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DISSECTING GENETIC CONTROL OF YIELD AND ASSOCIATED TRAITS IN ROSELLE (*HIBISCUS SABDARIFFA* L.) THROUGH HERITABILITY, CORRELATION, AND PATH ANALYSIS

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Abstract

Roselle (*Hibiscus sabdarifa* L.) is cultivated for its stem, leaves, and other parts in tropical and subtropical regions. The cleistogamous nature of the roselle plant makes it difficult for hybridization and further conventional improvement. Therefore, this study evaluated thirty-five roselle genotypes in order to sort-out the most performing genotype with high yield potential. The results revealed that genotype BUM-001 exhibited the highest fruits number per plant (290), weight of individual calyx (725 g), and maximum fruits weight per plant (1096.69g). The calyx ball and calyx fruit ratios were higher in the genotype VM-1 (1.17 and 0.53, respectively). The maximum fruit length (54.19 mm) and heaviest calyx (4.65 g) were recorded in the genotype BUM-007. The minimum duration for 100% flowering (71 days), 1st fruit maturity (56 days), 1st edible fruit maturity (110 days), and 50% fruit maturity (121 days) was found in genotype 4556. Maximum fruit width (26.37 mm) and fruit weight (11.18 g) were observed for the genotype BUM-004. High heritability, broad sense, and genetic gain were found in several branches, internode length, calyx yield, fruit yield per plant, and individual calyx weight. The values of genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficient, indicating a strong inherent association between various characters at the genetic level. Significant and positive correlation coefficients were observed for fruit yield per plant with days to 1st edible maturity fruit weight, fruits per plant, and fruit length. The results obtained from path analysis showed that 50% maturity (days) had the strongest influence on fruit yield per plant, followed by fruits per plant, fruit length, and first fruit setting (days). These results improve our understanding of crop improvement in roselle plants which could be further utilized for new varieties development.

Key words: Calyx yield; Heritability; Path coefficients; Roselle (*Hibiscus sabdariffa* L.)

Introduction

Globally, for ensuring food security and alleviating poverty require cultivation of alternate high revenue generating cash crops and their sustainable integration into modern commercially-oriented farming systems (Iqbal, 2019; Iqbal *et al*., 2020; 2022). Roselle (*Hibiscus sabdariffa* var *sabdariffa* L.) is an annual tropical plant species of the Malvaceae family having chromosome number 2n= 72 (tetraploid) which originated from West Africa (Shoosh, 1993). Roselle is commonly known as chukur in Bangladesh while it has many other names like sorrel, karkade, jelly okra, Asamsusur, Bissap, mesta, saril, etc. It is cultivated in tropical countries, predominantly in tropical Africa, Australia, Indonesia, Malaysia, Thailand, China, Philippines, and Brazil. Major producing countries are Sudan, Jamaica, and Mexico. Two prominent types of roselle including *Hibiscus sabdariffa* (cv. *Sabdariffa)* and *Hibiscus sabdariffa* (cv. *Altissima),* were identified and recognized by Purseglove (1974). Particularly, the variety altissima has been grown for fiber in India, Philippines and Java for many years. Primarily, it has been identified that it can be present in green, red, and dark red colors in the tropics (Purseglove, 1974). The tender leaves and stalks of Roselle find its use as a salad in many countries. Additionally, its roots have been reported to be aperients owing to the abundant presence of tartaric acid (Mclean, 1973). Overall, its economic importance lies in multiple uses of its seeds, leaves, fruits, and roots in human consumption, medicinal uses and livestock feed (Anon., 2012). In particular, its fleshy calyx is processed to prepare tasty and flavoring jams, pudding, jelly, squash, different types of cakes, syrup, gelatin, ice cream, and roselle tea (Mohamed *et al*., 2012).

Despite its enormous potential and immense economic pertinence, Roselle has not received due attention of researchers and resultantly serious research and knowledge gaps continue to prevail regarding crucial information about its genetic make-up, breeding needs, and production

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potential under varying agro-climatic and soil conditions. Its demand has persistently increased in Bangladesh owing to its fleshy calyces and leaves, whereas phloem fiber of Roselle has been finding extensive use at the homestead level. Recently, Roselle cultivation has increased (in terms on acreage and production) in many countries in the world like Senegal and Mali, however, whole produce of Roselle gets consumed domestically in these countries. China and Thailand have emerged as the largest producers of Roselle in Asia. Presently, Malaysia has also started Roselle cultivation on a medium scale in order to meet the demand of local industry, however, negligible produce becomes available for international trade every year (Mohammad *et al*., 2002). Therefore, keeping in view the multiple uses and increasing demand of Roselle locally in Bangladesh and globally, have necessitated conducting scientific studies to increase its productivity on per unit land area basis.

Globally, very small number of scientific studies have been executed to develop high-yielding varieties through genetic improvement especially research to sort-out the most performing genotypes of Roselle has been lacking in Bangladesh despite persistent increase in its demand in local small and medium industries. The net result is sub-optimal yields of calyx in Bangladesh, although the soil and climatic conditions are excellent to boost its yield. Moreover, critical information pertaining to genetic variability among Roselle genotypes and interrelationship among yield components have become crucial for plant breeders in order to develop potent and high potential varieties of Roselle. Therefore, in order to bridge this research gap, a trial was conducted to comparatively assess 35 genotypes of Roselle that were collected from local and exotic genetic pools. The ultimate aim of the study was to find-out the correlation and causation of yield and yield components in Roselle.

