Variability and Correlations among Groundnut Populations for Early Leaf Spot, Pod Yield, and Agronomic Traits

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Abstract: The present experiment was conducted in Mali to study the genetic variability and correlation of early leaf spot (ELS) resistance parameters and agro-morphological traits in groundnut using two F3 populations from crosses QH243C X NAMA and TS32-1 X NAMA. Estimates of genotypic coefficient of variation and phenotypic coefficient of variation revealed high value for pod yield, kernel yield, and ELS score at 60 and 80 days after sowing for the cross QH243C X NAMA. Low-to-moderate GCV and PCV were obtained for the remaining traits for both crosses. High heritability values coupled with high genetic advance as percentage of mean recorded for ELS_II, defoliation percent, pod yield in cross QH243C X NAMA; shelling percent for the cross TS32-1 X NAMA and ELS_III; and plant height, kernel yield in both crosses, indicate the significant role of additive gene action for inheritance of these traits. Correlation analysis indicated that pod and kernel yield were significant and positively correlated with 100 kernel weight and shelling percent. For cross QH243C X NAMA, kernel yield showed significant positive correlation with all ELS resistance components but the correlation was not significant for the cross TS32-1 X NAMA. Positive and significant correlation was observed between ELS resistance components themselves, suggesting that these components could be controlled by a similar polygenic system. The findings suggest that early generation selection should be effective for days to first flowering, days to 50% flowering, plant height, pod yield, kernel yield, 100 kernel weight and early leaf spot resistance which recorded the highest value of heritability in the two crosses.

Keywords: genetic variability; correlation; agronomical traits; early leaf spot; groundnut

1. Introduction

Groundnut (*Arachis hypogaea* L.), an annual leguminous crop, is one of the important oil seed crops in the world. It is a rich source of protein. Groundnut seed contains about 45–55% oil and 27–33% of protein [1]. Its seeds are also a source of minerals and vitamins like vitamin E, niacin, falcin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine, and potassium [2]. In addition, the haulm is used as animal feed and industrial raw material. Groundnut also contributes to maintaining soil fertility by fixing atmospheric nitrogen.

In 2014, groundnut was grown in more than 115 countries around the world, covering a total area of about 24.31 million (M) hectares (ha) with a global production of about 42.4 million tons [3]. The major producers were China and India with 15.7 M and 6.5 M tons, respectively, followed by Nigeria (3.4 M tons), the USA (2.4 M tons), and Sudan (1.8 M tons). Continent-wide, Africa ranks second accounting for over 29.8% of global production after Asia (59.8% of global production). However, Africa has the lowest average yield (964.8 kg/ha) compared to America (3333.4 kg/ha), Asia (2370.6 kg/ha), Oceania (1847.9 kg/ha), Europe (1158.5 kg/ha), and global average yield (1654.6 kg/ha). Several constraints like abiotic stress (e.g., drought) and biotic stress (e.g., diseases and pests) can explain the low productivity of groundnut in Africa.

Among the main foliar fungal diseases, early leaf spot (ELS) caused by *Cercospora arachidicola* Hori and late leaf spot (LLS) caused by *Phaeoisariopsis personata* (Bert and Curtis) Deigton are the more destructive diseases [4,5]. The two diseases combined can cause pod and fodder yield loss of over 50% to 70% [6,7]. In West Africa, yield loss due to ELS alone reaches up to 70% [8]. Development of high yielding cultivars with resistance to these diseases, particularly ELS, is an important breeding priority to reduce impact of disease and increase groundnut production in West Africa. Understanding the genetic underpinnings of early leaf spot resistance components and agronomic traits (yield and its components) is likely to contribute to enhancing breeding for these traits.

Effectiveness of selection is dependent upon the availability of large genetic variability present in the breeding material for the target character and the extent to which it is heritable [9,10]. It also depends on the direction and magnitude of association between the traits to be improved [11]. Therefore, plant breeders need to have a good knowledge about genetic variability—i.e., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense, genetic advance (GA), and genetic advance as percentage of mean (GAM)—and good understanding of correlation between the traits to be improved for the genetic material at hand. To this effect, the objective of the present study was to assess genetic variability of two F3 populations of groundnut based on ELS resistance components, agro-morphological traits (agronomic yield and yield components) and evaluate the relationships between these traits.

