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Genetic Variability, Heritability, Genetic Advance, Path Coefficient Analysis, and Inter-Character Relationships in Colocynth (*Citrullus colocynthis* [L.] Schrad.) from Southeastern Villages of the Benin Republic

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Abstract

Genetic improvement of crops for important traits requires reliable estimates of genetic variability. heritability and genetic advance of intending parent materials to identify traits useful in planning an efficient breeding program through selection. Hence, the effectiveness of genetic improvement of a crop depends on the variability in the morpho-agronomic traits of individual genotypes. Understanding the variation that exists will allow the breeder to determine strategies to be adopted in his breeding program. The objectives of the present study were to estimate the magnitude of genetic variability and advance, heritability and inter-character relationships by simple correlations and path coefficient analysis in 40 local colocynth genotypes from Southeastern Benin. The experiment was carried out in a randomized complete block design with three replications in three locations for three years. 34 morpho-agronomic traits were observed in each genotype. Analysis of variance revealed that effects of genotype, genotype by year or location and genotype by year by location interactions were significant ($p \leq 0.01$ or 0.05) for all the characters. Phenotypic coefficients of variation (PCV) values were relatively greater than genotypic coefficients of variation (GCV) for all traits. High magnitude of phenotypic and genotypic coefficients of variation as well as high heritability along with high genetic advance were recorded particularly for qualitative traits. All yield components, except time to emergence, time to tailspins, leaf limb width, fruit number per plant, fruit width, seed length, seed tegument percentage and stem pubescence texture, had significant and positive correlations with yield attributes represented by thousand-seed weight (TSW) and seed number per plant (SNP). Path coefficient analysis indicated that all the characters (except leaf pubescence texture, stem pubescence texture, fruit design produced by secondary skin color and male flower size) had positive direct effects on TSW and partly SNP. Results suggested that most of the 34 quantitative and qualitative traits studied could be effectively used as selection criteria in the breeding program of *Citrullus colocynthis* varieties with high yield.

Keywords: *Citrullus colocynthis*, Genetic advance (GA, GAM), Genetic variability, Genotypic coefficients of variation (GCV), Heritability, Phenotypic coefficients of variation (PCV), Path coefficient analysis

Introduction

The origin of colocynth [*Citrullus colocynthis* (L.) Schrad.] is thought to be Africa, where it emerged as an oilseed crop for human consumption. Distribution of the crop around the world was initially based on its use as a food. The crop is a good oil and protein source for segments of human populations. It is an ancient crop in West Africa, which is considered to be the center of diversity for the species (Achigan-Dako et al. 2015, Gama et al. 2013, Simonds 1979, Whitaker and Davis 1962). In Benin, it is annually cultivated traditionally on a family consumption basis. Ecologically, colocynth can be grown in a wide range of environments and is presently cultivated under diverse agro-climatic conditions in Benin. It can be grown under various rainfalls, temperatures and soil regimes. Depending on the location and maturity period of the cultivar, it is grown during the short rainy growing season between September and February. It is mainly cultivated under a multiple cropping system. Despite the aforementioned importance, its productivity is very low. Documentation on the contribution of plant breeding to a given crop yield improvement and evaluation of past gains are useful for identifying areas with potential for planning a future breeding program (Bishwas and Singh 2024, Mitra et al. 2023, Waddington et al. 1987). Evans (1993) advocated already that understanding of changes produced by crop breeding on seed yield and its determinants was important in evaluating the efficiency of past improvement work on the advances in genetic yield potential, and in defining also future selection criteria to facilitate further progress. Genotype, environment and management interact to determine the yield of a crop. However, no method of estimating long-term improvement progress can completely separate genetic effects per se and their interaction effects. Nevertheless, the evaluation of popular cultivars from different years in common environments is the most comprehensive and direct method that has been used to estimate progress in yield improvement (Mitra et al. 2023, Girmay 2013). Progress made in genetic yield potential and associated changes in morpho-physiological attributes produced by genetic improvement and benefits obtained, therefore, have been documented in different crops from diverse countries by comparing old and modern varieties (Bishwas and Singh 2024, Girmay 2013, Perry and d'Antuono 1989). Lipids are nutritionally important. They are either fat (solid) or oil (liquid) and contain fatty acids. A minimum amount of body fat is necessary to provide insulation that prevents heat loss and protects vital organs from shock due to ordinary activities (Anhwange et al. 2010). Deficiency of lipids in the body reflects the type of fatty acids that is lacking in the diet (Anhwange et al. 2010). Therefore, since the common dietary sources of lipids are of animal origin, which contains only saturated fatty acids, it will be of great significance if the essential components of lipids are from plant products, which have been known to contain them. The usefulness of essential lipids, which are needed for the proper body functioning and the expensiveness of their processed forms, let us think of providing a veritable channel for harnessing them from locally available vegetable sources like *Citrullus colocynthis*.

In low-input farming systems, farmers often use a wide range of crop varieties, to provide harvest security, yield stability and the possibility to adapt to changing ecological conditions (Bishwas and Singh 2024, Nuijten and van Treuren 2007, Teshome et al. 1999, Hardon and De Boef 1993). Farmers in these situations adopt modern varieties only to a limited extent, or not at all (Nuijten and van Treuren 2007). The main reason for not adopting modern varieties is that they do not meet farmers' requirements. In recent years, various participatory plant breeding initiatives have been set up to develop varieties to meet farmers' requirements better (Nuijten and van Treuren 2007, Almekinders and Elings 2001, Sperling et al. 2001). Some of these programs aim to collaborate with farmers in the very early stages of crop development, with the breeder acting more as a facilitator providing the raw genetic material. It is suggested that farmers maintain high levels of crop diversity by developing new varieties and by matching specific varieties to particular conditions (Nuijten and van Treuren 2007). How much genetic diversity, these varieties represent, however, has not often been studied and different processes seem to regulate the amount and development of genetic diversity in crops in low-input farming systems. Rather than continuing to assume that the obvious morphological diversity of traditional varieties assures a broad genetic base on-farm, diagnostic surveys of genetic variation and genetic distance between varieties are urgently needed (Nuijten and van Treuren 2007, Wood and Lenné 1997).

An important step in cultivar development is studying the genetic variability found in genetic resources. The use of genetic resources to create new varieties is important for obtaining higher yields and the technological transformations required for the modernization of agribusiness. It is a dynamic process, that requires continuous enrichment and characterization of the materials maintained in germplasm collections, or by farmers (Mitra et al. 2023, Gama et al. 2013, Valls 2007, Whitaker and Davis 1962). Attaching a value to genetic resources is a complex task. Describing the kinds of benefits associated with these resources is easier. The simplest benefit arises from the direct use of genetic resources to produce food and fiber or to help create new varieties of crops and livestock. The ultimate direct-use benefits of crop genetic resources are measured in the increased output, higher quality, better resistance to pests, diseases, and other stress as well as other characteristics found in improved crop varieties. These benefits derive not only from the genetic resources contained in precursor wild relatives but also from the efforts of farmers who domesticated the crop and developed landraces through many years of selection; works of collectors and gene banks that assembled and preserved genetic material in the form of landraces and wild relatives; and the work of plant breeders who have continued to develop and improve crop varieties.

Plant genetic resources used for various purposes (agronomy, industry, environment, ecology, medicine, etc.), and thus possessing an important economic and social value are essential for humanity’s survival. To satisfy the future needs for genetic resources, it is imperative to collect and conserve representative stocks of plant genetic diversity (Koffi et al. 2008, Given 1987). Indeed, the chance for fulfilling future demand for genetic resources is better whenever a high level of genetic diversity is conserved and made available for breeders. This challenge should not be missed, particularly for the crops such as neglected and underutilized by both national and international research programs, so-called minor or orphan crops (Koffi et al. 2008, Rasul et al. 2007). The indigenous edible-seeded colocynths are classified into minor crops. There are several species of cucurbits in tropical Africa and Asia, cultivated mainly for their oleaginous seeds that are important in the social and cultural life of several people (Achu et al. 2005, Zoro Bi et al. 2005, Enujiugha and Ayodele-Oni 2003, Das et al. 2002, Badifu, 1993). *Citrullus colocynthis* belonging to this category of crops, is one of the most widely distributed and consumed at both rural and urban levels in Sub-Saharan Africa. There, *C. colocynthis* is prized for its oleaginous seeds consumed as thickeners of a traditional soup called “Egusi” soup in Cameroon, Nigeria or Benin and pistachio soup in Côte d’Ivoire (Koffi et al. 2008, Loukou et al. 2007, Achu et al. 2005, Zoro Bi et al. 2005, Enujiugha and Ayodele-Oni 2003). This cucurbit is reported to be rich in nutrients (Achu et al. 2005, Enujiugha and Ayodele-Oni 2003, Badifu 1993), namely protein (2.17-36%) and fat (4.73-45.89%). Thus, *C. colocynthis* represents an excellent plant model for which improved cropping system implementation can ensure the economic prosperity of rural women from tropical Africa. In spite of the nutritional and agronomic potentials of *C. colocynthis*, in-depth basic investigations on the crop are scant (Koffi et al. 2008, Osuji et al. 2006). For example, to our knowledge, no detailed study has been devoted to genetic diversity, genetic parameters, and reproduction biology. However, investigations reported for other species, suggested that the cucurbit family is predominantly outcrossing (Koffi et al. 2008, Montes-Hernandez and Eguiarte 2002). Such expectations are based on the fact that indigenous edible-seeded cucurbits are generally monoecious and entomophilous (Gusmini 2003). The first step of such investigations is the documentation and the assemblage of genetic stocks representative of the total genetic diversity displayed by this species (Mahmoud et al. 2020, Koffi et al. 2008, Brown and Briggs 1991, Chapman 1989, Kjellqvist 1975). Results from such investigations are useful to improve both their quality and their productivity through selection and breeding, as well as to implement reliable genetic resource collections and conservation strategies (Tolera et al. 2024, Koffi et al. 2008).

