DIALLEL ANALYSIS FOR SEED YIELD AND ITS COMPONENT TRAITS IN *CUPHEA PROCUMBENS*

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The *Cuphea procumbens* Orteg. is an important annual plant source of medium chain fatty acids. The present study was conducted to estimate different gene systems involved in the inheritance of important quantitative traits viz. plant height, branches/plant, fruits/plant, seeds/fruit and seed yield/plant in F_1 and F_2 generations following 6 parents half diallel. Diallel assumptions were fulfilled for all the characters. Wr-Vr graph and component analysis revealed the major influence of over dominance for all the traits except branches/plant in F_1. The arrays scattered all along the regression line below limiting parabola in two groups, Dominance and recessive and was confirmed by standardized deviation graph. The ranking on the basis of breeding value (Yr) of the parents and per se performance was closely associated (r=0.83**). On the basis of ranking, parents 'NBC-01', 'NBC-25' and 'NBC-30' were found most promising and possessed more dominant alleles for most of the characters. Considering the gene action involved, the breeding plan was discussed

Key words: *Cuphea*, diallel, regression coefficient, combining ability, gene action, over-dominance

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INTRODUCTION

Vegetable oils and fats are an important source of human nutrition. Medium chain fatty acids (MCFA) are nutritionally more important than long chain fatty acids (LCFA). Short and medium chain fatty acids are easily absorbed for quick energy and contribute to health immune system (SINGH and RAMESHKUMAR 2003, RAMESHKUMAR and SINGH 2004). Research has indicated that heart disease; breast cancer and colon cancer are reduced when medium chain triglyceride (MCTG) are used as primary dietary lipid source (BABAYAN 1987; BACH and BABAYAN 1982; DEHESH 2001)). At present use of MCTGs in human diets is restricted because of high cost of synthesizing MCTG and lack of proper source. So developing an alternative cheep and renewable source can enhance the use of MCTG in human diet, which are essential for human well being (KABARA, 2000; THOMPSON, 1984).

At present coconut and palm kernel oils are only commercial source of lauric acid (C12: 1), which is perennial and restricted to specific ecogeographical region and has less scope for genetic improvement. The other MCTG caprylic acid (C 8:0) and capric acid (C10:0) are not found in above two species and are derived from either petrochemicals or by fractionating coconut and palm kernel oil, which is costly. Due to erratic and uncertain supply of medium chain fatty acids to the world market, possibilities have been explored for alternative annual crops to meet the demand of these fatty acids (ROBBELIN and HIRSINGER 1982; KHANNA and SINGH 1991) and number of species of *Cuphea* were discovered to possess dominant fatty acids in range of C8:0 to C14:0 and caught world wide attention for domestication and improvement. Some species have more than 70 percent of only one type MCFA. So lauric acid (C12:0) of *Cuphea* makes them potential substitute of coconut and palm kernel oil and high content of capric acid (C10:0) suggests that these could eventually replace or supplement petrochemicals. Thus *Cuphea* has potential to satisfy both industrial and domestic oil demands. It has potential for high yield, drought tolerant, adaptability to arid climates and genetic diversity but dormant seed, indeterminate growth; early seed shattering and sticky glandular hairs hinder its commercialization. The genetic improvement in *Cuphea* for high yield in relation to break the linkage of wild characters is very meager. However, some improvements have been reported in *Cuphea* for the loss of glandular hairs and early seed shattering by mutation (HIRSINGER, 1985). Hence to fill the lacunae and gather the different genetic system involved in the inheritance of component traits contributing towards seed yield, the present investigation was undertaken to study gene actions of the population in order to formulate an effective breeding programme in creeping wax weed (*Cuphea procumbens* Orteg.)

MATERIALS AND METHODS

Exotic and indigenous germplasm lines of *Cuphea procumbens* obtained from different ecogeographical origins viz. USA, Germany, U.K., NBPGR, India, were subjected to selection for pure and inbred lines during 1995-96 - 1997-98 (SINGH and SINGH 2004). Among these, 6 equally diversed genotypes were utilized in half diallel fashion to gets F_1 seed during 1998-99 and selfed to get F_2 seeds. A

