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Research Note

Genetic evaluation of *Salacia chinensis* L. accessions for yield and related traits

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Abstract

Thirteen accessions of *Salacia chinensis* L., a threatened species known for its medicinal properties, were evaluated in terms of variability, heritability and genetic advance for yield and other contributing traits. Genotypic and phenotypic coefficient of variation were highest for fruit yield per plant followed by plant spread, fruit weight and seed weight. High heritability were observed for fruit weight (99.1 %), fruit yield per plant (98.5 %), seed length (98.1 %), seed weight (97.2 %), leaf area (96.8 %), fruit length (96.8 %), plant spread (96.2 %), seed diameter (96.2 %), fruit diameter (94.2 %), leaf length (92.1 %), leaf width (86.4 %), plant height (85.1 %) and petiole length (84.1 %) thus indicating that these characters has additive gene effect and hence, they can be used for effective selection.

Keywords

Salacia chinensis, selection, crop improvement, fruit yield.

Salacia chinensis L. [Synonym-*Salacia prinoides* (Willd.) DC.], family - Celastraceae is an evergreen climbing shrub or a small tree occurring in India, Sri Lanka, China, Malaysia, Java and Philippines (Khare, 2007). It occurs in pockets mainly around the Sahyadri-konkan corridor area of the north western ghats. It is locally referred as Saptarangi, Ekanayakam, Ponkoranti, Saptachakri or Ingali. *S. chinensis* has gained importance as a rich repository of chemical constituents contributing to various medicinal properties. Phytochemical profiling reveals the presence of constituents such as salacinol (Yishikawa *et al*., 2003), kotalanol, neokotalanol, neosalacinol (Muraoka *et al*., 2011) and mangiferin (Deokate and Khadabadi, 2012). Though extracts of *S. chinensis* exhibit medicinal activity against tumors, mutagenicity, hepatitis, arthritis, cardiac disorders and mental disorders, traditional medicinal systems have restricted use of *Salacia* primarily as an anti-diabetic agent (Patwardhan *et al*., 2015).

As the roots are economic parts in the species, bulk harvesting of roots hinders the natural regeneration. Hence, the population of this plant has decreased exponentially in the last few years in their natural habitat. Due to several medicinal and commercial uses, the conservation of this medicinal plant is of utmost importance. Hence, selection of superior genotypes for improvement through morphological traits helps in further improvement and conservation. Thirteen different accessions of *Salacia chinensis* L. has collected from different region of country and established at the Field Gene Bank of Division of Plant Genetic Resources, ICAR-Indian Institute of Horticultural Research, Bengaluru. Magnitude of variability present in genetic stocks, heritability and genetic advance are important parameters for effective selection of genotypes and crop improvement. Therefore, the present study was undertaken with a view to assess the extent of genetic variation among the available *Salacia chinensis* L. accessions.

The present investigation was conducted in the Field Gene Bank of Division of Plant Genetic Resources, ICAR-Indian Institute of Horticultural Research, Bengaluru. Thirteen different accessions ACC-1, ACC-2, ACC-3, ACC-4, ACC-5, ACC-6, ACC-7 ACC-8 ACC-9, ACC-10, ACC-11, ACC-12 and ACC-13 were grown in Randomized Block Design (RBD) with three replication and 1mx1m spacing. Plants were maintained organically and recommended cultural practices were adopted for proper growth and stand of the plants. The observations were recorded on thirteen quantitative traits of the randomly selected plants from each of the accessions and its replications. The data were subjected to Analysis of Variance as per the procedure described by Panse and Sukhatme (1967). The co-efficient of phenotypic and genotypic variations were calculated according to Burton and Dewane (1953). Heritability, genetic advance and genetic gain were calculated according to the formula given by Johnson *et al.* (1955).

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied *viz.*, plant height, plant spread, leaf length, leaf width, leaf area, petiole length, fruit length, fruit diameter, fruit weight, seed length, seed diameter, seed weight and fruit yield (Table 1).

High genotypic and phenotypic coefficients of variation were recorded for fruit yield per plant (78.54 % and 79.13 %), plant spread (34.73 % and 35.41 %), fruit weight (25.57 % and 25.69 %) and seed weight (22.21 % and 22.53 %) (Table 2). This shows greater genetic variability among accessions for these characters, to carry out further improvement by selection. Phenotypic and genotypic coefficients of variation were quite low for leaf length, leaf width, leaf area and seed diameter. The result obtained revealed that the estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV). Although estimates of PCV were higher than that of GCV, they were close to one another which implies that the influence of environment on the expression of these characters were negligible and therefore selection based on phenotypic values is possible (Falconer, 1981). The lowest GCV was noticed for leaf length, leaf width, leaf area and seed diameter.

The amount of genetic variation present for different desirable traits can be known by the estimation of genetic coefficient of variation whereas the proportion of variation which is inherent can be estimated by heritability. Heritability alone can be used to gather information of relative value of selection, but Johnson *et al*., (1955) had shown that for better and reliable conclusion, both heritability and genetic advance should be considered.