Understanding the relationships between traits, for the selection of important ones, is of the utmost importance. The goal of the path analysis is that the acceptable descriptions of the correlation between the traits, based on a model of cause and effect, are presented, and the importance of the affecting traits on a specific one is estimated. In fact, the basic relationships between the traits are expressed by this analysis. So, the correlation coefficients divided into direct and indirect effects, affect the set of independent variables and dependent ones. Their relative importance is calculated (Tolera et al. 2024, Balqees and Mohammed 2022, Mahmoud et al. 2020, Rasaei et al. 2011). Several researches on the relationships among trait effects of plants have been reported (Parte et al. 2022, Rasaei et al. 2011, Amaranthath, and Viswantaha 1990).

The main objectives of the research report presented here were therefore to analyze: (i) the extent of genetic variability and advance; (ii) broad sense heritability and (iii) the correlations existing between seed yield and related traits in *C. colocynthis* by applying sequential path analysis and identifying traits of genotypes, which may be useful in breeding higher-yielding materials.

Materials and methods

Plant material

It consisted of forty accessions of *Citrullus colocynthis* collected from farmers in the Southeastern Benin Republic. Those materials are named CC 1 to CC 40 and were multiplied in Ko-Anagodo (in Ifangni Commune belonging to the Department of Plateau in Benin during the short rainy growing season from September 2013 to February 2014).

Study sites and experimental design

Experiments were laid out in a randomized complete block design with three replications at each location and every year. Experiment plots consisted of two rows, with each comprising five plants. The within and between rows were 2m respectively. Adjacent plots were also separated by 2m. One seed was sown per hole. Weeds were removed manually during the growing season. Field trials were carried out at three locations and during three years (2014-2017) in Southeastern Benin. The three locations were Ko-Anagodo – 02°72’E, 06°67N - (Ifangni), Késsounou - 02°55E, 06°58N - (Dangbo commune) and Idiotchè - 02° 64E, 06° 73N - (Sakété Commune), respectively in the Plateau Department for Ko-Anagodo and Idiotchè locations, and the Ouémé Department for Késsounou cited above. The soils at the three stations were well-drained sandy loams at all locations during the three years of experimentations.

Traits recorded

In total, 34 morpho-agronomic characters were recorded. Data were measured on a plot basis. Eight (8) plants from the central rows were used to obtain the plot mean. Characters observed, their codes and the measurement procedures are presented in Zanklan (2024, submitted). Among the traits recorded, 20 were quantitative and 14 qualitative. The qualitative characters were treated as quantitative since they showed continuous variation between the genotypes. Quantitative characters were: time to emergence (TE), time to tailspins (TT), time to male flowering (MF), time to female flowering (FF), time to fruit maturity (MT), limb peduncle length (LPL) in mm, leaf limb length (LLL) in mm, leaf limb width (LLW) in mm, number of fruits per plant (FN), plant height (PH) in m, internode length (IL) in cm, number of branches per node (NBN), fruit weight (FW) in g, fruit length (FL) in cm, fruit width (FWI) in cm, seed number per plant (SNP), seed length (SL) in mm, seed width (SWI) in mm, seed tegument percentage (TP) and thousand-seed weight (TSW) in g. Qualitative traits consisted of leaf shape (LS), leaf size (LSi), leaf color (LC), leaf pubescence density (LPD), leaf pubescence texture (LPT), internode length (ILq), stem pubescence density (SPD), stem pubescence texture (SPT), plant canopy coverage (PCC), fruit primary skin color (PSC), fruit secondary skin color (SSC), design produced by fruit secondary color (DPSC), female flower size (FFS) and male flower size (MFS). Qualitative traits were recorded on a score basis.

Statistical analyses

The mean value over all 9 environments (according to years and locations) for each trait evaluated was used to determine the minimum, maximum and range for different parameters. Data were subjected to analysis of variance (ANOVA) and covariance using JMP 7.0 (SAS Institute 2007) and Minitab 19 (Minitab 2019) statistical packages. The plot yield can be described as:

$$Y_{ijkl} = \mu_i + g_{ij} + j_{ik} + l_{il} + \varepsilon_{ijkl}$$

where Y_{ijkl} represents the observed value for the ith trait of the jth genotype for the kth location and the lth year. μi is the trial mean of a given trait; $g_{ij,}$ j_{ik} lil are respectively the effects of genotypes, years and locations; ε_{ijkl} is the error, comprising the genotype × location, genotype × year and genotype × year × location interactions, respectively, and the plot error.

Variance components were assessed from the mean squares in ANOVA (Becker 2011, Hill et al. 1998, Falconer 1989, Wricke and Weber 1986). The phenotypic variance of the means for genotypes over years, locations and replications σ^2_p, was calculated as:

$$\sigma^2_{p} = \sigma^2_g + \sigma^2_{gl}/Y + \sigma^2_{gk}/L + \sigma^2_{glk}/YL + \sigma^2_{glkr}/RYL$$

where σ^2_g represents the variance component due to genotypes, σ^2_{gl} is the variance components due to genotype by year interactions, σ^2_{gk} represents the variance components due to genotype by location interactions, σ^2_{glk} represents the variance components due to genotype by location within years, σ^2_{glkr} is the variance components due to genotype by replication within locations and years (pooled the whole plot error), while R, Y and L represent the number of replications, years and locations, respectively.

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated as:

$$PCV = (\sigma_p/\underline{X}) \times 100$$

$$GCV = (\sigma_g/\underline{X}) \times 100$$

where σ_p, σ_g and $\underline{X}$ are roots of the phenotypic, genotypic variances, and grand mean across years and locations, respectively.

Broad sense heritability (h^2) was estimated on the genotypic mean basis as described by Allard (1999), Hill et al. (1998) and Falconer (1989) as:

$$h^2 = \sigma^2_g / \sigma^2_p$$

Expected genetic advance (GA), and GA as a percent of the mean assuming selection of the superior 5% of the genotypes were estimated in accordance to Falconer (1989), Fehr (1987) and Johnson et al. (1955) as:

$$GA = k \times \sigma_p \times h^2$$
$$GA \text{ (in \% of the mean)} = (GA / \underline{X}) \times 100$$

where k is the selection differential (with 5% selection intensity, $k = 2.063$), σ_p is the phenotypic standard deviation, h^2 is the heritability, and $\underline{X}$ refers to the grand mean of a given trait.

The genetic correlation coefficient was estimated from the analysis of covariance as suggested by Miller et al. (1958) and Robinson et al. (1951), as applied by Tolera et al. (2024). Estimations of genetic correlation coefficient (r_g) for any two traits x and y are defined as:

$$r_g = \sigma_{g1/2} / \sigma_{g1} \text{ x } \sigma_{g2}$$

where $\sigma_{g1/2}$ is the genetic covariance between two traits, and σ_{g1}, σ_{g2} are the genotypic standard deviations of the first and second characters, respectively. Similarly, the phenotypic correlation (r_p) can be obtained (Falconer 1989).

Path analysis partitions the total correlation coefficients into direct and indirect effects of various characters and then helps to quantify the relationships among variables based on *a priori* model. Direct and indirect path coefficients were calculated as initially proposed by Dewey and Fu (1959) and earlier Wright (1921) as:

$$r_{yi} = P_{yi} + \sum_{i=1}^{n} r_{ii'} P_{yi'} \quad \text{for } i \neq i', \text{ and } i' \neq 1$$

where r_{yi} is the simple correlation coefficient between the i-th causal variable (x) and effect variable (y), $r_{ii'}$ is the simple correlation coefficient between the i-th and i'-th causal variables, P_{yi} is the path coefficient (direct effect) for the i-th causal variable (x), $r_{ii'}P_{yi'}$ is the indirect effect of the i-th causal variable via the i'-th causal variable. To determine P_{yi} values, square matrices of the correlation coefficient between independent traits in all possible pairs were inverted and then multiplied by the correlation coefficients among the independent and dependent traits.

Traits closely related to seed yield, namely seed number per plant (SNP) and thousand-seed weight (TSW) were used as dependent variables for path coefficient analysis in the present study.

Results

Variability, (phenotypic [PCV] and genotypic [GCV] coefficient of variation). heritability (h^2) and genetic advance (GA. GAM)

Descriptive statistics for the 20 quantitative and 14 qualitative characters in 40 *Citrullus colocynthis* collections including the minimum, maximum, mean and their standard deviations for data averaged over three locations in three years are summarized in Tables 1 and 2. In general, all the traits exhibited wide ranges of variation. Significant variation existed then in all traits.

Table 1. Descriptive statistics (range, mean and standard deviation SD) for 20 quantitative traits in 40 tested genotypes over three years and three locations in each year

Traits	Range		Mean	SD	Traits	Range		Mean	SD
	Minimum	Maximum				Minimum	Maximum		
TE*	0.00	9.00	2.66	1.49	IL	0.80	104.00	71.84	13.21
TT	1.00	9.00	2.38	1.35	NBN	0.40	3.12	1.48	0.43
MF	19.00	63.00	39.02	7.49	FW	50.00	231.00	158.28	35.92
FF	22.00	63.00	38.45	7.85	FL	10.50	40.80	24.14	6.01
MT	85.00	186.00	117.45	25.69	FWI	8.00	35.00	22.41	5.57
LPL	23.20	708.00	44.15	61.52	SNP	222.00	1571.00	710.99	241.18
LLL	1.50	203.00	117.62	25.02	SL	1.30	3.00	1.77	0.27
LLW	0.95	137.00	81.32	14.85	SWI	0.80	1.60	1.05	0.13
FN	2.00	24.00	8.94	3.47	TP	1.44	18.20	9.81	2.79
PH	1.40	16.40	8.52	2.21	TSW	4.40	96.6	60.03	2.83

The meaning of all abbreviations is indicated in the sections called „Traits recorded" in Materials and methods

Table 2. Descriptive statistics (range, mean and standard deviation SD) for 14 qualitative traits in 40 tested genotypes over three years and three locations in each year

Traits	Range		Mean	SD	Traits	Range		Mean	SD
	Minimum	Maximum				Minimum	Maximum		
LS*	3.00	9.00	6.65	1.70	SPT	3.00	7.00	4.96	1.57
LSi	3.00	7.00	6.18	1.04	PCC	3.00	7.00	5.65	1.37
LC	3.00	7.00	5.16	1.64	PSC	3.00	9.00	6.25	2.11
LPD	3.00	7.00	5.36	1.54	SSC	3.00	7.00	4.38	1.43
LPT	3.00	7.00	4.90	1.48	DPSC	1.00	5.00	2.51	1.57
ILq	3.00	5.00	4.16	0.98	FFS	3.00	7.00	5.60	1.35
SPD	3.00	7.00	4.70	1.52	MFS	3.00	7.00	4.10	1.33

The meaning of all abbreviations is indicated in the sections called „Traits recorded" in Materials and methods

Combined analysis of variance showed significant differences for all the parameters considered among the colocynth genotypes collected (Tables 3 and 4) ($p \leq 0.01$). It could be concluded that differences between colocynth collections may be due to genetic differences between cultivars. Those differences indicate a considerable amount of variation present in the material, and reveal a high level of diversity among the genotypes for the traits, except for the characters: number of branches per node (NBN), seed length (SL), seed tegument percent (TP) and most all the qualitative characters. Effects of the factors year (Y) and location (L) were quite non-significant for all the quantitative traits compared to qualitative ones. Furthermore, genotypic mean-variance significance was lower for qualitative traits than for quantitative characters (Tables 3 and 4). Interactions between genotypes and the factors of year and location were highly significant ($p \leq 0.05$ or 0.01) for all traits observed.