2. Results

2.1. Analysis of Variance

The results of analysis of variance for the measured characters are presented in Table 1. In the analysis of variance for all agro-morphological traits, the three stages of ELS and defoliation percent due to ELS effect in the two F3 populations revealed significant difference ($p < 0.05$) for all the traits except ELS score at 60 DAS (ELS_II) for the cross TS32-1 X NAMA. This indicated the presence of variability in the genetic materials for the traits studied.

The susceptible parents QH243C and TS32-1 had an average disease score of 7.35 and 8.052 at 80 days after sowing (ELS_III), while the resistant parent (NAMA) had an average disease score of 2.93 and 3.094 in crosses QH243C X NAMA and TS32-1 X NAMA, respectively. The susceptible and resistant parents also differed significantly in terms of infestation progress for ELS score at 60 (ELS_II) and 80 days after sowing (ELS_III). In a span of 20 days, the disease score for QH243C and TS32-1 increased from 4.32 to 7.35 and from 3.63 to 8.05, while that of the resistant parent (NAMA) rose from 2.02 to 2.93 and from 2.07 to 3.09 in crosses QH243C X NAMA and TS32-1 X NAMA, respectively. The two F3 populations significantly differed for all agro-morphological traits. The F3 population from cross QH243C X NAMA was distinct for its highest mean value for all agro-morphological traits including pod and kernel yield and its lowest mean value for the three stages of ELS incidence, whereas the one from TS32-1 X NAMA showed low mean for the agro-morphological traits and relatively higher value for ELS score.

Table 1. Mean performance of parents and F3 populations for ELS scores and agro-morphological trait.

Crosses	Source of Variation	DFF	D50F	ELS_I	ELS_II	ELS_III	PH	Defol%	Pyield	Kyield	Sh%	100 KW
QH243C X NAMA	NAMA	29.65	34.01	2.00	2.02	2.93	26.13	23.94	739.28	558.01	50.46	22.29
	QH243C	25.01	26.73	2.33	4.32	7.35	40.63	31.26	2360.37	1571.89	62.62	28.99
	F3pop	25.66	28.13	2.33	2.91	5.04	38.53	32.23	2409.20	1261.72	60.66	31.48
	Range	21–33	24–34	2–3	2–5	3–8	8–50	14.38–59.54	691.70–4387	514.60–2324	20–95	15–53
	Fproba	**	**	*	**	**	**	**	**	**	*	**
	CV%	7.7	6.78	13	23.17	26.31	18.24	16.08	22.97	20.66	10.76	12.78
TS32-1 X NAMA	NAMA	27.78	32.29	2.00	2.07	3.09	23.14	30.86	782	369.99	58.29	23.62
	TS32-1	23.39	25.74	2.33	3.63	8.05	38.42	51.78	1324	751.61	53.5	29.73
	F3pop	23.9	26.40	2.50	2.97	5.44	35.58	50.39	2111.25	1089.12	57.42	30.40
	Range	20–32	24–34	2–3	2–6	3–8	6.66–50	16.67–84.87	830–5099	269.8–2614	10–96	14–53
	Fproba	**	**	**	ns	**	**	**	**	**	**	**
	CV%	6.65	6.26	13.94	5.84	21.28	20.96	13.35	26.12	32.76	18.18	11.93

DFF: days to first flowering, D50F: days to 50 percent flowering, PH: plant height, Sh%: shelling percent, 100 KW: 100 kernel weight, Pyield: pod yield, Kyield: kernel yield, ELS_I: early leaf spot score at 40 days after sowing, ELS_II: early leaf spot score at 60 days after sowing, ELS_III: early leaf spot score at 80 days after sowing, Defol%: defoliation percent, *: significant at 0.05, **: significant at 0.01, ns: no significance.

