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Research Article

Analysis of genetic parameters, correlation and path coefficients in sesame (*Sesamum indicum* L.)

Zangui Hamissou[1*], Takvorian Najat[2,3], Naino Jika Abdel Kader[1] and Amoukou Adamou Ibrahim[1]

[1]Department of Plant Production, Faculty of Agronomy, Abdou Moumouni University, P.O. Box 10960, Niamey, Niger.
[2]Université Paris-Saclay, CNRS, AgroParisTech, Ecologie Systématique et Evolution, 91190, Gif-sur-Yvette, France
[3]Sorbonne Université, UFR Sciences de la Vie, UFR927, 4 Place Jussieu, 75005 F-75252 Paris Cedex 05, France
***E-Mail:** zanguiagro@gmail.com

Abstract
This study aimed to assess the genetic potential of 140 sesame genotypes from Niger to develop strategies for improving grain yields in the Sahelian region. The research combined an analysis of genetic parameters with an investigation into the interrelationships among yield components to advance selection criteria for local breeding programs. Using an Alpha-Lattice experimental design, eight key agronomic traits were measured. Analysis revealed significant genetic diversity among the accessions. High broad-sense heritability was found for yield (99.34%), days to maturity (82.60 %) and seeds per capsules (70.62 %), indicating strong genetic control and good potential for selective improvement. Conversely, the weight of 1,000 grains had very low heritability (9.24 %), suggesting major environmental influence. Path analysis identified the number of capsules per plant as having the most significant positive direct effect on yield (0.213). Consequently, the study concludes that breeding programs in Niger should prioritize the number of capsules per plant as the primary selection criterion for effectively increasing sesame yield.

Keywords : Sesame, genetic parameters, genetic and phenotypic correlations, path analysis,

INTRODUCTION

Sesame (*Sesamum indicum* L), one of the oldest and most highly regarded oilseed crops, is experiencing remarkable growth in West Africa. Praised for its refined oil, its high proportions of unsaturated fatty acids and antioxidant lignans (sesamin and sesamolin), sesame seeds are a product with high nutritional and economic value (Pathak *et al.,* 2020). In particular, Niger has distinguished itself as an important player in West African production, making sesame a strategic cash crop for enhancing the income of small farmers and national exports (Dossa *et al*., 2023). Nonetheless, the productivity potential of sesame in Niger remains underutilized.

The foundations of any successful genetic improvement program lie in an accurate assessment of the diversity and genetic parameters present in a local gene pool. By estimating genetic and phenotypic variance, broad sense heritability (H^2) and expected genetic gain (GS) the effeciency of selection for a particular trait may be predicted. High heritability in the broad sense indicates that the observed variance is mainly genetically driven, suggesting potential for selection response, although only the additive component is directly transmissible to subsequent generations (Parihar *et al*., 2022). Recent studie with sesame by Patel *et al*. (2022) indicated the presence of significant genetic diversity present for yield and architectural traits in ethnic collections, indicating successful selection is possible.

However, improving yield, which is a complex and polygenic trait, cannot occur by studying genetic parameters in isolation. There is a need to develop a better understanding of the interrelations of yield and its primary components, number of capsules per plant, number of seeds per capsule, and weight of 1000 seeds as well as secondary components such as plant height, number of branches, and cycle length. A first step in establishing these interrelations is phenotypic and genotypic correlation (Srikanth and Ghodke 2022). In particular, a strong positive correlation between yield and some components, for example number of capsules per plant, suggests that selection for that component could yield improvements in yield as well (Srikanth and Ghodke, 2022). However, simply focusing on correlation link can be misleading, as a simple correlation is the aggregate effect of a variable (or component) and any direct or indirect effects from other variables, thereby hiding the true causal patterns. Path analysis may be one of the best ways to overcome this limitation when studying the interrelationships between yield traits. Path analysis, which is an extension of multiple regression, resolves limitations in the simple correlation by separating the correlation coefficients into direct and indirect effects of independent variables (the components of yield) on the dependent variable (the yield) (Srikanth and Ghodke, 2022). Path analysis will also help identify the traits on which to focus selection efforts, based on their most immediate or significant impact. Several recent studies have highlighted the effectiveness of this method in determining the ranking of selection criteria in sesame, frequently indicating that the capsule number per plant and the weight of 1000 seeds are the most important for yield.

While these are worldwide tools for improving sesame, they have been rarely used to evaluate accessions adapted to the agroecological conditions of Niger and the Sahel. In order to develop an appropriate and effective selection strategy for farmers in Niger, an integrated analysis suggests that genetic parameters, correlations, and causal relationships should be examined. The expected results will identify the potential of local genetic resources and provide breeders with clear guidelines for improving the breeding program aimed at sustainably increasing sesame productivity in Niger.

