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Genetic Variability and Divergence studies in *Prosopis juliflora* DC

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Abstract

Variability in morphometric traits of thirty seed sources of *Prosopis juliflora* were collected from different agroclimatic zones of Tamilnadu state, India were assessed. There were significant differences among different growth parameters both at nursery level and in the field for plant height, collar diameter and number of branches and also for secondary parameters viz., Sturdiness quotient and volume index. Superiority in terms of growth parameters were recorded in four seed sources viz., Ramnad, Rameshwaram, Madurai and Keezhakarai. However, consistent performance in growth characters were depicted by two seed sources viz., Ramnad and Rameshwaram, throughout the study at nursery and field conditions. In general, phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicating the predominant role of environment. High heritability was recorded for plant height and volume index respectively (89.00% and 73.00%) and genetic gain as percentage of mean was high for volume index (65.50 %) followed by plant height (32.69%) indicating the additive gene action. Volume index had positive correlation and intercorrelation with plant height, collar diameter and number of branches. Path analysis indicated that collar diameter and plant height had positive effect on Volume index. Hence, these two parameters can be used as selection index for biomass production in *Prosopis juliflora*. On the basis of hierarchical Euclidian cluster analysis, two major clusters were obtained with highest number of sources falling under cluster A. These clusters were further branched into four sub clusters. The highest Euclidean distance was recorded between the sources of Pudukkottai and Tuticorin (30.33) followed by Pudukkottai and Pollachi of 29.95. The lowest genetic distance of 2.207 was observed between Virudhunagar and Tirupathur. Thus genetic divergence studies using biometric approach revealed similarity with geographic distribution of seed sources.

Keywords: Seed source, variability, heritability, correlation, path analysis, genetic divergence

1. Introduction

Prosopis juliflora is a deciduous thorny tree belonging to the family Leguminosae and sub-family Mimosoideae. It grows from mean sea level upto 1500m and is tolerant to very high temperatures (e.g. 48 °C) and annual rainfall range of 150 - 750 mm ^[1]. *Prosopis juliflora* is an indigenous species of Central America that has its genetic center in South America ^[2]. This species has been successfully introduced in the arid tracts of Asia, Australia, Sudan and South Africa where the rainfall varies from 10 to 20 cm ^[3]. *Prosopis* was first introduced into India during 1870's for meeting the fuel wood demand and also for stabilizing sand dunes ^[4]. This species is most common in the states of Punjab, Rajasthan, Gujarat, Haryana, Uttar Pradesh, Orissa, Tamil Nadu and West Bengal.

It is one of the most economically and ecologically important tree species distributed mainly in arid and semi-arid zones of the world ^[2]. It is a hardy, drought resistant and leguminous plant having immense potential to be used in the afforestation and reclamation of wastelands. It is also found to be tolerant to heavy metals and thus has the scope of exploiting for phytoremediation purposes. The fast growing habit, high coppicing potential and higher yield in terms of biomass production and carbon sequestration potential, besides being a high valued fuel wood makes it a suitable candidate for enhancing the economic status and for sustainable development of the region.

In Tamil Nadu, *Prosopis juliflora* was first introduced during 1960's into the composite Ramanathapuram and Tirunelveli districts for live fence because of its thorny nature. This has now spread to other district on account of its multifarious uses and covers an area of more than 2.5 lakhs hectares in this state ^[5]. Ever since, there has been repeated introductions in several regions of the country. The morphological differences in the plants growing under various climatic regions may be attributed to further introductions of seed material of various origins and possible hybridisation between them.

Despite the advantages of mesquite trees, there is a serious drive to eradicate the population

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as they are listed under most invasive species. Unlike any other invasive species, *Prosopis* has lots of evidences to prove that this species has a positive impact on the overall ecosystem of the region. This calls for more research and understanding of the species about its adaptability, root efficiency, stress tolerance strategy, invading power and genetic variability.

This paper concentrates on the genetic studies in *Prosopis juliflora*. Detailed studies on the distribution of genetic variability in *Prosopis* in India are however, limited. Genetically broad populations should be maintained as a basis for present and future conservation practices. Populations with low genetic variability have a reduced potential to adapt to environmental changes [6]. Thus, genetic variation is important to assess the long-term survival of a species [7].

