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FACTOR ANALYSIS IN CERTAIN WILD GENOTYPES OF *HEVEA BRASILIENSIS*

Saji T. Abraham, Panikkar, A.O.N., George, P.J., Ramesh, B. Nair, Reghu, C.P. and Annamma Varghese, Y.

Rubber Research Institute of India, Rubber Board, Kottayam - 686 009

ABSTRACT

Factor analysis is a useful statistical tool to reduce the total number of characters to be studied by identifying marker characters, which will accommodate the inheritance of a set of associated characters. A pooled factor analysis of 33 variables representing morphological, leaf and bark anatomical characters in the early growth phase of 80 wild genotypes of Natural Rubber (*Hevea brasiliensis*), with the popular clone RRII 105 as control, was carried out in an evaluation trial at the Central Experiment Station of Rubber Research Institute of India. Twelve factors were identified, influencing 12 groups of characters out of the total 33 characters subjected to the analysis.

Of the twelve factors identified, three factors controlled the morphological characters, five bark structural characters and four leaf anatomical characters. The characters identified with maximum factor loadings in each group include girth, total number of leaves per plant, petiole length, inter flush distance, number of stomata and number of epidermal cells per unit area of leaf lamina, single leaf area, thickness of lamina, number of cells per unit length of spongy layer, total bark thickness, total number of latex vessel rows, height of phloic rays, diameter and density of latex vessels. It can be seen that the 12 factors accounted for 82.30% of the total variance, which will sum up the information in the original data of the 33 selected characters. Thus the dimension of the data could be reduced to the 14 variables, controlled by 12 factors. This is of great significance in building up of core collections using data of selected marker characters and also in multivariate studies in germplasm evaluation trials to identify the main factors of divergence.

INTRODUCTION

The rubber plantations in the east, producing a major share of the total production of Natural Rubber, originated from a narrow genetic base. From this small genetic foundation, substantial improvement in productivity has already been achieved. However, there has been a slow down in genetic advance in the recent years, which is attributed mainly to the narrow genetic base. Hence, action was initiated at the international level for enriching the original gene pool by introducing a large quantity of wild germplasm from the center of diversity, in Brazil. These are being conserved, characterized, evaluated and documented in different rubber producing countries including India with the objective of utilizing them for broadening the genetic base and thereby achieving further genetic improvement of *Hevea*. The wild germplasm is a rich source of many potential genes resistant to various biotic and abiotic stresses. Hence, a systematic screening is essential for identification of valuable genotypes for direct use and / or incorporation into the breeding pool.

Evaluation of germplasm introduced and their incorporation in the breeding programmes are the two most important steps involved in broadening the genetic base. Evaluation includes biometric study of the morphological traits (Lesprit and Nouy, 1984) and related characters of individual genotypes. One of the constraints in the successful and quick utilization of the wild germplasm is the delay in characterization, evaluation and cataloguing of the wild germplasm. In the genetic evaluation of the wild germplasm of *Hevea*, large number of morphological and anatomical traits are recorded in the early years of its growth for estimation of the genetic variance, genetic parameters and genetic correlations among these characters. It gives an indication of the genetic worthiness of this wild material, in the immature phase itself. The recording of data on such large number of characters is very time consuming, especially when large number of genotypes evaluated. Interco-relations and interdependence exist among such variables in a multivariate data, which may be due to certain unobservable factors (Rugmini and Balagopalan, 1994). Application of multivariate data analysis has become a popular method mainly because it can provide information not otherwise accessible. Hence, in the present study, a factor analysis by means of principal component analysis method

was carried out to reveal such underlined factors in groups of related variables. Factor analysis is a useful statistical tool to reduce the total number of variables to be studied by identifying marker variables, which will accommodate the inheritance of a set of variables associated with it.

The study was carried out with the objective to analyze sets of related variables for identifying principal factors of divergence so as to short list the variables to be studied, in the future evaluation programmes involving genetic divergence estimations and for establishment of core collections from large number of wild accessions.

MATERIALS AND METHODS

Eighty genotypes belonging to the 1981 International Rubber Research and Development and Board (IRRDB) collection of wild *Hevea* germplasm planted in a field evaluation trial in 1992 at the Central Experiment Station, Chethakal was used for this study. The popular clone RRII 105 was used as the control. The selected genotypes represented accessions from the three provinces of Brazil - Acre (AC), Rondonia (RO) and Mato Grosso (MT) with 25, 27 and 28 genotypes respectively (Table 1).

