ASSESSING THE GENETIC DIVERSITY AND CHARACTER ASSOCIATION OF YIELD COMPONENTS IN LITCHI (*LITCHI CHINENSIS* SONN.)

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Keywords: Litchi, Genetic diversity, Heritability, Path analysis, Correlation

Abstract

Eighteen litchi genotypes were evaluated in this study for genetic advancement, heritability, variability, and association studies. The genotype 'CHL-4' exhibited maximum fruit weight (28.12 g), aril weight (14.00 g), aril thickness (9.65 mm) and seed weight (4.86 g). Fruit length (10.70 and 10.46%), panicle width (10.61 and 10.37%), and panicle length (15.75 and 15.45%) all had substantial phenotypic and genotypic coefficients of variation. All the metrics, with the exception of fruit diameter, aril thickness, seed weight, and number of fruits/panicle, showed higher heritability estimations with substantial genetic advances. In addition to being negatively correlated with fruit weight, aril weight, seed weight and pulp thickness, yield also showed a strong positive correlation with the number of fruits/panicle and aril percentage. Path analysis made the impact of different components on yield very evident. The maximum positive direct effect on yield at genotypic level was through fruit weight (10.120) followed by seed weight (4.070), panicle length (1.550), panicle girth (1.170) and negative direct effect via aril weight (-0.12.860) followed by panicle width (-11.830) and fruit length (-6.290). In order to select a diverse parent for a subsequent breeding effort, cluster analysis assists in classifying comparable objects into appropriate categories. Therefore, the goal of the study was to confirm the genetic variability across genotypes of litchi and identify prospective features for the selection of genotypes that are superior.

Introduction

The evergreen and highly significant fruit tree litchi (Litchi chinensis Sonn.) belongs to the Sapindaceae family. India grows relatively few commercial cultivars, indicating a limited genetic base. Litchi has been reported to contain genetic variants (Singh and Nath 2012). To increase the diversity of litchi, it may be helpful to select clones from various ecological zones. The most efficient and quickest method for creating new cultivars of litchi is to choose the most promising clones from the current population. Breeding and identification purposes might benefit from the presence of notable variation in appearance, biochemistry, and yield, among other features (Chandola and Mishra 2015). A successful breeding program requires a population of breeding material that is variable. Increased heritability in conjunction with variability gives crops more room to grow and improve. Improvements in crucial characteristics including fruit weight, quality, and yield open up opportunities to produce more high-quality litchis (Singh et al. 2012). Understanding genetic advancements, variability, and heritability is crucial because it offers insight into the several contributing factors that influence yield. Therefore, for successful breeding, investigations of variety based on genotypic coefficient of variation, heritability, and genetic advancements are crucial (Mishra et al. 2015). In order to significantly improve any crop, the methods of correlation and path analysis give information about the kind and amount of genetic variation found in quantitative traits. A breeder can create selection techniques for crop improvement by using trait relationship analysis, which provides a comprehensive picture of the interrelationships and relative contributions of independent features on dependent variables. By

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classifying similar objects into appropriate groups, cluster analysis facilitates the selection of a diversified clone or parent for a subsequent breeding cycle. Therefore, the goal of the study was to confirm the genetic heterogeneity among the litchi clones and identify potential attributes for the genotype selection that would lead to superiority.

Materials and Methods

At the ICAR-National Research Centre on Litchi in Muzaffarpur, Bihar, India, eighteen litchi genotypes were collected from various sources, preserved in a field gene bank, and assessed for fruit qualities that are economically significant. Every tree was exposed to the same cultural customs. Twelve fruit physico-chemical characteristics were observed over the course of two years (2018 and 2019), with three replications of each genotype. A digital weighing balance was used to measure the weight of the fruits, aril, and seed. A digital vernier calliper was used to record the physical parameters of the fruits, such as their size and thickness. Following randomized block design, the mean values of twelve attributes for both years were combined and put through analysis of variance (ANOVA) to determine whether there were any notable variations between the clones (Panse and Sukhatme 1954). WASP2 was used to evaluate the phenotypic and genotypic coefficients of variation, heritability, and genetic advancements. Standard techniques were used to estimate the direct and indirect effects of component characters on fruit weight, as well as the correlation study among the all possible combinations at genotypic, phenotypic and environmental levels. The software R was used to perform neighbor joining cluster analysis, which created a diverse group.