fresh F_1s were also made. Final experiment including 36 genotypes including 15 each F_1s and F_2s along with 6 parents were grown with 3 replications in following year at National Botanical Research Institute, Lucknow. The experimental site is situated at $26^\circ40'$ to $26^\circ45'$ N latitude and $80^\circ45'$ to $80^\circ53'$ longitude at an elevation of 129 m above sea level. The area fall under subtropical zone receiving annual rain fall of 80-100 cm. The rows were 3 m long while spacing between rows and within rows were 50 cm and 30 cm respectively. Parents and F_1s were sown in 3 m long single row while F_2s were sown in two rows. The fertilizer application of 90 kg nitrogen, 50 kg phosphorus and 40 kg potash per hectare was given. Half of the nitrogen and full amount of phosphorus and potash were applied as basal dressing while the rest of the amount of nitrogen was applied in two splits as top dressing. The ten plants in parents and F1s and twenty plants in F_2s per replications were selected at random before flowering to record the detailed observations on plant height (cm), branches/plant, fruits/plant, seeds/pod and seed yield/plant (g).

Statistical analysis
Statistical analysis was done on plot means basis. The differences among populations were tested by analysis of variance for individual characters. The data were subjected to graphical and component analyses according to Hayman (1954, 1957) and JINKS and HAYMAN (1953). Analysis of Yr, the standardized deviation graph (Wr+Vr) was done following JOHNSON and ASKEL (1959). The 't' test, which tests for overall assumptions of diallel was performed according to ALLARD (1956) to determine the adequacy of the model with respect to non-allelic interaction.

RESULTS

Analysis of plot means showed highly significant differences among parents and crosses indicating much scope for further genetic studies.