Genotypes were planted in a simple lattice design with 4 replications and 4 plants per plot in 2.5 x 2.5m spacing. In the first year after planting, morphological characters like girth, height, number of leaf whorls and total number of leaves per plant, inter-whorl distance, length of the petiole, total leaf area and leaf area index were recorded. In the third year after planting, data on number of stomata and number of epidermal cells per mm^2 of the leaf surface, stomatal index, leaf structural characters like thickness of the leaf blade, midrib, palisade layer and spongy layer of cells, number of cells per 0.01mm length of the palisade and spongy layers, thickness of the epicuticular wax layer and single leaflet area were recorded. In the same year, bark structural characteristics viz., bark thickness, thickness of soft bark and hard bark, number of latext vessel rows of soft bark and hard bark regions, total number of latex vessel rows, average distance between the latex vessel rows in the soft bark region, density of latex vessels per row per mm circumference of the plant, diameter of the latex vessels, total cross sectional area of the latex vessels, frequency, length, width and length-width ratio of the phloic rays were recorded.

Factor analysis was done using principal component analysis method since it is used widely (Harman, 1976 and Rencher, 1998). The factors were subjected to varimax rotation.

RESULTS AND DISCUSSION

Factor analysis refers to the statistical techniques whose common objective is to represent a set of variables in terms of a smaller number of hypothetical variables. Hence, the complexity of recording, analyzing and interpreting a host of multivariate data in field experiments, especially in a perennial tree crop like rubber, can be lessened by adopting factor analysis whereby the breeder benefits from this character reduction technique, to concentrate on selected independent marker characters which also represents other characters related by their likeness in inheritance. This will be of great importance in the development of core collections of wild *Hevea* germplasm from the available large gene pool.

Factor analysis is the most common method used for identifying the factors of divergence in a multivariate data. In this study, a pooled set of 33 characters representing the morphological, leaf and bark anatomical characters in the wild *Hevea* germplasm used for factor analysis to get a set of reduced number of new orthogonal variables. Mydin (1992) reported factor analysis in two genetically divergent clusters of Wickham clones wherein the yield factors comprising dry rubber yield, latex flow rate, volume of latex, length of tapping panel and plugging index were identified as the main factors of divergence.

Factor analysis carried out in the above set of variables identified 12 factors, which accounted for 82.30% variability in these 33 variables. It should be stressed that this method estimates only mathematical associations among the multivariates. The most important aspect is that this should be supplemented with biological interpretation of these associations, which should

Table 1. List of the 80 wild genotypes selected for the study

Sl. No.	National Accession number	International genotype code	Sl. No.	National Accession number	International genotype code
1	AC 426	AC/F/5/117	41	RO 369	RO/C/8/130
2	AC 453	AC/F/5/220	42	RO 380	RO/C/8/177
3	AC 604	AC/S/11/1	43	RO 381	RO/C/8/179
4	AC 624	AC/S/11/107	44	RO 395	RO/C/8/302
5	AC 626	AC/S/11/111	45	RO 399	RO/C/8/327
6	AC 627	AC/S/11/113	46	RO 859	RO/CM/12/26
7	AC 629	AC/S/11/155	47	RO 868	RO/CM/12/44
8	AC 632	AC/S/11/198	48	RO 876	RO/CM/12/91
9	AC 644	AC/S/11/282	49	RO 879	RO/CM/12/100
10	AC 647	AC/S/11/327	50	RO 883	RO/CM/12/110
11	AC 650	AC/S/11/348	51	RO 886	RO/CM/12/115
12	AC 654	AC/S/9/5	52	RO 894	RO/CM/12/136
13	AC 657	AC/S/10/15	53	MT 899	MT/IT/16/2
14	AC 706	AC/S/12/18	54	MT 901	MT/IT/16/6
15	AC 733	AC/S/10/21	55	MT 906	MT/IT/16/12
16	AC 754	AC/S/10/79	56	MT 920	MT/IT/16/81
17	AC 953	AC/F/6B/11	57	MT 922	MT/It/16/94
18	AC 959	AC/F/6B/21	58	MT 929	MT/IT/16/135
19	AC 963	AC/F/6B/27	59	MT 931	MT/It/16/138
20	AC 966	AC/F/6B/35	60	MT 935	MT/IT/16/174
21	AC 979	AC/F/6B/79	61	MT 944	MT/IT/16/208
22	AC 986	AC/F/6B/104	62	MT 945	MT/IT/16/210
23	AC 995	AC/F/6B/169	63	MT 947	MT/IT/16/212
24	AC 1043	AC/S/12/365	64	MT 948	MT/IT/16/213
25	AC 1090	AC/F/6A/121	65	MT 1005	MT/C/1/60
26	RO 254	RO/OP/4/12	66	MT 1007	MT/C/1/68
27	RO 255	RO/OP/4/15	67	MT 1008	MT/C/1/69
28	RO 256	RO/OP/4/27	68	MT 1011	MT/C/1/75
29	RO 257	RO/OP/4/49	69	MT 1021	MT/C/1/91
30	RO 287	RO/OP/4/139	70	MT 1024	MT/C/1/99
31	RO 311	RO/C/9/127	71	MT 1025	MT/C/1/102
32	RO 316	RO/C/9/141	72	MT 1028	MT/C/1/108
33	RO 317	RO/C/9/142	73	MT 1029	MT/C/1/109
34	RO 319	RO/C/9/152	74	MT 1030	MT/C/1/113
35	RO 322	Ro/C/9/157	75	MT 1031	MT/C/1/116
36	RO 328	RO/C/9/174	76	MT 1055	MT/C/10/20
37	RO 330	RO/C/9/179	77	MT 1057	MT/C/10/24
38	RO 338	RO/C/9/203	78	MT 1063	MT/C/10/94
39	RO 352	RO/C/9/308	79	MT 1064	MT/C/10/102
40	RO 364	RO/C/8/98	80	MT 1077	MT/C/7/37