Results and Discussion

Table 1 presents quantitative trait data for the genotypes of litchi under study. Significantly highest panicle length was noted in CSL-9 (45.85 cm), CSL-3 and CHL-8 (45.35 cm). Panicle girth was observed maximum in CHL-4 (4.97 mm). The number of fruits per bunch differed considerably between genotypes as well; the highest number was recorded in CSL-12 (14.12) and the lowest in CHL-4 (5.68). The genotypes under investigation showed considerable variation in fruit size with CHL-4 exhibiting the highest fruit weight (28.12 g). Fruit length was maximum in CHI-4 (42.56 mm) followed by CSL-2 (38.45 mm). CHL-4 also exhibited maximum aril weight (14. 00 g), aril thickness (9.65 mm), seed weight (4.86g) and minimum aril (49.79%) and yield (22.56 kg/plant). The maximum yield (kg/plant) was recorded in CSL-18 (32.56), followed by CSL-2 (31.45). The genotypes responsible for this variation in the current investigating corroborate the conclusion drawn by Rai et al. (2002), and Singh and Nath (2015). The minimum, maximum, standard deviation, coefficient of variation, phenotypic and genotypic coefficients of variation, heritability and genetic advances exhibited a wide range of variability for most of the characters studied (Table 2). Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were high for panicle length (15.75% and 15.45%), panicle width (10.61%) and 10.37%), and fruit length (10.70% and 10.46%) and low to moderate for the remaining attributes. For the majority of the features, there is moderate variation in the population, as indicated by the estimations of GCV, which were less in magnitude than PCV and range. These conclusions corroborate the prior research by Lal et al. (2022), which found that the length of panicle had high PCV and GCV (23.67 and 23.44%). Therefore, these traits would be helpful in choosing favourable genotypes for litchi. Higher improvement may be expected through selection based on these features, as evidenced by the high values of PCV and GCV for various traits like fruit length and width as well as panicle length and width. It is obviously important to evaluate heritability because the genotypic coefficient of variation does not provide a complete framework for estimating variations that are heritable in nature.

Since environment has a significant influence on yield, which is the most desirable quantitative trait complex in inheritance, heritability is a useful tool for estimating the potential for improvement through selection. Selection would be particularly successful for traits with high heritability because of the strong affinity between genotypes and phenotypes resulting from reduced environmental effects. With the exception of the number of fruits/panicle (38.23), fruit diameter (14.64), aril thickness (48.85), and seed weight (47.38), the heritability in the broadest sense was greater than 80% for every measure. The high heritability suggests that there was a lot of room for genetic improvement in the traits being studied. Rajan et al. (2009) discovered that mangos have higher heritability for a variety of characteristics. With the exception of fruit diameter, aril thickness, seed weight, and number of fruits/panicle, higher heritability estimates with high genetic advancements were found in the current study. This suggests that phenotypic selection may be more successful for all of these traits as these characters are exhibiting additive gene action. The traits with the highest heritability values were those that were least influenced by environment, indicating that phenotypic performance-based selection would be a dependable method of selection. Several researchers (Rajan et al. 2009, Srivastava et al. 2014) observed high heritability with stronger genetic gain for several qualities in other fruits crops and they reported similar findings.