The magnitude of phenotypic variation does not reveal the relative amount of genotypic and non-genetic components of variation. Moreover, it is difficult to compare the variances between various traits because they are not unit-free. Thus, variance components, estimates of the phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), broad sense heritability, genetic advance (GA) and genetic advance as a percentage of the mean (GAM) were calculated and compared (Tables 5 and 6). In general, higher PCV values than GCV were obtained for all the characters. For quantitative traits, PCV was very high and ranged from 76.251 (leaf limb width - LLW) to 839.988 % (thousand-seed weight - TSW). It ranged from 74.275 (leaf size - LSi) to 284.484 % (design produced by fruit secondary skin color - DPSC) for qualitative characters. Quantitative characters were observed to have the highest PCV. The genotypic coefficient of variation (GCV) measures the genotypic variance relative to the mean of a given character and is independent of the units of measurement. These values allow direct comparison of various characters. GCV showed similar trends as PCV and ranged from 15.906 (time from sowing to maturity - MT) to 291.046 % (limb peduncle length) concerning quantitative characters. For qualitative traits, GCV ranged from 44.830 (leaf size - LSi) to 213.666 % (DPSC).

Table 3. Mean squares from combined analysis of variance for 40 *Citrullus colocynthis* genotypes evaluated by 20 quantitative morpho-agronomic characters across three years and three locations within each year in Southeastern of Benin Republic

Traits	**Sources of variation**						
	Year (Y)	**Location (L)**	**Genotype (G)**	**G × Y**	**G × L**	**G × Y × L**	**Pooled error**
TE	65.878	54.269	5,778*	2.883**	3.044**	2.104**	1.879
TT	65.389	0.889	5.510*	2.556**	2.922**	1.624**	1.567
MF	6166.80	482.70	94.56**	58.470**	130.034**	60.874**	42.14
FF	11840.9	1263.5	63.9**	76.505**	19.220**	60.463**	36.6
MT	249905	12983	349**	220.385**	89.643**	284.309**	167
LPL	63.9**	61916.3	16513.0**	6594.196**	772.358**	6974.364**	3206.9
LLL	5087.68	460.08	2224.70**	1683.827**	1290.289**	1224.217**	558.49
LLW	376.88	1181.35	587.43**	556.858**	535.366**	402.374**	204.84
FN	62.381	5.458	35.580**	16.808**	17.594**	9.541**	11.115
PH	1.684**	7.374**	14.537**	12.408**	5.963**	5.320**	4.570
IL	9743.7	328.1	560.7**	228.053**	470.018**	183.130**	141.3
NBN	0.571	0.177	0.675	0.354**	0.280**	0.230**	0.171
FW	9743.7	562.4	5681.9**	3481.922**	2587.484**	1200.447**	1104.9
FL	16.015**	2.842**	178.942**	85.309**	56.615**	42.714**	31.001
FWI	530.219	170.553	131.834**	93.386**	41.457**	28.417**	26.094
SNP	146689	33892	129509**	105449.743**	72934.410**	109837.211**	55456
SL	15.682	2.150	0.086	0.093**	0.063**	0.055**	0.040
SWI	3.808	0.761	0.012	0.008**	0.010**	0.013**	0.008
TP	1587.00	242.95	7.23	11.578**	3.806**	5.168**	4.34
TSW	2167.2	420.6*	834.0**	93487.179**	74548.564**	82046.698**	801.4

and ** : significant at 0.05 and 0.01. respectively

Table 4. Mean squares from combined analysis of variance for 40 *Citrullus colocynthis* genotypes evaluated by 14 qualitative characters across three years and three locations within each year in Southeastern of Benin Republic

Traits	**Sources of variation**						
	Year (Y)	**Location (L)**	**Genotype (G)**	**G × Y**	**G × L**	**G × Y × L**	**Pooled error**
LS	0.000**	0.900**	30.146*	0.000**	25.207**	0.000**	0.000
LSi	0.000**	1.200	7.684	0.000**	11.353**	0.000**	0.856
LC	0.000**	0.300**	34.923**	0.000**	19.992**	0.000**	1.508
LPD	0.000**	0.300**	23.353**	0.000**	21.530**	0.000**	1.624
LPT	0.000**	0.000**	18.800	0.000**	20.923**	0.000**	1.578
ILq	0.000**	0.300**	9.418	0.000**	7.513**	0.000**	0.659
SPD	0.000**	0.000**	37.507**	0.000**	13.230**	0.000**	0.998
SPT	0.000**	0.300**	36.892	0.000**	15.684**	0.000**	1.183
PCC	0.000**	0.000**	15.069	0.000**	18.461**	0.000**	1.392
PSC	0.000**	0.900**	77.038	0.000**	23.361**	0.000**	1.762
SSC	0.000**	0.300**	34.700	0.000**	11.069**	0.000**	0.835
DPSC	0.000**	1.200	28.915	0.000**	19.661**	0.000**	1.483
FFS	0.000**	0.000**	22.646	0.000**	14.153**	0.000**	1.067
MFS	0.000**	0.000**	23.107	0.000**	13.230**	0.000**	0.998

** significant at 0.01

Broad sense heritability (h^2) has also to be considered to predict the amount of progress from farmer selection in the present study. Broad sense heritability was generally low and showed values under 50 % for all 20 quantitative traits (Table 5). In general, values estimated for qualitative characters were higher than for quantitative traits. It ranged from 0.132 (Time to maturity - MT) to 43.281 % (fruit length - FL). For qualitative traits, heritability ranged from 36.429 (leaf size - LSi) to 95.859 % (male flower size - MFS). Obtained results showed that qualitative characters are highly heritable, and almost all traits presented high heritability around 50 % (Table 6). This fact is maybe interesting as it shall be possible to select for them limiting costs involved in research activities. Heritability estimates along with genetic advances are more helpful in foreseeing the genetic gain under selection than heritability estimates alone. High genetic advance (GA) and genetic advance related to trait mean (GAM) joined with high heritability was observed for all quantitative traits, particularly leaf peduncle length (LPL), leaf limb length (LLL), leaf limb width (LLW), fruit weight (FW), fruit length and width (FL and FWI) and seed number per plant (SNP). Therefore, the selection of genotypes based on these indicated traits will be effective. Nevertheless, GA and GAM were relatively low for thousand-seed weight (TSW) in spite of their importance in enhancing seed yield in colocynth (Table 5). For qualitative characters, GA was relatively low. However, GAM was higher, and sometimes above 100 % (Table 6).

Table 5. Variability (phenotypic [PCV] and genotypic [**G**CV] coefficient of variation). heritability (h^2) and genetic advance (GA. GAM) for 40 farmers' genotypes of *Citrullus colocynthis* tested by 20 quantitative traits

Traits	PCV (%)	GCV (%)	h^2 (%)	GA	GAM
TE	437.055	90.140	4..253	1.022	38.353
TT	376.500	98.528	6..848	1.267	53.192
MF	214.934	24.917	1..344	2.325	5.959
FF	300.581	20.786	0..478	1.140	2.965
MT	437.483	15.906	0..132	1.401	1.193
LPL	701.903	291.046	17..193	109.925	248.969
LLL	95.167	40.101	17..756	41.002	34.860
LLW	76.251	29.803	15..277	19.543	24.032
FN	140.721	66.677	22..451	5.830	65.177
PH	84.489	44.734	28..033	4.164	48.862
IL	150.268	32.959	4..810	10.714	14.913
NBN	105.820	55.453	27..461	0.888	59.950
FW	98.613	47.623	23..322	75.098	47.446
FL	84.213	55.402	43..281	18.155	75.193
FWI	142.644	51.233	12..900	8.507	37.961
SNP	113.722	50.615	19..809	330.436	46.475
SL	240.097	16.518	0..473	0.041	2.344
SWI	204.310	10.412	0..259	0.011	1.094
TP	439.848	27.407	0..388	0.345	3.523
TSW	839.988	48.103	0..327	3.411	5.683

Table 6. Variability (phenotypic [PCV] and genotypic [**G**CV] coefficient of variation). heritability (h^2) and genetic advance (GA. GAM) for 40 farmers' genotypes of *Citrullus colocynthis* tested by 14 qualitative traits

Traits	PCV (%)	GCV (%)	h^2 (%)	GA	GAM
LS	112.784	82.564	53.590	8.291	124.690
LSi	74.275	44.830	36.429	3.451	55.820
LC	145.770	114.378	61.567	9.566	185.148
LPD	127.482	90.046	49.892	7.041	131.214
LPT	131.154	88.487	45.519	6.034	123.163
ILq	101.511	73.653	52.643	4.593	110.246
SPD	153.036	130.304	72.498	10.757	228.887
SPT	148.036	122.292	68.243	10.351	208.416
PCC	104.592	68.705	43.150	5.260	93.107
PSC	162.430	140.434	74.749	15.655	250.482
SSC	156.242	134.387	73.980	10.452	238.462
DPSC	284.484	213.666	56.409	8.331	331.063
FFS	109.884	84.978	59.805	7.592	135.574
MFS	119.748	117.243	95.859	9.709	236.812

Correlations between characters

Correlation analysis figures out the intensity of the relationship between two traits. For the present breeding material, genotypic correlations were computed among yield-contributing components and are presented in Table 7.