be done based on logics. All the variables were grouped with respect to the factors identified and marker variables were identified based on the factor loadings for each character (Table 2 and 3). In the present study, the first factor was found to be associated with six of the growth characters - height, girth, number of leaf flushes/plant, total number of leaves per plant, total leaf area and leaf area index with factor loadings of 0.8439, 0.8793, 0.9067, 0.9630, 0.9482 and 0.9475 respectively. This factor had the maximum contribution of 18.1% to the total variance. All these six variables can be expected to behave alike in their inheritance, as a single factor is believed to control the inheritance of these variables. Of these variables, the maximum factor loading was recorded for the total number of leaves per plant, which could be treated as a marker variable in this group representing all the other five variables in any future study involving these variables. However, girth of the plants has to be singled out even though it comes alongwith the other five growth characters, as the uniqueness of girth as the most important indicator of vigor in rubber has been proved beyond doubt.

The second factor was found to be associated with a set of five bark structural characters viz. - number of latex vessel rows in the hard bark and in the soft bark, total number of latex vessel rows in the bark, average distance between the latex vessel rows in the soft bark and laticifer area index contributing 12.2% of the total variance. Total number of latex vessel rows was identified as the marker character to represent the remaining four structural traits, as it carried the maximum factor loading of 0.9531.

Factor three with 9% contribution to the total variance was associated with the characters related to the thickness of the bark i.e., total bark thickness, thickness of the soft bark and hard bark. Here, total bark thickness was found to have the maximum factor loading of 0.9409 and can represent the thickness of soft bark and hard bark in their inheritance pattern.

Two leaf structural characters identified with the factor four were the number of epidermal cells per unit area of leaf lamina and stomatal index contributing 7.5% to the total variance. Number of epidermal cells per unit area had a factor loading of 0.9266 and hence can be identified as the marker character.

Four of the important leaf structural traits - thickness of the lamina, thickness of leaf midrib, thickness of palisade and thickness of spongy layers - were associated with the factor five, accounting for 6.5% of the variance. Thickness of the lamina could be identified as the marker trait in this group with the maximum factor loading of 0.9045.

Factor six was associated with two traits - petiole length and single leaflet area. These two traits contributing 5.5% of the total variance, carried almost equal factor loadings of 0.7530 and 0.7590 respectively and may be considered as two independent traits as the factor seems to have an equal control in their inheritance.

Three leaf structural traits were associated with the factor seven viz. number of cells per unit length of palisade layer and spongy layer and thickness of the cuticle. The maximum factor loading (0.7706) was for the number of cells per unit length of spongy layer, identifying it as the prominent character among the three variables. This factor also had a similar contribution like the previous factor with 5.3% contribution.