In order to determine the sort of link that exists between the individual traits, correlations at the genotypic, phenotypic, and environmental levels were established among the 18 litchi genotypes for all traits under study (Table 3). Significant correlations between the traits of the litchi clones included in the study were shown by the correlation coefficient between the various traits. At the phenotypic and genotypic levels, yield was extremely significant and inversely connected with fruit weight, aril weight, aril thickness, and seed weight, and positively correlated with number of fruits/panicle and aril percentage. Strong relationship between the traits was shown by the genotypic correlation value, which was higher than the phenotypic correlation value. To choose appropriate clones for litchi breeding, it may be helpful to understand the relationships between the characters. Additionally, favourable correlations between the characters show that a character's development can benefit another character (Yucel et al. 2006). For instance, a positive correlation between the quantity of fruits/panicle and yield indicates that increasing the quantity of fruits can also increase the yield of litchi. A dependent trait is an interaction product of multiple mutually related component qualities, and a change in any one feature may disrupt the total. The correlation coefficient tells us about the relationship between traits. Direct and indirect association is an efficient way to partition data, according to path coefficient analysis. To evaluate the direct and indirect effects of various features on fruit weight, path analysis was done (Table 4). Correlation analysis does not explain the rationale for the link; it merely measures the strength of the relationship between two features. Therefore, it is not possible to infer that there is no functional link between two qualities based on a non-significant correlation value. However, by dissecting the entire correlation coefficient into components of direct and indirect effects, path coefficient analysis makes this clear. The path analysis result shows the relative contributions of several traits to fruit weight. Table 4 shows that fruit weight (10.120) had the most positive direct effect on yield at the genotypic level, followed by seed weight (4.070), panicle length (1.550), and panicle girth (1.170). On the other hand, aril weight (-0.12.860) had the lowest positive direct effect, followed by panicle width (-11.830), and fruit length (-6.290). Fruit length (0.256) showed the most beneficial direct influence at the phenotypic level, followed by aril weight (0.147) and number of fruits/panicle (0.106). The present study's features include limits that require additional morpho-physiological traits to fully characterize the range of variation, as demonstrated by the high size of residual effect at the phenotypic level (Table 3).

Genotype	Panicle length (cm)	Panicle width (cm)	Panicle girth (mm)	Number of fruits/bunch	Fruit weight (g)	Fruit length (mm)	Fruit diameter (mm)	Aril weight (g)	Aril thickness (mm)	Aril (%)	Seed weight (g)	Yield (kg/plant)
CSL-1	43.57	24.58	4.18	11.45	19.85	35.68	31.56	10.47	7.12	52.76	4.12	25.65
CSL-2	40.15	20.15	4.56	13.25	20.05	38.45	32.75	10.82	6.48	53.94	3.76	31.45
CSL-3	45.35	25.32	4.25	12.65	18.75	34.56	31.56	10.47	7.38	55.85	4.15	26.48
CSL-4	39.57	19.86	4.57	13.75	19.63	37.26	32.47	10.56	6.38	53.80	3.84	28.46
CSL-5	40.45	20.35	4.6	13.68	19.61	37.58	32.68	10.55	6.75	53.79	3.92	28.35
CSL -6	41.25	24.86	4.23	11.56	19.65	35.45	31.57	10.47	7.46	53.28	4.13	27.68
CSL -7	45.16	25.12	4.21	12.24	18.79	34.62	31.68	10.30	7.52	54.79	4.27	26.75
CHL-8	45.35	25.32	4.22	11.45	19.55	34.67	30.86	10.37	7.28	53.04	4.17	27.82
CSL -9	45.85	24.86	4.23	12.35	19.05	34.25	31.67	10.47	7.34	54.98	4.26	26.38
CSL -10	39.67	19.76	4.58	13.78	19.55	37.62	32.57	10.56	6.64	54.03	3.75	27.46
CSL-11	40.15	20.15	4.6	13.67	19.67	37.24	32.45	10.56	6.57	53.70	3.67	27.45
CSL-12	40.25	20.37	4.56	14.12	19.14	37.56	32.26	10.40	6.45	54.34	3.58	28.67
CSL-13	44.35	25.35	4.2	11.45	19.63	35.65	31.86	10.37	7.16	52.83	4.24	26.45
CSL-15	44.85	25.16	4.19	12.35	19.13	34.56	31.57	10.28	7.68	53.75	4.18	26.85
CSL-16	45.15	24.95	4.21	11.76	19.35	34.52	31.68	10.37	7.46	53.61	3.98	26.37
CSL-18	40.25	20.15	4.55	13.47	19.32	37.86	32.34	10.56	6.57	54.66	3.76	32.56
CSL-19	45.24	25.13	4.2	11.35	19.39	35.24	30.76	10.37	7.62	53.48	4.15	26.45
CHL-4	26.45	16.78	4.97	5.68	28.12	42.56	34.26	14.00	9.65	49.79	4.86	22.56
SE (d)	0.76	0.48	0.10	0.30	0.36	0.73	0.67	0.19	0.13	1.43	0.07	0.58
CD (0.05)	1.56	0.99	0.22	0.61	0.74	1.50	1.37	0.39	0.27	N/A	0.160	1.185

