Studies on genetic variability, heritability, correlation and path coefficient analysis in betel vine (*Piper betle* L.) genotypes.

ABSTRACT

An experiment was conducted on thirty seven betel vine genotypes to assess the variability and correlation among different twenty one qualitative traits. Analysis of variance was revealed that the genotypes significantly differed for all the characters studied. The results showed that phenotypic coefficient of variations values were higher than the genotypic coefficient of variation for all the characters studied. The values of heritability in broad sense were observed very high for all the twenty one traits. Correlation studies revealed that total yield per vine was significantly and positively correlated with plant height (0.918), number of laterals per vine (0.988), number of leaves per lateral (0.827), total number of leaves per vine (0.863), clinging roots (0.887), petiole length (0.814) and path analysis showed that the traits such as number of laterals per vine (0.6350), total number of leaves per vine (0.2601), clinging roots (0.0839), leaf area (0.2091) and petiole length (0.2696) had direct and positive effect on total yield per vine. Hence, direct selection would be more effective in improving these traits.

Comment [mm1]: Add background, problems, aims.

Keywords: Variability, GCV, PCV, heritability, genetic advance

INTRODUCTION

Betel vine (*Piper betel L*.) is the perennial dioecious climber and shade loving plant, belongs to the family piperaceae and believed to have originated in Central and eastern Malaysia. It is mainly cultivated in Southeast Asian countries that are India, Bangladesh, Sri Lanka, Malaysia, Thailand, Philippines *etc*. for its leaves, which mainly used as stimulant. In Indian subcontinent it is known as pan in Hindi, Tambula in Sanskrit, Villayadela in Kannada, Vettilakkoti in Malyalam, Vettilai in Tamil, Tamalapaku in Telugu, Videch-pan in Marathi, Nagarbel in Gujrati and pan in Bangala.

In India, it is one of the important commercial crops grown mostly by small and marginal farmers in the states of Assam, West Bengal, Bihar, Andhra Pradesh, Karnataka, Tamil Nadu, Maharashtra, Madhya Pradesh, Kerala, Uttar Pradesh and Orissa with an estimated area of 53,539 ha and annual production worth Rs. 9,000 million (Ray, 2008) [1].

In India, during 2011-12, it was grown in an area of 6,988 ha with a production of 1,31,795 lakh leaves with a productivity of 18.86 lakh leaves/ha. It has exported 13,195.43 MT of betel leaves to the world for the worth of Rs. 46.75 crores/ 6.74 USD Millions in 2018-19 (APEDA agriXchange)[2]. In Karnataka, it is mainly grown in districts of Haveri, Davanagere, Tumkur, Bengaluru Rural, Mysuru, Dharwad, Shivamogga, Chikkamagaluru, North Canara, Belagavi, Bagalkot and Vijayapur.

The presence of variability in the breeding population is prerequisite for boosting production and assigning characteristics, necessitates its assessment. The plant's phenotypic expression is mostly determined by its genetic makeup and the environment in which it grows. As a result, using appropriate parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advance, it becomes important to divide observed phenotypic variability into heritable and non-heritable components.

Improvement made in crop varieties is primarily focused on enhancing yield and yield attributing characters. A study of the correlation between several quantitative aspects that give an insight of their relationship and may be used to develop selection methods to improve yield and quality. However, the direct and indirect impact of individual character to yield is not shown by correlation studies. It would be useful to analyse the relative size of various features contributing to yield in order to obtain an accurate picture of yield components for an efficient selection procedure. The path coefficient technique established by Wright (1921) [3] and Dewey and Lu (1959)[4]aids in assessing the direct and indirect contributions of various components in constructing yield correlations. On the basis of these studies, the quantitative relevance of specific features is underlined to aid the selection programme in crops, as well as in betel vine also.

2.MATERIAL AND METHODS

2.1 Experimental site and location

The present study on “Genetic variability in thirty seven betel vine genotypes” was carried out during 2019-21 at farmer’s field, Badami. The experimental plot was laid out in Randomized Block Design with three replications and 1.5 m × 0.45 m spacing was followed and the field was provided with the adequate quantity of farm yard manure (40 t/ha). A total of 100 kg nitrogen, 50 kg P_2O_5 and 50 kg K_2O per hectare was applied through different organic manures viz., FYM, neem cake groundnut cake and vermicompost along with chemical fertilizers. Fifty per cent of nitrogen was applied at the time of lowering, twenty five per cent at four months after lowering and remaining twenty five per cent at six months after lowering. Observations were recorded from five selected plants in each genotype and each replication in two month interval.