Graphical analysis
The non-significant 't' test showed that assumptions underlying diallel analysis are fulfilled and the additive-dominance model gives an adequate description of data. The linear regression of Wr against Vr, the limiting parabola (Wr²) and scatter of parents along the regression line and standardized deviation graph are presented in Fig 1 to Fig. 5.
1. Plant height: The regression of Wr against Vr was significantly different from zero (0-b) but not from unity (1-B) indicating the absence of epistasis. The regression line passed the Wr axis much below the origin indicating over dominance in both F_1 and F_2. In F_1 parents scattered all along the regression line below the limiting parabola indicating much diversity among parents while in F_2 parents grouped into two groups. Parents 'NBC-20', 'NBC-12', 'NBC-3' possessed maximum dominant gene and 'NBC-25, maximum recessive alleles in F_1 while in F_2, 'NBC-3','NBC-30' and 'NBC-1' possessed maximum dominant alleles for plant height. The pattern of parental order of dominance was almost the same from Wr-Vr graph and standard deviation graph.
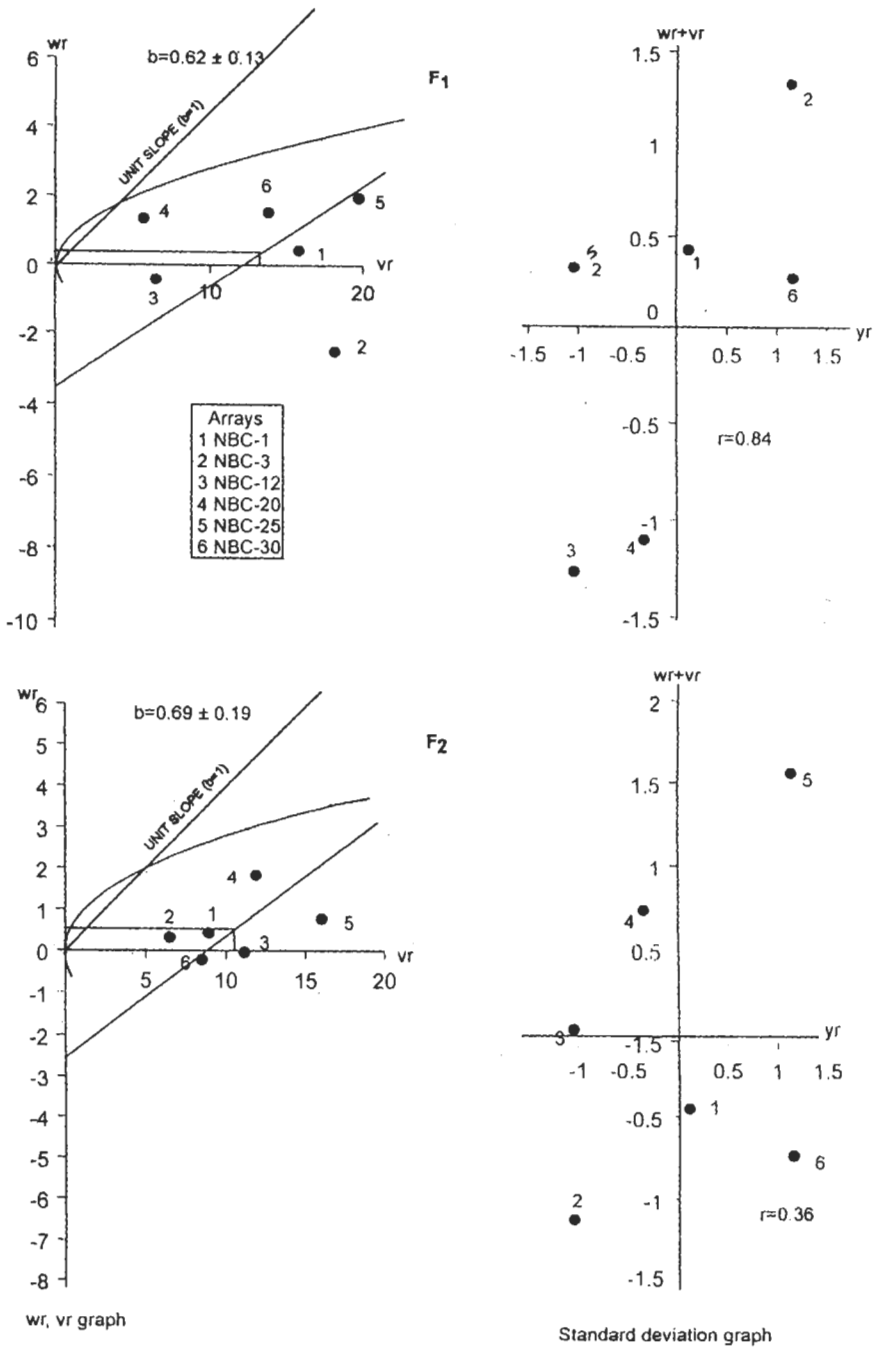
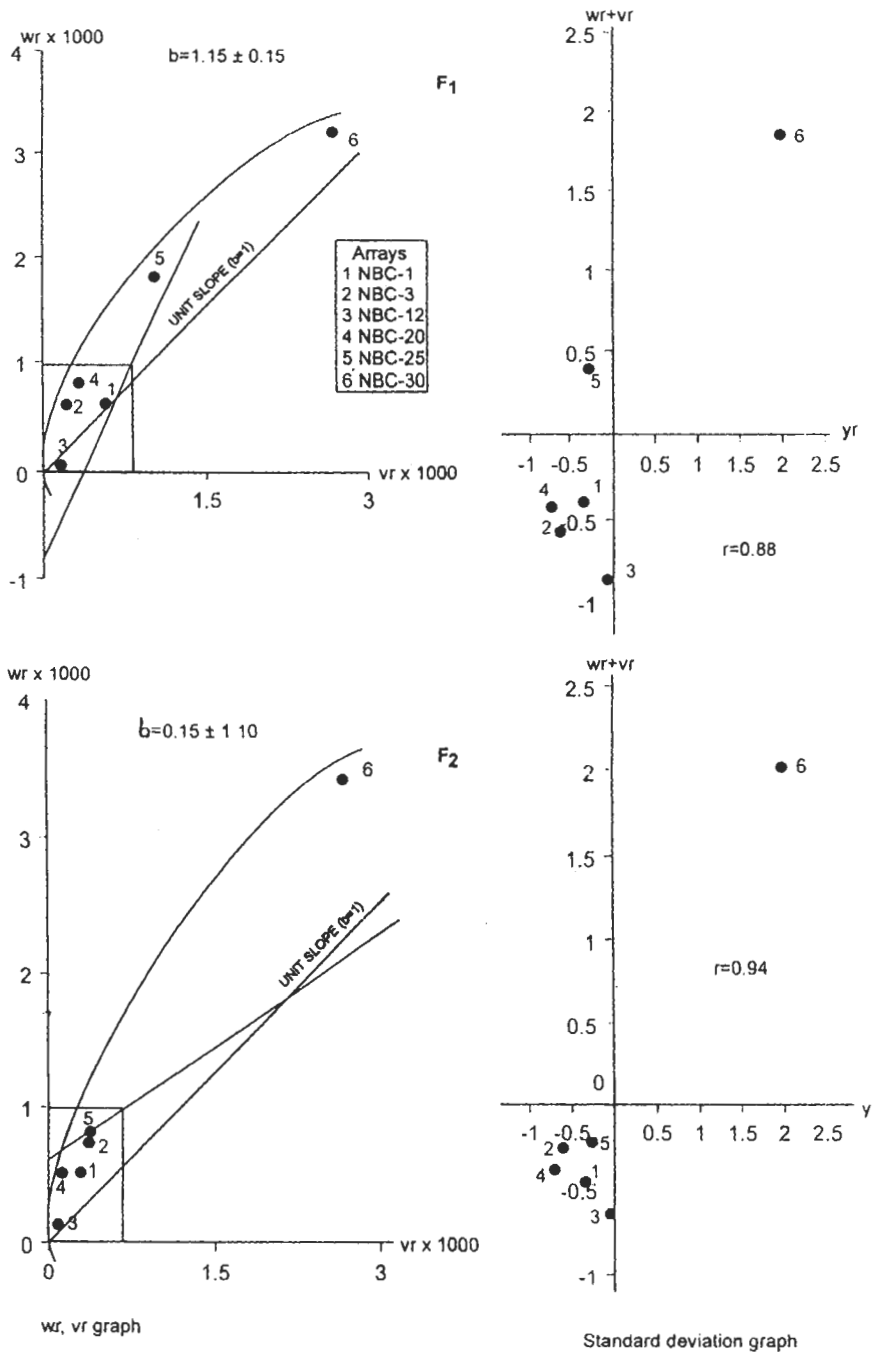Fig. 1. - Wr-Vr and standard deviation graph of plant heigh