Materials and Methods

Plant materials: Thirty-five genotypes of Roselle from 15 countries (Australia, Bangladesh, Brazil, Indonesia, Kenya, Malaysia, Nepal, Niger, Cameroon, Nigeria, Pakistan, Poland, Sudan, Thailand, USA, and Zambia) were collected from different sources. Roselle seeds of 28 genotypes were collected from the GRS Division of Bangladesh Jute Research Institute, Dhaka, Bangladesh, whereas seven genotypes were acquired from the germplasm maintained in the Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh (Currently, Gazipur Agricultural University). In this way, a trial was conducted to comparatively assess thirty-five roselle genotypes in terms of their agronomic yield attributes, genotypic variability, and fifteen yield attributes association with each other. The location of the trial was the experimental field of the Department of Genetics and Plant Breeding, BSMRAU, Gazipur, Bangladesh during August 2015 to February 2016. The experimental design was randomized complete block design (RCBD) with regular arrangement and there were three replications maintained for every genotype of Roselle under investigation.

Data collection: Sampling was done by selecting ten random plants from each plot for data collection. Data were recorded for plant height (cm), first, 50% and 100% flowering (days), fruit setting (first, 50% and edible maturity in days), branches and fruits number per plant, internodal length (cm), length and width of fruit (mm), fruit and calyx weight (g), calyx fruit ratio, calyx ball ratio, fruit and calyx yield (g/plant Data were measured at different growth stages of plants and harvesting.

Statistical analysis

Statistical analysis was conducted using the Satistix10 program (Michigan State University, USA). Data were subjected to analysis of variance for mean comparison, and significant differences were calculated according to Fisher's LSD test. Differences at $p<0.05$ were considered to be statistically significant. Mean square (MS) at error and phenotypic variances was determined by following the procedure described by Johnson *et al*., (1995). Likewise, genotypic variance (GMS= σ^2_g) was estimated by subtracting the MS error from the genotypic MS error (EMS) and dividing it by the replication number (r) by following the equation 1.

$$\sigma^2_g = \frac{GMS - EMS}{r} \quad (1)$$

Phenotypic variance (σ^2_p) was calculated by adding genotypic variance (σ^2_g) with error variances (σ^2_e), as described in equation 2.

$$\sigma^2_p = \sigma^2_g + \sigma^2_e \quad (2)$$

Estimation of GCV and PCV: The genotypic coefficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were estimated according to the formula given by Burton (1952):

$$GCV = \frac{\sigma_g \times 100}{\bar{x}}$$

$$PCV = \frac{\sigma_p \times 100}{\bar{x}}$$

Where,
σ_g = genotypic standard deviation and
σ_p = phenotypic standard deviation
X = population mean

Estimation of heritability: The broad sense heritability was determined by following the protocol as suggested by Lush (1949), Hanson *et al*., (1956) and Johnson *et al*., (1955):

$$h^2_{b\,\%} = \frac{\sigma^2_g}{\sigma^2_p} \quad (3)$$

where,
h^2_b = Broad sense heritability
σ^2_g = Variance (genotypic)
σ^2_p = Variance (phenotypic)

Estimation of genetic advance: The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson *et al*., (1995).
Genetic advance (GA) = $K.h^2.\sigma_p$

$$= K.[\sigma^2_g \div \sigma^2_p \,].\sigma_p \qquad (4)$$

Where,
K = 2.06 at 5% selection intensity (selection differential)
σ_p = phenotypic standard deviation

Genetic advance as a mean percentage was estimated by using equation 5.

$$\text{Genetic advance (\% mean)} = \frac{\text{Genetic advance}}{\text{Population advance}} \times 100 \qquad (5)$$

Estimation of the correlation coefficient: Genotypic and phenotypic correlation coefficients (r_g and r_p, respectively) were determined in all possible combinations using the formula suggested by Johnson *et al*., (1955) and Hanson *et al*., (1956).

The covariance component was used to compute r_g and r_p between the pairs of the characters as follows:
Genotypic correlation,

$$r_g = \frac{\sigma^2_{gxy}}{\sqrt{\sigma^2_{gx} \times \sigma^2_{gy}}}$$

Where,
σ^2_{gxy} = genotypic covariance between the traits x and y
σ^2_{gx} = genotypic variance of the traits x
σ^2_{gy} = genotypic variance of the traits y

Phenotypic correlation

$$r_p = \frac{\sigma^2_{phxy}}{\sqrt{\sigma^2_{phx} \times \sigma^2_{phy}}}$$

Where,
σ^2_{phxy} = phenotypic covariance between the traits x and y
σ^2_{phx} = phenotypic variance of the traits x
σ^2_{phy} = phenotypic variance of the traits y

Estimation of path coefficient: Path coefficient was estimated for further partition of correlation coefficients into direct and indirect effects following the method originally described by Wright (1921) and later illustrated by Dewey & Lu (1959).

Results and Discussion

The analysis of variance (ANOVA) showed highly significant ($p<0.01$, $p<0.05$) mean square value due to growth and yield contributing characters (Tables 1 and 2) among 35 genotypes of roselle. The highly significant results indicated genetic differences among genotypes for different growth and yield contributing traits.

Mean performance of Roselle for growth and yield characters: The 50% flowering's minimum duration (64 days) was observed for genotype 4602 (Table 3). Mohamed *et al*., (2013) reported that some accessions flowered within 60 days. It could be inferred that robust genotype was responsible behind the minimum duration taken to 50% flowering by genotype 4602. The minimum duration for 100% flowering (71 days), 1st fruit setting (56 days), 1st edible fruit maturity (110 days), and 50% fruit maturity (121 days) was found in genotype 4556 (Table 3). The shortest internode length (3.78 cm), maximum fruit width (26.37 mm) (Table 3), and weight of fruit (11.18 g) (Fig. 3) were observed in the genotype BUM-004. The highest branches number per plant was produced by the genotype BUM-001 (27) (Fig. 1). Falusi *et al*., (2013) found similar results, and the highest number of branches per plant was observed in the genotype NG002 (24.50).

The highest plant height was measured in genotype 4385 (249.36 cm) (Fig. 2). Falusi *et al*., (2013) also reported variation in plant height (74.16-154 cm). The maximum fruit length (54.19 mm) and heaviest (4.65 g) calyx (Figa. 3 and 4) were recorded in the genotype BUM-007. The greatest fruits number per plant (290) was produced by the genotype BUM-001 (Fig. 5), along with maximum calyx yield per plant (725g) and fruit yield per plant (1096.69g) (Table 3). Osman *et al*., (2011) obtained the maximum fruits per plant (182.8) in roselle accession UKMR-3. The calyx ball and calyx fruit ratios (1.17 and 0.53, respectively) were higher in the genotype VM-1.

