

Original Research

DOI : <http://doi.org/10.22438/jeb/43/5/MRN-3057>

Assessing genetic diversity in rough lemon (*Citrus jambhiri* Lush) using morphological characters

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Received: 22.09.2021

Revised: 02.01.2022

Accepted: 16.03.2022

Abstract

Aim: To assess genetic diversity and relationship among important horticultural traits in rough lemon (*Citrus jambhiri* Lush).**Methodology:** The study was conducted at Punjab Agricultural University, Ludhiana on seventeen strains of rough lemon. Data was recorded for vegetative, fruiting and productivity parameters. Genetic variability and relationship among important horticultural traits were assessed by analyzing data with Microsoft Excel and Minitab 18 software.

Results: There was wide variability among seventeen genotypes of rough lemon. Little difference between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for majority of traits confirmed low environmental influence on the characters under study. High heritability with high to moderate genetic gain for fruit weight (69.49% and 36.50%), fruit length (95.24% and 40.62%), fruit diameter (93% and 32.23%), spine length (98.30% and 70.56%), acidity (95.07% and 40.18%) and fruit axis diameter (94.71% and 64.14%) suggested additive gene action and ability of improvement through selection. Strong character association of fruit number/tree and fruit axis diameter with yield revealed that these are the most important characteristics to be considered for effective selection in favour of high yield. Similarly, Principal Component Analysis showed high association between leaf lamina length and fruit size characters.

Seventeen genotypes of rough lemon selected for diversity analysis



Data recorded for vegetative, fruiting and productivity traits



Diversity analysis comprising genotypic and phenotypic coefficients of variability, heritability, genetic advance, paths analysis, principal component analysis and cluster analysis were performed using Microsoft Excel and Minitab 18 software.



High genetic diversity between genotypes and desirable character associations were recorded.

Interpretation: This research suggests a high genetic diversity among the genotypes of rough lemon and valuable correlations were observed between different traits of economic significance. The findings of this study can be used in future crop improvement programmes for developing desirable varieties.**Key words:** *Citrus jambhiri*, Cluster analysis, Genetic diversity

How to cite : Rattanpal, H.S., G.S. Uppal, M. Gupta and B.S. Gill: Assessing genetic diversity in rough lemon (*Citrus jambhiri* Lush) using morphological characters. *J. Environ. Biol.*, **43**, 651-659 (2022).

Introduction

Citrus is an important fruit crop of tropical and sub-tropical region of the world. It is reported to be grown in every tropical country and in those regions of sub-tropical countries, where winter temperature does not fall below 0°C (Reitz, 1984). As per the citrus classification, important centres of origin of citrus are South-east Asia, Islands between Asia and Australia, Australia and Central Africa (Swingle and Reece, 1967; Tanaka, 1958). Knowledge of genetic diversity in a crop species is fundamental to its improvement. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny. The vast amount of genetic diversity present in wild and semi-wild citrus germplasm in India has been utilized minimally in the genetic improvement programmes, because there exists little information regarding the relationship that exist between different morphological traits (Sharma *et al.*, 2004). Morphological traits have been used as main characters for identification and description of plant taxa (Dwari and Mondal, 2011) and till now these traits are used to describe genetic diversity present in various crops (Mathew *et al.*, 2007; Prabalee *et al.*, 2007).

Morphological characters are easy to observe and there are well-established descriptors present for citrus and other crops. This makes it easy for determining the amount of genetic diversity present in a species (Szczeplaniak and Cieslak, 2011). Several researchers have studied genetic diversity in different citrus species using morphological traits. Vegetative characters of plant, leaves, flower and fruits were described to distinguish mandarin varieties and their hybrids (Domingues *et al.*, 1999). Variation within Rough lemon and Kinnow mandarin was assessed phenotypically (Altaf *et al.*, 2014; Altaf and Khan, 2008). Similarly, morphological markers were used to determine the diversity among Himalayan citrus species (Sharma *et al.*, 2004). Their objective was to exploit these genotypes in breeding programs or to release these genotypes as new varieties (Koehler, 2003). However, in the present study morphological traits were used to determine correlation between traits and relative contribution of different traits to yield.