The genotypic correlation coefficients among 34 morpho-agronomic quantitative and qualitative characters in colocynth in nine environments (three years and three locations per year) are presented in Table 7. Seed number per plant (SNP) and thousand-seed weight (TSW) are important components of seed yield. SNP presented significant positive genotypic correlations with all traits studied, except time to emergence (TE), time to tailspins appearance (TT), leaf limb width (LLW), fruit number per plant (FN), fruit width (FWI), seed length (SL), seed tegument percentage (TP) and stem pubescence density (SPD). Apart from TE, TT, MF, FF, MT, FL, SL, LPT, SPD and MFS, TSW exhibited positive associations with the remaining 24 characters (Table 7). From Table 7, the differences in both the magnitude and direction of correlation coefficients were observed considering the nine environments taken in the present study for some of the characters. Positive significant correlation coefficients were observed for most traits except for those cited above.

Table 7. Associations of 20 morpho-agronomic quantitative and 14 qualitative characters in 40 genotypes of *Citrullus colocynthis* evaluated across three years (2014-2017) and three locations each year in Southeastern Benin

Traits	**TE**	**TT**	**MF**	**FF**	**MT**	**LPL**	**LLL**	**LLW**	**FN**	**PH**	**IL**	**NBN**
TE	-											
TT	0.540**	-										
MF	0.236**	0.182**	-									
FF	0.224**	0.179**	0.795**	-								
MT	0.202**	0.233**	0.476**	0.633**	-							
LPL	0.165**	0.144**	-0.013	-0.032	-0.015	-						
LLL	-0.081*	-0.176*	-0.078*	-0.094*	-0.099*	-0.370**	-					
LLW	-0.028	-0.141**	0.027	0.027	0.025	-0.454**	0.518**	-				
FN	0.266**	0.152*	0.076*	0.082*	0.071	0.078*	0.032	0.079*	-			
PH	-0.058	-0.095*	-0.055	-0.012	-0.032	-0.255**	0.242**	0.293**	0.320**	-		
IL	0.091*	0.115**	0.185**	0.251**	0.359**	-0.620**	0.240**	0.359**	0.032	0.262**	-	
NBN	0.031	0.042	0.051	0.077*	0.050	0.025	-0.112*	-0.060	-0.134*	0.000	0.024	-
FW	0.001	0.023	0.001	0.023	0.127*	-0.081*	0.127*	0.176*	0.045	0.124*	0.138*	0.005
FL	-0.049	-0.065	-0.061	-0.083*	-0.025	0.063	0.047	-0.134*	-0.121*	-0.139*	-0.141*	0.104*
FWI	0.032	0.007	0.030	0.080*	0.120*	0.080*	0.118*	0.023	-0.162**	-0.062	-0.089*	0.188**
SNP	-0.056	-0.024	0.036	0.004	0.044	0.019	0.014	-0.034	-0.035	0.012	0.043	0.020
SL	0.161*	0.191**	0.386**	0.458**	0.601**	-0.009	0.011	0.121*	0.067	0.022	0.231**	0.051
SWI	0.180**	0.160*	0.322**	0.450**	0.626**	0.011	-0.061	0.005	0.065	-0.025	0.228**	0.022
TP	-0.182**	-0.152**	-0.296**	-0.368**	-0.547**	-0.018	-0.021	-0.117*	-0.073*	-0.027	-0.220**	-0.042
TSW	-0.042	-0.020	-0.009	-0.026	-0.051	-0.013	0.012	0.005	-0.019	0.026	-0.028	0.009
LS	0.003	-0.046	0.064	0.013	-0.010	-0.019	0.087*	0.036	0.026	0.032	0.052	-0.016
LSi	-0.048	-0.029	-0.094*	-0.079	0.017	0.033	-0.021	-0.071*	-0.065	0.002	-0.033	0.073*
LC	0.049	0.037	-0.000	-0.012	-0.008	-0.015	0.062*	0.053	-0.047	-0.053	0.007	-0.080*
LPD	0.018	-0.031	-0.028	-0.007	-0.015	-0.006	0.069*	0.040	-0.003	-0.051	-0.018	-0.013
LPT	0.042	0.019	0.052	0.004	0.013	0.043	0.087*	0.005	0.043	-0.016	0.001	-0.025
ILq	-0.020	0.007	-0.036	-0.047	-0.004	-0.033	0.000	-0.019	-0.049	0.008	-0.018	0.029
SPD	0.127*	0.101*	0.063	0.038	-0.021	0.082*	-0.014	-0.016	-0.034	-0.064	-0.051	0.011
SPT	-0.108*	-0.120*	-0.005	0.003	0.021	-0.076*	-0.013	0.037	0.049	0.072*	0.033	0.003
PCC	-0.030	-0.046	-0.008	-0.038	-0.007	-0.017	-0.026	0.028	0.020	0.016	0.028	-0.002
PSC	-0.053	-0.034	-0.003	0.022	-0.018	-0.023	-0.014	0.054	0.002	0.091*	0.018	-0.011
SSC	-0.123*	-0.114*	-0.047	-0.043	-0.017	-0.019	0.043	0.052	0.059*	0.090*	0.003	0.001
DPSC	-0.071*	-0.038	-0.063*	-0.050	-0.000	0.040	0.043	0.018	0.043	0.040	-0.042	-0.002
FFS	-0.012	0.010	-0.052	-0.051	-0.025	-0.004	0.023	-0.026	-0.003	-0.018	0.004	-0.050
MFS	-0.080*	-0.043	-0.052	-0.042	0.003	-0.025	0.048	0.006	0.007	0.073*	0.034	0.080*

Table 7. Continued

Traits	**FW**	**FL**	**FWI**	**SNP**	**SL**	**SWI**	**TP**	**TSW**	**LS**	**LSi**	**LC**	**LPD**
FW	-											
FL	-0.089*	-										
FWI	-0.071*	0.306**	-									
SNP	0.061*	0.008	-0.031	-								
SL	0.103*	-0.021	0.133*	-0.006	-							
SWI	0.079*	-0.006	0.093*	0.015	0.566**	-						
TP	-0.140*	-0.004	-0.123*	-0.039	-0.573**	-0.532**	-					
TSW	0.025	-0.002	0.002	0.012	-0.041	-0.039	0.054	-				
LS	0.004	0.114*	0.018	0.069*	0.004	-0.051	0.000	0.006	-			
LSi	0.050	0.024	0.007	0.054	-0.019	-0.018	-0.042	0.016	0.008	-		
LC	-0.055	-0.030	0.021	-0.009	0.060	-0.015	-0.012	0.041	-0.169*	-0.114*	-	
LPD	-0.034	0.008	0.084	-0.026	-0.031	0.014	0.017	0.031	-0.078*	0.041	0.028	-
LPT	-0.023	0.078*	0.044	0.031	0.053	-0.021	0.011	-0.005	0.422**	0.012	0.048	0.060*
ILq	-0.057*	0.050	0.025	0.029	0.003	-0.039	0.004	0.016	0.045	-0.142*	0.127*	-0.171*
SPD	-0.037	0.055	0.029	-0.039	-0.050	-0.070*	0.086*	-0.017	0.229**	0.076*	0.033	0.061*
SPT	0.053	-0.006	-0.057	0.081*	-0.040	0.059*	-0.061*	-0.009	-0.203**	0.044	-0.230**	-0.036
PCC	-0.030	0.010	-0.022	0.027	-0.012	-0.070*	0.009	0.038	0.354**	0.091*	0.129*	-0.112*
PSC	0.031	0.057	0.010	0.028	-0.030	-0.009	-0.043	0.051	-0.008	-0.021	-0.165*	0.023
SSC	-0.007	0.052	0.082*	0.018	-0.082*	-0.013	-0.041	0.057	0.007	-0.246**	-0.268**	-0.048
DPSC	0.025	0.020	0.067*	0.011	-0.039	0.010	-0.042	0.043	-0.113*	-0.037	-0.214**	-0.023

FFS	-0.046	0.028	0.064*	0.007	0.074*	0.007	-0.042	0.031	-0.212**	0.204**	0.403**	0.133*
MFS	-0.023	-0.010	0.024	0.045	-0.007	-0.027	0.007	-0.034	0.212**	0.070*	-0.265**	0.191**

Table 7. Continued

Traits	LPT	ILq	SPD	SPT	PCC	PSC	SSC	DPSC	FFS	MFS
ILq	0.148*	-								
SPD	0.076*	-0.100*	-							
SPT	-0.303**	-0.083*	-0.367**	-						
PCC	0.131*	0.228**	-0.002	-0.176**	-					
PSC	-0.312**	-0.076*	0.272**	-0.068*	-0.073*	-				
SSC	0.018	-0.033	-0.376**	0.213**	0.051	0.144*	-			
DPSC	0.065*	-0.088*	-0.298**	0.169*	-0.133*	0.102*	0.816**	-		
FFS	0.229**	-0.050	-0.301**	-0.319**	0.059*	-0.087*	-0.015	0.042	-	
MFS	0.258**	0.240**	-0.182**	-0.268**	0.210**	-0.168*	0.041	-0.033	0.077*	-

Path coefficient analysis

Path coefficients are the separation of correlation coefficients into components of direct and indirect effects. The use of those methods needs cause and effect situations among the variables and direction in the causal system is assigned, based upon experimental evidence. Tables 8 and 9 present estimates of direct and indirect contributions of 33 traits to seed yield contributing components represented in this study by seed number per plant (SNP) and thousand-seed weight (TSW). Simple correlation coefficients indicate only the general association between any two traits without possible causes of such association. Path coefficient analysis presents a better understanding of cause-and-effect relationships among different characters and plays therefore an important role in determining the degree of relationships between yield and its components. Thus, the path coefficient analysis was performed to partition the correlation coefficient into direct and indirect effects of various characters on yield. Results of path coefficient analysis are presented in Tables 8 and 9. Path coefficient analysis based on SNP and TSW as dependent variables was then studied. It revealed a positive direct effect on SNP for most of the traits except for TE, MF, FF, LLW, FN, PH, FWI and SL (Table 8). Moreover, indirect effects of SNP via the remaining 33 independent characters were positive or negative and often very high and then considerable. Because of those indirect effects, this trait should be considered along with direct effects on seed yield. TSW as a dependent variable, showed a high positive direct effect with all traits apart from LPT, SPT, DPSC and MFS. Its indirect effects via all remaining 33 characters were very varied, positive or negative, and need careful analyses for the use of those traits as selection criteria.