Prosopis juliflora exhibited general inherent variations in various growth parameters. As an introduced species, neither knowledge nor records of the genetic base of the population is known for the breeders and the foresters. *Prosopis* species are essentially cross pollinated, which result in a high degree of variation and have excellent scope for tree improvement. Progeny test of *Prosopis juliflora* will provide a quick and cheap way of identifying superior progenies for improvement programmes. However, the attempt to improve the species in India is dismally modest.

Study of morphometric characters in field trials was earlier the dominating technique and it is still today the most robust and valid way of assessing genetic variation. Information from field experiments is very valuable, because assessed adaptive genetic variation is still the best input for breeding and conservation activities [8]. However, variation studies using biometric attributes in *Prosopis juliflora* is less attempted and thus need research.

For provenance trials, it is essential to know the magnitude and type of association between growth and its component characters. Knowledge on association among components of economic importance can help in improving the efficiency of selection. In the integrated structure of plant, path coefficient analysis measures the direct influence of one variable upon another and permits the separation of correlation coefficients into components of direct and indirect effects [9]. However, association studies in *Prosopis juliflora* among various growth attributes of different progenies are very scant and thus underscore investigations.

It is important that centers are identified as reference points for researchers and anyone using *Prosopis* for any purpose [10]. It was recognized that a lot more work is needed on the genetic understanding of the genus in order to obtain information on the biodiversity. Genetic diversity studies will help the breeders in avoiding closely related seed sources and developing hybrids and its derivatives in future endeavours. Such studies are limited in *Prosopis juliflora*.

2. Materials and Methods

The experimental material for the present study consisted of 30 seed sources of *Prosopis juliflora* collected from 30 districts of Tamil Nadu and maintained at the regulations for seed source sampling concerning minimum number of trees and distance between parent trees, were followed [11]. The details of the seed sources are dealt in table 1.

2.1 Nursery Experiment

The seedlings of thirty seed sources were made into three replications each and studied at Nursery level at different periods viz., 90 DAS, 180 DAS, 270 DAS. The growth

attributes viz., (i) shoot length, (ii) root length, (iii) collar diameter, (iv) sturdiness quotient and (v) Volume index, were recorded on five randomly selected seedlings in each replication.

2.2 Field Experiment

Seedlings of 30 different seed sources were planted in a randomized block design (RBD) with five replications. The spacing adopted was 1 x 1 m and with 9 seedlings per plot. The observations were recorded on all 9 seedlings at 3 MAP. The trial was laid out in Randomized Block Design (RBD) with five replications and spacing adopted was 1 x 1 m with nine plants per plot. Recommended silvi cultural operations were carried out uniformly. Data were recorded for the species under consideration at 3 MAP and were used for the present study. The following growth attributes were recorded on all thirty seed sources in each replication. (a) Plant Height (b) Basal diameter (c) Number of branches (d) Volume index.

2.3 Statistical analysis

The data gathered from the field experiments were subjected to analysis of variance (ANOVA) to establish the significance of differences between the seed sources. Estimates of mean, variance and standard error were worked out [12]. The significance test was carried out by referring to the standard 'F' table [13].

Phenotypic and genotypic variances were estimated as per the method described by [14]. Phenotypic and genotypic coefficients of variances (PCV and GCV) were computed following [15]. Heritability (h^2) in the broad sense was calculated according to [16]. Genetic advance was worked out after [17]. Phenotypic and genotypic correlation coefficients were calculated according to the method suggested by [18]. Path co-efficient analysis was estimated after [18] to apportion the genotypic correlation coefficients into direct and indirect effects. Data from the nursery and field experiment were subjected to genetic diversity estimation through cluster analysis by Neighbour joining method [19].

3. Results and Discussion

3.1 Mean Performance

Genetic parameter estimates of growth traits are essential for the breeder to identify superior genotypes. The morphological traits of the all seed sources indicated wide variability for all the characters studied and hence ample opportunities exists for genetic improvements of the crop through selection directly from the seed sources for improvement programme

Two seed sources viz., Ramnad and Rameshwaram showed consistent superior performance for all the biometric traits over the different growth periods both in nursery (Table 2) and under field conditions (Table 3). Variations in growth attributes due to progenies and provenances were also earlier reported in other species also [20, 21].