Heritability broad or narrow sense were high for characters like fruit weight (99.1 %), fruit yield per plant (98.5 %), seed length (98.1 %), seed weight (97.2 %), leaf area (96.8 %), fruit length (96.8 %), plant spread (96.2 %), seed diameter (96.2 %), fruit diameter (94.2 %), leaf length (92.1 %), leaf width (86.4 %), plant height (85.1 %) and petiole length (84.1 %). From the above heritability values, it can be concluded that these characters are less influenced by the environmental factors and are controlled by additive gene effect (Table 2). In confirmation with the obtained results, Yadav *et al*. (2007), Singh *et al*. (2004), Kakaraparthi *et al*. (2013) and Chitra and Rajamani (2010) have also reported higher heritability values for these traits in medicinal crops like Safed musli, Opium poppy, Ashwagandha and Glory lily, respectively.

In the present experiment high genetic advance over mean, coupled with high heritability was observed in characters like fruit yield per plant (160.58 %), Plant spread (70.18 %), fruit weight (52.43 %), seed weight (45.10 %), plant height (31.55 %), petiole length (29.96 %), fruit diameter (23.25 %), fruit length (22.47 %) and seed length (21.65 %). Moderate estimates of genetic advance as per cent of mean were recorded in seed diameter (20.03 %), leaf length (17.66 %) and leaf width (14.84 %) whereas, lowest genetic advance as percent of mean was observed in leaf area (8.29 %) which suggests that existing variability among the accessions with respect to these traits is mainly due to additive type of genes (Panse, 1957 and Thombre and Joshi, 1981). These traits can be improved through simple individual plant selection to bring out genetic improvement in desired selection.

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Table 1. Analysis of variance (mean sum of square) for growth and yield parameters of *Salacia chinensis* L.

Sl. No.	Sources of variation/characters	Replication	Treatments(genotypes)	Error	S. Em ±	CD (5%)
	Degrees of freedom	2	12	24		
1	Plant height (m)	0.1067	0.3773	0.0208	0.0832	0.2431
2	Plant spread (m)	0.0924	1.5487	0.0200	0.0817	0.2386
3	Leaf length (cm)	0.0758	1.2298	0.0340	0.1064	0.3108
4	Leaf width (cm)	0.0002	0.2069	0.0102	0.0585	0.1708
5	Leaf area (cm^2)	0.0619	5.0813	0.0552	0.1356	0.3960
6	Petiole length (cm)	0.0236	0.0412	0.0024	0.0285	0.0834
7	Fruit length (cm)	0.0018	0.0880	0.0009	0.0178	0.0520
8	Fruit diameter (cm)	0.0124	0.0727	0.0014	0.0220	0.0642
9	Fruit weight (g)	0.0101	0.4282	0.0013	0.0211	0.0617
10	Seed length (cm)	0.0002	0.0223	0.0001	0.0069	0.0202
11	Seed diameter (cm)	0.0001	0.0145	0.0001	0.0079	0.0231
12	Seed weight (g)	0.0011	0.0118	0.0001	0.0061	0.0180
13	Fruit yield/plant (kg/plant)	0.0172	2.9720	0.0148	0.0704	0.2055

Table 2.Estimates of mean, components of variance, heritability and genetic advance for growth and yield parameters of *Salacia chinensis* L.

Sl. No.	Characters	Mean	GV	PV	GCV	PCV	h^2 (%)	GAM (%)
1	Plant height (m)	2.076	0.119	0.140	16.606	18.001	85.1	31.55
2	Plant spread (m)	2.055	0.510	0.530	34.735	35.411	96.2	70.18
3	Leaf length (cm)	7.066	0.399	0.433	8.936	9.309	92.1	17.66
4	Leaf width (cm)	3.304	0.066	0.076	7.750	8.335	86.4	14.84
5	Leaf area (cm^2)	31.622	1.675	1.731	4.093	4.160	96.8	8.29
6	Petiole length (cm)	0.717	0.013	0.015	15.864	17.303	84.1	29.96
7	Fruit length (cm)	1.537	0.029	0.030	11.089	11.270	96.8	22.47
8	Fruit diameter (cm)	1.325	0.024	0.025	11.627	11.977	94.2	23.25
9	Fruit weight (g)	1.475	0.142	0.144	25.575	25.695	99.1	52.43
10	Seed length (cm)	0.810	0.007	0.008	10.614	10.717	98.1	21.65
11	Seed diameter (cm)	0.699	0.005	0.005	9.912	10.105	96.2	20.03
12	Seed weight (g)	0.281	0.004	0.004	22.212	22.535	97.2	45.10
13	Fruit yield/plant (Kg)	1.264	0.986	1.001	78.540	79.131	98.5	160.58

Where,

GV : Genotypic variance
PV : Phenotypic variance
GCV: Genotypic coefficient of variation
PCV : Phenotypic coefficient of variation
h^2 : Broad sense heritability
GAM : Genetic advance as per cent of mean