2.2 Analysis of variances

Analysis of variance was carried out as per the procedure given by Panse and Sukthame (1967) [5] using the mean values of random plants in each replication from all treatments to find out the significance of treatment effects.

2.3 Estimates of genetic variability

Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) [6] based on estimate of genotypic and phenotypic variance. Burton and Devane (1953) [6] classified GCV and PCV as follows, Low: Less than 10%; Moderate:10-20%; High: More than 20%. Heritability in broad sense was estimated as the ratio of genotypic variance to phenotypic variance and expressed in percentage (Falconer,1981) [7]. Robinson *et al*. (1949) [8] classified heritability percentage as follows, Low: Less than 30%; Moderate:30-60%; High: More than 60%. Genetic advance over mean was calculated according to Johnson *et al*. (1955) [9]. Classified genetic advance as percentage over mean as follows, Low: Less than 10%; Moderate: 11-20%; High-More than 20%.

2.4 Correlation analysis

To examine the degree of association of traits with growth, yield and also among the yield components between the genotypes, the correlation coefficient were estimated and tested as per procedures given by Panse and Sukhatme (1967) [5].

2.5 Path coefficient analysis

The concept of path coefficient analysis was developed by Wright (1921) [3] and illustrated by Dewey and Lu (1959) [4] was carried out separately to know the direct and indirect effects of the important components, which are the standardized partial regression.

3.RESULTS

3.1 Analysis of variance

Mean sum of squares due to replication, genotypes and error of the experiment was calculated and presented in table 1. The analysis of variance showed highly significant differences among the genotypes for all the parameters such as Plant height (cm), Number of laterals per vine, Number of leaves per lateral, Number of leaves per vine, Clinging roots, Leaf length (cm), Leaf width (cm), Leaf area (cm^2), Petiole length (cm), Internodal length (cm), Spike length (cm), Peduncle length (cm), 100 leaves weight (g), Total yield per vine, Total yield per hectare, Total chlorophyll content (mg/g), Antioxidants (mg/g), Total phenolics (mg/g), Essential oil (%), Eugenol (%).

3.2 Estimates of genetic variability parameters in betel vine genotypes

3.2.1 Genotypic (GCV) and Phenotypic (PCV) coeffiecient of variation

The genetic variability study, estimates of PCV for all the characteristics were greater than the estimates of GCV (Table 2)

The highest estimates of coefficients of variations was recorded for spike length (GCV=53.26 % and PCV=59.54 %), followed by number of spikes (GCV=50.52 % and PCV=53.78 %), peduncle length (GCV=46.57 % and PCV=46.90 %), essential oil (GCV=34.83 % and PCV=35.82 %), internodal length (GCV=31.18 % and PCV=31.75 %), number of laterals per vine (GCV=29.54 % and PCV=33.12 %), antioxidants (GCV=27.31 % and PCV=28.04 %), petiole length (GCV=26.77 % and PCV=28.37 %), total chlorophyll content (GCV=23.63 % and PCV=24.29 %) and leaf area (GCV=21.91 % and PCV=23.04 %). Moderate estimates of genotypic coefficient of variation and highest phenotypic coefficient of variation was registered for total yield per vine (GCV=19.65 % and PCV=20.00%) followed by total yield per hectare (GCV=19.65 % and PCV=20.00 %) and plant height (GCV=18.87 % and PCV=20.49 %). Moderate coefficient of variations was recorded for number of leaves per vine (GCV=17.80 % and PCV=18.79 %), eugenol (GCV=16.55 % and PCV=17.82 %), clinging roots (GCV=16.09 % and PCV=17.31 %), hundred leaf weight (GCV=13.94 % and PCV=15.25 %), leaf width (GCV=13.38 % and PCV=14.46 %), number of leaves per lateral GCV=12.09 % and PCV=14.24 %) and leaf length (GCV=10.63 % and PCV=11.65 %).Lowest estimates of genotypic coefficients of variations and moderate estimates of phenotypic coefficient of variation was noticed for total phenolics (GCV=8.81 % and PCV=10.17 %).