3.2 Variability studies

Volume index had recorded high phenotypic and genotypic coefficient of variation of 43.86 and 37.34 followed by collar diameter (35.82 and 31.25), sturdiness quotient (21.90 and 19.61), plant height (17.93 and 16.87) and number of branches (16.72 and 13.55) (Table 4). Volume index recorded heritability of 0.73 and highest genetic gain as percentage of mean was 65.50. Plant height recorded highest heritability of 0.89 and genetic gain as percentage of mean of 32.69. Number of branches recorded lowest heritability and genetic gain as per cent as percentage of mean (Table 4).

Among morphometric traits investigated, though volume index and sturdiness quotient displayed high phenotypic and genotypic coefficient of variation and genetic advance as percentage of mean, it cannot be relied upon for selection because it involves laborious estimation. Therefore, the primary parameters such as plant height and collar diameter which possessed high PCV and GCV, high heritability and genetic advance as percentage of mean were taken into account (Table 4). The results are in close association with the findings in *Bambusa balcoona* [22], in *Madhuca latifolia* [23] and in *Simarouba Glauca* [24].

3.3 Association studies

3.3.1 Correlation studies

Correlation studies indicated that volume index exhibited a positive and highly significant association with plant height and collar diameter at genotypic level and a negative correlation with collar diameter at phenotypic level (Table 5), whereas number of branches and sturdiness quotient showed non-significant negative correlation with volume index at both levels. Further, the plant height exhibited positive phenotypic and genotypic *inter* correlations with collar diameter and sturdiness quotient (Table 5). Similar correlation and intercorrelation were observed in *Simarouba glauca* [24] and in *Albizia lebbek* [25].

3.3.2 Path analysis

Plant height and collar diameter exhibited highest positive direct effect on volume index followed by plant height and number of branches (Fig. 1). Collar diameter exercised the highest indirect effect on volume index via plant height and sturdiness quotient (Fig. 1). Plant height also exhibited its influence indirectly on volume index through collar diameter. Similar results were documented in Teak [26].

3.4 Estimation of genetic diversity using biometric traits

Euclidean distance for all the pairwise combinations of seed sources was computed and the highest Euclidean distance was recorded between the sources of Pudukkottai and Tuticorin (30.33) followed by Pudukkottai and Pollachi (29.95). The lowest genetic distance was observed between Virudhunagar and Tirupathur (2.20). The phenetic tree constructed through hierarchical analysis revealed that the thirty seed sources were

grouped into two major clusters A and B at a coefficient level of 105 (Fig.2). Cluster A was the largest with 21 seed sources and cluster B had nine seed sources. At a coefficient level of 50.5, the cluster A was resolved into two sub-clusters (A1 and A2). Among the sub-clusters, A1 was the largest with 16 seed sources and A2 had only five seed sources. Similarly, at a coefficient level of 22.5, cluster B was resolved into two sub-cluster (B1 and B2) with six seed sources in B1 and three seed sources in B2 (Fig.2). Similar results were confronted with genetic divergence studies in *Simarouba Glauca* [24], *Tectona grandis* [26], *Albizia lebbek*, [27] and *Eucalyptus* spp [28-30] as well.

Table 1: Details of the seed sources

Source No.	Seed source	Latitude	Longitude
S ₁	Bodi	10°01'N	77°00'E
S ₂	Vellore	12°55'N	79°11'E
S ₃	Madurai	9°58'N	78°10'E
S ₄	Theni	9°68'N	79°86'E
S ₅	Kancheepuram	12°50'N	79°45'E
S ₆	Dindigul	10°22'N	78°00'E
S ₇	Chengam	12°15'N	79°07'E
S ₈	Tuticorin	8°48'N	78°11'E
S ₉	Pollachi	10°39'N	77°03'E
S ₁₀	Tirunelveli	8°44'N	77°44'E
S ₁₁	Coimbatore	11°00'N	77°10'E
S ₁₂	Villupuram	11°57'N	79°32'E
S ₁₃	Tirupathur	11°68'N	79°25'E
S ₁₄	Sivaganga	10°62'N	79°15'E
S ₁₅	Trichy	10°50'N	78°46'E
S ₁₆	Pudukkottai	10°23'N	78°52'E
S ₁₇	Chennai	12°42'N	80°01'E
S ₁₈	Sivakasi	9°27'N	77°36'E
S ₁₉	Cuddalore	11°43'N	76°58'E
S ₂₀	Virudhunagar	9°35'N	77°57'E
S ₂₁	Aruppukkottai	9°31'N	78°08'E
S ₂₂	Erode	11°20'N	77°46'E
S ₂₃	Perambalur	11°14'N	78°56'E
S ₂₄	Keezhakarai	9°14'N	78°50'E
S ₂₅	Sankarankoil	9°10'N	77°35'E
S ₂₆	Salem	11°39'N	78°12'E
S ₂₇	Rameshwaram	9°17'N	79°22'E
S ₂₈	Dharmapuri	12°08'N	78°13'E
S ₂₉	Ramnad	9°22'N	78°52'E
S ₃₀	Nagercoil	8°11'N	77°29'E