Table 1. Analysis of variance for nine growth characters of 35 genotypes of roselle.

Source of variation	df	Days to 1st flowering	Days to 50% flowering	Days to 100% flowering	Days to 1st fruit setting	Days to 50% maturity	Days to 1st edible maturity	Branches per plant (no.)	Plant height (cm)	Internodal length (cm)
Replication	2	11.429	12.007	1.207	17.857	1.400	11.429	0.0395	185.66	0.04951
Genotype	34	630.73**	561.33**	495.218**	553.33**	575.51**	630.73**	73.29**	5352.70**	2.99**
Error	68	4.811	5.934	12.060	5.784	12.003	4.811	1.5225	71.26	0.16591

ns= Non-significant, * and ** Significant at 5% and 1% level of significance, respectively

Table 2. Analysis of variance for ten yield characters of 35 genotypes of roselle.

Source of variation	df	Length of fruit (mm)	Width of fruit (mm)	Weight of fruit (g)	Weight of calyces (g)	Fruits per plant (no.)	Calyces fruit ratio	Calyces ball ratio	Fruit yield per plant (g/plant)	Calyx yield per plant (g/plant)
Replication	2	20.234	7.0819	2.0871	0.69806	19.64	0.00122	0.0028	4929	1262.5
Genotype	34	193.46**	20.33**	12.66**	3.06**	9219.24**	0.017**	0.119**	307663**	51617.2**
Error	68	8.438	1.4095	0.6263	0.16036	40.80	0.0017	0.011	6569	1772.4

ns= Non-significant, * and ** Significant at 5% and 1% level of significance, respectively

Table 3. Morpho-agronomic and yield performance of 35 roselle genotypes.

Genotype	DOF	DFF	DHF	DOM	DEM	DFM	ILT	LOF	WOF	CYP	FYP	CFR	CBR
1740	69.0	70.5	76.5	119.0	74.0	126.5	3.81	45.93	23.70	273.67	619.3	0.46	0.85
2060	106.0	107.5	111.0	156.0	111.0	161.0	5.05	26.44	25.19	125.44	375.8	0.34	0.51
2065	68.0	71.0	76.0	120.0	73.0	126.0	5.50	42.21	21.68	158.01	333.3	0.45	0.83
2934	69.0	73.5	79.0	119.0	74.0	129.0	4.06	32.31	19.27	177.95	545.0	0.32	0.47
3372	89.0	101.5	104.0	139.0	94.0	154.0	5.42	38.87	16.87	73.75	223.7	0.43	0.58
3574	87.0	91.0	98.0	135.5	92.0	148.0	5.94	35.98	19.95	132.03	345.9	0.38	0.62
3692	85.5	87.5	89.0	134.0	90.5	139.0	6.11	38.09	18.52	213.11	545.0	0.40	0.66
3994	68.0	71.0	76.0	119.0	73.0	126.0	4.17	21.95	22.74	211.98	598.3	0.23	0.30
4373	112.0	112.0	112.0	162.0	117.0	166.0	5.67	30.25	24.55	202.27	666.1	0.32	0.48
4381	85.5	95.5	99.0	130.0	90.5	149.0	6.28	33.17	19.61	79.25	226.9	0.33	0.50
4385	76.0	78.5	81.0	126.5	81.0	131.0	6.78	35.64	22.60	169.12	435.2	0.39	0.64
4390	77.0	85.5	89.5	127.0	82.0	139.5	8.14	35.49	20.83	132.81	305.8	0.44	0.78
4398	79.5	95.0	99.0	130.0	84.5	149.0	7.28	31.01	20.04	100.92	271.4	0.38	0.62
4537	81.0	84.0	84.0	131.0	86.0	134.0	5.57	38.04	18.14	290.72	832.4	0.31	0.45
4544	93.0	96.0	105.0	143.0	98.0	155.0	6.50	28.12	23.89	126.77	346.5	0.37	0.59
4556	51.0	66.0	71.0	101.0	56.0	121.0	4.67	24.14	15.17	28.56	134.9	0.22	0.28
4561	86.0	89.5	91.0	134.0	91.0	141.0	4.92	39.33	20.06	341.32	853.2	0.39	0.65
4601	74.0	78.0	86.0	124.5	79.0	136.0	6.22	40.41	18.91	262.16	1038.2	0.27	0.36
4602	62.0	64.0	66.0	112.0	67.0	116.5	5.33	44.97	20.79	245.25	627.3	0.41	0.69
4605	56.5	68.5	71.0	106.5	61.5	122.0	5.81	43.60	22.15	332.65	706.6	0.47	0.91
4611	70.0	70.0	72.0	120.0	75.0	122.0	6.64	45.51	22.30	418.22	838.3	0.51	1.08
4613	62.0	66.0	71.0	112.0	67.0	122.0	5.11	39.19	21.36	252.87	645.0	0.43	0.77
4765	81.0	84.0	90.0	131.0	86.0	140.0	6.57	47.24	20.14	381.1	790.0	0.43	0.77
4904	101.5	101.5	101.5	151.5	106.5	155.0	4.95	30.89	24.51	98.25	295.8	0.36	0.50
4920	90.0	91.5	92.5	137.5	95.0	142.5	5.71	41.58	21.69	326.0	735.2	0.28	0.39
5020	68.5	71.5	72.5	118.0	73.5	122.5	5.36	43.58	22.56	379.59	877.7	0.45	0.82
5022	86.5	91.5	93.0	136.5	91.5	142.5	6.72	26.07	21.21	135.23	345.0	0.38	0.62
BUM-001	111.0	111.0	111.0	151.0	116.0	170.5	5.83	30.28	25.75	725.0	1896.6	0.38	0.62
BUM-002	70.0	71.0	82.0	120.5	75.0	132.0	5.78	39.11	24.99	251.59	624.4	0.40	0.67
BUM-003	70.5	73.5	78.5	121.0	75.5	128.5	4.22	50.86	23.46	202.0	552.5	0.47	0.87
BUM-004	69.5	73.0	80.5	122.0	74.5	130.5	3.78	47.81	26.37	199.23	535.1	0.39	0.64
BUM-005	69.5	73.5	76.5	119.0	74.5	122.0	4.72	47.81	23.58	154.97	409.6	0.37	0.61
BUM-006	68.0	70.0	78.0	120.0	73.0	128.0	4.97	42.88	24.35	150.78	393.0	0.38	0.61
BUM-007	67.5	73.5	78.5	117.5	72.5	128.5	4.94	54.19	24.36	122.87	304.0	0.44	0.80
VM-1	74.5	82.5	87.0	126.5	79.5	137.0	6.58	46.99	20.72	337.23	707.8	0.53	1.17
Mean	78.14	82.59	86.53	127.80	83.14	136.94	5.57	38.29	21.77	223.22	570.87	0.38	0.65
CV (%)	2.81	2.95	4.01	1.88	2.64	2.53	7.34	7.59	5.45	18.86	14.20	10.6	16.06
LSD (0.05)	1.79	1.99	2.84	1.96	1.79	2.82	0.33	2.37	0.97	34.37	66.17	0.033	0.853