Yield is the most important trait that cannot be ignored in breeding program of any crop. Though rough lemon is commonly used as a rootstock, yet high yield is required even for a new rootstock to be commercially viable. Brinton and Uauy (2019) suggested that there might not be a single gene for the yield and yield is the result of interaction between different yield components. A crop breeding programme, intended at increasing plant productivity necessitates consideration not only of yield but also of components that have direct or indirect effect on yield (Rao *et al.*, 2004). Correlation coefficient enables a breeder to discern the degree of association between the dependent and independent variables. Path coefficient analysis is used in crop breeding programs to measure the relationships between yield and its contributing components and also to ascertain the components which have significant effects on yield (Sood *et al.*,

2011). Keeping in view the above facts, the present study was undertaken on seventeen rough lemon genotypes representing high the most of genetic variability present in the species in India were selected with specific objective to observe variability present for morphological traits and to determine the most important characters contributing towards yield.

Materials and Methods

The research work was carried out on 11-year-old trees of seventeen genotypes of rough lemon introduced viz. 14-9-13, 58-III-IV, Abohar, Assam, Australia, Brazilian, Chase, Chethali, Florida, Katazamir, Limmonaria Assam, Limmonaria Rugosoda, Nagpur, South Africa, Schaoub, Sohmyndog and Tharsa. These genotypes were introduced from J.C. Bakshi Regional Research Station, Abohar, India; Central Citrus Research Institute, Nagpur, India and Assam Agricultural University, Tinsukia, Assam, India. The investigation was carried out at Punjab Agricultural University, Ludhiana during the year 2019-20. The experiment was laid out in RBD as described by Singh *et al.* (1998) with three replications for each strain and one plant per replication. Morphological diversity was analyzed using a set of fourteen quantitative characters, recorded based on descriptors for citrus developed by International Plant Genetic Resources Institute, Italy (IPGRI) in the year 1999. Morphological characters are easy to record, differ between the genotypes and are part of the plant phenotype. These comprised leaf lamina length (cm), leaf lamina width (cm), spine length (cm), chlorophyll, pollen viability (%), Total Soluble Solids (°Brix), acidity (%), rind thickness (mm), fruit axis diameter (mm), fruit length (cm), fruit diameter (cm), fruit weight (g), fruit No./ tree and yield/ tree (kg). Chlorophyll content was estimated in ten intact leaves per plant using a portable chlorophyll meter (SPAD-502).

The Genotypic and Phenotypic Coefficients of variability (GCV and PCV) were calculated by the formula proposed by Burton and Devane (1953). Heritability in broad sense and genetic advance were calculated by using the formulae of Allard (1960). Genetic gain expressed as per cent ratio of genetic advance and population mean was calculated by the method given by Johnson *et al.* (1955). The genotypic and phenotypic correlations were calculated as per method described by Al-Jibouri *et al.* (1958). The direct and indirect effected were calculated by following Akintunde (2012) method of Path analysis. Cluster analysis was used to classify 17 rough lemon genotypes based on Ward's clustering method (Ward, 1963) and squared Euclidean distance. Principal Component Analysis was performed using Minitab 18 software.

Results and Discussion

All the strains included in the study differed significantly for all the horticultural traits (Table 1) as observed from analysis of variance. Maximum variability was observed for fruit number per tree followed by fruit weight, yield per tree and fruit length. These results support the selection programme for better yield in rough

lemon. The mean leaf lamina length ranged from 62.80-87.00 cm. The range of variation for spine length, chlorophyll, pollen viability, TSS and acidity was 8.20-33.50 cm, 49.10-62.70, 44.90-85.70 %, 5.60-9.00 °Brix and 2.80-5.30%, respectively. Similarly, fruit characters like rind thickness, fruit diameter, fruit length, fruit weight, fruit number per tree and yield per tree ranged from 2.30-14.00 mm, 7.80-27.30 cm, 39.90-105.00 cm, 55.90-106.40 cm, 81.60-385.10 g, 42.10-377.40 and 11.11-100.01 kg per tree, respectively. The range and mean differences of studied traits indicated the existence of genetic variability among genotypes for the majority of the characters, which reflect the potential of improvement in rough lemon. Similar variability for horticultural traits in different varieties of citrus have also been reported by Shrestha *et al.* (2012) in Nepal and by Dubey *et al.* (2013) under New Delhi conditions. Our study confirms the existence of a large morphological variability in the collection of Rough lemon. The accessions evaluated in this present research represent an interesting starting point for a future plant breeding programme aimed at the development of new varieties.