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Characters	Mean	Max	Min	n	2	200	PCV	711	GA	GA%
Panicle length (cm)	41.84	45.85	26.45	4.55	10.88	15.45	15.74	96.35	3.82	31.25
Panicle width (cm)	22.68	25.35	16.78	2.86	12.59	10.37	10.61	95.58	4.16	20.89
Panicle girth (mm)	4.40	4.97	4.18	0.23	5.23	5.56	60.9	83.39	3.81	10.47
Number of fruits/bunch	12.22	14.12	5.68	1.90	15.55	2.02	3.27	38.23	0.83	2.58
Fruit weight (g)	19.90	28.12	18.75	2.08	10.45	7.79	8.10	92.49	1.65	15.44
Fruit length (mm)	36.41	42.56	34.25	2.09	5.74	10.46	10.70	95.58	1.52	21.07
Fruit diameter (mm)	32.03	34.26	30.76	0.80	2.51	1.36	3.55	14.64	0.58	1.07
Aril weight (g)	10.66	14.00	10.28	0.84	7.90	7.30	7.68	90.48	0.58	14.31
Aril thickness (mm)	7.20	9.65	6.38	0.76	10.54	2.53	3.62	48.85	0.75	3.64
Aril (%)	53.69	55.85	49.79	1.25	2.33	5.57	5.84	90.90	1.35	10.93
Seed weight (g)	4.04	4.86	3.58	0.30	7.43	2.48	3.60	47.38	0.02	3.51
Yield (kg/plant)	27.44	32.56	22.56	2.15	7.85	7.70	8.13	89.82	4.13	15.04