Factor eight was associated with the width of phloic rays and diameter of latex vessels, more factor loading (0.8917) being for the diameter of latex vessels which becomes the marker character in this group. This factor accounted for 4.6% variance. Height of phloic rays and the height/ width ratio of phloic rays were associated together by the ninth factor with a contribution of 3.7% and the height of phloic rays having more factor loading (0.8515). Factor ten contributing 3.6% to the total variance, was associated with a single character - the inter-flush distance with a loading of 0.8208, which can be considered as an independent trait. Frequency of phloic rays and density of latex vessels were associated together with the next factor, which accounted for 3.2% variance and more factor loading was seen for density of latex vessels (0.8490). The last factor was associated with only a single character, the number of stomata per unit area of the lamina, with a factor loading of 0.9501 contributing 3.2% of the total variance.

Table 2. Factor loadings of the pooled characters

SL. No.	Character	Factor Loadings											
		F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12
1	Girth of the plants (cm)	0.8439	0.0978	0.1094	-.0093	-.0009	0.2675	0.0858	-.0067	0.0122	0.0517	0.0067	0.0172
2	Height of the plants (cm)	0.8793	0.0304	0.0559	-.0591	-.0252	0.0680	0.0111	-.0134	-0.050	0.3135	-.0172	0.0148
3	Number of leaf flushes/plant	0.9067	0.0782	-.1407	-.798	0.0525	-.1215	0.0057	-.0523	0.0446	-.0775	0.0147	-.0119
4	Total number of leaves/plant	0.9630	0.0880	-.1407	-.0307	0.0240	0.0521	0.0450	0.0363	-.0078	-.0920	-0.022	-.0638
5	Total leaf area (cm^2)	0.9482	-0.0440	0.0157	0.0590	0.0019	0.1511	0.0314	0.0398	-.0498	0.0050	0.0060	0.0378
6	Leaf area index	0.9475	-.0400	0.0161	0.0576	0.0018	0.1489	0.0312	0.0405	-.0469	-.0006	0.0089	0.0419
7	Inter flush distance (cm)	0.0143	-.1876	0.1905	0.0393	-.1268	0.1806	0.0475	0.0546	0.0348	0.8208	-.0408	0.0624
8	Petiole length (cm)	0.1590	-.0178	-.2217	-.0401	0.1068	0.7530	0.0962	0.1048	0.1881	0.1829	0.0457	-.0743
9	No. of stomata/mm^2 of leaf area	0.0245	-.0294	0.0109	-.0191	0.0364	-.0759	0.0923	-.0233	0.0048	0.0354	0.0032	0.9501
10	No. of epidermal cells/mm^2 of leaf area	-.0050	-.0218	-.0419	0.9266	0.0373	-.0222	0.0026	-.0572	-.0353	0.0175	0.0488	0.2730
11	Stomatal index	0.0138	0.0175	0.0879	-0.8758	0.0072	-.0617	0.0750	0.0536	0.0269	-.0145	-.0614	0.4015
12	Single leaflet area (cm^2)	0.3586	0.0118	-.0183	0.0499	0.0062	0.7590	-.0792	-.0941	0.0996	0.0570	-.0897	-.0850
13	Thickness of leaf blade (µm)	0.0851	0.0503	0.0964	0.1655	0.9045	-.0365	0.0371	-.0835	-.0838	.07585	-.1410	-.0335
14	Thickness of midrib (mm)	-.1861	-.1124	0.1762	0.0006	0.5597	0.0533	0.2069	0.1180	0.0243	-.4430	0.0622	0.1628
15	Thickness of palisade layer (µm)	0.0890	0.1763	0.0712	0.3852	0.5530	-.1844	-.3791	0.0057	-.3108	0.1104	-.1803	-.1341
16	Thickness of spongy layer (µm)	0.0050	-.0278	-.0117	-.2086	0.7795	0.1697	0.1398	0.1019	-.0506	-.1887	0.0268	0.0530
17	No. of cells/mm of palisade tissue	-.0643	0.1465	-.2434	-0.0647	-.0226	-.1769	0.5930	0.0820	0.1661	-.0773	-.1974	0.1912
18	No. of cells/mm of spongy tissue	0.1338	0.1389	-.0257	0.1363	0.2340	0.0420	0.7706	-.1439	0.1041	0.0010	-.1538	0.0426
19	Thickness of cuticle (µm)	-.1384	0.2179	-.0757	0.1652	-.0195	-.0617	-0.7021	0.0768	0.1314	-.0831	-.2210	0.0542
20	Total bark thickness (mm)	0.0142	0.2047	0.9409	-.0425	0.0824	-.0195	-.0551	-.0151	-.0169	.0507	0.0444	0.0842
21	Soft bark thickness (mm)	0.2001	0.1480	0.5214	0.0074	0.0252	0.4545	-.1377	-.1250	-.1055	-.1506	-.0978	0.2288
22	Hard bark thickness (mm)	-.0817	0.1666	0.8427	-.0525	.0842	-.2427	0.0027	0.0434	0.0301	0.1332	0.0995	-.0129
23	No. of latex vessels in hard bark	0.0113	0.7759	0.1494	0.0534	0.0331	0.0124	-.0197	0.1819	-.0091	0.0355	0.0163	-.1606
24	No. of latex vessels in soft bark	0.0697	0.8861	0.1375	0.0017	0.0460	-.0976	-.0408	-.0793	-.0501	-.0518	0.0228	0.0963
25	Total no. of latex vessel rows	0.0391	0.9531	0.1492	0.0298	0.0391	-.0405	-.0310	0.0235	-.0526	-.0184	0.0226	-.0069
26	Density of latex vessels/mm circumference	0.0130	0.1363	0.1194	0.0329	-.1271	-.0992	0.0102	-.0253	0.1312	-0.062	0.849	-.0209
27	Diameter of latex vessels (µm)	0.0825	0.1031	-.1009	-0.1813	0.0543	-.0211	-.1135	0.8917	0.0358	0.1055	0.0015	-.0098
28	Total CSA of latex vessels (mm^2)	0.3421	0.6400	0.0542	-.0611	-.0146	0.0204	-.0514	0.5295	0.0338	0.0530	0.3087	0.0085
29	Av. distance between latex vessels (mm)	0.0448	-0.6477	0.0602	0.1508	0.1278	-.2296	-.2021	0.1213	0.0604	0.2012	-.0893	-.0538
30	Frequency of phloic rays/0.01mm^2 area	-.0850	0.1216	-.0604	0.1075	0.0285	0.1127	-.2457	0.0110	-.4873	-.0642	0.4916	0.0522
31	Height of phloic rays (mm)	-.1558	-.0790	0.0346	0.0890-1399		0.2292	0.0236	0.1608	0.8515	-.0535	0.0195	-.0100
32	Width of phloic rays (mm)	-.2340	-.1006	0.1838	0.4233	-.0034	0.0034	-.0136	0.6111	-.0877	-.3929	-.1894	-.0350
33	Height/width ratio of phloic rays	.0698	-.0269	-.1663	-.2843	-.0644	0.0889	-.0072	-.3670	0.7154	0.2946	0.2590	0.0631