DOF= Days to 1st flowering, DFF= Days to 50% flowering, DHF= Days to 100% flowering, DOM= Days of maturity, DEM= Days to 1st edible maturity, DFM= Days to 50% maturity, ILT= Internodal length (cm), LOF= Length of fruit (cm), WOF= Width of fruit (cm), CYP= Calyx yield per plant (g/plant), FYP= Fruit yield per plant (g/plant), CFR= Calyces fruit ratio and CBR= Calyces ball ratio

Estimation of genetic parameters for 16 characters in Roselle: The highest genotypic (δ^2g) and phenotypic (δ^2p) variances (2889.6, 2959.26, respectively) were found for fruit yield per plant (Table 4). The lowest magnitude of δ^2g (0.58) and δ^2p (0.63) were observed in weight of individual calyx. High genotypic (GCV) and phenotypic (PCV) coefficient of variation were obtained from fruit weight per plant (224.983 and 227.679, respectively) followed by 1st edible maturity (162.716 and 171.404). The GCV and PCV of branches per plant, days to 1st flowering, 50% flowering, 100% flowering, and 1st maturity were the same, indicating that these characteristics had no environmental influence. The highest heritability (99.104%) was recorded for branches per plant, followed by fruit weight per plant (97.646), 1st flowering (96.279), 100% flowering (95.14), fruits per plant (94.928), calyx yield per plant (94.384), 1st fruit maturity (93.908), 50% flowering (93.284), 50% maturity (93.091). Sabiel *et al*., (2014) observed high heritability for 50% flowering in Roselle. The highest genetic advances were recorded for calyx yield per plant (681.665), followed by fruit yield per plant (310.983), 1st edible maturity (291.448), branches per plant (129.714), weight of individual calyx (122.459). The lowest genetic advance was recorded for length of fruit (11.21), width of fruit (11.228), and 50% flowering (25.645). Rani (2005) and Ibrahim and Hussein (2006) reported high heritability and moderate genetic advance for days to 50% flowering. The highest GA (% of mean) was recorded for the yield of fruits per plant (457.98), followed by 1st edible maturity (318.21) and internode length (144.68). According to Panse (1957), the characters have a high Hb value and high GA due to additive genetic components. The high Hb and GA results in this study for branches per plant, internode length, calyces yield (g/plant), yield of fruit (g/plant), and weight of single calyx. High heritability and high genetic advance as a percent of the mean for plant height were reported by Bandi *et al*., (2014).

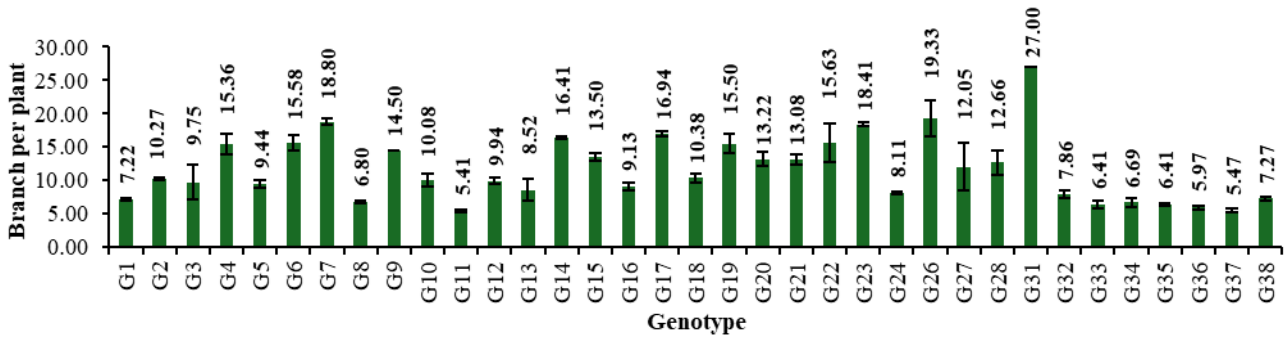

Fig. 1. Variations among different genotypes of Roselle for branches per plant.