MATERIALS AND METHODS

The experiment was conducted during 2023-2024 winter season at the experimental station of the Faculty of Agronomy of Abdou Moumouni University in Niamey. The experimental design was an Alpha-Lattice with 140 sesame genotypes from a national collection. The design included two replicates. Each replicate consisted of ten blocks, with fourteen elementary plots each. The essential principle of this method is to establish a configuration that allows each accession to be present exactly once in each replicate. This has the advantage of keeping the experimental field small enough to limit the impact of soil heterogeneity while evaluating a large number of genotypes. Within each replicate and each block, the accessions (which were not repeated at the same time in a given replicate) were randomly distributed across the elementary plots. The plots measure 2 m long and 1.5 m wide. The spacing maintained within each plot was 0.5 m between rows and between holes, resulting in a density of twenty holes per elementary plot. At emergence, the plots were thinned to one plant per hole. Replicates were separated by a distance of 2 m. A localized fertilization of 150 kg/ha in the form of NPK (15-15-15) was made immediately after the first weeding and after enough rain. The genetic components of variance were calculated using mean squares. The genetic components of the variance were calculated using the method made by Robinson *et al.* (1951). The genotypic and phenotypic correlations between yield and yield component traits were calculated using the method made by Johnson *et al.* (1955) and Al-Jibouri *et al*. (1985). The significance of the correlation coefficient was tested by referring to the standard table of Fisher and Yates (1938). The association between yield and yield component traits were estimated by the correlation coefficient using the method made by Miller *et al*. (1958). Direct and indirect effects are estimated using path coefficient analysis using the method made by Dewey and Lu (1959). All suggested practices according to necessity and timing were applied, including plant protection practices. Data on five randomly chosen plants were collected for the following parameters: date with 50% flowering, number of branches per plant, height, number of capsules per plant, number of seeds per capsule, days to maturity, thousand seed weight, and potential yield (kg/ha). Statistical analysis at the association level and path analysis were calculated using the “Lavaan” package of the statistical software R version 4.5.1.

RESULTS AND DISCUSSION

Analysis of variance for seed yield and its components in sesame: Analysis of variance (ANOVA) partitioned the variation among 140 sesame genotypes into components due to genotypes, blocks (replications) and residual error (environment plus G×E interaction). All traits, except thousand-seed weight, showed a significant mean sum of squares for genotypes, indicating significant genetic variability among the Nigerien sesame genotypes. Similar results were reported by Disowja *et al*. (2020) in India in a study on evaluation of sesame based on correlation and path analysis. Repeatability was significant for days to 50% flowering and days to maturity, reflecting consistent measurements among blocks. In contrast, thousand-seed weight showed non-significant differences among genotypes (0.094570), which is consistent with its very low genetic variance (σ^2G = 0.01, **Table 1**) and its heritability (H^2 = 9.24%; **Table 1**), suggesting that direct selection for this trait would not be effective. The significant genotypic differences observed for most traits confirm a genetic basis for the variation, thus providing a reliable foundation for further genetic analyses, including correlations, heritability estimates and path coefficient analysis.

Table 1. Analysis of variance of eight quantitative characters of sesame genotypes

S. No.	Characters	Mean sum of square			
		Replication (df=1)	Block (df=9)	Genotype (df=139)	Residuals (df=139)
1	Seed Yield	315	297.72***	95193***	315
2	Date of 50% flowering	2772.00***	1.3828	44.37***	18.28
3	Number of branches per plant	5.201	1.4875	55.197***	16.926
4	Plant height	109.15	1.4110	965.56**	595.88
5	Number of capsules per plant	8166.5	1.3303	12242.1**	7701.6
6	Number of seeds per capsule	79.289	2.2763	177.059***	30.484
7	Days to maturity	248.914***	4.9666***	193.395***	18.425
8	1000 seed weight	0.000707	0.8536	0.094570	0.078642

** = Significant at P = 0.01 and *** = Significant at P = 0.001

Genetic parameters: The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimated for the eight traits studied are reported in **Table 2**. The genotypic coefficient of variation ranged from 2.49 % (thousand-seed weight) to 38.34 % (number of branches per plant), while the phenotypic coefficient of variation ranged from 8.18 % (thousand-seed weight) to 52.63 % (number of branches per plant). Broad-sense heritability for the eight quantitative traits, calculated from variance components ranged from 9.24 % for thousand-seed weight to 99.34 % for seed yield. Consequently, the following traits showed high heritability: seed yield (99.34%), days to maturity (82.60%), number of seeds per capsule (70.62%) and number of branches per plant (53.06%). This indicates that a large portion of the observed variation for these four traits was genetic (additive) and therefore heritable. Subsequently, the response to selection on these traits will be strong and reliable. For high heritability, there is additive action of the genes involved, which can therefore be improved by selecting plants individually. In comparison, the heritability of plant height (23.68 %), number of capsules per plant (22.77 %) and thousand-seed weight (9.24 %) is low, meaning that the environment greatly affects the expression of each phenotype. Thus, selection for these traits will be much less effective.

