Table 3. **Spectral reflectance (%) in four bands for *kharif* rice varieties at flowering stage (60 DAT)**

Varieties	Blue	Green	Red	Infra red
ASD 18	9.87	11.86	11.21	65.90
ADT 36	9.68	12.05	7.24	73.82
IR 50	10.37	12.78	10.87	71.37
IR 60	9.23	12.30	14.34	59.91
IR 64	11.84	13.50	5.71	84.21
JJ 92	10.57	11.22	10.84	67.60
TKM 9	9.61	11.35	12.07	61.71
CO 37	10.56	13.17	6.36	76.48
SEd	1.22	1.13	0.71	2.82
CD (0.05)	2.73	2.43	1.52	6.06

Table 4. **Vegetation indices for *kharif* rice varieties computed at flowering stage (60 DAT)**

Varieties	IR/R	IR-R	ND	TVI	PVI
ASD 18	8.59	65.52	0.79	1.14	51.97
ADT 36	9.98	68.68	0.72	1.10	51.41
IR 50	5.99	55.19	0.71	1.10	48.84
IR 60	6.01	55.52	0.43	0.96	48.41
IR 64	11.76	77.00	0.84	1.16	52.03
JJ 92	7.97	63.32	0.58	1.03	47.57
TKM 9	8.77	62.00	0.58	1.04	48.95
CO 37	8.33	67.01	0.79	1.13	53.79
SEd	0.82	2.95	0.05	0.03	3.04
CD (0.05)	1.75	6.32	0.11	0.06	6.51

SUMMARY

The spectral studies conducted with ground truth radiometer demonstrated the potentiality of discriminating important *kharif* rice varieties *viz.,* ADT 36, IR 50, IR 60 and JJ 92. The best period of discriminating the rice varieties is the flowering stage (60 DAT). Red and infrared bands and vegetation indices like IR/R and IR-R were more effective in the discrimination study. However, these findings have to be confirmed with satellite data before satellite based remote sensing is employed for the identification of rice varieties in the command areas.

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GENETIC ANALYSIS IN A DIALLEL CROSS OF INBRED LINES OF CASSAVA

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ABSTRACT

A study to determine gene action, heritability and number of effective genes controlling 13 traits utilizing Jinks - Hayman diallel analysis of the populations raised by a 6x6 diallel cross of fourth generation inbred lines of cassava showed that overdominance governed most of the traits including yield and yield components. The number of gene groups controlling various traits was estimated and root yield was found to be controlled by 3 gene groups. Very low narrow sense heritability obtained for yield and its components also revealed the preponderance of non-additive gene action. The (Vr, Wr graph confirmed the role of overdominance for yield and its major components. The standardised deviation graph was used to identify superior parents. The study indicated the possibility of genetic improvement in cassava through heterosis breeding.

KEY WORDS : Cassava, diallel, overdominance, yield components

Cassava (*Manihot esculenta* Crantz) is a subsidiary food crop of vital importance for nearly 500 million people of the tropics. In addition to its use as human food, cassava serves as an ideal substitute for carbohydrates in animal feed and as raw material for various industries. In a world of shrinking agricultural land, cassava also is confronted with considerable fall in the cultivated area necessitating the development of high yielding varieties to increase the productivity of the crop. Eventhough several high yielding hybrids have been released in cassava, information on the genetic systems controlling complex traits like yield and quality are still obscure. Cassava shares a common gene pool in the genus *Manihot* and free gene flow among the species made it highly heterozygous and unsuitable for direct genetic studies. It is in this context that the efforts of the Central Tuber Crops Research Institute for the production of successive generation of inbred lines of cassava assumes significance. The inbred lines being reasonably homozygous, forms the ideal material for genetic studies. A diallel cross of cassava involving 6 fourth generation inbred lines as parents was employed to ascertain the gene action for root yield and yield attributing characters of cassava.

MATERIALS AND METHODS

Three indigenous and two exotic accessions of cassava formed the original parents (S_0 parents) of the inbred lines used in the diallel cross. Interclonal plants of these accessions were subjected to four successive cycles of selfing to raise the fourth generation inbred lines. Six S_4 lines designated as P_1, P_2, P_3, P_4, P_5 and P_6 and their all possible 30 F_1 hybrids including reciprocals formed the materials for this study. Fifty plants from ten randomly selected first clonal genotypes from each of the 30 cross combinations and the inbred parents were grown in a randomised block design with two replications in 1991-92. The package of practices recommended by the Central Tuber Crops Research Institute was followed for raising the experimental material. Observations on 13 metric traits were recorded from 5 randomly selected plants per treatment per replication. The data were subjected to analysis of variance and test of significance to meet the pre-requisite for further analysis. The genetic parameters *viz.*, D, F, H1, H2, h^2, E and the standard ratios of these genetic parameters were worked out by component of variance method using the 2nd degree statistic and error mean square. The data for root yield and yield components were also subjected to (Vr, Wr) graph analysis following Jinks and Heyman (1953) and Hayman (1954, 1957). Analyses of parental mean (Vr) and parental order of dominance (Wr + Vr) as standardised deviation graph were done following Johnson and Aksel (1959).