3.2 Estimation of heritability and genetic advance

3.2.1 Heritability

The estimates of heritability (broad sense) ranges from 74.99 % to 98.61 % for various characters under investigation (Table 2). It was found maximum for peduncle length (98.61 %) followed by total yield per vine (96.59 %), total yield per hectare (96.59 %), internodal length (96.46 %), total antioxidants (94.87 %), total chlorophyll content (94.64 %), essential oil (94.56 %), leaf area (90.47 %), number of leaves per vine (89.71 %), petiole length (89.03 %), number of spikes (88.24 %), clinging roots (86.41 %), eugenol (86.18 %), leaf width (85.56 %), plant height (84.89 %), hundred leaf weight (83.61 %), leaf length (83.31 %), spike length (80.01 %), total phenolics (74.99 %) and number of leaves per lateral (72.10 %).

3.2.2 Genetic advance as per cent of mean

Genetic advance as per cent of population mean was low to high in nature and ranged from 15.71 to 98.13% for different characters under study (Table 2). It was found high for the characters *viz*. spike length (98.13 %), number of spikes (97.76 %), peduncle length (95.26 %), essential oil (69.77 %), internodal length (63.09 %), antioxidants (54.80 %), number of laterals per vine (54.26%), petiole length (52.04 %), total chlorophyll content (47.36 %) and leaf area (42.94 %). Moderate genetic advance was recorded for total yield per hectare (39.79 %), total yield per vine (39.79 %), plant height (35.82 %), number of leaves per vine (34.72 %), eugenol (31.65 %), clinging roots (30.81 %), hundred leaf weight (26.27 %), leaf width (25.49 %) and number of leaves per lateral (21.15 %). Whereas it was low for leaf length (19.99 %) and total phenolics (15.71 %).

3.3 Correlation

The genotypic and phenotypic association of different betel vine genotypes during 2019-21 is presented in Table 3 and 4.

At genotypic level, total yield per vine was found to have highly positive significant correlation with number of laterals per vine (0.988), plant height (0.918), clinging roots (0.887), total number of leaves per vine (0.863), number of leaves per lateral (0.827) and petiole length (0.814) and highly significant and negative correlation with internodal length (-0.925), leaf width (-0.298), hundred leaf weight (-0.292), leaf area (-0.237) and leaf length (-0.1458).

At phenotypic level, total yield per vine was found to have highly positive significant correlation with clinging roots (0.924), total number of leaves per vine (0.919), petiole length (0.911), number of laterals per vine (0.910), number of leaves per lateral (0.860), plant height (0.836) and highly significant and negative correlation with internodal length (-0.955). While it had significant negative correlation with leaf width (-0.263), hundred leaf weight (-0.250), leaf area (-0.196) and non significant negatively associated with leaf length (-0.1417).

3.4 Path analysis

Genotypic path coefficients for total yield per vine with 11 independent characters are presented in table 5. During experiment, number of laterals per vine (0.6350) revealed high positive and direct effect on total yield per vine whereas, petiole length (0.2696), total number of leaves per vine (0.2601) and leaf area (0.2091) had moderate and clinging roots (0.0839) had negligible positive effect at 240 DAL. Number of leaves per lateral (-0.3244) had high and negative direct effect on total yield per vine, while internodal length (-0.2442) had moderate negative and direct effect and plant height (-0.1554), leaf width (-0.1057) revealed low negative and direct effect. Whereas negative negligible and direct effects were seen in leaf length (-0.0664) and hundred leaf weight (-0.0423) for total yield per vine (Table 5).

4. DISCUSSION

4.1 Analysis of variance

The analysis of variance during 2019-21 data (Table 1) revealed highly significant (both at p=0.01 and p=0.05) variation among the genotypes for growth, yield and quality parameters in betel vine. It is indicated that, sufficient genetic variability is present in the betel vine genotypes for various characters studied. Hence, considerable crop improvement can be achieved. The results of the study are in harmony with the findings of Laxmi and Naidu (2010) [10], Hegde *et al*. (2012) [11], Pariari and Imam (2012) [12] and Pradhan *et al*. (2013) [13]. However, analysis of variance by itself is not enough and conclusive to explain all the inherent genotypic variances in the genotypes.