The expected selection gain for yield (68.33 % of the mean) and number of branches per plant (57.53 %) is very high, supporting the improvement potential of these traits. Little genetic gain was achieved for thousand-seed weight (1.56 %), which corresponds to its low heritability. Yield was found to have very high heritability, but it is not a simple trait. It would be more effective to select for yield indirectly by selecting alternative traits that have high heritability and a strong genetic correlation with yield, or for traits that showed high direct effects on yield in the path analysis. High genetic gain was achieved for both seed yield (68.33%) and number of branches per plant (57.53%) as a percentage of the mean.

Table 2. Genetic variability parameters of eight quantitative traits in 140 sesame genotypes

S. No.	Characters	σ_e^2	σ_g^2	σ_p^2	GCV (%)	PCV (%)	h^2 (broad sense (%))	Genetic advance	Genetic advance as % mean
1	Seed Yield	315.03	47438.96	47754.00	33.28	33.39	99.34	447.20	68.33
2	Date of 50% flowering	18.28	13.04	31.33	5.71	8.85	41.63	4.80	7.59
3	Number of branches per plant	16.93	19.14	36.06	38.34	52.63	53.06	6.56	57.53
4	Plant height	595.88	184.84	780.72	9.61	19.76	23.68	13.63	9.64
5	Number of capsules per plant	7701.64	2270.23	9971.87	23.41	49.05	22.77	46.83	23.01
6	Number of seeds per capsule	30.48	73.29	103.77	12.50	14.88	70.62	14.82	21.65
7	Days to maturity	18.43	87.49	105.91	7.57	8.33	82.60	17.51	14.18
8	1000 seed weight	0.08	0.01	0.09	2.49	8.18	9.24	0.06	1.56

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, h^2 = Heritability

The extent of genetic diversity for most studied agronomic traits, specifically yield (99.34 %), number of seeds per capsule (70.62 %) and number of branches per plant (53.06 %), is remarkable. These high estimates of (broad-sense) heritability suggest that the variations are almost entirely due to additive genetic variances, thus indicating reasonable estimates of presumed genetic gains under selection. These results are consistent with those of Boru (2020), where heritability was also high (78-92 %) for the same traits reported. Thousand-seed weight has low heritability (9.24 %), indicating high sensitivity to the environment, especially under stress. Misganaw (2015) also concluded that the expression of this trait was largely determined by genotype-by-environment interaction under Sahelian conditions. Jeyaraj and Beevy (2024) noted that thousand-seed weight was stable under normal growth conditions, but when subjected to water and heat stress the trait was less stable, which they attributed to its low heritability. Heritability is high and significant genetic gain is noted for yield (68.33 %) and number of branches per plant (57.53 %), suggesting considerable improvement potential for these traits.

Phenotypic and genotypic correlation: The correlation analysis (**Fig. 1**) showed that a strong positive correlation (0.73) between the number of branches per plant and the number of capsules per plant, which is biologically sensible because more branches mean more potential sites for capsules. Plant height is also significantly correlated with the number of branches per plant (0.43) and the number of capsules per plant (0.57), suggesting that taller plants are both more branched and more productive in terms of capsules. These results are consistent with those of Sumathi *et al*. (2007) in terms of plant height and number of capsules per plant. The number of branches per plant (0.37) is significantly correlated with days to maturity, indicating that more-branched plants tend to have a longer lifecycle. A similar observation was made between days to maturity and plant height, with a positive and significant correlation (0.28). The positive and significant correlation (0.46) between days to 50% flowering and days to maturity seems logical, because plants that flower earlier should reach maturity earlier. The yield showed a small but significant positive correlation with PH (0.15). It is noteworthy that the correlation with thousand-seed weight is also positive but non-significant (0.09), and with the number of capsules per plant it is negative but non-significant (-0.05). This suggests that yield results from the interaction of multiple traits rather than from a single trait. The negative non-significant correlation between yield and days to maturity: (-0.07) might suggest a trend that early-maturing accessions tend to have slightly higher yields; however, this relationship is weak and not statistically significant.