The genotypic variation for these characters indicated that the investigated genotypes comprised of phenotypically different individuals. These differences could be assigned to mutations and cross-pollination (due to male sterility and self-incompatibility). It has been reported that natural hybridization and the occurrence of spontaneous mutations are very common in citrus species. Furthermore, cross-pollination and the occurrence of zygotic twins have resulted in considerable variation in plant types (Das *et al.*, 2007). The genetic constitution in combination with biotic and abiotic stresses also cause variation in the germplasm. These conclusions could be supported by the hypothesis of Paudyal and Haq (2008) who stated that ecological factors contributed to 40% variation in pummelo accessions in an un-controlled field survey. Similarly, Dorji and Yapwattanaphun (2011a) reported that morphological variability could be assigned to mutations, cross-pollination and environment interactions. The bud sport, introduction of materials in a location different from its original habitat and lack of reproductive barriers (Self or cross-incompatibility, male sterility, synchronization of flowering) both within species and genus might have recurrently supplemented to its variation and heterogeneity (Dorji and Yapwattanaphun, 2011b). The degree of variability shown by different characters can be judged by phenotypic (PCV) and genotypic coefficient of variation (GCV). A little difference was observed between Genotypic and Phenotypic coefficients thereby indicating that environment had little influence on the horticultural traits investigated.

This suggests that selection will be effective on the basis of genotype alone with equal chance of success. The PCV and GCV ranged from 7.75 to 76.75 and 6.34 to 48.44 per cent, respectively (Table 2). The maximum PCV and GCV were observed for yield per tree (76.75 and 48.44), fruit number per tree (66.98 and 39.62) and rind thickness (57.14 and 45.73) reflecting the presence of high genetic variability among all the genotypes for studied characters, respectively. The results

obtained in our study is in agreement with the findings of Akter *et al.* (2013) suggesting that high GCV is the indication of exploitable genetic variability for selection, whereas, high PCV is an indication of the existence of wide scope of selection for the improvement from a considerable amount of variability present in the traits. In the present study it means that successful selection can be made for fruit yield, fruit number per tree and rind thickness in the breeding population. The estimate of heritability gives the idea of reliability of phenotypic value. Therefore, a breeder can select a specific character when the heritability is high. Genetic advance indicates the expected progress that can result from making the selection on applicable population.

The heritability was very high for all the traits studied, except for fruit number per tree (34.99%) and yield per tree (39.84) indicating less influence of environment on expression of these traits (Table 2). Heritability along with genetic gain is more accurate than heritability alone in estimating the results of selection as it indicates the presence of additive gene effects. High heritability with moderate genetic gain leaf lamina width, spine length, fruit axis diameter, fruit length and fruit diameter indicate that heritability of these traits is mainly due to additive effects and thus, genetic gain is anticipated under such situation. The estimate of heritability gives the idea of reliability of phenotypic value. Therefore, a breeder can select a specific character when the heritability is high. Genetic advance indicates the expected progress that can result from making the selection on applicable population. The heritability was very high for all the traits studied, except for fruit number per tree (34.99%) and yield per tree (39.84) indicating less influence of environment on expression of these traits (Table 2). Heritability along with genetic gain is more accurate than heritability alone in estimating the results of selection as it indicates the presence of additive gene effects. High heritability with moderate genetic gain leaf lamina width, spine length, fruit axis diameter, fruit length and fruit diameter indicate that heritability of these traits is mainly due to additive effects and thus, genetic gain is anticipated under such situation. Better heritability values recorded point to the possibility of improvement in these parameters (Ahmed and Khaliq, 2007; Songsri *et al.*, 2008). Further explanation by Sardana *et al.* (2007), suggested that high heritability may not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm. Association among different components of characters is due to linkage or pleiotropic gene action or both. Phenotypic correlation comprises environmental and genetic effects, which gives idea about total association between desirable characters.