2.2. Estimation of Genetic Variability Parameters

The genotypic (Vg) and phenotypic variance (Vp), genotypic (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (H^2), and genetic advance as percent of mean (GAM) for all the traits studied are presented in Table 2. Genotypic variances ranged from 0.03 (ELS_I) to 176,529 (pod yield) and from 0.001 (ELS_II) to 48,847 (pod yield) in crosses QH243C X NAMA and TS32-1 X NAMA, respectively. For phenotypic variance, the minimum value was recorded for ELS_I (0.09) and ELS_II (0.02) in crosses QH243C X NAMA and TS32-1 X NAMA and the maximum for pod yield in both crosses (276,560.3 and 72,159). Almost all traits related to ELS resistance (ELS_I, ELS_II and ELS_III) presented low genotypic and phenotypic variances, except defoliation percent in both crosses.

Table 2. Genetic variability parameters for different traits in F_3 population of a groundnut.

Variable	Mean	Vg	Vp	GCV	PCV	H^2 (%)	GA	GAM
Cross QH243 X NAMA								
DFF	25.71	3.3	3.81	7.07	7.59	86.73	3.49	13.56
D50F	28.19	3.24	3.64	6.38	6.77	88.98	3.5	12.4
ELS_I	2.33	0.03	0.09	7.87	13.16	35.77	0.23	9.7
ELS_II	2.93	0.31	0.46	19.03	23.19	67.36	0.94	32.17
ELS_III	5.04	1.49	1.79	24.18	26.56	82.85	2.29	45.34
PH	38.41	42.2	49.25	16.91	18.27	85.69	12.39	32.25
Defoliation%	32.12	16.54	26.01	12.66	15.88	63.60	6.68	20.8
PYield (kg/ha)	2387.72	176,529	276,560.3	17.6	22.02	63.83	691.49	28.96
Kyield (kg/ha)	1256.74	82,476	108,412.7	22.85	26.2	76.08	516.01	41.06
Shelling%	60.56	17.71	40.35	6.95	10.49	43.89	5.74	9.48
100 KW (g)	31.34	11.06	15.43	10.61	12.53	71.68	5.8	18.51
Cross TS32-1 X NAMA								
DFF	23.95	1.91	1.96	5.76	5.85	97.08	2.80	11.70
D50F	26.47	2.24	2.29	5.66	5.72	97.98	3.05	11.54
ELS_I	2.50	0.03	0.04	6.80	7.62	79.70	0.31	12.51
ELS_II	2.97	0.001	0.02	1.90	4.96	14.72	0.04	1.50
ELS_III	5.45	0.64	0.69	14.64	15.28	91.69	1.57	28.87
PH	35.46	42.58	43.48	18.40	18.60	97.93	13.30	37.51
Defoliation%	50.18	23.45	25.78	9.65	10.12	90.97	9.51	18.96
PYield (kg/ha)	2085.00	48,847	72,159	10.60	12.88	67.69	374.59	17.97
Kyield (kg/ha)	1076.24	34,357	39,948.33	17.22	18.57	86.00	354.11	32.90
Shelling%	57.39	37.40	42.60	10.66	11.37	87.79	11.80	20.57
100 KW (g)	30.32	3.97	4.66	6.57	7.12	85.25	3.79	12.50

DFF: days to first flowering, D50F: days to 50 percent flowering, PH: plant height, Shelling%: shelling percent, 100 KW: 100 kernel weight, Pyield: pod yield, Kyield: kernel yield, ELS_I: early leaf spot score at 40 days after sowing, ELS_II: early leaf spot score at 60 days after sowing, ELS_III: early leaf spot score at 80 days after sowing, Defoliation%: defoliation percent, Vg: genotypic variance, Vp: phenotypic variance, GCV: genotypic coefficient of variance, PCV: phenotypic coefficient of variance, H^2: heritability in broad sense, GA: genetic advance, GAM: genetic advance as percent of mean.

Genotypic coefficient of variance (GCV) varied from 6.38 (D50F) to 24.18 (ELS_III) and phenotypic coefficient of variance (PCV) varied from 6.77 (D50F) to 26.56 (ELS_III) in the cross QH243C X NAMA (Table 2). For cross TS32-1 X NAMA, the maximum values of GCV and PCV were recorded for plant height (18.40 and 18.60) and the minimum values for ELS_II (1.90 and 4.96). High GCV and PCV (>20%) were observed only in the cross QH243C X NAMA for ELS_II, ELS_III, kernel yield and pod yield. Moderate estimates of PCV and GCV were observed for 100 KW in the cross QH243C X NAMA; ELS_III, pod yield, and kernel yield in the cross TS32-1 X NAMA; and plant height, defoliation percent, and shelling percent in both crosses. The days to first flowering (DFF), days to 50% flowering (D50F), and ELS score at 40 days after sowing (ELS_I) recorded low value (<10%) of GCV and PCV in the two crosses. GCV and PCV estimates for all traits were higher in the cross QH243C X NAMA relative to cross TS32-1 X NAMA. In addition, PCV estimates were higher than GCV estimates for all the traits in both crosses. However, the magnitude of difference was low for all the traits.