4.2 Coefficients of variation

The phenotypic coefficients of variation (PCV) were found high for plant height, number of laterals per vine, leaf area, petiole length, internodal length, number of spikes, spike length, peduncle length, total yield per vine, total yield per hectare, total chlorophyll, antioxidants and essential oil. Whereas, moderate phenotypic coefficients of variation (PCV) were recorded for number of leaves per lateral, number of leaves per vine, clinging roots, leaf length, leaf width, 100 leaves weight, total phenolics and eugenol. The genotypic coefficients of variation (GCV) were recorded high for number of laterals per vine, leaf area, petiole length, internodal length, number of spikes, spike length, peduncle length, total chlorophyll content, antioxidants and essential oil. Whereas, moderate genotypic coefficients of variation (GCV) were recorded for plant height, number of leaves per lateral, number of leaves per vine, clinging roots, leaf width, hundred leaf weight, total yield per vine, total yield per hectare and eugenol while genotypic coefficient of variation (GCV) recorded low for total phenolics. Earlier researchers like Bekele *et al*. (2017) [14] and Shivakumar*et al*. (2020) [15] in black pepper; Shobha *et al*. (2020) [16] and Chittaragi*et al*. (2022) [17] in curry leaf; Tak and Maurya (2015) [18], Selvakumari and Ponnuswami (2017) [19] and Priya *et al*. (2019) [20] in drumstick had also reported similar phenotypic and genotypic coefficients of variation for different traits under study.

4.3 Heritability

As the genotypic coefficient of variation does not furnish complete details to determine the variations that are heritable nature. Hence, the heritability estimate become inevitable as this governs the variations due to genetic factors. This heritability helps for direct selection of characters, one should concentrate on these traits which are possessing high heritability. In addition to this, Burton (1952) [21] proposed that the GCV along with heritability estimates will provide the clearer image of the improvement to be expected by phenotypic selection. The heritability in broad sense comprises both additive and non-additive gene effects (Hanson *et al.,* 1956) [22].

The estimates of heritability (broad sense) varied from 74.99 to 98.61 per cent for different characters under study. It was found high for the characters *viz.,* plant height, number of laterals per vine, number of leaves per lateral, number of leaves per vine, clinging roots, leaf length, leaf width, leaf area, petiole length, internodal length, number of spikes, spike length, peduncle length, hundred leaf weight, total yield per vine, total yield per hectare, total chlorophyll content, antioxidants, total phenolics, essential oil and eugenol, which indicates that the expression of heritability in these characters might be due to additive gene effects and less influence of environment, suggesting that the simple directional selection would be effective for improvement. These results are in compliance with Bekele *et al*. (2017) [14] and Shivakumar*et al*. (2020) [15] in black pepper; Shobha *et al*. (2020) [16] and Chittaragi*et al*. (2022) [17] in curry leaf; Lakshmi *et al*. (2019) [23], Priya *et al*. (2019) [20] and Varma *et al*. (2019) [24] in drumstick.

High heritability estimates coupled with high genetic advance were observed for plant height, number of laterals per vine, number of leaves per lateral, number of leaves per vine, clinging roots, leaf width, leaf area, petiole length, internodal length, number of spikes, spike length, peduncle length, 100 leaves weight, total yield per vine, total yield per hectare, total chlorophyll content, antioxidants, total phenolics, essential oil and eugenol,which indicated that these characters are under additive gene effects and these characters are more reliable for effective selection. These results are in accordance with Bekele *et al*. (2017) [14] and Shivakumar*et al*. (2020) [15] in black pepper; Shobha *et al*. (2020) [16] and Chittaragi*et al*. (2022) [17] in curry leaf; Lakshmi *et al*. (2019) [23], Priya *et al*. (2019) [20] andBalaguru*et al*. (2020) [25] in drumstick..

4.4 Correlation and path-coefficient analysis

Knowledge of degree of association of yield with its components is of great importance, because yield is not an independent character, but it is the resultant of the interactions of a number of component characters among themselves as well as with the environment in which the plant grow. Further each character is likely to be modified by action of genes present in the genotypes of plant and also by the environment and it becomes difficult to evaluate this complex character directly. Therefore, correlation study of yield with its component traits has been executed, to find out the yield contributing traits.