Table 3. Distribution of various characters among the 12 factors identified

Factor	Per cent of variance	Characters associated
1	18.1	**Total no. of leaves** (0.9630), **girth** (0.8439), height (0.8739), no. of leaf whorls (0.9067), total leaf area (0.9482) and Leaf area index (0.9475)
2	12.2	**Total no. of latex vessel rows** (0.9531), Latex vessels in hard bark (0.7759), LV in soft bark (0.8861), average distance between latex vessel rows in soft bark (0.6477), total cross sectional area of latex vessels (0.6400)
3	9.0	**Bark thickness** (0.9409), thickness of soft bark (0.5214), thickness of hard bark (0.8427)
4	7.5	**No. of epidermal cells per unit area of leaf lamina** (0.9266), stomatal index (0.8758)
5	6.5	Thickness of - lamina (0.9045), midrib (0.5597), palisade layer (0.5530) and spongy layers (0.7795)
6	5.5	**Length of petiole** (0.7530), **Single leaflet area** (0.7590)
7	5.3	No. of cells per unit length of - **spongy layer** (0.7706), palisade layer (0.5930) and thickness of cuticle (0.7021)
8	4.6	**Diameter of latex vessels** (0.8917) and width of phloic rays (0.6111)
9	3.7	**Height of phloic rays** (0.8515) and height/width ratio of phloic rays (0.7154)
10	3.6	**Inter flush distance** (0.8205)
11	3.2	**Density of latex vessels** (0.8490), frequency of phloic rays (0.4916)
12	3.2	**No. of stomata per unit area of leaf lamina** (0.9501)

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