Broad sense heritability (H^2) represents the relative strength of the traits and indicates the efficiency of selection systems [10]. H^2 estimates varied from 35.77% (ELS_I) to 88.98% (D50F) in the cross QH243C X NAMA and from 14.72 (ELS_II) to 97.98% (D50F) in the cross TS32-1 X NAMA. High H^2 (>60%) was observed for the days to first flowering (86.77% and 97.08%), days to 50% flowering (88.98% and 97.98%), ELS_III (82.85% and 91.69%), plant height (85.69% and 97.93%), defoliation percent (63.60% and 90.97%), pod yield (63.83% and 67.69%), kernel yield (76.08% and 86%), and 100 kernel weight (71.68% and 85.25%) in the crosses QH243C X NAMA and TS32-1 X NAMA, respectively. Moderate H^2 (30–60%) was recorded for ELS score at 40 days after sowing (ELS_I) and shelling percent in the cross QH243C X NAMA with 35.25% and 43.89%, respectively. Low H^2 (14.72%) was recorded for ELS score at 60 days after sowing (ELS_II) in the cross TS32-1 X NAMA. Contrary to GCV and PCV estimates, H^2 values were high in the cross TS32-1 X NAMA compared to H^2 in the cross QH243C X NAMA for all traits studied except ELS score at 60 days after sowing (ELS_II).

Genetic advance (GA) estimates ranged from 0.23 for ELS_I to 691.49 for pod yield in the cross QH243C X NAMA and from 0.04 for ELS_II to 374.59 for pod yield in the cross TS32-1 X NAMA. The highest GA was recorded for pod yield and kernel yield in both crosses. For genetic advance as percent of mean (GAM), high (>20%) values were recorded for ELS_II (32.17%), defoliation percent (20.80%), and pod yield (28.96%) in the cross QH243C X NAMA; shelling percent (20.57%) in the cross TS32-1 X NAMA; and ELS_III (45.34% and 28.87%), plant height (32.25% and 37.51%), and kernel yield (41.06% and 32.90%) in both crosses. Moderate GAM (10–20%) was observed for the remaining traits except ELS_I (9.7%) and shelling percent (9.48%) in the cross QH243C X NAMA and ELS_II (1.50%) in cross TS32-1 X NAMA.

2.3. Correlation

Results of correlation analysis between all agro-morphological traits and ELS resistance parameters in the two crosses (QH243C X NAMA and TS32-1 X NAMA) are presented in Table 3. Days to 50% flowering showed significant and negative correlation with all traits except with days to first flowering in both crosses. Shelling percent and ELS resistance parameters (ELS_I, ELS_II, ELS_III, and defoliation percent) showed positive correlation with all traits except with days to first flowering and days to 50% flowering in the two crosses. Pod yield showed positive correlation with kernel yield ($r = 0.8661$ and $r = 0.7648$), 100 kernel weight ($r = 0.475$ and $r = 0.1125$) and shelling percent ($r = 0.3223$ and $r = 0.0486$) in both crosses. For cross QH243C X NAMA, kernel yield showed significant positive correlation with all ELS resistance components ($r = 0.29$ ** with ELS_I, $r = 0.36$ ** with ELS_II, $r = 0.48$ ** with ELS_III) but the correlation was not significant for the cross TS32-1 X NAMA. All components of ELS resistance were positively correlated among themselves in the two crosses. Correlation of plant height in cross QH243C X NAMA with 100 kernel weight ($r = 0.2463$) and kernel yield ($r = 0.3948$) were significant and positive, while in cross TS32-1 X NAMA these correlations were not significant and took negative direction ($r = -0.0157$ and $r = -0.0448$, respectively).