Genotypic correlations (above the diagonal) are higher than phenotypic correlations (below the diagonal) (**Table 3**). For example, between days to 50% flowering and the number of branches per plant, r_g = 0.706 versus r_p = 0.215, was observed respectively which suggests that the phenotypic association was somewhat attenuated by the environment, but the underlying genetic association among lines is very strong. The strong positive genetic correlation between number of branches per plant and the number of capsules per plant, r_g = 0.854, is the genetic equivalent of the strong phenotypic association (**Fig. 1**). That is, the genes underlying plant branching also have a strong influence on the increased capacity of plants to produce more capsules. The yield showed a positive and statistically significant genetic correlation with plant height = 0.287, and a negative genetic correlation with days to 50% flowering (r_g = -0.208). The phenotypic correlation for thousand-seed weight is weak and positive r_p = 0.064, creating a situation where yield and thousand-seed weight have a strong negative genotypic correlation

Table 3. Phenotypic correlation (at the bottom of the diagonal) and genotypic correlation (at the top of the diagonal) of eight quantitative parameters of sesame genotypes

	Yield	DF	NBP	PH	NCP	NSC	DM	WTG
Yield	**1,000**	-0.208**	-0.048	0.287**	0.188**	-0.120*	-0.078	0.231**
FD	-0.139*	**1,000**	0.706**	0.515**	0.612**	-0.114	0.841**	-0.192**
NBP	-0.047	0.215**	**1,000**	0.404**	0.854**	-0.168**	0.541**	-0.264**
PH	0.145*	-0.065	0.435**	**1,000**	0.123*	0.113	0.627**	0.083
NCP	0.091	0.036	0.733**	0.569**	**1,000**	-0.015	0.286**	-0.561**
NSP	-0.096	-0.041	-0.054	0.066	0.059	**1,000**	-0.080	-0.346**
DM	-0.070	0.479**	0.371**	0.283**	0.146*	-0.082	**1,000**	0.050
WTG	0.064	-0.050	-0.018	0.022	-0.081	0.005	-0.040	**1,000**

(DF: Date of 50% flowering, NBP: Number of branches per plant, PH: Plant height, NCP: Number of capsules per plant, NSC: Number of seeds per capsule, DM: Days to maturity, WTG: 1000 seed weight), * Significance at P = 5% level; ** Significance at P = 1% level.

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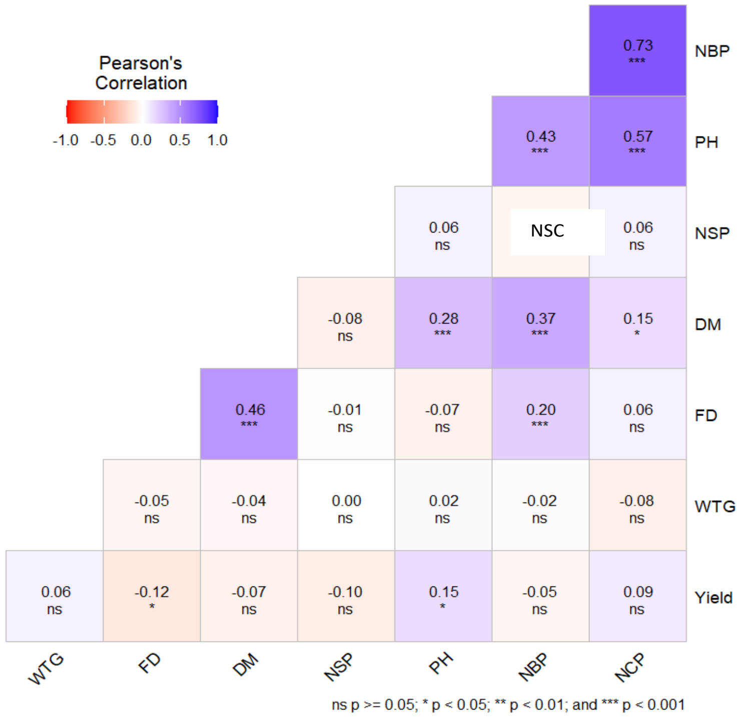

Fig. 1. Pearson's correlation coefficients between the seven quantitative parameters studied

(NBP: Number of branches per plant, PH: Plant height, NSP: Number of seeds per capsule, DM: Days to maturity, FD: Date of 50% flowering, WTG: 1000 seed weight, NCP: Number of capsules per plant)

while the phenotypic correlation is not substantial and is positive. This suggests that environmental effects on phenotypic expression are strong relative to the actual negative genetic association between seed weight and yield. Selection on one trait such as the number of branches per plant will produce a correlated response in the other trait, for example the number of capsules per plant, because these traits are genetically correlated. It also showed that one should be cautious about relying solely on phenotypic correlations because they can be misleading. The substantial difference between genotypic and phenotypic correlations found in the present study, particularly for connections involving yield, demonstrates how environmental conditions can mask trait expression. The strong genotypic correlation between number of branches per plant and number of capsules per plant ($r_g = 0.854$) shows there is a genetic association between vegetative architecture and reproductive structures. This finding corroborates the results of Zhou *et al*. (2018), who discovered shared genetic loci governing these two traits via a genome-wide association study (GWAS).