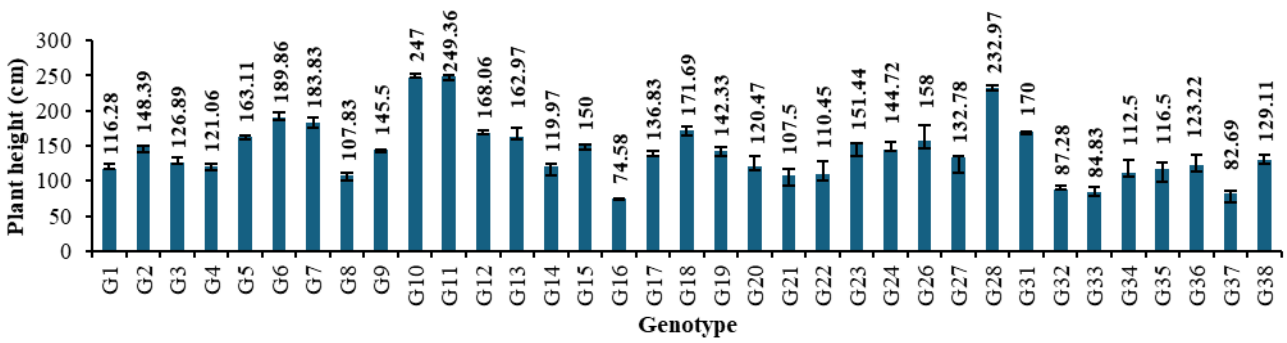

Fig. 2. Variation among different genotypes of Roselle for plant height.

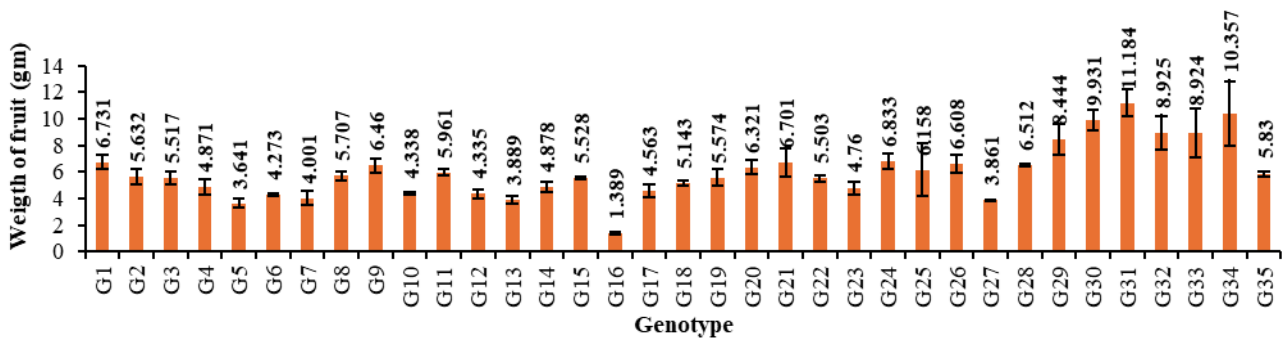

Fig. 3. Variation in weight of fruit observed in different genotypes of Roselle.

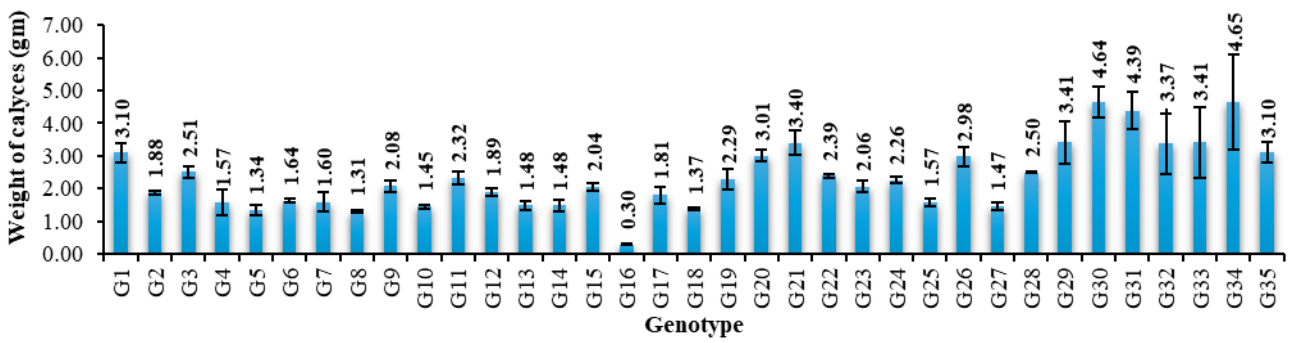

Fig. 4. Variation in weight of calyces observed in different genotypes of Roselle.

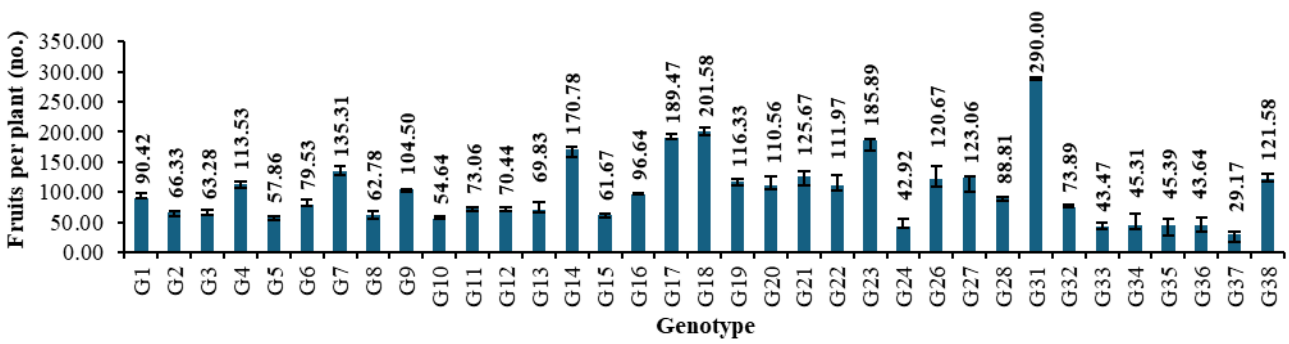

Fig. 5. Variation in the number of fruits per plant was observed among 35 genotypes of Roselle.