Table 3. Correlation coefficients among agro-morphological traits and ELS resistance parameters for two crosses.

Traits	D50F	Sh%	Defol%	ELS_I	ELS_II	ELS_III	DFF	PH	100 KW	Pyield
Cross QH243C X NAMA										
D50F	-									
Sh%	−0.45 **	-								
Defol%	−0.55 **	0.17 ns	-							
ELS_I	−0.29 **	0.15 ns	0.29 *	-						
ELS_II	−0.43 **	0.15 ns	0.56 **	0.54 **	-					
ELS_III	−0.65 **	0.30 *	0.66 **	0.37 **	0.75 **	-				
DFF	0.93 **	−0.43 **	−0.56 **	−0.30 *	−0.46 **	−0.66 **	-			
PH	−0.51 **	0.39 **	0.50 **	0.43 **	0.64 **	0.75 **	−0.57 **	-		
100 KW	−0.29 **	0.43 ns	0.06 ns	0.34 **	0.21 ns	0.11 ns	−0.24 *	0.25 *	-	
Pyield	−0.63 **	0.32 ns	0.15 ns	0.31 **	0.36 **	0.40 **	−0.55 **	0.36 **	0.47 **	-
Kyield	−0.61 **	0.45 ns	0.20 ns	0.29 **	0.36 **	0.48 **	−0.54 **	0.39 **	0.47 **	0.87 **
Cross TS32-1 X NAMA										
D50F	-									
Sh%	−0.46 **	-								
Defol%	−0.38 **	0.39 **	-							
ELS_I	−0.42 **	0.25 *	0.42 **	-						
ELS_II	−0.46 **	0.12 ns	0.26 *	0.19 ns	-					
ELS_III	−0.56 **	0.41 **	0.48 **	0.52 **	0.35 **	-				
DFF	0.89 **	−0.38 **	−0.37 **	−0.38 **	−0.39 **	−0.51 **	-			
PH	−0.58 **	0.39 **	0.47 **	0.44 **	0.28 *	0.55 **	−0.63 **	-		
100KW	−0.22 *	0.24 *	0.27 *	0.004 ns	0.22 ns	0.06 ns	−0.22 ns	−0.02 ns	-	
Pyield	−0.31 **	0.05 ns	0.16 ns	0.19 ns	0.11 ns	0.30 **	−0.21 ns	0.02 ns	0.11 ns	-
Kyield	−0.38 **	0.22 ns	0.15 ns	0.13 ns	0.18 ns	0.15 ns	−0.22 *	−0.05 ns	0.10 ns	0.76 **

DFF: days to first flowering, D50F: days to 50 percent flowering, PH: plant height, Sh%: shelling percent, 100 KW: 100 kernel weight, Pyield: pod yield, Kyield: kernel yield, ELS_I: early leaf spot score at 40 days after sowing, ELS_II: early leaf spot score at 60 days after sowing, ELS_III: early leaf spot score at 80 days after sowing, Defol%: defoliation percent, *: significant at 0.05, **: significant at 0.01, ns: no significant.

3. Discussion

In the present study, significant differences among the F3 progenies in the two crosses were observed for all the traits indicating the presence of genetic variability for disease score and agronomic traits in the populations. High variability values for these traits were previously reported including leaf spot disease resistance [12–14] in F2 populations; and days to first flowering, days to 50% flowering, pod yield, kernel yield, shelling percent, and 100 kernel weight in cultivated groundnut [2,12,15,16].

Estimation of GCV and PCV revealed high value for kernel yield, pod yield and ELS score at 60 and 80 days after sowing (ELS_II and ELS_III) in cross QH243C X NAMA, suggesting the presence of considerable variation among the population. Similar findings of higher estimates of GCV and PCV were reported for kernel yield and pod yield [2,9,10,15,17–19], ELS score at 60 and 80 days after sowing [13,14,18,20–23]. Moderate PCV and GCV were observed for 100 kernel weight (cross QH243C X NAMA); pod yield, kernel yield, and ELS score at 80 days after sowing (cross TS32-1 X NAMA), plant height, shelling percent, and defoliation percent (in both crosses) indicating presence of moderate levels of variability for these traits in the populations. These results are similar to the findings of Maurya et al. [24] and Patil et al. [25] for plant height and shelling percent, and Hamasselbe et al. [22] for defoliation percent. Days to 50% flowering and days to first flowering showed low GCV and PCV, indicating the presence of narrow genetic variability for these traits. These results are in accordance with previous findings [10,18,26,27]. The difference between PCV and GCV was small, indicating low effect of environment on the expression of these traits.