Table 2: Seed source variation for biometrical attributes under nursery condition

Seed Sources	270 DAS				
	Shoot length (m)	Root length (cm)	Collar diameter (mm)	Sturdiness quotient	Volume index
S ₁	71.40	52.28	5.13	139.13	18.808
S ₂	71.53	54.20	5.30	135.03	20.177
S ₃	99.93*	74.42*	4.83	206.68*	23.390
S ₄	85.00*	64.54*	5.03	168.45*	21.948
S ₅	73.33	56.45	5.10	143.65	19.128
S ₆	61.97	63.47*	5.00	123.87	15.558
S ₇	68.17	55.53	5.07	134.37	17.583
S ₈	76.63	59.65	5.60	136.80	24.089
S ₉	72.20	60.05	5.07	142.59	18.540
S ₁₀	69.80	47.47	5.27	132.96	19.513
S ₁₁	71.07	50.40	5.13	138.50	18.744
S ₁₂	62.33	50.00	5.13	121.45	16.420
S ₁₃	70.53	55.23	5.23	134.88	19.333
S ₁₄	63.63	59.33	4.73	134.98	14.354
S ₁₅	71.17	53.90	5.20	137.07	19.278
S ₁₆	68.17	57.28	5.23	130.30	18.660
S ₁₇	67.53	54.94	4.80	140.73	15.654
S ₁₈	64.80	60.22	4.93	131.25	15.845

S ₁₉	76.10	54.48	5.67	134.30	24.422
S ₂₀	79.33	60.02	5.57	143.60	25.302
S ₂₁	73.67	60.82	4.87	151.44	17.518
S ₂₂	71.80	57.54	5.23	137.22	19.678
S ₂₃	68.33	51.48	5.83*	117.11	23.283
S ₂₄	87.23*	66.39*	5.80	152.77*	29.953*
S ₂₅	83.63*	59.13	5.63	148.39	26.564
S ₂₆	81.00	56.32	5.63	144.27	25.686
S ₂₇	98.38*	77.97*	5.83*	168.74*	33.440*
S ₂₈	66.40	50.53	5.77	115.64	22.063
S ₂₉	94.49*	78.38*	6.97*	135.57	45.900*
S ₃₀	79.00	65.90*	5.90*	133.85	27.527
Mean	73.86	58.94	5.35	138.74	24.488
Sed	3.75	1.24	0.24	6.59	2.696
CD	7.51	2.48	0.47	13.19	5.397

*Significant at 5% level.