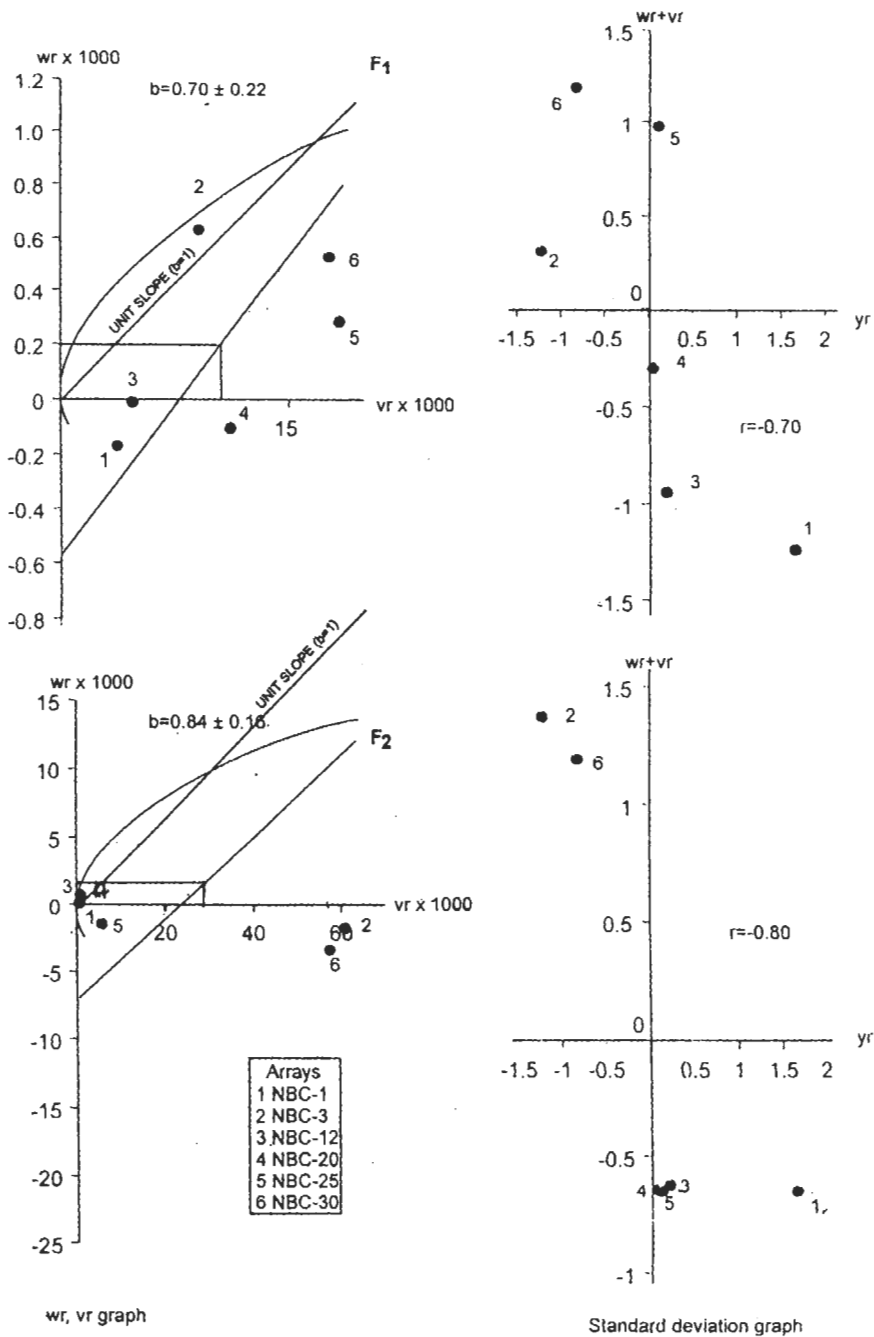Fig. 2. - Wr-Vr and standard deviation graph of number of branches/plant