Most of the traits studied were highly heritable as indicated by high broad sense heritability estimates. Heritability estimates for ELS resistance were consistent over the two crosses and were generally high for all scores (ELS_ I, ELS_II, ELS_III, and defoliation percent) indicating that selection based on ELS score and defoliation percent would be useful for ELS resistance. These results also indicate a high response to selection for ELS resistance due to reduced environment influence in these crosses. Similar findings were obtained for ELS score [18,23,28] and for ELS score and defoliation

percent [22]. The authors concluded that individual plant selection for early and late leaf spot diseases would be effective in early generations. High heritability was also obtained for the agro-morphological traits like days to first flowering, days to 50% flowering, plant height, pod yield, kernel yield, and 100 kernel weight in both crosses. Similar results were also reported for days to first flowering, days to 50% flowering and plant height [9,15], for pod yield and kernel yield [10,15,29], and for pod yield and 100 kernel weight [18].

Broad sense heritability is an important parameter for breeding. It provides useful information on genetic variability, however, when coupled with genetic advance as a percent of mean it provides a better prediction of expected gain under selection than heritability alone. Estimates of both parameters help to understand the type of gene action involved in the expression of traits studied, particularly for polygenic traits. High heritability values coupled with high GAM were recorded for ELS_II, defoliation percent, pod yield in cross QH243C X NAMA; shelling percent in cross TS32-1 X NAMA; and ELS_III, plant height, kernel yield in both crosses. In addition, high heritability values with moderate GAM were obtained for ELS_I, pod yield in cross TS32-1 X NAMA and for days to first flowering, days to 50% flowering, 100 kernel weight in the two crosses. This indicates a significant role of additive gene action for inheritance of these traits. Classical selection methods would be effective for improvement of these traits including ELS resistance from these crosses. Similar results were reported for plant height, pod yield, kernel yield [10,25], days to first flowering, days to 50% flowering [9,21,26], and ELS resistance [13,14,18]. Moderate heritability values coupled with low GAM were obtained in cross QH243C X NAMA for shelling percent. This indicates that additive and non-additive gene effects are playing an important role in the expression of this character. Therefore, selection for this character is not effective in early segregating generations. This finding is in agreement with previous results [14]. The correlation analysis in the present study revealed significant and negative correlation between flowering parameters (days to first flowering and days to 50% flowering) with pod yield and kernel yield in the two crosses, suggesting that early flowering and high yield could be simultaneously selected. These results are in accordance with previous results [30,31]. Pod yield presented a positive correlation with kernel yield, 100 kernel weight, and shelling percent in both crosses, indicating a favorable association between yield and its components. Similar findings were also previous reported [9,13]. In the two crosses, ELS resistance parameters were positively and significantly associated among themselves. These results suggest that all ELS resistance parameters could be controlled by a similar polygenic system. Early research reported similar results for ELS components [20] and leaf spot diseases including ELS [18,31]. Correlations between ELS resistance parameters and kernel yield and its components were positive in cross QH243C X NAMA, revealing the linkage of high productivity with ELS susceptibility. These results are in agreement with [13,22,31]. Several studies revealed the possibility of breaking undesirable linkages between yield and diseases susceptibility by reshuffling of genes through multiple crosses [32]. ELS resistance combined with high yield could be bred through back crossing in multiple ways. Plant height presented a positive correlation with pod and kernel yield in cross QH243C X NAMA, whereas these correlations were negative in cross TS32-1 X NAMA, suggesting the possibility of identifying desirable recombinants in one of the crosses.

4. Materials and Methods

4.1. Study Area

The study was carried out in 2014 at ICRISAT West Africa Regional hub Research Station based at Samanko in Mali. Samanko is located at 25 km from Bamako near Niger River. The station is located between 12°54′ N, and 8°4′ W at an altitude of 330 m above sea level.