RESULTS AND DISCUSSION

The non significant t^2 values indicated the adequacy of the model for all the traits except

Table 1. Estimates of genetic parameters in the F_1 of a diallel cross of inbred lines of Cassava

Characters	D	F	H_1	H_2	h^2	E
Height at first branching	108.16** ± 29.75	119.15 ± 72.68	252.08** ± 75.52	203.26** ± 67.46	151.73** ± 45.41	5.76 ± 11.24
Plant height	481.69** ± 84.42	520.67*± 206.23	949.53 ± 214.30	798.27** ± 191.44	1736.36** ± 128.85	21.61 ± 31.91
Petiole length	6.48** ± 0.75	1.19 ± 1.83	12.21** ± 1.90	10.11** ± 1.70	20.56** ± 1.14	1.07** ± 0.28
Length of middle leaflet	4.37** ± 0.32	-0.59 ± 0.78	1.12 ± 0.81	1.02 ± 0.72	0.74 ± 0.49	0.36** ± 0.12
Breadth of middle leaflet	0.59** ± 0.06	0.01 ± 0.15	0.53** ± 0.15	0.43** ± 0.14	0.28** ± 0.09	0.05* ± 0.02
Spread of foliage	343.98** ± 48.57	26.83 ± 118.66	929.90** ± 123.30	767.57** ± 110.15	1262.55** ± 74.14	44.75* ± 18.36
Number of roots	-0.12 ± 0.36	-1.16 ± 0.87	3.42** ± 0.91	3.09** ± 0.8	10.58** ± 0.54	0.50** ± 0.13
Length of root	15.66** ± 1.62	11.45** ± 3.96	25.31** ± 4.11	23.70** ± 3.67	86.54** ± 2.47	2.15** ± 0.61
Girth of root	0.42* ± 0.19	-0.18 ± 0.46	0.78 ± 0.48	0.71 ± 0.42	1.32** ± 0.29	0.38** ± 0.07
Mean weight of root	328.21±844.39	915.11±2062.84	4597.13*±2134.56	4473.81*±1914.89	7611.81**±1288.85	855.34**±319.15
Total biomass	0.46** ± 0.13	0.09 ± 0.31	1.24** ± 0.32	1.19 ± 0.28	3.56** ± 0.19	0.06 ± 0.05
Harvest index	-0.51 ± 13.96	8.79 ± 34.10	95.22** ± 35.44	72.81* ± 31.66	133.01** ± 21.31	20.61** ± 5.28
Root yield	0.04 ± 0.05	-0.12 ± 0.13	0.46** ± 0.13	0.45** ± 0.12	1.33** ± 0.08	0.04* ± 0.02

* Significant at 5% level ; ** Significant at 1% level

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Table 2. Ratios of Genetic Parameters in the F_1 of a diallel cross of inbred lines of cassava