Table 4. Genetic variability estimates for 16 yield-related traits in Roselle.

Characters	$\delta^2 g$	$\delta^2 p$	GCV (%)	PCV (%)	Hb (%)	GA	GA (%) mean
Branches per plant (no.)	5.81	5.86	70.491	70.809	99.104	129.714	144.56
Fruits per plant (no.)	16.00	16.86	40.118	41.175	94.928	35.422	80.52
Fruit length (cm)	2.36	2.79	24.838	26.988	84.698	11.21	47.09
Fruit width (cm)	10.52	11.37	69.502	72.261	92.508	11.228	137.71
Fruit weight (g)	1.58	1.77	51.458	54.430	89.378	2.788	100.22
Weight of calyces (g)	0.58	0.63	49.535	51.648	91.983	122.459	97.87
Plant height (cm)	10.21	11.37	26.762	28.239	89.816	44.551	52.25
1st flowering (days)	2.11	2.19	16.422	16.737	96.279	27.236	33.19
50% flowering (days)	1.86	1.99	15.003	15.534	93.284	25.645	29.85
100% flowering (days)	2.04	2.14	15.352	15.739	95.14	37.705	30.85
1st fruit setting (days)	1.33	1.42	10.184	10.543	93.908	27.528	20.27
50% maturity (days)	8.99	9.66	25.628	26.562	93.091	45.996	50.94
Edible maturity (days)	220.13	244.27	162.716	171.404	90.119	51.595	318.21
Internode length (cm)	2.98	3.22	73.064	76.011	92.397	291.448	144.68
Calyx yield/plant (g)	90.76	96.15	63.763	65.632	94.384	681.665	127.61
Fruit yield /plant (g)	2889.6	2959.2	224.983	227.679	97.646	310.983	457.98

Correlation analysis: The results of correlation analysis demonstrated that estimates of genetic correlation coefficient were generally higher than their parallel phenotypic correlation coefficient, indicating powerful genetic association among different traits at the genotypic level. Estimates of correlation coefficients are given in Table 5. First flowering (days) showed positive and highly significant genotypic and phenotypic correlation with fifty percent flowering (days), fruit setting (days), 100% flowering (days), and 50% maturity (days). A non-significant association was recorded for fruit yield (g/plant) at the genotypic and phenotypic levels. Fifty percent flowering (days) showed highly significant positive genotypic and phenotypic correlation with days to 1st fruit setting, days to 100% flowering, and days to 50% maturity. A non-significant positive association was noted with calyx yield per plant at both genotypic and phenotypic levels. A non-significant negative correlation was observed with fruit yield per plant at both genotypic and phenotypic levels. Days to 50% flowering and calyx yield per plant showed a highly significant and negative correlation, as reported by Abdelatif *et al*., (2009).

Positive and highly significant genotypic and phenotypic correlation coefficients were observed for hundred percent flowering (days) with days to 1st fruit setting, internode length, and calyx yield (g/plant). It also revealed a negative and highly significant correlation with fruit yield (g/plant). Days to first fruit setting exhibited positive and considerably strong association at genotypic and phenotypic levels with 50% maturity (days), calyx yield (g/plant), and negative significant correlation with fruit yield (g/plant). Days to 50% maturity positive and highly significant correlation with days to 1st edible maturity, fruit yield (g/plant). It also revealed a negative and significant association both at genotypic and phenotypic levels with internode length and calyx yield (g/plant). The highly effective and positive genotypic and phenotypic correlation was observed with days to 1st edible maturity and fruit yield (g/plant). It also depicted a negative genotypic and phenotypic association with internode length and calyx yield (g/plant).

A highly significant and positive correlation was observed for branches per plant with calyx yield (g/plant) and internode length at the genotypic and phenotypic levels. It showed positive genotypic correlation and negative phenotypic correlation with fruits per plant. A highly significant positive correlation between the number of branches and calyx yield per plant was found by Abdelatif *et al*., (2009) at the phenotypic level.

Similarly, significantly positive correlation at genotypic and phenotypic levels was observed for fruit numbers per plant, fruit yield (g/plant), fruit width, fruit weight, days to 1st edible maturity, and fruit length (Table 5). Fruit length revealed a positive and highly significant association with fruit width, yield (g/plant), weight, days to 1st edible maturity, plant height, and fifty percent maturity (days) at phenotypic and genotypic points. It is negatively and significantly associated with calyx weight, 100% flowering (days), internode length, and calyces yield (g/plant) at the genotypic and phenotypic stages. Similar to these findings, Gasim *et al*., (1998) found a significant positive association between calyx yield (g/plant) and fruit length at the genotypic and phenotypic levels. Likewise, the width of fruit showed positive and highly effective association both at genotypic and phenotypic with days to 1st edible maturity, fruit weight, fruit yield (g/plant), fifty percent maturity (days), and plant height. In this study, we found that fruit width remained highly negatively correlated with calyx weight and 100% flowering (days) at the genotypic and phenotypic levels.

Table 5. Genotypic (r_g) and phenotypic (r_p) correlation coefficient of 16 different characters in Roselle.