Phenotypic correlation gives estimate of association between two characters whereas genotypic correlation gives estimate of magnitude of genetic association between the characters. Genetic and phenotypic correlation for yield per tree and their components in rough lemon are presented in Table 3. In general, genotypic correlations were higher than their corresponding phenotypic correlation coefficients for most of the traits studied indicate strong inherent association between these

Table 1: Mean square of different traits for rough lemon genotypes

Source of variation	Degree of freedom	Leaf lamina length (cm)	Leaf lamina width (cm)	Spine length (cm)	Chlorophyll	Pollen viability (%)	TSS (°Brix)	Acidity (%)	Rind thickness (mm)	Fruit dia. (cm)	Fruit length (cm)	Fruit dia. (cm)	Fruit wt. (g)	Fruit No. /tree	Yield/ tree (kg)
Replications	2	2.3	0.7	2.8	1.5	9.3	0.03	0.05	0.02	0.5	4.0	1.9	93.1	66.1	13.7
Genotypes	16	111.6**	43.5**	175.3**	40.2**	329.0**	1.81**	1.95**	20.44**	84.7**	825.7**	503.1**	20253.1**	27666.2**	1952.4**
Error	32	13.7	3.6	5.7	6.4	10.0	0.12	0.04	0.79	1.6	15.2	21.7	294.1	332.3	180.3

** Significant at 1% level

Table 2: Range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic gain in rough lemon

Traits	Range	Mean $\pm$ SE	Coefficient of variability (%)		Heritability (%)	Genetic gain mean (%)
			Phenotypic	Genotypic		
Leaf lamina length (cm)	62.80-87.00	77.14 $\pm$ 0.927	8.71	7.45	73.16	13.13
Leaf lamina width (cm)	29.00-45.30	39.61 $\pm$ 0.56	10.22	9.19	80.86	17.03
Spine length (cm)	8.20-33.50	23.47 $\pm$ 1.12	34.85	34.55	98.30	70.56
Chlorophyll	49.10-62.70	53.86 $\pm$ 0.57	7.75	6.34	67.01	10.70
Pollen viability (%)	44.90-85.70	68.66 $\pm$ 1.49	15.85	15.19	91.79	29.97
TSS ($^{\circ}$ Brix)	5.60-9.00	7.53 $\pm$ 0.11	10.99	10.06	83.80	18.97
Acidity (%)	2.80-5.30	3.99 $\pm$ 0.11	20.51	20.00	95.07	40.18
Rind thickness (mm)	2.30-14.00	5.27 $\pm$ 0.36	57.14	45.73	64.03	75.38
Fruit axis diameter (mm)	7.80-27.30	16.95 $\pm$ 0.75	32.87	31.99	94.71	64.14
Fruit length (cm)	39.90-105.00	81.65 $\pm$ 2.32	20.70	20.20	95.24	40.62
Fruit diameter (cm)	55.90-106.40	81.16 $\pm$ 1.87	16.82	16.22	93.00	32.23
Fruit weight (g)	81.60-385.10	237.22 $\pm$ 11.47	25.50	21.26	69.49	36.50
Fruit No./ tree	42.10-377.40	195.94 $\pm$ 13.60	66.98	39.62	34.99	48.28
Yield/ tree (kg)	11.11-100.01	44.29 $\pm$ 3.61	76.75	48.44	39.84	62.98

Table 3: Phenotypic and genotypic coefficients of correlation among different traits in rough lemon