In the present investigation, at both genotypic and phenotypic level, total yield per vine exhibited positive significant correlation with plant height, number of laterals per vine, number of leaves per lateral, total number of leaves per vine, clinging roots and petiole length at 240 DAL and significant negative correlation with leaf length, leaf width, leaf area, internodal length and hundred leaf weight at 240 DAL. Selection of parameters that are positively associated with yield helps in crop improvement by enhancing the yield of the genotypes. Selection with greater efficiency was practiced through these positively correlated traits on yield. Negatively related traits with yield influence other parameters that are positively correlated with yield factor. Parallel findings were obtained by in Tirkey*et al*. (2019) [26] in betel vine; Kurian *et al.* (2002) [27];Bhagavantagouda*et al*. (2008) [28]; Krishnamurthy *et al*. (2010) [29], Bekele *et al*. (2017) [14] and Preethy*et al*. (2018) [30] in black pepper;Indhumati*et al*. (2020) [31] and Shobha *et al*. (2020) [16] in curry leaf.

Although correlation studies are helpful in determining the components of yield but it does not provide a clear picture of nature and extent of contributions made by number of independent traits. Path coefficient analysis devised by Dewey and Lu (1959) [4], however, provides a realistic basis for allocation of appropriate weightage to various attributes while designing a pragmatic programme for the improvement of yield. Path coefficient analysis depicts the effects of different independent characters individually and in combination with other characters on the expression of different characters on marketable yield per vine.

In the current research, among 11 traits chosen for path analysis which revealed that, at genotypic level, number of laterals per vine at 240 DAL recorded high positive and direct effect on total yield per vine followed petiole length, total number of leaves per vine, leaf area and clinging roots at 240 DAL. Number of leaves per lateral, internodal length, plant height, leaf width and leaf length revealed high negative direct effect on yield per vine (Table 5). Selection for these parameters causes considerable improvement in yield due to positive direct and indirect effect through different traits. Comparable findings were given by Tirkey*et al*. (2019) [26] in betel vine; Shivakumar and Saji (2019) [32]in black pepper; Chittaragi*et al*. (2022 [17]; Selvakumari and Ponnuswami (2017) [19], Karunakar*et al*. (2018) [33] and Varma *et al*. (2019) [24] in drumstick.

Comment [mm2]: Add discussion

Table 1: Analysis of variance (ANOVA) for growth, yield and quality parameters in betel vine genotypes

Sl.No.	Source	Replication	Treatment	Error
	Degrees of freedom	2	36	72
1	Plant height (cm) 240 DAL	984.46*	5450.68**	305.42
2	No. of laterals per vine 240 DAL	0.74**	14.72**	0.14
3	No. of leaves per lateral 240 DAL	0.27	6.16**	0.46
4	No. of leaves per vine 240 DAL	7.03	3360.06**	123.67
5	Clinging roots 240 DAL	1.76	20.55**	1.02
6	Leaf length (cm) 240 DAL	0.08	5.80**	0.36
7	Leaf width (cm) 240 DAL	0.40	3.47**	0.19
8	Leaf area (cm^2) 240 DAL	76.14	807.24**	68.09
9	Petiole length (cm) 240 DAL	0.38	8.23**	0.32
10	Internodal length (cm)	0.01	11.88**	0.14
11	Spike length (cm)	1.35	13.05**	0.33
12	Peduncle length (cm)	0.08*	0.31**	0.02
13	100 leaves weight (g)	31.64	518.39**	31.79
14	Total yield per vine	611.30	35828.51**	552.13
15	Total yield per hectare	0.0170	786.581**	1.327
16	Total chlorophyll content (mg/g)	0.05**	0.31**	0.01
17	Antioxidants (mg/g)	197.29**	941.47**	16.66
18	Total phenolics (mg/100g)	43.37	287.92**	28.80
19	Essential oil (%)	0.33**	0.56**	0.01
20	Eugenol (%)	2.17	20.74**	1.05

Table 2: Mean, coefficient of variation, heritability (broad sense), genetic advance and genetic advance as per cent of mean for various characters of betel vine germplasm 240 DAL