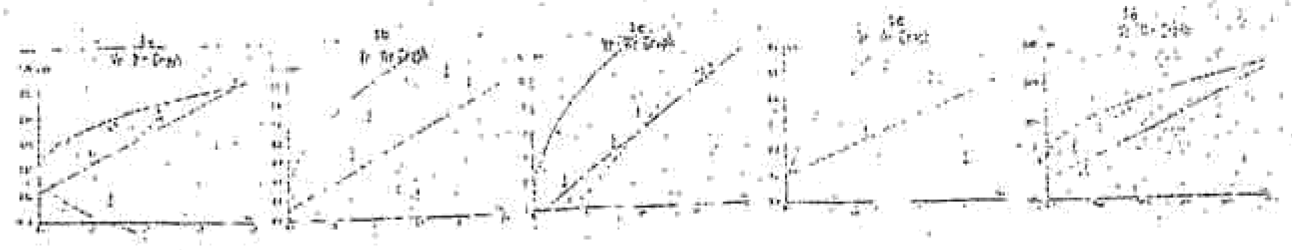
Characters	$(H1/D)^{1/2}$	H2/4HI	K.D./K.R.	h^2/H2	h^2	(Wr + Vr) Vs Yr
Height at first branching	1.53	0.20	2.13	0.75	40.95	-0.35
Plant height	1.40	0.21	2.25	2.18	48.32	-0.58
Petiole length	1.37	0.21	1.14	2.03	29.75	-0.21
Length of middle leaflet	0.51	0.23	0.76	0.73	58.26	-0.77
Breadth of middle leaflet	0.94	0.20	1.02	0.66	45.93	-0.32
Spread of foliage	1.64	0.21	1.05	1.64	24.12	-0.19
No.of roots	0.00	0.23	0.00	3.42	-1.87	-0.01
Length of root	1.27	0.23	1.81	3.65	41.09	- 0.97**
Girth of root	1.36	0.23	-1.72	1.85	14.50	-0.34
Mean weight of root	3.74	0.24	0.46	1.70	3.54	-0.65
Total Biomass	1.64	0.24	1.13	2.99	25.14	-0.83
Harvest index	0.00	0.19	0.00	1.83	-0.30	-0.69
Root yield	3.44	0.25	0.37	2.95	5.05	-0.65

** Significant at 1% level

length of root. The regression of Wr on Vr did not deviate significantly from unity, but did so from zero for petiole length, breadth of middle leaflet, spread of foliage and total biomass indicating the absence of non allelic interaction for these traits. The genetic parameters were estimated using the F_1 means of 30 crosses and 6 parents and presented in tables 1 and 2.

The component of variation due to additive effect, D was found to be highly significant for all the characters except stem girth, number of roots, mean weight of roots, harvest index and root yield. The 'F' component was significant only for plant height and length of roots. The positive sign of F for majority of the traits indicated a greater frequency of dominant alleles in the parents for those traits. However, yield and its components like number of roots and girth of roots were found to be governed by recessive alleles than by dominant ones. The dominant genetic variance parameters H1 and H2 were also significant for all the traits other than stem girth, length of middle leaflet and girth of roots. H1 was greater than H2 for all the traits indicating that the positive and negative alleles at the loci for these traits were not equal in proportion in the parents. H1 was also greater than D in most of the cases. This suggests that dominant genetic variance (overdominance) was more important for most of the traits than additive genetic variance. The estimate of the component, h^2 which shows the net dominance effect was significant for all the traits except length of middle leaflet. The environmental component of variation, E, was found to play an important role for majority of the traits.

Various genetic ratios were calculated to provide further information about gene action. The value of $(H1/D)^{1/2}$ reveals mean degree of dominance over all loci. With average partial dominance this value is expected to fall within the range of 0 to 1 and with overdominance to be 1. In this study, it ranged from 0 to 3.74 for different traits with 9 of the 13 traits studied including the major yield and yield components being in the overdominance range. The ratio H2/4HI indicated that the parents were with asymmetrical distribution of positive and negative alleles as the ratio is not equal to 0.25 for most of the traits. Interestingly, symmetrical distribution of positive and negative alleles was noticed for root yield. However, the proportion of dominant and recessive alleles was lesser in controlling yield and yield components *viz.*, number of roots, girth of roots and mean weight of roots as indicated by the ratio KD/KR being less than 1. This was also confirmed by the negative sign of F estimates for these traits. The ratio h^2 / H_2 determines the number of gene groups that control the trait. At least, 3 gene groups were found to control root yield and total biomass as the ratio being nearest to 3, whereas 4 gene groups were involved in the inheritance of number and length of roots.



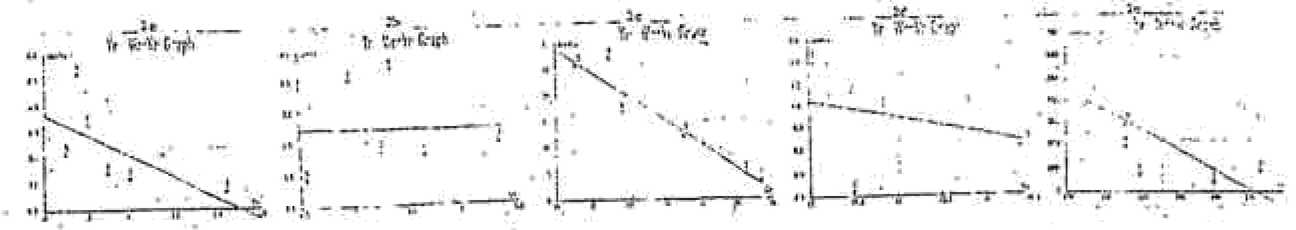


Fig. 1. Wr-Vr graphs for Root yield and its componants in Cassava.