4.2. Breeding Population

Two Spanish bunch ELS susceptible varieties (i.e., QH243C and TS32-1) obtained from INERA and resistant local cultivar (NANA—a Virginia bunch) grown in Burkina Faso were used as parents to develop two populations (Pop1 = QH243 X NAMA and Pop2 = TS32-1 X NAMA). The F3 populations of the two crosses, comprised of 82 individuals per population, were used for early leaf spot resistance and agronomic trait evaluations.

4.3. Experimental Design and Traits Measured

The two F3 populations with 82 individuals each were grown in two different trials during the 2014 rainy season. Each entry was sown in one row of 4 m length by adopting spacing of 50 × 15 cm in an augmented design with three replications for checks. Seeds were treated using a fungicide (APRON STAR 42 WS) before sowing. The screening of the progenies and their parental lines was carried out under natural infestation. Samanko station is a hotspot for leaf spot diseases including ELS. Normal cultural practices were followed during the growing season. Observations were recorded for seven agro-morphological traits viz., days to first flowering (DFF, days after sowing), days to 50 percent flowering (D50F, days after sowing), plant height (PH, cm), shelling percent (Sh%), 100 kernel weight (100 KW, g), pod yield (Pyield, kg/ha), and kernel yield (Kyield, kg/ha). Also, at 40 days (ELS_I), 60 days (ELS_II), and 80 days (ELS_III) after planting, ELS incidence was scored using the 9-point field scale of ICRISAT [33]. Score of 1 was given if there was 0 % infection; 2 for 1–5%; 3 for 6–10%; 4 for 11–20%, 5 for 21–30%; 6 for 31–40%; 7 for 41–60%; 8 for 61–80%; and 9 for 81–100% infection. According to Pande and Rao [34], genotypes with a disease score of 1 to 3, 4 to 6 and 7 to 9 were designated as being resistant, tolerant, and susceptible, respectively. In addition, to evaluate the incidence of ELS in the F3 progenies, we also estimated the defoliation percent (Defol%) at 80 days after sowing. It was computed as follows based on the main stem of 10 plants

$$Defoliation\ percent = \frac{Number\ of\ leaflets\ lost}{Total\ leaflets} \times 100$$

4.4. Statistical Analysis

Analysis of variance (ANOVA) was carried out on the agro-morphological traits and ELS incidence parameters to access the genotype effect for all traits using Genstat 14th edition. Phenotypic and genotypic coefficients of variance were estimated according to Burton [35] to quantify the genetic variance among the genotypes. The heritability in broad sense and genetic advance as a percent of mean were estimated using the formula given by Johnson et al. [36] and Burton and De Van [37], respectively.

Phenotypic and genotypic variances were estimated using the formula

$$V_g = \frac{MS_g - MS_e}{r}$$

$$V_p = V_g + MS_e$$

Vg = genotypic variance; *Vp* = phenotypic variance; *MSg* = mean square of genotypes, *MSe* = mean square of error; and *r* = number of replications.

$$GCV = \frac{\sqrt{V_g}}{X} \times 100$$

$$PCV = \frac{\sqrt{V_p}}{X} \times 100$$

GCV = genotypic coefficient of variability; *PCV* = phenotypic coefficient of variability; $\sqrt{V_g}$ = genotypic standard deviation; $\sqrt{V_p}$ = phenotypic standard deviation; and X = general mean of the character.

Heritability in broad sense (H^2) was computed as the ratio of genetic (Vg) variance to the total phenotypic variance (Vp).

$$H^2 = \frac{V_g}{V_p} \times 100$$

$$GA = H^2 k \sqrt{V_p}$$

$$GAM = \frac{GA}{X} \times 100$$

GA = genetic advance; *GAM* = genetic advance as percent of mean; *k* = Selection differential, which is equal to 2.06 at 5% intensity of selection; X = general mean of the character.

Correlation analysis among all the traits studied was computed using Genstat 14th edition.

5. Conclusions

The present study indicated that most of traits were under influence of genetic control and could be improved through classical selection. Results suggest that early generation selection should be effective for days to first flowering, days to 50% flowering, plant height, pod yield, kernel yield, 100 kernel weight, and early leaf spot resistance which recorded highest value of heritability in the two crosses.

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