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Table

Characters	Correla-	Panicle	Panicle	Panicle	Number	Fruit	Fruit	Fruit	Aril	Aril	Aril (%)	Seed	Yield
	tion	length	width	girth	of fruits/	weight	length	diameter	weight	thickness		weight (g)	(kg/plant)
		(cm)	(cm)	(mm)	bunch	(g)	(mm)	(mm)	(g)	(mm)			
Panicle	G	1.000											
length (cm)	Р	1.000											
	Щ	1.000											
Panicle width	ŋ	0.873**	1.000										
(cm)	Р	0.840^{**}	1.000										
	Щ	0.078 ^{NS}	1.000										
Panicle girth	U	-0.976**	-1.059**	1.000									
(mm)	Р	-0.797***	-0.861**	1.000									
	Щ	0.144 ^{NS}	0.187^{NS}	1.000									
Number of	ŋ	0.516^{**}	0.041^{NS}	-0.179 ^{NS}	1.000								
fruits/bunch	Р	0.497**	0.051 ^{NS}	-0.147 ^{NS}	1.000								
	Ы	0.028^{NS}	0.301^{*}	0.022^{NS}	1.000								
Fruit weight	IJ	-0.887**	-0.573**	0.714^{**}	-0.858**	1.000							
(g)	Р	-0.861**	-0.545**	0.576**	-0.822**	1.000							
	Щ	-0.292*	0.082 ^{NS}	-0.156 ^{NS}	0.034 ^{NS}	1.000							
Fruit length	G	-0.996	-0.974**	1.032^{**}	-0.366**	0.808^{**}	1.000						
(mm)	Р	-0.897	-0.849**	0.824^{**}	-0.350**	0.744^{**}	1.000						
	Щ	-0.068 ^{NS}	0.257 ^{NS}	0.106^{NS}	-0.287*	0.264^{NS}	1.000						
Fruit	IJ	-1.123**	-1.121**	1.287^{**}	-0.359**	0.869**	1.203^{**}	1.000					
diameter	Р	-0.698	-0.681	0.567	-0.206 ^{NS}	0.588	0.636	1.000					
(mm)	Щ	-0.115 ^{NS}	-0.019 ^{NS}	-0.265 ^{NS}	0.082 ^{NS}	0.381	-0.137 ^{NS}	1.000					
Aril weight	IJ	-0.905	-0.606	0.759**	-0.826	1.016	0.852**	0.996	1.000				
(g)	Р	-0.861	-0.593	0.609	-0.773	0.940	0.716**	0.524**	1.000				
	Щ	-0.147 ^{NS}	-0.398	-0.079 ^{NN}	0.134 ^{NS}	-0.279	-0.288	-0.317	1.000				
Aril	G	-0.409	0.061 ^{NS}	0.095 ^{NS}	-0.958	0.765	0.238 ^{NS}	0.240 ^{NS}	0.749	1.000			
thickness	P I	-0.390	0.055 ^{NS}	0.054 ^{MS}	-0.917	0.730	0.195 ^{NS}	0.173^{NS}	0.708	1.000			
(mm)	Щ	0.047	-0.086	-0.221	0.048	-0.026	-0.208	0.171	0.068	1.000			
Aril (%)	Ċ	1.164	0.585	-0.835	1.389	-1.453	-1.090	-1.049	-1.295	-1.057	1.000		
	Ь	0.446	0.230	-0.179 ^m	0.524	-0.552	-0.337	-0.199 ^{us}	-0.506	-0.457	1.000		
	Щ	0.055 ^{NS}	0.057 ^{NS}	0.192 ^{NS}	0.014 ^{NS}	-0.046 ^{NS}	0.117 ^{NS}	0.068 ^{NS}	-0.118 ^{NS}	-0.316	1.000		
Seed weight	G	-0.234 ^{NS}	0.233 ^{NS}	-0.092 ^{NS}	-0.912	0.638	0.060 ^{NS}	0.097 ^{NS}	0.624	0.947	-1.001	1.000	
(g)	Р	-0.233 ^{NS}	0.211 ^{NS}	-0.094 ^{NS}	-0.863	0.608	0.071 ^{NS}	0.055 ^{NS}	0.569	0.885	-0.339	1.000	
	Щ	-0.238 ^{NS}	-0.105 ^{NS}	-0.123 ^{NS}	-0.206 ^{NS}	0.223 ^{NS}	0.146 ^{NS}	-0.006 ^{NS}	-0.023 ^{NS}	0.073 ^{NS}	0.088 ^{NS}	1.000	
Yield	IJ	0.198^{NS}	-0.192 ^{NS}	0.072^{NS}	0.737**	-0.536**	-0.002 ^{NS}	-0.043 ^{NS}	-0.499**	-0.788	0.957**	-0.783**	1.000
(kg/plant)	<u>ч</u> ,	0.172 ^{NS}	-0.180 ^{NS}	0.084 ^{NS}	0.690	-0.485	-0.005 ^{NS}	-0.074 ^{NS}	-0.443	-0.749	0.312 [*]	-0.715	1.000
	Т	-0.183	-0.039	0.152	0.073	0.176	-0.027	-0.195	0.140^{-12}	-0.282	-0.118.	-0.089-0-	1.000

Table 3. Correlation coefficients for genotypic (G), phenotypic (P) and environmental (E).