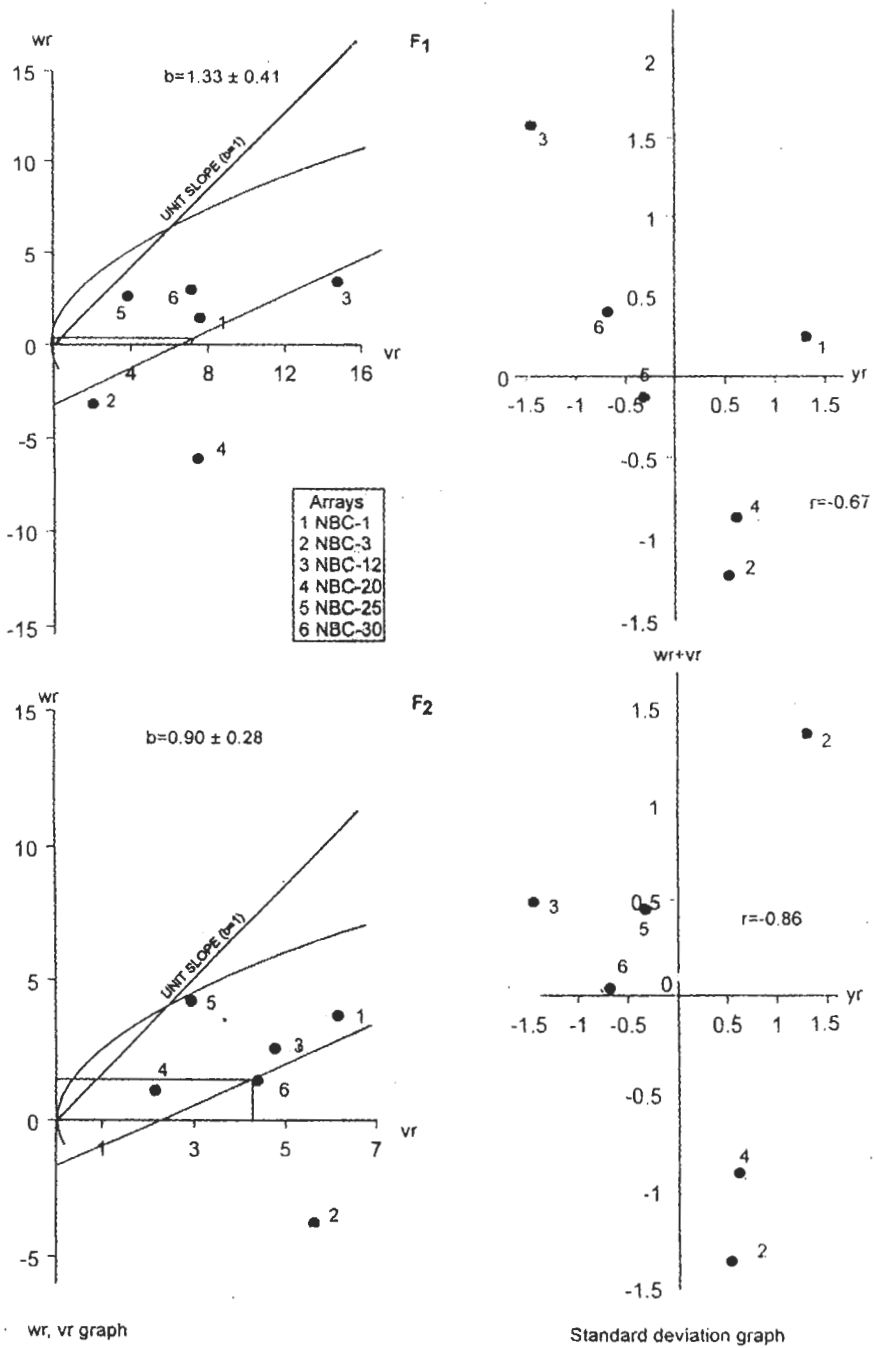Fig. 3. - Wr-Vr and standard deviation graph of number of fruits/plant