Traits		FPP	LDF	WDF	WTF	WTC	PHT	DOF	DFF	DHF	DFS	DFM	DEM	ILT	CYP	FYP
BPP	r_g	0.417**	-0.520**	-0.577**	-0.540**	0.463**	-0.273**	0.221*	0.169ns	0.481**	0.272**	-0.271**	-0.509**	0.874**	0.897**	-0.460**
	r_p	-0.405**	-0.476**	-0.554**	-0.510**	0.438**	-0.255**	0.218*	0.165ns	0.467**	0.263**	-0.258**	-0.480**	0.835**	0.866**	-0.452**
FPP	r_g		0.700**	0.823**	0.804**	-0.713**	0.456**	-0.319**	-0.336**	-0.731**	-0.400**	0.494**	0.746**	-0.346**	-0.280**	0.873**
	r_p		0.671**	0.801**	0.770**	-0.689**	0.461**	-0.318**	-0.323**	-0.714**	-0.391**	0.458**	0.721**	-0.326**	-0.269**	0.854**
LDF	r_g			0.856**	0.806**	-0.653**	0.620**	-0.143ns	-0.159ns	-0.599**	-0.186ns	0.614**	0.716**	-0.376**	-0.268**	0.823**
	r_p			0.853**	0.792**	-0.660**	0.635**	-0.157ns	-0.149ns	-0.597**	-2.00*	0.626**	0.731**	-0.339**	-0.246*	0.797**
WDF	r_g				0.903**	-0.793**	0.685**	-0.107ns	-0.124ns	-0.656**	-0.178ns	0.707**	0.910**	-0.463**	-0.360**	0.888**
	r_p				0.888**	-0.787**	0.690**	-0.122ns	-0.118ns	-0.654**	-0.187ns	0.712**	0.902**	-0.432**	-0.344**	0.872**
WTF	r_g					-0.744**	0.420**	-0.278**	-0.291**	-0.621**	-0.326**	0.444**	0.679**	-0.280**	-0.237**	0.715**
	r_p					-0.707**	0.422**	-0.275**	-0.267**	-0.600**	-0.303**	0.444**	0.659**	-0.259**	-0.228**	0.694**
WTC	r_g						-0.387**	0.356**	0.350**	0.721**	0.393**	-0.399**	-0.714**	0.362**	0.299**	-0.712**
	r_p						-0.425**	0.357**	0.332**	0.721**	0.393**	-0.429**	-0.729**	0.336**	0.283**	-0.707**
PHT	r_g							0.567**	0.543**	-0.095ns	0.481**	0.996**	0.805**	-0.322**	-0.206**	0.683**
	r_p							0.509**	0.501**	-0.130ns	0.417**	0.992**	0.817**	-0.305**	-0.204*	0.676**
DOF	r_g								0.986**	0.720**	0.982**	0.562**	0.058ns	0.112ns	0.149ns	-0.117ns
	r_p								0.960**	0.717**	0.963**	0.520**	0.026ns	0.111ns	0.148ns	-0.125ns
DFF	r_g									0.724**	0.985**	0.534**	0.042ns	0.068ns	0.103ns	-0.150ns
	r_p									0.699**	0.980**	0.503**	0.033ns	0.053ns	0.088ns	-0.147ns
DHF	r_g										0.771**	-0.106ns	-0.613**	0.455**	0.415**	-0.711**
	r_p										0.756**	-0.132ns	-0.623**	0.438**	0.402**	-0.711**
DOM	r_g											0.476**	-0.040ns	0.180ns	0.220*	-0.207*
	r_p											0.427**	-0.068ns	0.162ns	0.202*	-0.211**
DFM	r_g												0.821**	-0.323**	-0.203*	0.712**
	r_p												0.829**	-0.307**	-0.201*	0.708**
DEM	r_g													-0.531**	-0.436**	0.902**
	r_p													-0.498**	-0.416**	0.887**
ILT	r_g														0.955**	-0.491**
	r_p														0.948**	-0.473**
CYP	r_g															-0.370**
	r_p															-0.360**

*Indicates significant at 5% level of significance, **Indicates significant at 1% level of significance,

r_g= Genotypic correlation coefficient, r_p= Phenotypic correlation coefficient, BPP= Branches per plant, FPP= Fruits per plant, LDF= Length of fruit, WDF= Width of fruit, WTF= Weight of individual fruit, WTC= Weight of individual calyx, PHT= Plant height, DOF= Days to 1st flowering, DFF= Days to 50% flowering, DHF= Days to 100% flowering, DFS= Days to 1st fruit setting, DFM= Days to 50% maturity, DEM= Days to 1st edible maturity, ILT= Internode length, CYP= Calyx yield per plant, FYP= Fruit yield per plant

Table 6. Path co-efficient analysis showing direct (bold) and indirect effects of different characters on yield of Roselle.

Traits	BPP	FPP	LOF	WOF	WTF	WTC	PHT	DOF	DFF	DFS	DFM	DED	ILT	CYP	FYP
BPP	**-0.011**	-0.124	-0.136	0.209	0.023	-0.011	0.466	0.011	-0.212	0.049	-0.614	-0.009	-0.154	0.103	-0.452**
FPP	0.005	**0.307**	-0.191	-0.301	-0.034	0.017	-0.842	-0.016	0.324	-0.073	1.154	0.014	0.060	-0.032	0.854**
LOF	0.006	0.206	**0.285**	-0.322	-0.035	0.017	-1.160	-0.008	0.271	-0.037	1.490	0.015	0.063	-0.030	0.797**
WOF	0.007	0.246	0.243	**-0.378**	-0.040	0.020	-1.261	-0.006	0.297	-0.035	1.693	0.018	0.080	-0.041	0.872**
WTF	0.006	0.237	0.226	-0.336	**-0.045**	0.018	-0.771	-0.014	0.272	-0.057	1.057	0.013	0.048	-0.027	0.694**
WTC	-0.005	-0.212	-0.188	0.298	0.031	**-0.025**	0.777	0.018	-0.328	0.073	-1.021	-0.015	-0.062	0.034	-0.707**
PHT	0.003	0.142	0.181	-0.261	-0.019	0.010	**-1.827**	0.026	0.059	0.078	2.360	0.017	0.056	-0.024	0.676**
DOF	-0.003	-0.098	-0.045	0.046	0.012	-0.009	-0.930	**0.051**	-0.326	0.179	1.237	0.001	-0.020	0.018	-0.125ns
DFF	-0.002	-0.099	-0.042	0.045	0.012	-0.008	-0.915	0.048	-0.318	0.183	1.200	0.0007	-0.010	0.010	-0.147ns
DHF	-0.005	-0.219	-0.170	0.247	0.027	-0.018	0.238	0.036	**-0.455**	0.141	-0.314	-0.013	-0.081	0.048	-0.711**
DFS	-0.003	-0.120	-0.057	0.070	0.013	-0.009	-0.762	0.048	-0.343	**0.187**	1.015	-0.002	-0.030	0.024	-0.211*
DFM	0.003	0.149	0.179	-0.269	-0.020	0.010	-1.813	0.026	-0.125	0.060	0.080	**2.378**	0.017	0.057	-0.030	0.708**
DEM	0.006	0.223	0.208	-0.341	-0.029	0.018	-1.494	0.001	-0.008	0.283	-0.012	1.970	**0.020**	0.092	-0.050	0.887**
ILT	-0.010	-0.100	-0.097	0.163	0.012	-0.008	0.557	0.006	-0.013	-0.199	0.030	-0.730	-0.010	**-0.185**	0.113	-0.473**
CYP	-0.010	-0.083	-0.070	0.130	0.010	-0.007	0.373	0.007	-0.022	-0.183	0.038	-0.479	-0.008	-0.175	**0.119**	-0.360**