In general, results of the direct and indirect path coefficients that estimated the extent of the relationships between seed yield (number) per plant or thousand-seed weight and 33 yield-related characters using the genotypic correlation values are presented here. All traits evaluated in this study were genotypically significantly correlated with seed yield in both directions. Path analysis partitioned these correlation coefficients into their components. Thus, it gives an insight into which traits can be selected for improvement in seed yield.

Table 8. Path coefficient analysis (direct and indirect effects) of component traits on seed yield parameter represented by seed number per plant (SNP) for data recorded across three different years and three locations in each year.

Traits	**Direct effect**	**Indirect effect via**										
		TE	TT	MF	FF	MT	LPL	LLL	LLW	FN	PH	IL
TE	-0.040	-	0.059	0.389	0.267	0.495	0.454	-0.864	-0.785	0.078	-1.172	1,087
TT	0.000	-0.059	-	0.329	0.156	0.291	0.298	-0.215	0.070	-0.072	-0.378	0,582
MF	-0.170	-0.329	-0.040	-	0.016	1.307	0.282	-2.592	-0.934	0.436	0.037	-0,313
FF	-0.005	-0.111	-0.153	0.063	-	-0.468	-0.106	-1.407	-0.475	-0.666	0.155	0,207
MT	0.003	-0.185	-0.373	-0.010	-0.063	-	1.666	0.303	-3.120	-1.112	1.000	-0,002
LPL	0.061	-0.138	-0.236	0.021	-0.023	-1.666	-	0.013	0.116	-0.692	0.027	-0,038
LLL	0.021	-0.129	-0.208	0.027	-0.015	-2.000	-0.013	-	-0.092	-1.531	-0.008	0,120
LLW	-0.061	-0.040	0.054	0.088	0.060	-2.200	-0.143	0.092	-	-0.012	0.156	0,214
FN	-0.047	-0.038	0.060	0.089	0.061	-2.266	-0.145	0.094	0.012	-	0.146	2,437
PH	-0.011	-0.125	-0.197	0.030	-0.012	-2.133	-0.018	0.003	-0.582	-0.146	-	0,118
IL	0.028	-0.183	-0.368	-0.008	-0.061	-0.066	0.064	-0.055	-0.974	-0.243	-0.118	-
NBN	0.029	-0.140	-0.241	0.020	-0.025	-1.600	0.002	-0.011	-0.683	-0.171	-0.030	0,958
FW	0.060	-0.216	-0.467	-0.031	-0.090	1.133	0.113	-0.090	-1.202	-0.300	-0.187	-0,750
FL	0.023	-0.118	-0.175	0.035	-0.006	-2.400	-0.029	0.011	-0.531	-0.134	0.015	1,458
FWI	-0.086	-0.046	0.038	0.084	0.055	0.200	-0.135	0.086	-0.037	-0.012	0.164	3,083
SL	-0.017	-0.092	-0.098	0.052	0.015	-2.333	-0.067	0.038	-0.354	-0.090	0.068	2,041
SWI	0.016	-0.131	-0.214	0.026	-0.017	-1.933	-0.010	-0.001	-0.620	-0.156	-0.011	1,166
TP	-0.000	-0.031	0.082	0.094	0.067	-2.533	-0.156	0.102	0.063	0.012	0.194	3,416
TSW	0.038	-0.125	-0.197	0.030	-0.012	-2.133	-0.018	0.003	-0.582	-0.146	0.000	1,291
LS	0.088	-0.231	-0.510	-0.041	-0.102	1.666	0.135	-0.106	-1.303	-0.325	-0.217	-1,083
LSi	0.083	-0.203	-0.428	-0.022	-0.078	0.666	0.094	-0.077	-1.113	-0.278	-0.160	-0,458
LC	0.058	-0.087	-0.428	-0.022	-0.078	0.666	0.094	-0.077	-1.113	-0.278	-0.160	-0,458
LPD	0.011	-0.055	0.010	0.077	0.047	-4.666	-0.121	0.077	-0.101	-0.028	0.145	2,875
LPT	0.081	-0.161	-0.302	0.006	-0.042	-0.866	0.032	-0.032	-0.822	-0.206	-0.072	0,500
ILq	0.050	-0.157	-0.291	0.008	-0.039	-1.000	0.027	-0.028	-0.797	-0.200	-0.064	0,583
SPD	0.038	-0.157	-0.291	0.008	-0.039	-1.000	0.027	-0.028	-0.797	-0.200	-0.064	0,583
SPT	0.116	-0.253	-0.576	-0.056	-0.121	2.466	0.167	-0.129	-1.455	-0.362	-0.263	-1,583
PCC	0.054	-0.153	-0.280	0.011	-0.036	-1.133	0.021	-0.025	-0.772	-0.193	-0.057	0,666
PSC	0.069	-0.153	-0.280	0.011	-0.036	-1.133	0.021	-0.025	-0.772	-0.193	-0.057	0,666
SSC	0.039	-0.137	-0.230	0.022	-0.022	-1.733	-0.002	-0.007	-0.658	-0.165	-0.022	1,041
DPSC	0.030	-0.124	-0.192	0.031	-0.011	-2.200	-0.021	0.005	-0.569	-0.143	0.003	1,333
FFS	0.020	-0.116	-0.170	0.036	-0.004	-2.466	-0.032	0.013	-0.518	-0.131	0.019	1,500
MFS	0.061	0.187	0.379	0.011	0.064	-0.066	-0.070	0.059	1.000	0.250	0.125	0,083

Table 8. Continued

Trait	**Direct effect**	**Indirect effect via**											
		NBN	**FW**	**FL**	**FWI**	**SL**	**SWI**	**TP**	**TSW**	**LS**	**LSi**	**LC**	**LPD**
TE	-0.040	2.451	1.700	-1.306	0.781	0.310	0.394	-0.093	-1.619	1.666	-2.291	0.959	1,666
TT	0.000	1.047	2.695	-0.492	-1.000	0.094	0.243	0.098	-1.800	-2.021	-2.689	0.405	0,064
MF	-0.170	2.500	0.459	-2.233	-0.108	-0.065	0.253	2.666	0.515	-0.191	0.000	2.214	-0,096
FF	-0.005	2.478	-0.048	-0.437	-0.021	0.024	0.116	-0.307	2.500	-0.632	1.083	2.285	1,750
MT	0.003	-0.480	0.133	1.440	-0.625	-0.083	-0.046	0.151	0.627	-2.500	0.588	2.625	1,666
LPL	0.061	0.040	-0.518	-0.174	-0.625	2.777	-0.363	2.222	0.538	-2.631	1.060	1.866	2,500
LLL	0.021	-0.053	0.370	-0.127	-0.381	-1.818	-0.016	2.523	-0.166	0.632	-1.904	-0.370	-0,579
LLW	-0.061	-0.900	0.539	-0.313	0.130	0.231	2.800	0.042	2.400	2.861	-1.239	0.471	0,200
FN	-0.047	-0.410	2.133	-0.355	-0.024	0.432	0.769	0.054	-2.473	2.000	-1.369	-0.553	-3,000
PH	-0.011	0.000	0.395	0.028	0.693	-0.818	-0.120	1.888	0.000	1.781	2.100	0.396	0,745
IL	0.028	-0.958	0.130	0.248	0.831	-0.212	-0.122	0.372	1.107	0.500	-0.333	-7.428	2,833
NBN	0.029	-	2.200	-0.115	-0.271	-0.509	-0.227	1.404	-0.888	-3.062	0.465	0.362	2,538
FW	0.060	-1.200	-	0.595	1.295	-0.650	-0.582	0.714	-1.960	2.000	-0.140	1.272	2,558
FL	0.023	2.400	-0.595	-	-0.127	0.666	-1.166	1.750	-2.000	0.535	1.916	0.566	-2,250

FWI	-0.086	1.200	-1.033	0.127	-	1.233	1.333	0.747	1.500	2.722	2.428	2.476	1,369
SL	-0.017	2.200	-0.752	0.045	0.806	-	0.037	0.057	-0.439	2.750	-3.157	-0.050	0,645
SWI	0.016	1.000	-0.516	-0.022	1.483	-0.037	-	0.101	0.076	-1.058	-2.166	1.600	-2,928
TP	0.000	1.800	-1.123	0.153	-0.258	0.058	-0.101	-	0.944	0.000	-2.214	-2.500	0,764
TSW	0.038	1.600	-0.550	-0.013	1.387	-0.031	-0.005	-0.944	-	2.500	2.625	-0.512	-1,225
LS	0.088	-2.800	0.089	-0.199	3.225	-0.132	0.101	-2.000	-2.500	-	-1.875	0.461	1,217
LSi	0.083	-2.800	-0.078	-0.150	2.741	-0.106	0.073	-1.722	-2.000	1.875	-	0.552	-1,951
LC	0.058	-2.800	-0.078	-0.150	2.741	-0.106	0.073	-1.722	-2.000	1.875	0.000	-	-2,857
LPD	0.011	2.200	-0.977	0.111	0.161	0.035	-0.077	-0.240	2.333	1.875	-0.701	0.607	-
LPT	0.081	-2.200	-0.337	-0.075	2.000	-0.065	0.030	-1.296	-2.166	2.750	-0.201	-1.428	-0,950
ILq	0.050	-1.800	-0.359	-0.068	1.935	-0.061	0.026	-1.259	-2.833	2.000	-0.219	-1.357	-0,916
SPD	0.038	-1.800	-0.359	-0.068	1.935	-0.061	0.026	-1.259	-2.833	2.000	-0.219	-1.357	-0,916
SPT	0.116	-2.200	0.224	-0.238	3.612	-0.153	0.124	-2.222	-1.500	-1.500	0.236	-2.214	-1,783
PCC	0.054	-1.400	-0.382	-0.062	1.870	-0.058	0.022	-1.222	-2.500	2.250	-0.236	-1.285	-0,883
PSC	0.069	-1.400	-0.382	-0.062	1.870	-0.058	0.022	-1.222	-2.500	2.250	-0.236	-1.285	-0,883
SSC	0.039	0.400	-0.483	-0.032	1.580	-0.042	0.005	-1.055	-1.000	2.375	-0.315	-0.964	-0,733
DPSC	0.030	1.800	-0.561	-0.009	1.354	-0.030	-0.007	-0.925	0.166	3.250	-0.377	-0.714	-0,616
FFS	0.020	2.600	-0.606	0.003	1.225	-0.022	-0.015	-0.851	0.833	2.750	-0.412	-0.571	-0,550
MFS	0.061	2.000	0.179	0.120	-2.451	0.090	-0.056	1.555	2.500	-3.000	0.078	1.928	1,183

