indicated by their high broad sense heritability estimates. High heritability may be attributed to additive and non additive (dominance and epistasis) gene action that could make selection for such traits effective in improving resistance to *Cercospora* leaf spots (Ozveren et al., 2006). Ghizan and Nour (2000) also found high broad sense heritability estimates for 100-seed weight and number of pods per groundnut plant.

Low genetic gain values obtained for most of the characters studied indicated low levels of additive gene action. Genetic gain is low where the genes governing a character showed dominance (Kulbe et al., 2000). In contrast, Kahrizi et al. (2010) obtained high genetic gain for some morpho-physiological variables of durum wheat (*Triticum turgidum* var. durum).

Heritability along with genetic gain is more useful in predicting the resultant effect from selecting best genotypes (Kahrizi et al., 2010). Pod yield had high heritability along with genetic gain, indicating that selection based on phenotypic performance could be effective for this character (Ozveren et al., 2006).

Associations between percent defoliation with other characters studied were non-genetic in nature except for *Cercospora* severity and fodder yield at harvest, which

had significant genotypic correlation coefficients. Low inherent associations are probably due to the lack of pleiotropic gene action and/or linkage between genes governing these characters (Ghizan and Nour, 2000). These results are at variance with those of Ait Abd et al. (2010) who found higher genotypic than phenotypic correlations in Agran trees,

Cercospora severity and fodder yield at harvest showed significant positive and negative inherent associations with percent defoliation, respectively. Selection for one character will result in a progress for all positively but in a regress to all negatively correlated characters (Gomez and Lopez, 2005). These results indicate that resistance to *Cercospora* could be improved through selection for genotypes which had low disease severity scores and high fodder yield at harvest. However, fodder yield showed low heritability along with genetic gain that could make selection for this character difficult (Ghizan and Nour, 2000). Anderson et al. (1991) obtained positive and significant correlation between percent defoliation in field with late leaf spot lesion number and early leaf spot lesion size in groundnut.

Conclusion

The results of this study revealed that improvement of resistance to *Cercospora* leaf spots in the genotypes tested could be limited by the low levels of genetic variability of the traits measured. Selection based on phenotypic performance could be effective for pod yield. Resistance to *Cercospora* leaf spots in groundnut could be improved through selection for low *Cercospora* severity and high fodder yield at harvest.

Since correlation coefficient analysis provides limited genetic information on the relationships between quantitative traits, a path coefficient analysis is required to estimate the direct and indirect contributions of the characters studied to groundnut resistance to *Cercospora* leaf spots.

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