*Indicates significant at 5% level of significance, **Indicates significant at 1% level of significance,
BPP= Branches per plant, FPP= Fruits per plant, LOF= Length of fruit, WOF= Width of fruit, WTF= Weight of fruit, WTC= Weight of calyces, PHT= Plant height, DOF= Days to 1st flowering, DFF= Days to 50% flowering, DHF= Days to 100% flowering, DFS= Days to 1st fruit setting, DFM= Days to 50% maturity, DEM= Days to 1st edible maturity, ILT= Internode length, CYP= Calyx yield per plant, FYP= Fruit yield per plant.

The weight of the fruit gave positive and highly significant genotypic and phenotypic association with fruit yield (g/plant) and first edible maturity (days). It showed a positive and significant association at genotypic and phenotypic levels with 50% maturity (days) and plant height. Fruit weight also had a negative and highly significant association with calyx weight and 100% flowering (days) both at the genotypic and phenotypic levels (Table 5). The significant negative association of this trait at both levels was estimated for first flowering (days), 50% flowering (days), internode length, and calyces yield (g/plant). Ibrahim *et al*., (2013) and Mohamed and Gabri (2013) reported that fruit weight had a significant negative association with days to 50% flowering at both genotypic and phenotypic levels. A highly significant and positive association was observed with 100% flowering (days) at the genotypic and phenotypic levels. Calyx weight showed positive and significant association both at genotypic and phenotypic levels with first maturity (days), first flowering (days), 50% flowering (days), length of internode, and fruit yield (g/plant). Highly significant and positive association both at genotypic and phenotypic level was found for plant height with days to 50% maturity (days), first edible maturity (days), fruit yield (g/plant), first flowering (days), 50% flowering (days), first fruit setting (days). Length of internode gave positive and highly significant genotypic and phenotypic association with calyx's yield (g/plant). It had significant negative genotypic and phenotypic associations with fruit yield (g/plant). Calyx yield (g/plant) showed significant negative genotypic and phenotypic association with fruit yield (g/plant). Ibrahim *et al*., (2013) found a significant and positive association of calyx yield (g/plant) with fruit weight both at genotypic and phenotypic levels.

Path co-efficient analysis: The correlation coefficient of each yield-contributing trait on yield may not accurately depict the proportional importance of direct and indirect effects. To find out a clear illustration of the relationship between yield and yield components, direct effects were estimated with the help of path analysis using genotypic correlation coefficients, which also calculated the comparative significance of each element. Calyx yield per plant was considered as a resultant (dependent) variable, and branches per plant, fruits per plant, fruit length, fruit width, individual fruit weight, weight of individual calyx, plant height, 1st flowering, 50% flowering, 100% flowering, first fruit setting, 50% maturity, first edible maturity, internode length, calyces yield per plant as causal (independent) variables. The results of the path analysis have been presented in Table 6. The result obtained from path analysis showed that days to 50% maturity (2.38) had the highest and positive magnitude direct effect on fruit yield (g/plant), followed by fruits per plant (0.307), fruit length (0.285), days to 1st fruit setting (0.187), calyx yield (g/plant) (0.119), first fruit maturity (days) (0.051), first edible fruit maturity (0.020). Plant height (-1.827) had the highest magnitude of negative direct effect on fruit yield (g/plant), followed by 100% flowering (-0.455), fruit width (-0.378), days to 50% flowering (-0.248), internode length (-0.185), weight of fruit (-0.045), weight of calyx (-0.025), number of branches in each plant (-0.011).

Maximum indirect effect in a positive direction was observed for branches per plant through plant height (0.467), weight of individual fruit (0.209), and calyx yield (g/plant) (0.103). Gasim *et al*., (1998) also found the highest indirect effect for branches per plant on calyx yield, followed by calyx weight per fruit. They also reported a negative indirect effect of number of branches per plant on fruits per plant (-0.348). Plant height (0.373), width of fruit (0.130), 1st fruit setting (0.038), weight of fruit (0.010), and 1st flowering (0.007) showed positive indirect effects on calyx yield (g/plant). Sabiel *et al*., (2014) described positive indirect effects of the number of branches in each plant and plant height on calyx yield. The residual effect was observed at 0.023, which revealed a 99.97% contribution of characters to the calyx yield per plant under study.

Conclusion

The recorded findings were in agreement with the study hypothesis as there was significant genetic variance among Roselle genotypes under investigation and there was atypical association among yield attributes. This study identified the genotype BUM-001, VM-1, BUM-004, and BUM-007 with high yield potential characters. The values of genotypic characters and correlation coefficients analysis indicate a strong inherent association between various characters at the genetic level. These results improve our understanding of crop improvement in roselle plants which could be further utilized for new varieties development. These findings might serve as baseline to conduct further in-depth studies to study. The cleistogamous nature of the Roselle planta that has restricted the success of hybridization and further conventional genetic improvement techniques.

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