Table 8. Continued

Traits	**Direct effect**	**Indirect effect via**									
		LPT	**ILq**	**SPD**	**SPT**	**PCC**	**PSC**	**SSC**	**DPSC**	**FFS**	**MFS**
TE	-0.040	2.071	-2.250	0.133	-1.268	-2.766	-1.584	-0.601	-0.943	-2.250	-1,262
TT	0.000	2.894	2.571	-0.148	-0.875	-1.108	-1.529	-0.368	-0.921	2.100	-1,604
MF	-0.170	0.194	-1.190	-1.000	1.125	2.666	0.382	0.396	0.557	-0.173	0,045
FF	-0.005	-0.531	-1.131	2.666	-0.605	1.090	-0.325	-0.14	-0.058	-0.976	0,045
MT	0.003	-1.000	1.750	1.952	1.761	2.428	0.888	1.529	0.000	1.48	0,333
LPL	0.061	0.279	-0.303	-0.707	-0.815	-0.470	-0.391	0.052	-0.200	2.000	-1,040
LLL	0.021	0.195	0.000	1.785	-2.153	-0.500	-1.000	0.093	-0.069	-0.304	0,645
LLW	-0.061	1.300	-2.315	0.312	2.108	2.178	1.148	1.000	2.500	-1.576	3,166
FN	-0.047	1.534	-1.306	0.117	2.367	2.100	2.000	0.898	1.069	-2.400	2,428
PH	-0.011	-1.187	2.125	0.796	0.958	0.937	0.175	0.066	-0.025	0.277	0,452
IL	0.028	-1.200	0.777	1.607	1.151	-0.571	-0.833	-2.333	0.761	-2.000	0,058
NBN	0.029	-0.440	0.310	-2.363	2.333	-2.500	-0.727	-2.000	2.500	0.260	0,312
FW	0.060	1.304	0.561	2.702	0.377	1.133	-1.064	6.142	-2.000	1.173	0,695
FL	0.023	0.294	0.420	-0.854	-2.166	1.900	0.350	0.192	0.150	-0.035	-2,700
FWI	-0.086	1.704	2.240	2.068	0.456	-0.409	2.100	1.378	1.462	1.484	2,291
SL	-0.017	0.698	1.666	0.660	-2.175	-2.750	-1.133	-0.292	-0.435	0.175	-2,285
SWI	0.016	-0.761	-0.358	0.771	1.118	-0.171	-1.444	-0.230	-0.400	-1.142	-1,111
TP	0.000	2.363	1.700	0.000	-1.967	2.333	-1.558	-1.390	-1.190	-1.095	1,200
TSW	0.038	-2.800	1.062	2.000	-2.666	0.394	0.313	0.105	-0.023	-0.161	-0,970
LS	0.088	-0.090	-0.888	-0.471	-0.059	-0.118	2.125	-2.285	0.513	0.292	-0,113
LSi	0.083	-1.916	0.176	-1.223	0.613	-0.296	1.238	0.146	1.162	-0.230	-0,128
LC	0.058	-0.479	-0.196	-2.818	-0.117	-0.209	0.157	0.134	0.200	-0.116	0,033
LPD	0.011	0.950	-0.321	-0.213	-2.972	-0.473	2.347	-0.916	-1.608	0.248	0,371
LPT	0.081	-	-0.013	-0.921	-0.165	-0.030	0.009	-0.722	-0.307	-0.104	0,054
ILq	0.050	0.013	-	0.680	-0.626	-0.008	0.013	0.333	0.204	0.440	0,066
SPD	0.038	0.013	0.000	-	-0.141	1.000	-0.003	0.029	0.060	0.073	-0,087
SPT	0.116	-0.337	0.520	0.326	-	0.306	0.779	-0.295	-0.414	0.231	0,134
PCC	0.054	0.027	-0.020	0.179	-0.306	-	-0.013	-0.176	0.120	-0.338	0,085
PSC	0.069	0.027	-0.020	0.179	-0.306	-0.013	-	-0.176	0.120	-0.338	0,085
SSC	0.039	0.087	-0.110	0.155	-0.357	-0.123	0.069	-	-0.008	0.733	0,658
DPSC	0.030	0.135	-0.180	0.136	-0.397	-0.219	0.118	0.008	-	-0.095	-1,030
FFS	0.020	0.162	-0.220	0.125	-0.420	-0.273	0.145	0.013	0.095	-	0,493
MFS	0.061	0.094	-0.160	-0.228	0.204	-0.246	0.118	0.033	0.809	0.493	-

Table 9. Path coefficient analysis (direct and indirect effects) of component traits on seed yield parameter represented by thousand-seed weight (TSW) for data recorded across three different years and three locations in each year.

Trait	Direct effect	Indirect effect via											
		TE	TT	MF	FF	MT	LPL	LLL	LLW	FN	PH	IL	NBN
TE	0.034	-	-0.040	-0.139	-0.071	0.044	-0.175	0.666	1.678	-0.086	1.172	-0.153	-1,645
TT	0.066	0.040	-	-0.060	0.033	0.133	-0.048	0.181	0.177	-0.006	0.484	0.069	-0,690
MF	0.124	0.061	0.060	-	0.021	0.088	-0.307	0.269	-0.518	0.131	0.636	0.102	-0,352
FF	0.112	0.029	-0.032	-0.021	-	0.039	0.406	0.404	-1.148	-0.085	2.333	0.007	-0,454
MT	0.066	-0.016	-0.170	-0.052	-0.039	-	1.187	0.670	-2.074	-0.390	2.416	-0.091	-0,779
LPL	0.038	0.053	0.038	-0.005	0.020	-2.533	-	0.067	0.039	0.076	0.152	-0.024	-0,880
LLL	0.045	0.100	0.175	0.026	0.060	-2.200	-0.067	-	0.013	0.968	-0.057	0.166	-0,026
LLW	0.046	0.087	0.137	0.017	0.048	-1.733	-0.048	-0.013	-	0.303	-0.071	0.091	0,066
FN	0.019	0.042	0.005	-0.012	0.011	-2.133	0.016	-0.059	-0.303	-	-0.140	0.281	0,208
PH	0.068	0.125	0.252	0.044	0.082	-2.133	-0.105	0.027	0.265	0.140	-	0.206	0,000
IL	0.035	0.025	-0.043	-0.023	-0.003	-1.533	0.040	-0.077	-0.417	-0.028	-0.206	-	-1,541
NBN	0.058	0.094	0.159	0.022	0.055	-2.000	-0.059	-0.005	0.050	0.087	-0.064	1.541	-
FW	0.079	0.124	0.247	0.042	0.080	2.000	-0.102	0.025	0.253	0.137	-0.003	2.208	2,200
FL	0.028	0.074	0.098	0.008	0.037	1.000	-0.029	-0.027	-0.088	0.053	-0.106	1.083	-2,200
FWI	0.046	0.081	0.120	0.013	0.044	-1.533	-0.040	-0.019	-0.037	0.065	-0.091	1.250	-1,400
SNP	0.052	0.100	0.175	0.026	0.060	-2.200	-0.067	0.000	0.088	0.096	-0.053	1.666	0,600
SL	0.056	0.001	-0.115	-0.040	-0.023	-0.666	0.075	-0.102	-0.582	-0.068	-0.255	-0.541	-1,000
SWI	0.056	0.005	-0.104	-0.037	-0.020	-0.800	0.070	-0.098	-0.556	-0.062	-0.248	-0.458	-2,600
TP	0.106	0.177	0.406	0.079	0.126	-2.000	-0.181	0.081	0.620	0.228	0.106	3.416	2,000
LS	0.066	0.088	0.142	0.018	0.050	-1.800	-0.051	-0.011	0.012	0.078	-0.076	1.416	-0,600
LSi	0.025	-1.208	-1.241	-0.265	-0.531	1.941	0.878	-0.190	-0.154	-0.538	-3.000	-1.333	0,095
LC	0.051	1.693	1.648	0.000	-2.583	-2.150	-2.600	0.467	0.679	-1.276	-0.283	2.857	-0,400
LPD	0.042	2.055	-1.645	-1.428	-3.142	-2.466	-2.333	0.275	0.650	-1.666	-0.098	-3.277	-1,692
LPT	-0.377	-2.611	0.774	2.035	1.285	1.200	2.000	-1.333	-0.250	2.000	-0.215	0.333	-1,538
ILq	0.021	-2.900	2.142	-0.694	-0.893	-2.750	-0.878	0.000	-0.578	-0.714	-1.250	-2.444	0,241
SPD	0.000	0.196	0.029	-0.126	0.236	-1.619	-0.048	2.071	1.375	-0.058	0.671	-0.215	-2,363
SPT	-0.017	-0.305	-0.091	0.000	2.666	2.000	-0.052	1.615	-0.378	0.204	-0.486	0.575	-2,000
PCC	0.033	-2.666	-1.260	-2.875	-1.684	-2.714	-3.000	-1.000	1.178	2.850	0.750	2.357	-2,500
PSC	0.042	-1.754	-2.088	-2.000	2.500	-1.666	-2.782	-2.785	0.851	2.750	0.274	2.388	-1,818
SSC	0.013	-0.804	-0.675	-1.404	-1.930	-2.352	-1.684	1.046	1.000	1.288	0.344	2.833	1,000
DPSC	-0.004	-1.394	-2.026	-1.047	-1.660	0.000	1.750	1.046	2.888	1.767	0.775	-2.023	-2,400
FFS	0.010	-2.083	1.100	-0.769	-1.117	-1.280	-2.000	0.826	-1.000	-2.666	-0.277	2.750	-0,440
MFS	-0.052	-0.100	0.325	0.480	0.190	2.666	0.840	-0.958	-2.500	-2.142	-0.821	-0.176	-0,537