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Characters	Correlation	Panicle length (cm)	Panicle width (cm)	Panicle girth (mm)	Number of fruits/bunch	Fruit weight (g)	Fruit length (mm)	Fruit diameter (mm)	Aril weight (g)	Aril thickness (mm)	Aril (%)	Seed weight (g)
Panicle length (cm)	IJ	1.55	-10.32	-1.15	0.3	-8.97	6.27	2.84	11.64	-0.16	-0.84	-0.95
	Р	-0.064	-0.008	0.038	0.053	0.250	-0.229	0.036	-0.126	0.195	-0.001	0.028
Panicle width (cm)	ŋ	1.350	-11.830	-1.240	0.020	-5.800	6.130	2.840	7.790	0.020	-0.420	0.950
	Р	-0.054	-0.009	0.041	0.005	0.158	-0.217	0.035	-0.087	-0.028	0.000	-0.025
Panicle girth (mm)	IJ	-1.510	12.530	1.170	-0.100	7.220	-6.490	-3.260	-9.760	0.040	0.600	-0.370
	Ь	0.051	0.008	-0.047	-0.016	-0.167	0.210	-0.030	060.0	-0.027	0.000	0.011
Number of	ŋ	0.800	-0.480	-0.210	0.580	-8.680	2.300	0.910	10.620	-0.380	-1.000	-3.710
fruits/bunch	Ρ	-0.032	0.000	0.007	0.106	0.239	-0.089	0.011	-0.114	0.460	-0.001	0.103
Fruit weight (g)	IJ	-1.370	6.780	0.840	-0.500	10.120	-5.080	-2.200	-13.070	0.310	1.050	2.600
	Р	0.055	0.005	-0.027	-0.087	-0.290	0.190	-0.031	0.138	-0.366	0.001	-0.072
Fruit length (mm)	IJ	-1.540	11.520	1.210	-0.210	8.180	-6.290	-3.040	-10.960	0.100	0.790	0.250
	Ρ	0.057	0.008	-0.039	-0.037	-0.216	0.256	-0.033	0.105	-0.098	0.000	-0.008
Fruit diameter (mm)	ŋ	-1.740	13.260	1.510	-0.210	8.800	-7.570	-2.530	-12.810	0.100	0.760	0.390
	Ρ	0.045	0.006	-0.027	-0.022	-0.171	0.162	-0.052	0.077	-0.087	0.000	-0.007
Aril weight (g)	IJ	-1.400	7.170	0.890	-0.480	10.290	-5.360	-2.520	-12.860	0.300	0.940	2.540
	Ρ	0.055	0.006	-0.029	-0.082	-0.273	0.183	-0.027	0.147	-0.355	0.001	-0.068
Aril thickness (mm)	IJ	-0.630	-0.720	0.110	-0.560	7.740	-1.500	-0.610	-9.630	0.400	0.760	3.850
	Ρ	0.025	-0.001	-0.003	-0.097	-0.212	0.050	-0.00	0.104	-0.501	0.001	-0.106
Aril (%)	IJ	1.800	-6.910	-0.980	0.810	-14.700	6.860	2.650	16.660	-0.420	-0.720	-4.070
	Ρ	-0.028	-0.002	0.008	0.056	0.160	-0.086	0.010	-0.074	0.229	-0.001	0.040
Seed weight (g)	IJ	-0.360	-2.760	-0.110	-0.530	6.450	-0.380	-0.240	-8.030	0.380	0.720	4.070
	Р	0.015	-0.002	0.004	-0.092	-0.176	0.018	-0.003	0.084	-0.444	0.000	-0.119

Twelve qualities served as the basis for the cluster analysis (Fig. 1). The evolutionary link between the 18 genotypes of litchi was represented by the dendrogram. Analysing the genetic and phenotypic diversity of germplasm is crucial when using the hierarchical clustering method. Based on the traits they possessed, the genotypes of litchi were grouped using the clustering approach. The primary cluster, which had the largest panicle girth, fruit weight, pulp weight, and seed weight, split off from CHL-4. Ten genotypes that represented comparable types of features (seeded weight, width, and panicle length) made up Cluster-I. Cluster-II, with eight genotypes, had greater panicle girth and yield.