		LLL	LLW	SPL	CHL	PVI	TSS	ACI	RDT	FAD	FRL	FRD	FWT	FNT	YLT
LLL	G	1	0.742**	-0.107	0.335*	0.016	0.516**	-0.186	0.228	0.356*	0.429**	0.470**	0.427**	-0.052	0.212
	P	1	0.695**	-0.170	0.162	-0.099	0.437	-0.299	0.218	0.341	0.396	0.426	0.426	-0.094	0.205
LLW	G		1	0.131	0.113	-0.058	0.738**	-0.249	0.398**	0.396**	0.474**	0.578**	0.542**	-0.235	0.105
	P		1	0.101	-0.075	-0.160	0.702	-0.345	0.400	0.382	0.445	0.548*	0.545*	-0.284	0.088
SPL	G			1	0.074	-0.424**	0.466**	0.066	0.119	0.400**	-0.032	0.203	0.170	-0.337*	-0.363**
	P			1	0.028	-0.465	0.460	0.048	0.112	0.392	-0.051	0.186	0.161	-0.348	-0.373
CHL	G				1	0.010	0.337*	0.199	0.443**	-0.114	0.350*	0.361**	0.228	-0.159	-0.102
	P				1	-0.122	0.213	0.129	0.466	-0.195	0.306	0.299	0.205	-0.224	-0.151
PVI	G					1	-0.255	0.104	-0.246	-0.410**	-0.247	-0.235	-0.280*	0.218	0.062
	P					1	-0.366	0.063	-0.271	-0.454	-0.303	-0.303	-0.315	0.206	0.048
TSS	G						1	0.005	0.600**	0.466**	0.478**	0.757**	0.709**	-0.353*	-0.009
	P						1	-0.061	0.613**	0.456	0.450	0.744**	0.720**	-0.403	-0.032
ACI	G							1	0.114	-0.338*	-0.362**	-0.195	-0.248	0.084	-0.242
	P							1	0.103	-0.368	-0.408	-0.245	-0.273	0.071	-0.259
RDT	G								1	0.046	0.694**	0.768**	0.740**	-0.341*	-0.005
	P								1	0.038	0.695**	0.773**	0.738**	-0.349	-0.009
FAD	G									1	0.441**	0.554**	0.506**	0.126	0.469**
	P									1	0.430	0.545*	0.500*	0.119	0.465
FRL	G										1	0.872**	0.872**	-0.258	0.309*
	P										1	0.867**	0.873**	-0.277	0.303
FRD	G											1	0.968**	-0.196	0.347
	P											1	0.974**	-0.219	0.342
FWT	G												1	-0.273	0.309
	P												1	-0.284	0.305
FNT	G													1	0.787**
	P													1	0.786**
YLT	G														1
	P														1

*Significant at 5% level of significance; **Significant at 1% level of significance; P, phenotypic coefficients of correlation; G, genotypic coefficients of correlation; LLL, Leaf lamina length (cm); LLW, Leaf lamina width (cm); SPL, Spine length (cm); CHL, Chlorophyll; PVI, Pollen viability (%); TSS, TSS ($^{\circ}$ Brix); ACI, Acidity (%); RDT, Rind thickness (mm); FAD, Fruit axis diameter (mm); FRL, Fruit length (cm); FRD, Fruit diameter (cm); FWT, Fruit weight (g); FNT, Fruit No./ tree; YLT, Yield/ tree (kg)

Table 4: Estimates of direct (bold) and indirect genotypic effects of different traits on fruit yield per plant in rough lemon

	LLL	LLW	SPL	CHL	PVI	TSS	ACI	RDT	FAD	FRL	FRD	FWT	FNT
LLL	-0.227	-0.168	0.024	-0.076	-0.004	-0.117	0.042	-0.052	-0.081	-0.097	-0.107	-0.097	0.012
LLW	0.160	0.215	0.028	0.024	-0.012	0.159	-0.054	0.086	0.085	0.102	0.124	0.117	-0.051
SPL	0.033	-0.041	-0.311	-0.023	0.132	-0.145	-0.021	-0.037	-0.124	0.010	-0.063	-0.053	0.105
CHL	0.065	0.022	0.014	0.194	0.002	0.065	0.039	0.086	-0.022	0.068	0.070	0.044	-0.031
PVI	0.000	-0.001	-0.007	0.000	0.016	-0.004	0.002	-0.004	-0.007	-0.004	-0.004	-0.004	0.003
TSS	-0.075	-0.107	-0.068	-0.049	0.037	-0.145	-0.001	-0.087	-0.068	-0.069	-0.110	-0.103	0.051
ACI	0.017	0.022	-0.006	-0.018	-0.009	0.000	-0.089	-0.010	0.030	0.032	0.017	0.022	-0.007
RDT	-0.010	-0.017	-0.005	-0.019	0.011	-0.026	-0.005	-0.043	-0.002	-0.030	-0.033	-0.032	0.015
FAD	0.124	0.138	0.139	-0.040	-0.143	0.162	-0.118	0.016	0.348	0.153	0.193	0.176	0.044
FRL	-0.072	-0.079	0.005	-0.058	0.041	-0.080	0.060	-0.116	-0.074	-0.167	-0.146	-0.146	0.043
FRD	-0.160	-0.197	-0.069	-0.123	0.080	-0.257	0.066	-0.261	-0.188	-0.296	-0.340	-0.329	0.067
FWT	0.398	0.505	0.158	0.212	-0.261	0.660	-0.231	0.689	0.471	0.812	0.901	0.931	-0.254
FNT	-0.041	-0.186	-0.267	-0.126	0.172	-0.279	0.066	-0.270	0.100	-0.204	-0.155	-0.216	0.791