Path coefficient analysis: The number of capsules per plant had the strongest positive direct effect (0.213) on yield (**Table 4**). Plant height also shows a positive direct effect (0.144). Therefore, these traits contribute most to improving yield. The number of branches per plant and the number of seeds per capsule both have negative direct effects (-0.249 and -0.135, respectively). In other words, all else equal, increasing these traits would be detrimental to yield. The fact that there is an overall positive correlation with yield (**Table 3**) is entirely attributable to positive indirect effects associated with these traits, primarily via the number of capsules per plant for the number of branches per plant. A similar counterintuitive effect was observed in the date of 50% flowering and yield relationship when considering the negative correlation in **Table 3** ($r_g = -0.208$) despite the observed positive direct effect. The reality is that the cumulative negative indirect effects (with the number of capsules per plant representing a contribution of -0.017) outweigh the positive direct effects on yield. Path analysis explores the complexity and sometimes contradictions in relationships among yield components. It shows that the number of capsules per plant is the primary lever to improve yield. It clarifies why selection for more branches might not be beneficial (negative direct effect), and why it is essential to examine thousand-seed weight independently of correlations, since the direct effect of this trait is positive. The path analysis applied in the study illustrated the complexity of relationships established among yield components. The dominant direct effect

Table 4. Direct (diagonal) and indirect (off-diagonal) effects of different characters on seed yield in sesame

Characters	Date of 50% flowering	Number of branches per plant	Plant height	Number of capsules per plant	Number of seeds per capsule	Days to maturity	1000 seed weight
Date of 50% flowering	**-0,061**	-0,050	-0,010	0,012	0,001	-0,013	-0,003
Number of branches per plant	-0,012	**-0,249**	0,062	0,156	0,007	-0,011	-0,001
Plant height	0,004	-0,108	**0,144**	0,121	-0,009	-0,008	0,002
Number of capsules per plant	-0,004	-0,183	0,081	**0,213**	-0,008	-0,004	-0,006
Number of seeds per capsule	0,001	0,013	0,009	0,013	**-0,135**	0,002	0,000
Days to maturity	-0,028	-0,093	0,040	0,032	0,010	**-0,029**	-0,003
1000 seed weight	0,003	0,005	0,003	-0,017	-0,001	0,001	**0,070**

Residual effect = 0.128

of the number of capsules per plant on yield (0.213) demonstrated its centrality in explaining a component of productive potential. Kumar and Vivekanandan (2009) reported similar results in a study on correlation and path analysis for seed yield in sesame in India. The negative direct effect (-0.249) of the number of branches per plant contrasts with its positive phenotypic correlation with yield, which is explained by strong positive indirect effects via the number of seeds per pod. However, path analysis showed that any selection for number of branches per plant should still be done cautiously because of the negative direct effect on yield. Yemata and Bekele (2024) suggested using indirect selection, possibly employing multi-trait indices to maximize selective response. Thousand-seed weight showed moderate heritability, suggesting that improvement of this difficult trait is more likely to involve management practices or selection for phenotypic stability. In this study, the residual effect is relatively small (0.128), which means that these selected traits can contribute effectively to yield.

This study indicates that there is potential genetic diversity among sesame accessions from Niger for most traits except for one, which is 1000 seed weight. Analysis of path coefficients showed that the number of capsules per plant and plant height were the traits with the most significant positive direct effects on yield. The opposite is true for the number of branches which had a negative direct effect, although number of branches per plant positively correlated with yield, the association was entirely indirect via number of capsules per plant. Heritability estimates indicate that yield, number of branches per plant and number of seeds per capsule are particularly additive and thus responsive to selection as breeding traits, while plant height and number of capsules per plant are highly environmentally determined. In light of this, breeding for yield will best reflect direct selection for number of capsules per plant and plant height. Selection for added branches may function in the right direction, but given the negative direct effect of number of branches per plant would defeat the objective of direct selection for yield. The results provide a clear direction for rational and effective selection towards utilizing the production potential within Nigerien sesame.

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