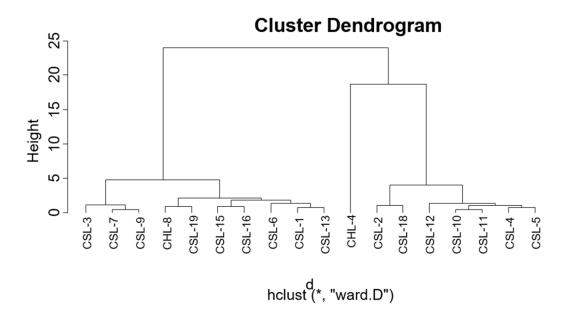


Fig. 1. Dendrogram of grouping for 18 genotypes of litchi based on 12 traits of panicle and fruit.

The findings of this study indicate that the number of panicles' length, girth, fruits/bunch, fruit weight, and seed weight all directly and favourably affected yield. In terms of fruit qualities, the genotypes examined showed genetic variation as well as morphological variability. Future breeding programs for litchi will benefit greatly from this diversity and variability. Selection based on these features would be more reliable because high heritability estimates and high genetic advancements seen for fruit weight, fruit length, panicle width, and aril weight were indicative of additive gene action. Characters with strong genetic advancement and high heritability further suggested that choices could have been made in previous generations. For a breeding program, representative genotypes from each cluster might be chosen.

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References

- Chandola JC and Mishra DS 2015. Morphological and biochemical characterization of litchi cultivars. Hort. Flora Research Spectrum **4**(4): 361-365.
- Lal N, Singh A, Kumar A, Marboh ES, Gupta AK, Pandey SD and Nath V 2022. Genetic variability, correlation and path-coefficient studies in litchi (*Litchi chinensis* Sonn.) for plant growth, panicle and yield attributes. Intl. J. Bio-resource Stress Manag. **13** (1): 29-36.
- Mishra PK, Ram Badan, Ram RA and Kumar N 2015. Genetic variability, heritability, and genetic advance in strawberry (*Fragaria* × *ananassa* Duch.). Turkish J. Agric. Forest. **39**: 451-458.
- Panse VG and Sukhatme PV 1954. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi. Pp. 361.
- Rai M, Das B, Nath V, Kumar M and Kumar RR 2002. Fruit characteristics of litchi genotypes under Chotanagpur conditions. Orissa J. Hort. 30 (2): 1-5.
- Rajan S, Yadava LP, Kumar R and Saxena SK 2009. Genetic divergence in mango varieties and possible use in breeding. Indian J. Hort. 66: 7-12.
- Singh A and Nath V 2012. Variability in fruit physico-chemical characters of litchi (*Litchi chinensis* Sonn.): an index for selection of improved clones for processing and value addition. Indian J. Genet. **72**(2): 143-147.
- Singh A and Nath V 2015. Variability in fruit physico-chemical characteristics of litchi (*Litchi chinensis*) in Tripura and Assam. Indian J. Agric. Sci. **85** (2): 261-265.
- Singh A, Pandey SD and Nath V 2012. The world litchi cultivars. Technical Bulletin 007. NRC for Litchi, Mushahari, Muzaffarpur. Pp. 1-65.
- Srivastava KK, Verma MK, Ahmad N, Razvi SM and Shabeer A 2014. Genetic diversity and divergence analysis in sweet cherry (*Prunus avium* L.). Indian J. Hort. **71**(2):156-161.
- Yucel DO, Anlarsal AE and Yucel C 2006. Genetic variability, correlation and path analysis of yield, and yield components in chickpea (*Cicer arietinum* L.). Turkish J. Agric. Forest. **30**: 183-188.

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