Sl. No.	Characters	Mean	Range		Coefficient of variation		Heritability (%)	Genetic advance (%)	Genetic advance as per cent of mean (%)
			Min.	Max.	Genotypic (%)	Phenotypic (%)			
1	Plant height (cm)	219.44	110.17	270.33	18.87	20.49	84.89	78.61	35.82
2	Number of laterals per vine	7.20	2.33	10.77	29.54	33.12	79.51	3.90	54.26
3	Number of leaves per lateral	11.21	7.93	13.20	12.09	14.24	72.10	2.37	21.15
4	Total number of leaves per vine	184.56	138.53	247.97	17.80	18.79	89.71	64.08	34.72
5	Clinging roots	15.87	11.60	20.12	16.09	17.31	86.41	4.89	30.81
6	Leaf length (cm)	12.66	9.57	14.23	10.63	11.65	83.31	2.53	19.99
7	Leaf width (cm)	7.83	5.93	9.43	13.38	14.46	85.56	2.00	25.49
8	Leaf area (cm^2)	68.12	39.81	90.67	21.91	23.04	90.47	29.25	42.94
9	Petiole length (cm)	6.06	3.47	8.37	26.77	28.37	89.03	3.16	52.04
10	Internodal length (cm)	6.34	3.07	9.69	31.18	31.75	96.46	4.00	63.09
11	Number of spikes	2.41	0.00	3.93	50.52	53.78	88.24	2.36	97.76
12	Spike length (cm)	3.79	0.00	7.33	53.26	59.54	80.01	3.72	98.13
13	Peduncle length (cm)	2.15	0.00	3.37	46.57	46.90	98.61	2.05	95.26
14	Hundred leaf weight (g)	91.33	70.40	110.10	13.94	15.25	83.61	23.99	26.27
15	Total yield per vine(no of leaves per vine)	216.23	145.40	286.80	19.65	20.00	96.59	86.04	39.79
16	Total yield per hectare(lakh leaves per hectare)	32.03	21.54	42.49	19.65	20.00	96.59	12.75	39.79
17	Total chlorophyll content (mg/g)	1.34	0.84	1.88	23.63	24.29	94.64	0.64	47.36
18	Antioxidants (mg/g)	64.28	35.10	93.31	27.31	28.04	94.87	35.23	54.80
19	Total phenolics (mg/100g)	105.51	90.30	131.80	8.81	10.17	74.99	16.58	15.71
20	Essential oil (%)	0.41	0.17	0.65	34.83	35.82	94.56	0.29	69.77
21	Eugenol (%)	15.48	11.07	19.90	16.55	17.82	86.18	4.90	31.65

Table 3: Genotypical Correlation coefficients between different growth and yield components in betel vine germplasm

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
1	1.0000	0.974**	0.910**	0.863**	0.937**	0.0192	-0.1709	-0.0765	0.917**	-0.925**	-0.1111	0.918**
2		1.0000	0.812**	0.943**	0.992**	-0.0183	-0.189*	-0.1050	0.970**	-0.970**	-0.1650	0.988**
3			1.0000	0.956**	0.924**	-0.0073	-0.1750	-0.1121	0.977**	-0.991**	-0.1517	0.827**
4				1.0000	0.887**	-0.207*	-0.339**	-0.286*	0.827**	-0.888**	-0.338**	0.863**
5					1.0000	-0.1447	-0.292*	-0.233*	0.807**	-0.728**	-0.292*	0.887**
6						1.0000	0.778**	0.945**	-0.1655	0.1460	0.859**	-0.1458
7							1.0000	0.983**	-0.301*	0.295*	0.912**	-0.298*
8								1.0000	-0.251*	0.228*	0.857**	-0.237*
9									1.0000	-0.815**	-0.304*	0.814**
10										1.0000	0.279*	-0.925**
11											1.0000	-0.292*
12												1.0000

*Significant at 5 % probability level, **Significant at 1 % probability level, Correlation value=0.2006 (5 %) and 0.2617 (1 %)

1. Plant height 2. Number of laterals per vine 3. Number of leaves per lateral
4. Total number of leaves per vine 5. Clinging roots 6. Leaf length (cm)
7. Leaf width 8. Leaf area 9. Petiole length
10. Internodal length 11. 100 leaf weight 12. Total yield per vine

Table 4: Phenotypic Correlation coefficients between different growth and yield components in betel vine germplasm