Table 3: Seed source variation for biometrical attributes under field condition

Seed Sources	3 MAP				
	Plant height (m)	Collar diameter (cm)	No. of branches	Sturdiness quotient	Volume index
S ₁	6.25	1.75	5.50	366.67	1931.25
S ₂	5.09	1.50	7.50*	339.00	1144.13
S ₃	7.38*	2.58*	5.50	286.41	4890.08*
S ₄	4.63	1.70	4.50	276.75	1346.63
S ₅	5.63	1.99	4.00	285.18	2262.81
S ₆	5.50	1.40	5.50	392.31	1097.50*
S ₇	7.45*	2.65*	2.50	281.93	5252.50
S ₈	4.80	1.83	6.50*	265.72	1610.21
S ₉	6.93	1.83	4.50	379.93	2312.41
S ₁₀	4.80	1.68	3.50	286.34	1356.94
S ₁₁	6.25	2.20	2.00	285.20	3020.25
S ₁₂	6.18	2.15	2.50	289.19	2857.00
S ₁₃	7.38*	1.60	5.50	467.26*	1925.50
S ₁₄	8.93*	1.70	4.50	526.88*	2592.08
S ₁₅	6.75	2.17	3.00	310.94	3235.84
S ₁₆	5.30	1.95	3.00	278.34	2019.20
S ₁₇	5.75	1.85	2.00	312.14	1955.50
S ₁₈	7.25*	1.98	3.50	370.46	2886.88
S ₁₉	5.00	1.43	4.00	352.21	1014.89
S ₂₀	5.50	1.62	3.50	339.08	1470.78
S ₂₁	5.88	1.75	4.50	345.83	1803.13
S ₂₂	6.88	1.75	4.00	400.00	2159.38
S ₂₃	5.65	1.55	3.50	368.91	1363.15
S ₂₄	7.38*	2.40*	4.50	307.61	4261.38*
S ₂₅	6.98	2.00	4.50	352.15	2819.90
S ₂₆	8.88*	1.60	3.50	562.50*	2315.50
S ₂₇	7.57*	1.75	7.50*	432.57*	2318.33
S ₂₈	6.17	2.05	4.50	301.36	2591.00
S ₂₉	7.51*	2.80*	8.50*	268.52	5862.92*
S ₃₀	5.75	1.90	4.50	302.78	2091.00
Mean	6.25	1.86	4.37	344.09	2250.22
Sed	0.38	0.18	0.76	33.56	517.56
CD	0.77	0.37	1.56	68.64	1058.55

*Significant at 5% level

Table 4: Genetic estimates for seedling attributes under field condition

Traits	PCV	GCV	Heritability	GA as (%) of mean
Plant height	17.93	16.87	0.89	32.69
Collar diameter	35.82	31.25	0.76	56.17
No. of branches	16.72	13.55	0.66	22.62
Sturdiness quotient	21.90	19.61	0.80	36.17
Volume index	43.86	37.34	0.73	65.49

Table 5: Genotypic and Phenotypic correlation coefficient for morphometric attributes under field condition – 3 MAP

Traits	Collar diameter	No. of branches	Sturdiness quotient	Volume index
Plant height	0.260	-0.184	0.761**	0.591**
	0.289	-0.119	0.657**	0.600**
Collar diameter		-0.442	-0.438	0.919**
		-0.327	-0.517	-0.916
No. of branches			0.114	-0.425
			0.132	-0.310
Sturdiness quotient				-0.067
				-0.175