Table 9. Continued

Traits	Direct effect	Indirect effect via											
		FW	FL	FWI	SNP	SL	SWI	TP	LS	LSi	LC	LPD	LPT
TE	0.034	-2.000	0.816	-1.375	0.964	-0.006	-0.016	0.527	-1.600	1.208	-1.693	-2.055	-0,880
TT	0.066	-1.956	0.276	-3.142	1.333	0.109	0.118	0.486	0.565	1.241	-1.648	1.645	-0,789
MF	0.124	-3.400	0.114	-0.366	-0.583	0.082	0.093	0.212	0.326	0.862	-1.351	1.290	-0,210
FF	0.112	-2.217	0.289	-0.350	-2.500	0.032	0.028	0.217	-2.461	0.531	1.583	2.142	-2,250
MT	0.066	-1.304	0.590	-0.662	-2.750	-0.021	-0.026	0.285	2.700	-0.941	1.150	2.466	-1,538
LPL	0.038	0.469	-0.174	-0.187	-1.315	-1.111	2.363	1.722	1.000	-0.878	1.600	7.333	-0,186
LLL	0.045	-0.102	0.297	0.084	0.000	1.818	-0.836	2.000	0.068	0.190	-0.467	-0.275	0,195
LLW	0.046	-0.113	-0.052	0.130	0.205	0.380	2.800	0.418	-0.027	0.154	-0.679	-0.650	2,000
FN	0.019	-0.977	0.140	0.129	0.885	0.328	0.307	1.000	-0.961	0.538	1.276	2.666	-0,325
PH	0.068	0.008	-0.201	-0.387	1.166	3.045	-2.600	1.037	0.625	2.000	0.283	0.098	-1,937
IL	0.035	-0.384	0.184	0.337	-0.930	0.056	0.048	0.372	-0.653	1.333	-1.857	1.277	-2,300
NBN	0.058	-2.200	0.105	0.037	-0.150	0.980	2.181	1.071	-0.187	-0.095	0.400	1.692	-0,560
FW	0.079	-	-0.303	-0.323	0.213	0.640	0.810	0.207	1.750	0.180	0.290	0.176	-1,304
FL	0.028	0.303	-	-0.013	-1.750	-1.857	-1.166	1.400	-0.070	-0.750	1.433	-1.125	0,038
FWI	0.046	0.258	0.013	-	0.322	0.323	0.440	0.422	-0.222	-2.000	-1.857	-0.345	0,159
SNP	0.052	0.146	0.045	-0.322	-	-2.833	1.400	1.076	0.086	-0.074	1.222	0.730	0,548
SL	0.056	0.741	-0.127	1.387	1.833	-	-0.003	0.165	-1.750	1.500	-1.366	2.322	-0,679
SWI	0.056	0.719	-0.120	1.322	2.500	0.003	-	0.174	0.882	3.055	2.333	-2.000	1,619
TP	0.106	-0.325	0.183	-1.677	-2.000	0.167	-0.174	-	0.000	-0.904	-1.083	1.352	1,363

LS	0.066	0.213	0.026	-0.129	1.000	0.083	-0.084	0.000	-	-1.250	0.207	0.320	0,026
LSi	0.025	-0.180	0.750	2.000	0.074	-2.000	-3.055	0.904	1.250	-	0.219	-0.365	1,750
LC	0.051	-0.290	-1.433	1.857	-3.222	1.366	-5.333	1.083	1.375	-0.219	-	0.357	0,958
LPD	0.042	-0.176	2.125	0.345	-0.730	-2.322	2.000	-1.352	3.125	-0.131	-0.357	-	0,600
LPT	-0.377	-0.529	-1.370	-0.583	1.384	1.870	1.142	-0.941	-2.375	0.149	-1.892	-1.083	-
ILq	0.021	0.157	0.360	0.560	0.137	1.900	-1.410	-2.500	0.222	0.000	-0.196	0.087	0,141
SPD	0.000	1.135	-0.272	-0.655	0.743	-0.480	-0.314	-0.825	-0.100	-0.434	-1.757	-0.786	-0,157
SPT	-0.017	-0.641	1.166	0.192	-0.259	-0.800	0.508	1.032	0.073	-0.568	0.217	1.111	0,013
PCC	0.033	-0.433	2.000	-1.636	0.962	-2.583	-1.100	-1.777	0.090	0.241	-0.023	-0.062	0,328
PSC	0.042	0.838	0.929	2.900	1.392	-1.066	-1.000	0.069	-1.625	-1.666	-0.060	0.869	-0,179
SSC	0.013	-1.571	1.134	0.670	2.500	-1.195	-1.384	-0.073	1.285	-0.166	-0.059	-0.541	3,444
DPSC	-0.004	1.280	1.950	0.820	2.090	-2.512	1.600	-0.071	-0.451	-1.108	-0.074	-1.130	0,953
FFS	0.010	-0.130	1.178	0.453	1.714	0.972	1.000	0.547	-0.117	0.073	-0.024	0.000	0,157
MFS	-0.052	2.565	1.200	-1.500	-1.022	-1.000	-0.185	-1.571	-0.188	-0.714	0.283	-0.340	-0,112

Table 9. Continued

Trait	**Direct effect**	**Indirect effect via**								
		ILq	**SPD**	**SPT**	**PCC**	**PSC**	**SSC**	**DPSC**	**FFS**	**MFS**
TE	0.034	1.900	-0.196	0.305	2.666	1.754	0.804	1.197	1.083	0,100
TT	0.066	-1.142	-0.029	0.091	1.260	2.088	0.675	1.657	-2.100	-0,325
MF	0.124	-1.571	0.079	0.000	1.021	1.764	0.578	1.368	-2.000	-0,581
FF	0.112	0.893	-0.236	-1.666	1.684	-2.500	1.930	1.380	1.117	-0,190
MT	0.066	1.675	1.619	-2.000	1.714	1.666	1.352	0.000	1.280	-2,666
LPL	0.038	0.878	0.048	0.052	3.000	2.782	1.684	-1.400	1.100	-0,840
LLL	0.045	0.000	-2.071	-1.615	1.000	2.785	-1.046	-0.720	-0.826	0,958
LLW	0.046	0.578	-1.375	0.378	-1.178	-0.851	-1.000	-2.111	1.000	2,500
FN	0.019	0.714	0.058	-0.204	-2.850	-3.500	-1.288	-1.441	1.666	2,142
PH	0.068	1.250	-0.671	0.486	-0.750	-0.274	-0.344	-0.425	0.277	0,821
IL	0.035	2.444	0.215	-0.575	-2.357	-1.388	-2.833	1.690	-2.750	0,176
NBN	0.058	-0.241	2.363	2.000	1.450	1.818	-2.480	1.700	0.440	0,537
FW	0.079	-0.157	-1.135	0.641	0.433	-0.838	1.571	-0.720	0.130	-2,565
FL	0.028	-0.36	0.272	-1.166	-2.000	-0.929	-1.134	-2.250	-1.178	-1,200
FWI	0.046	-0.56	0.655	-0.192	1.636	-1.900	-0.670	-0.611	-0.453	1,500
SNP	0.052	-0.137	-0.743	0.259	-0.962	-1.392	-2.500	-2.818	-2.714	1,022
SL	0.056	-1.900	0.480	0.800	1.583	1.066	1.195	2.153	-0.972	1,000
SWI	0.056	1.410	0.314	-0.508	1.100	1.000	7.384	-2.200	-1.000	0,185
TP	0.106	2.500	0.825	-1.032	1.777	-0.069	0.073	-0.261	-0.547	2,571
LS	0.066	-0.222	0.100	-0.073	-0.090	1.625	-1.285	0.327	0.117	0,188
LSi	0.025	0.000	0.434	0.568	-0.241	1.666	0.166	0.729	-0.073	0,714
LC	0.051	0.196	1.757	-0.217	0.023	0.060	0.059	0.009	0.024	-0,283
LPD	0.042	-0.087	0.786	-1.111	0.062	-0.869	0.541	0.521	0.000	0,340
LPT	-0.377	-1.033	-1.065	-0.983	-1.038	-0.983	-1.277	-1.076	-1.021	-1,019
ILq	0.021	-	-0.330	-0.301	-0.096	0.460	1.242	0.306	0.300	0,208
SPD	0.000	0.330	-	0.021	1.750	-0.250	0.196	0.201	0.159	-0,093
SPT	-0.017	0.301	-0.021	-	0.267	0.882	-0.309	-0.307	0.125	-0,093
PCC	0.033	0.096	-2.750	-0.267	-	0.178	-0.372	0.037	0.118	0,342
PSC	0.042	-0.460	0.250	-0.882	-0.178	-	-0.041	0.078	-0.229	-0,505
SSC	0.013	-1.242	-0.196	0.309	0.372	0.041	-	0.017	-1.733	2,219
DPSC	-0.004	-0.465	-0.248	0.390	-0.142	0.058	0.000	-	0.619	-2,757
FFS	0.010	-0.300	-0.159	-0.125	-0.118	0.229	1.733	-0.285	-	0,844
MFS	-0.052	-0.208	0.093	0.093	-0.342	0.505	-2.219	2.333	-0.844	-

Discussions

Genetic variability

Significant differences were observed among the genotypes for all the traits. These differences indicated the presence of high variability and opportunity for improvement. A wide range of variation for all traits under observation in colocynth was noted under different environmental conditions.

Such results had been reported by Tolera et al. (2024) in sugarcane, Jamshidian et al. (2013), Cervenski et al. (2011), Singh et al. (2011), Sharma (2010), Kaygısız (2009), Meena et al. (2009) and Balkaya et al. (2005) in cabbage., In *Citrullus colocynthis*, studies on that item are scarce. Highly significant mean squares for genotypic differences were found in the combined analysis of variance for all traits observed, confirming the possibility of improving those traits through selection. Also, genotypes responded differently to changes in years and locations, as genotype × year, genotype × location and genotype × year × location interactions mean squares were highly significant ($p \leq 0.05$ or $p \leq 0.01$) for all characters. This indicates that ranking between genotypes was affected significantly by differences in environments even if those genotypes were tested at three various locations during three different years.