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
1	1.0000	0.884**	0.814**	0.771**	0.805**	0.0190	-0.1361	-0.0610	0.794**	-0.822**	-0.0930	0.836**
2		1.0000	0.902**	0.880**	0.908**	-0.0124	-0.1737	-0.0924	0.900**	-0.940**	-0.1434	0.910**
3			1.0000	0.825**	0.832**	-0.0044	-0.1331	-0.0344	0.839**	-0.882**	-0.1160	0.860**
4				1.0000	0.877**	-0.1844	-0.290*	-0.235*	0.898**	-0.939**	-0.289*	0.919**
5					1.0000	-0.1343	-0.256*	-0.188*	0.908**	-0.949**	-0.232*	0.924**
6						1.0000	0.663**	0.805**	-0.1489	0.1307	0.683**	-0.1417
7							1.0000	0.891**	-0.288*	0.258*	0.886**	-0.263*
8								1.0000	-0.221*	0.201*	0.877**	-0.196*
9									1.0000	-0.932**	-0.263*	0.911**
10										1.0000	0.261*	-0.955**
11											1.0000	-0.250*
12												1.0000

*Significant at 5 % probability level, **Significant at 1 % probability level, Correlation value=0.1865 (5 %) and 0.3081 (1 %)

1. Plant height 2. Number of laterals per vine 3. Number of leaves per lateral
5. Total number of leaves per vine 5. Clinging roots 6. Leaf length (cm)
8. Leaf width 8. Leaf area 9. Petiole length
10.Internodal length 11. 100 leaf weight 12. Total yield per vine

Table 5: Genotypic direct and indirect effects on different growth and yield related traits in betel vine germplasm

Traits	1	2	3	4	5	6	7	8	9	10	11	rP
1	**-0.1554**	0.6184	-0.3262	0.2244	0.0786	-0.0013	0.0181	-0.0160	0.2472	0.2257	0.0047	0.918**
2	-0.1513	**0.6350**	-0.3291	0.2454	0.0832	0.0012	0.0200	-0.0220	0.2614	0.2369	0.0070	0.988**
3	-0.1563	0.6442	**-0.3244**	0.2487	0.0857	0.0005	0.0185	-0.0234	0.2635	0.2419	0.0064	0.827**
4	-0.1340	0.5989	-0.3101	**0.2601**	0.0882	0.0137	0.0359	-0.0598	0.2740	0.2485	0.0143	0.863**
5	-0.1456	0.6298	-0.3315	0.2737	**0.0839**	0.0096	0.0308	-0.0487	0.2778	0.2509	0.0124	0.887**
6	-0.0030	-0.0116	0.0024	-0.0538	-0.0121	**-0.0664**	-0.0822	0.1976	-0.0446	-0.0356	-0.0363	-0.1458
7	0.0265	-0.1202	0.0568	-0.0882	-0.0245	-0.0517	**-0.1057**	0.2056	-0.0810	-0.0721	-0.0433	-0.298*
8	0.0119	-0.0667	0.0364	-0.0744	-0.0195	-0.0628	-0.1039	**0.2091**	-0.0677	-0.0557	-0.0438	-0.237*
9	-0.1425	0.6157	-0.3170	0.2643	0.0864	0.0110	0.0318	-0.0525	**0.2696**	0.2478	0.0128	0.814**
10	0.1436	-0.6161	0.3214	-0.2648	-0.0862	-0.0097	-0.0312	0.0477	-0.2736	**-0.2442**	-0.0118	-0.925**
11	0.0173	-0.1048	0.0492	-0.0879	-0.0245	-0.0571	-0.1082	0.2165	-0.0819	**-0.0681**	**-0.0423**	-0.292*

*Significant at 5 % probability level, **Significant at 1 % probability level, Correlation r value= 0.1865 (5 %) and 0.3081 (1 %)
rP- Phenotypic correlation with total yield per vine Residual value – 0.180 **Bold diagonal figures indicate direct effect**

1.Plant height
2. Number of laterals per vine
3. Number of leaves per lateral
4.Total number of leaves per vine
5. Clinging roots
6. Leaf length (cm)
7.Leaf width
8. Leaf area
9. Petiole length
10.Internodal length
11. 100 leaf weight

CONCLUSION

The present investigation thus, showed high variability and diversity among all the genotypes. The correlation and path analysis findings indicated the nature of association and also its extent.

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