Fig. 2. Yr, Wr+Vr standardized deviation graphs for Root yield and its components in Cassava.
(a - Root yield, b - No. of roots, c - Length of root, d - Girth of root, e - Mean weight of root)

The narrow sense heritability was estimated to be very low for root yield (5.05) and its major components. This further confirmed the nonadditive gene action indicating the scope for exploitation of heterosis in cassava. The negative sign of 'r'' for all the characters other than breadth of middle leaflet indicates that dominance operated in positive direction for these traits.

The graphical analysis provides information about the additive dominance model, the average degree of dominance and characterises the parents containing most of the dominant and recessive genes. In the present study, the graphical analysis was also carried out to unravel the nature of gene action for yield and its major components in cassava. The (Vr, Wr) graph for root yield (Fig.1a) on cassava revealed overdominance as the regression line had cut the Wr axis below the point of origin. This was confirmed by the mean degree of dominance being more than one (3.44). The array points 1 and 2 are nearer to the origin. Therefore these parents appear to posses most of the dominant genes for root yield. On the other hand, points of arrays 5 and 6 are away from the origin indicating that these parents posses most of the recessive genes with regard to this trait. However, the standardised deviation graph (Fig.2a) shows that the recessive genes governing yield in these arrays (5 and 6) have positive effect leading to increase in yield. The dominant genes in array 1 acted in the negative direction. The recessive genes in parents 5 and 6 and the dominant genes in parents 2 and 3 mainly contributed for the increase in yield.

The important yield components viz. number of roots (Fig. 1 b), length of root (Fig. 1 c) and mean weight of root (Fig 1e,) also exhibit overdominance. The proportion of dominant genes was higher in arrays 4 and 1 for number of roots, in 3 for length of root and in 1, 2 and 6 for mean weight of root. The parents 2 and 6 ; 5,4 and 6 and 5 respectively possessed most of the recessive genes with regard to these characters. However, the standardised deviation graphs showed that the recessive genes in array 6 for number of roots and length of root were positive while the dominant genes in arrays 1 and 6 for mean weight of root functioned in the negative direction (Fig. 2e). Of all the yield components, only girth of root showed partial dominance (Fig. 1d). For this traits, the proportion of dominant genes is maximum in array 3 and they are positive in nature (Fig.2d).

The study on standardised deviations showed that the parent 3 possessed dominant genes having positive effects for all the traits.

Combining ability analysis in cassava (Easwari Amma *et al.*, 1995) also revealed P3 as the best general combiner for root yield. The parents 5 and 2 had higher proportion of genes having positive effects irrespective of whether they are dominant or recessive in nature. In general, the parents 5, 3 and 2 are better than the other inbred lines.

The present study revealed the predominance of non-additive gene action emphasizing the role of overdominance in the expression of yield and its components in cassava. Therefore, crop improvement in cassava through a hybrid breeding programme to exploit heterosis would be a paying prospective. With respect to the choice of parents inclusion of inbred parents P2, P3 and P5 appears to be beneficial.

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BIOMASS PRODUCTION AND NITROGEN ACCUMULATION OF VELVET BEANS, SUNNHEMP AND PILLIPESARA AS INFLUENCED BY PLANT DENSITY AND PHOSPHORUS APPLICATION

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ABSTRACT

Field experiments were conducted at Tamil Nadu Agricultural University during the NEM season of 1993-94 and SWM season of 1994 to study the effect of different spacings and phosphorus application on biomass production and nitrogen (N) accumulation of three green manure crops, pillipesara, sunnhemp and velvet beans. Velvet beans produced the highest biomass of 27.6 t/ha in the SWM season followed by Sunnhemp and pillipesara. Biomass production and N accumulation were higher at closer spacing (30x20cm). Application of 50 kg P_2O_5/ha significantly increased the growth of all the three crops. Interaction between spacing and P levels was significant and highest biomass (10.0, 11.2 and 35.9 t/ha for pillipesara, sunnhemp and velvet beans respectively) was achieved in the treatment combination of 50 kg P_2O_5/ha and closer spacing (30 x 20 cm). Velvet beans and sunnhemp produced higher biomass in SWM season (27.6 and 10.1 t/ha) while NEM season was more favourable for pillipesara (8.5 t/ha).

KEY WORDS : Velvet beans, sunnhemp, pillipesara, biomass, N accumulation