The magnitude of phenotypic variation does not reveal the relative amount of genotypic and non-genotypic components of variation (Falconer 1989). Furthermore, it is difficult to compare variations for various characters because they are not unit-free. Since most of the economic characteristics (grain or seed yield) are complex in inheritance and greatly influenced by several genes interacting with various environmental conditions. The study of the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very necessary to estimate the scope for improvement by selection (Bello et al. 2012). The reliability of a parameter to be selected for breeding programs among other factors is dependent on the magnitude of its coefficient of variations, especially the GCV. However, Differences between genotypic and phenotypic coefficient of variability indicate the environmental influence (Bello et al. 2012). While a lower value for the coefficient of variation (CV) generally depicts low variability among the tested samples, a high proportion of GCV to the PCV is desirable in breeding works. Results given in Tables 5 and 6 depicted that phenotypic variances and PCVs were slightly higher than genetic variances and GCVs for all the characters, suggesting the least influence of environment in the expression of these characters Similar results have also been reported by Tolera et al. (2024) and Bello et al. (2012). Estimates of genotype × year, genotype × location and genotype × year × location interaction variances for the traits in most instances were low considering qualitative characters. This result tends to support the notion that greater heterozygosity confers a buffering effect or stability over a wide range of environments, whereas inbreeding leads to increased homozygosity and less buffering capacity (Nigussie and Saleh 2007, Falconer 1989). High genetic variability for seed yield in the genotypes over years recorded in the test materials suggested that it could be further exploited through improvement and selection programs (Wannows et al. 2010, Najeeb et al. 2009, Kashiani et al. 2008, Aziz et al. 1998).

High values of PCV and GCV observed in most of the traits show that selection can be effective for these traits, but also indicate the existence of substantial variability, ensuring ample scope for their improvement through selection. These observations are in confirmation with the findings of Bishwas and Singh (2024), Mitra et al. (2023) and Bello et al. (2012) in wheat, tomato and maize, respectively.

A high magnitude of broad sense heritability estimates were noted in all qualitative characters (Table 6). This implied the possibility of effective selection for genetic improvement of these traits. Values of genetic advance as a percentage of the mean (GAM) ranged from 1.094 for seed width (SWI) to 248.969 % for leaf peduncle length (LPL) considering quantitative traits. For qualitative characters, GAM ranged from 55.820 in leaf size (LSi) to 331.063 % in fruit design produced by secondary skin color (DPSC). High heritability estimates coupled with high estimates of genetic advance expected in the next generation in several traits indicate the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generations. This also provides evidence that a larger proportion of phenotypic variance has been attributed to genotypic variance, and reliable selection could be made for these traits based on phenotypic expression (Bello et al. 2012). These results find support from the earlier studies by Akbar et al. (2008) and Kashiani et al. (2008) even though it was on another crop. Those authors suggested that the concerned parameters were under the control of additive genetic effects. Tolera et al. (2024) and Sumathi et al. (2005) suggested also that these parameters could be manipulated according to requirements, and worthwhile improvement could be achieved through selection. Those authors concluded that the selection at an early segregating generation will prove beneficial for selecting superior varieties of maize. Such conclusions should also be made in the study presented in the current report. To sum up, it can be concluded that heritability estimates along with genetic advances are more helpful in predicting the genetic gain under selection than heritability estimates alone as mentioned in Akbar et al. (2008) in maize.

Correlations among traits

In plant breeding, correlation coefficient analysis measures the mutual relationships between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield (Tolera et al. 2024, Cousin et al. 1985). **The** genotypic correlation coefficient is the heritable association between two variables (Hussain et al. 2011). However, phenotypic correlation includes both phenotypic and environmental effects. Hence, significant phenotypic correlation without significant genotypic correlation has no value (Parte et al. 2022, Bello et al. 2012, Falconer 1989). In the present study, correlations showed positive and significant association between traits contributing to yield (TSW and SNP) and most of the other characters at the genotypic level (Table 7).

Phenotypic correlation is a composite of genotypic and environmental correlations. In this study, it was observed that the genotypic correlation coefficients were, in most cases, lower than their corresponding phenotypic correlation coefficients, indicating that the inherent association between the characters is governed largely by environmental causes. These findings were not similar to those earlier observed by Balqees and Mohammed (2022), Adekoya et al. (2014) and Scod et al. (1995) in rice and okra, respectively. Characters that are phenotypically correlated but not genotypically correlated will not produce repeatable estimates of inter-character associations, and any selection based on the relationships is likely to be unreliable.

Path coefficient analysis

Correlation measures mutual association with no regard to causation, whereas path analysis specifies causes and measures their relative importance (Dewey and Lu, 1959). Time to emergence (TE), time to male flowering (MF), time to female flowering (FF), leaf limb width (LLW), fruit number per plant (FN), plant height (PH), fruit width (FWI), seed length (SL) and thousand-seed weight (TSW) had a negative direct effect on seed number per plant (SNP). However, apart from leaf pubescence texture (LPT), stem pubescence texture (SPT), design produced by secondary skin color (DPSC) and male flower size (MFS), all other traits showed positive direct effects on TSW. These observations suggested the inefficiency of selection based on correlation alone. In conclusion, the above-mentioned findings illustrated that the performance of genotypes varied from one location and year to another (Ogunniyan et al. 2015, Adekoya et al. 2014).

Understanding the relationships between the traits, for the selection of the important ones, is of crucial importance. The goals of the path analysis are that the acceptable descriptions of the correlation between the traits, based on a model of cause and effect, are presented. The importance of the affecting traits on a specific one is estimated. In fact, the basic relationships between the traits are expressed by this analysis (Tolera et al. 2024, Becker 2011, Falconer 1989). So, the correlation coefficients dividing to the direct and the indirect effects of the set of independent variables on a dependent, and their relative importance are calculated. Several researches on the relationships among characters and their effects in crop plants have been reported (Ogunniyan et al. 2015, Bello et al. 2012). In soybean, the number of pods per plant, the weight of 100 seeds and the number of seeds per plant compared to other traits had the most direct effect on the yield as reported in Edache (1996).

In an experiment that was performed on pea plants, it was clear that, there were positive and significant correlations between seed yield and number of pods per plant, weight of 100 seeds and number of lateral branches. Also, it was indicated that the number of pods per plant, the pod length and the vine length had the most direct effect on the seed yield of peas (Rasaei et al. 2011, Ghobary 2010, Amaranthath and Viswaantaha 1990). From these reports, pea seed yield had a positive correlation with plant height, number of pods per plant, number of seeds per pod and pod yield Furthermore, pod yield showed a high direct effect on the seed yield of the crop (Rasaei et al. 2011).

Moreover, the use of simple correlation analysis cannot fully explain the relationships among characters. Therefore, path coefficient analysis has been used by many researchers for a more complete impact determination of an independent variable on a dependent one (Tolera et al. 2024, Balqees and Mohammed 2022, Parte et al. 2022, Mahmoud et al. 2020, Bello et al. 2012, Udensi and Ikpeme 2012, Majid et al. 2011, Karademir et al. 2009, Zhao et al. 2008, Lal 2007, Akinyele and Osekita, 2006) in sugarcane, rice [*Oryza sativa*], peanut, okra, fennel, wheat, cotton, potato and *Cajanus cajan*, respectively). Path coefficient analysis helps the breeder to explain direct and indirect effects which have been extensively used in breeding works of different crop species by various researchers (Bishwas and Singh 2024, Tolera et al. 2024, Mitra et al. 2023, Adekoya et al. 2014). The knowledge of inter-character relationships is very important in plant breeding for indirect selection for characters that are not easily measured and for those that exhibit low heritability. A path coefficient analysis simultaneously captures the effects of intricate relationships among various traits under investigation (Falconer 1989). Information obtained from correlation coefficients can be enhanced by partitioning them into direct and indirect effects for a set of *a priori* cause–effect interrelationships. Such reports have been demonstrated in various crops (Tolera et al. 2024, Adekoya et al. 2014). However, there has been relatively little information on some of the newly collected genotypes of colocynth in Africa. A careful study of relationships among quantitative characters is necessary in order to ascertain the magnitude and direction of changes to be expected during selection in *Citrullus colocynthis*. Knowledge of relationships between yield and its components is essential as it may help in constructing suitable selection criteria for yield. In order to determine the relationships between yield and other examined traits, correlation coefficients were calculated. Simple correlation coefficients estimated among examined traits are shown in Table 7. Results suggested that any positive increase in these traits will accelerate the yield potential of colocynth. So, these traits should be paid attention in breeding programs. Positive and significant correlations between yield and yield components in colocynth were also reported.

Conclusions

The study presented here revealed that information about the extent of variation, estimates of heritability and expected genetic advance with respect to the performance of colocynth and particularly its yield contributing characters represents the basic requirement for a crop improvement program. Broad sense heritability is useful for measuring the relative importance of additive portions in genetic variance that can be transmitted to the offspring. The preponderance of additive gene effects controlling a trait usually resulted in both high heritability and genetic advance, while those governed by non-additive gene actions could give high heritability with low genetic advance. However, in the present research, expected genetic advance values were based on broad sense heritability, which integrates an additive portion of the total phenotypic variance. Effective selection for superior genotypes is possible considering some of the quantitative and especially qualitative characters investigated. Those traits could be sources of alleles that can be manipulated with other promising cultivars from farmers' origin in Benin and West Africa. The yield components except time to emergence (TE), time to tailspins (TT), leaf limb width (LLW), fruit number per plant (FN), fruit width (FW), seed length (SL), seed tegument percentage (TP) and stem pubescence texture (SPT) had significant and positive correlations with yield attributes represented by thousand-seed weight (TSW) and seed number per plant (SNP). Path coefficient analysis indicated that all the characters [except leaf pubescence texture (LPT), stem pubescence texture (SPT), fruit design produced by secondary color (DPSC) and male flower size (MFS)] had a positive direct effect on TSW and partly SNP. Results suggested that most of the 34 quantitative and qualitative traits studied could be effectively used as selection criteria in the breeding program of *Citrullus colocynthis* varieties with high yield. More collections in the whole Benin and West Africa are needed for the selection of high genotypes useful for breeding success in the crop under investigation. The current study is giving the first results in the variability existing in the crop and will help in future research activities, as it determines most of the characteristics necessary to be recorded for success. Furthermore, fruit and seed quality analyses are ongoing, and will be used together with morpho-agronomic traits to refine breeding strategies in *Citrullus colocynthis*.

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