** Significant at 1% level

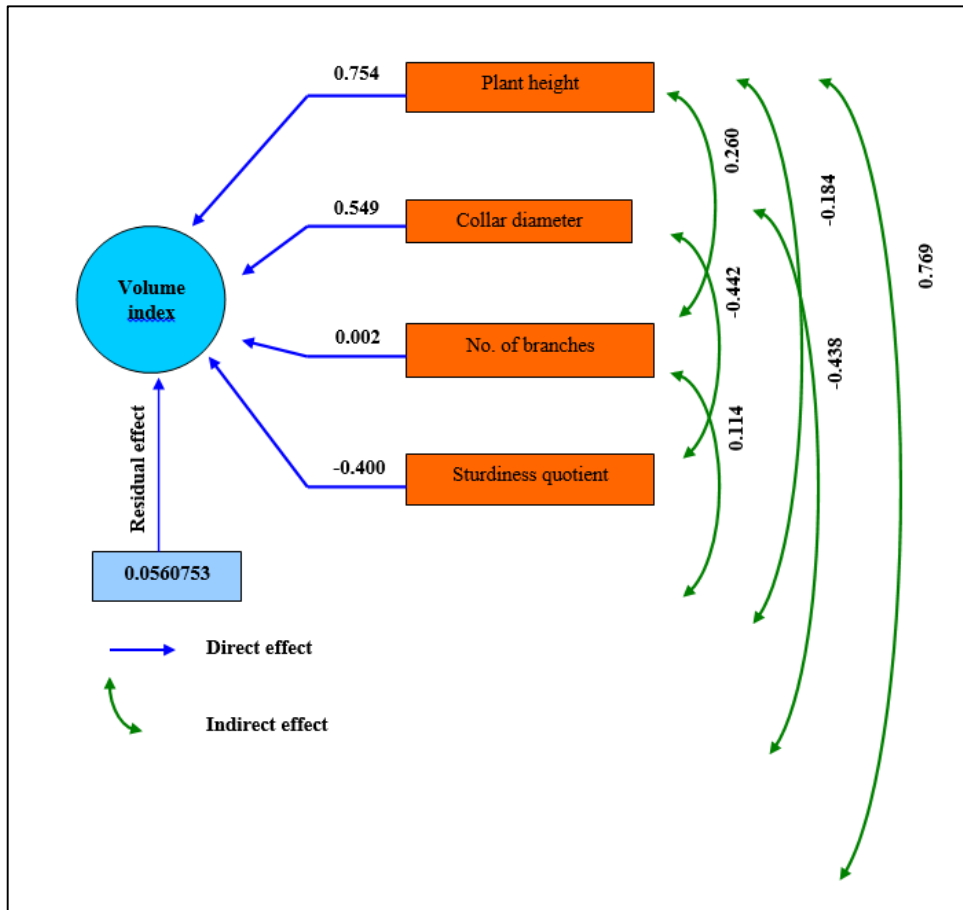


Fig 1: Path diagram showing relationship between volume index and biometric attributes

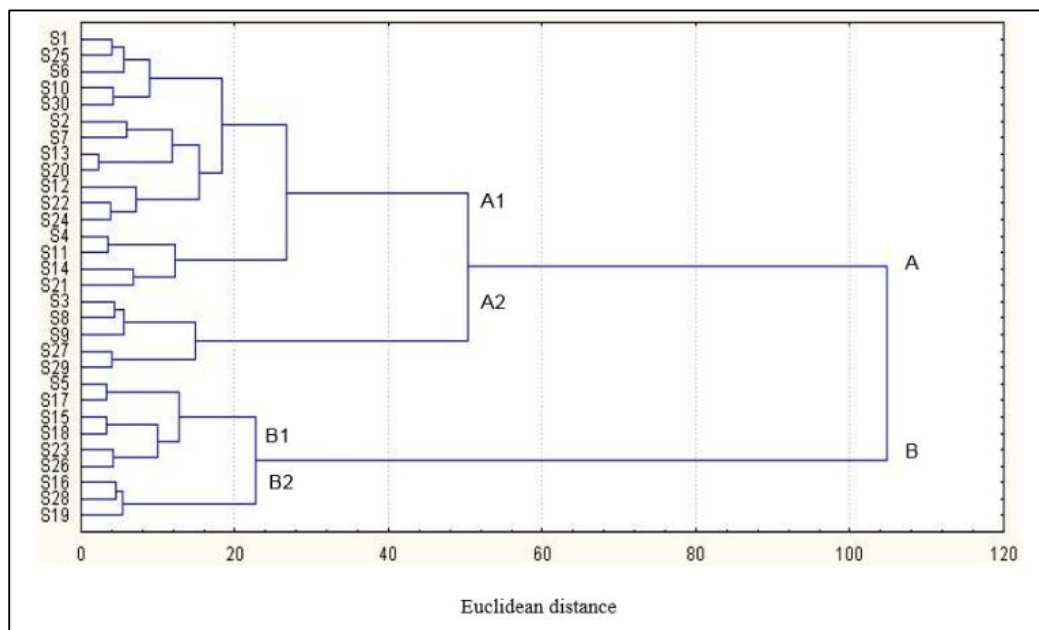


Fig 2: Phenetic tree constructed from biometric similarity matrix of seed sources

5. Conclusion

The present investigation envisaged that seed sources viz., Ramnad, Rameshwaram, Keezhakarai and Madurai expressed superiority over others for all the biometrical characters used in the study. The consistency and reliability expressed by the seed sources could be used for further improvement studies in the species. High and positive association coupled with intensive direct effect of collar diameter followed by plant height could be used as valuable, reliable and relevant yardsticks for selection in tree improvement programme. Genetic divergence studies expressed similarity with geographic distribution of seed sources. This might be due to the similarity of the nature of selection pressure operating under the respective habitat conditions. However, this helps to select the most divergent parents for crossings in order to provide greater variability in future generations.

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