Residual effect: 0.232. LLL, Leaf lamina length (cm); LLW, Leaf lamina width (cm); SPL, Spine length (cm); CHL, Chlorophyll; PVI, Pollen viability (%); TSS, TSS (°Brix); ACI, Acidity (%); RDT, Rind thickness (mm); FAD, Fruit axis diameter (mm); FRL, Fruit length (cm); FRD, Fruit diameter (cm); FWT, Fruit weight (g); FNT, Fruit No./ tree; YLT, Yield/ tree (kg)

Table 5: Clustering pattern of seventeen genotypes of rough lemon on the basis of genetic divergence of traits

Cluster	Number of genotypes	Genotypes
I	9	Assam, Chase, Florida, Katzamazir, Limmonaria Assam, Nagpur, South Africa, Schaoub, Sohmyndog
II	8	14-9-13, 58-III-IV, Abohar, Australia, Brazilian, Chethali, Limmonaria Rugosoda, Tharsa

Table 6: Cluster means for different traits in seventeen genotypes of rough lemon

Traits	Cluster I	Cluster II
Leaf lamina length (cm)	74.7	79.9
Leaf lamina width (cm)	38.1	41.3
Spine length (cm)	23.4	23.5
Chlorophyll	53.8	53.9
Pollen viability (%)	69.3	67.9
TSS (° Brix)	7.2	7.9
Acidity (%)	4.1	3.8
Rind thickness (mm)	4.0	3.1
Fruit axis diameter (mm)	15.1	19.1
Fruit length (cm)	71.7	92.9
Fruit diameter (cm)	71.8	91.8
Fruit weight (g)	173.1	309.4
Fruit No./ tree	198.0	193.7
Yield/ tree (kg)	33.1	56.9

traits. Genetic relation of traits may result from pleiotropic effects of a gene, linkage of two genes, chromogema and regimental affiliation or due to the environmental influences (Sgro and Hoffmann, 2004). The perusal of data indicates that yield per tree displayed significant positive correlation with fruit number/tree, fruit axis diameter and fruit length at genotypic level and these characters may be considered as yield contributing traits in rough lemon. Hence, for effective crop yield improvement selection

should be oriented towards the higher value for these component characters. Spine length showed significant and negative genotypic correlation with yield, indicating that plants with long spines should be discarded. TSS was significantly and positively correlated with fruit length, fruit diameter and fruit weight.

This implies that the value increase of one of this parameter leads to an increase in the parameter to which it is significantly correlated (Shivananda *et al.*, 2013; Kasu-Bandi *et al.*, 2019). Indeed, the positive link between this parameter is an important indicator in the conduct of the Rough lemon. Path coefficient analysis is a valuable tool for separating the correlation coefficient into direct and indirect effect of independent variables on dependent variable. The presence of multiple variables in correlation study make their indirect correlation more complex. Correlation may be observed between two characters only because they are correlated to third common character. Under these conditions, path coefficient analysis offers an effective tool of examining forces acting to produce a given correlation and get idea of relative importance of each character.

In this study, fruit yield per plant was taken as dependent variable and the remaining characters were taken as independent variables. Path coefficient analysis separates the total correlation and coefficient of different characters in direct and indirect effects on fruit yield, so that the sum of direct and indirect effect remains equal to genotypic correlation (Table 4). The data indicates that fruit weight showed the maximum positive direct effect ($r = 0.931$)

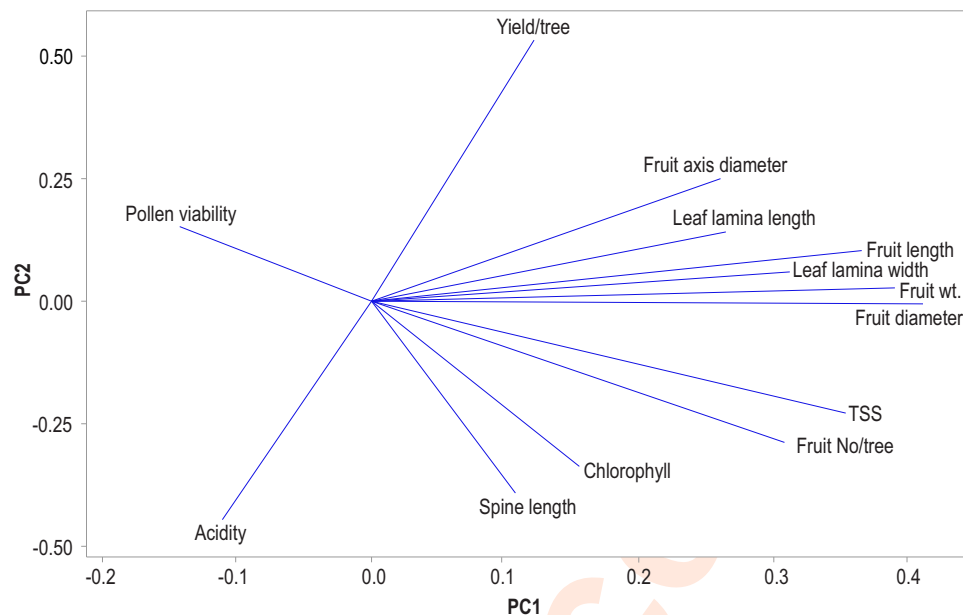


Fig.1: Graph for two Principal Components, PC1 and PC2 for rough lemon characters.

on yield per tree followed by fruit number per tree ($r = 0.791$), fruit axis diameter ($r = 0.348$) and leaf length width ($r = 0.215$). Fruit diameter ($r = -0.340$) and spine length ($r = -0.311$) negatively affected the fruit yield per tree. High positive direct effect on yield per plant fruit number per and its significant and positive correlation with yield as well as moderate heritability with genetic gain suggest it to be the most important components for yield and thus, more weight value should be given to these traits in improvement programmes. Similarly, negative direct effect of spine length on fruit yield and its significant negative correlation with fruit yield along with high heritability with genetic gain makes it an important trait to discard plants at early stage of selection. The unexplained variation in genotypic path coefficient was 0.232. It indicated that cause of 0.768% variation at genotypic level had been determined and further indicated that there were some more components which contributed to fruit yield per plant had not been included in the investigation, therefore some more traits may be considered while selecting the genotypes for high yield in rough lemon for Punjab region. In the system of two Principal components, the eigenvectors of studied characters are presented in Fig. 1.

The longest vectors were of fruit weight, fruit length and fruit diameter, which was expected as these are related characters. However, leaf lamina width was also positively correlated with fruit size parameters and this observation can be used to make selection of fruit size in young seedling, which otherwise take 6 to 8 years to come into first bearing in rough lemon. The least correlated characteristic with variables PC1 and PC2 was acidity. The principal component analysis made it possible to assess the analysis of genotype relatedness for

different characters in rough lemon and other crops (Muqaddasi *et al.*, 2017). Cluster analysis was carried out based on Ward's clustering method and squared Euclidean distance. Seventeen diverse genotypes of rough lemon were clustered into 2 major clusters as presented in Table 5.

Fruit weight, fruit length and fruit diameter made significant contribution to clustering. Cluster I accommodated 9 genotypes and Cluster II accommodated 9 genotypes. The cluster means of different traits are presented in Table 6. Higher mean pollen viability, acidity and rind thickness fruit length were observed in cluster I and other parameters were higher in cluster II. In some of these traits, selection is not effective and under such circumstances, genetic divergence allows further partitioning of variability. In the present investigation, the cluster II was found more divergent and had higher fruit length, fruit diameter and yield per tree. Consequently, hybridization between the genotypes of this group can be highly effective in breeding of rough lemon for fruit size and yield.

It is concluded that substantial amount of variability is present among the rough lemon strains. The study led to identification of many new relationships between the different traits of rough lemon that can be exploited for targeted development of new promising lines through targeted breeding under Punjab conditions.

Acknowledgment

This work was partially financially supported by the All India Coordinated Research Project on Fruits, Bangalore.

Add-on Information

Authors' contribution: H.S. Rattanpal: Planting of planning trial; G.S. Uppal: Recording of analysis of data; M. Gupta: Recording of data; B.S. Gill: Guidance in analysis and writing.

Research content: The research content of manuscript is original and has not been published elsewhere.

Ethical approval: Not applicable.

Conflict of interest: The authors declare that there is no conflict of interest.

Data from other sources: Not applicable.

Consent to publish: All authors agree to publish the paper in *Journal of Environmental Biology*.

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