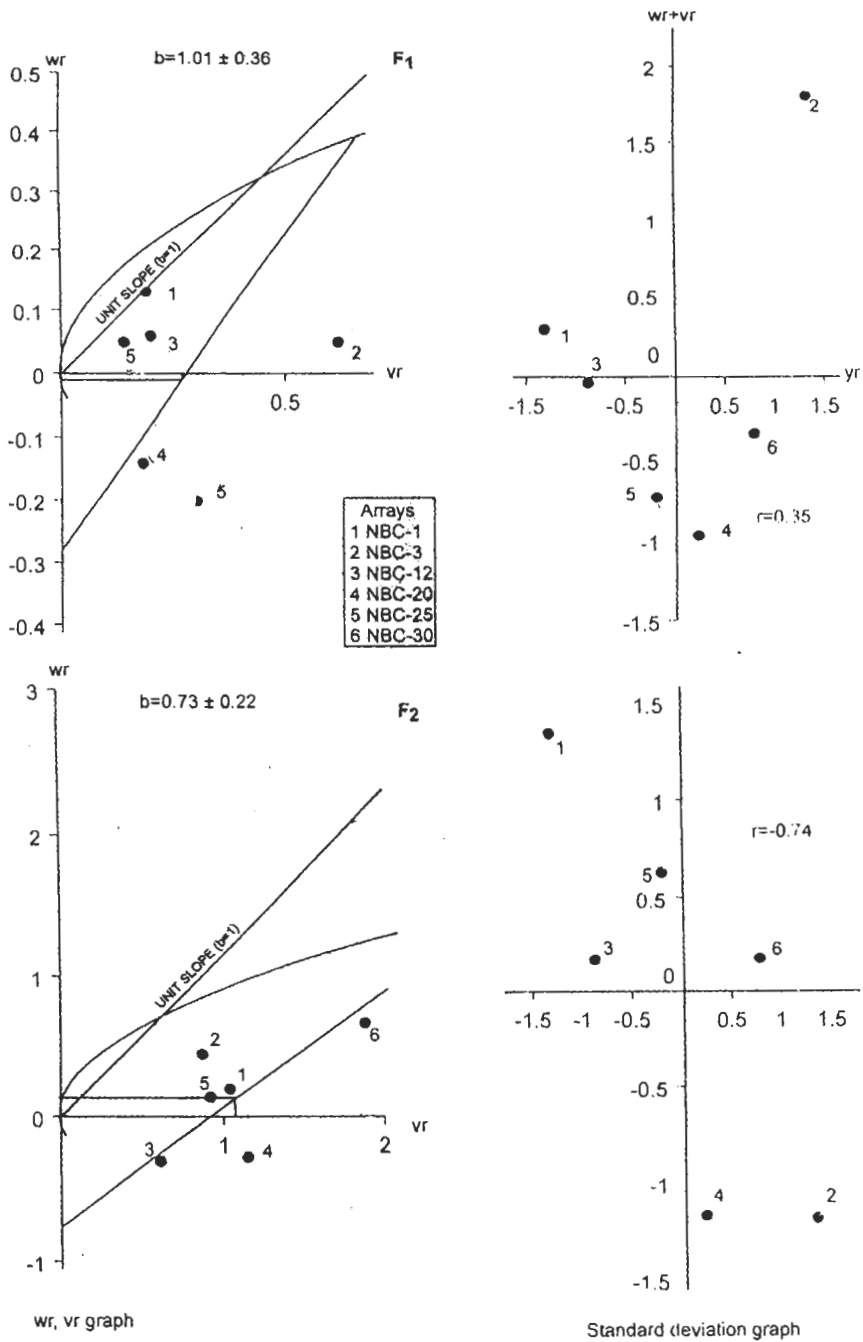Fig. 4. - Wr-Vr and standard deviation graph of seeds/fruit

Fig. 5. - Wr-Vr and standard deviation graph of seeds yeld/plant

2. Branches/plant: The Y intercepted the regression line on Wr axis below the origin in F_1 and above the origin in F_2 indicating the prevalence of over-dominance and partial dominance respectively. The regression coefficient (b) did not differ significantly from unity indicating the absence of epistasis or non-allelic interaction in both the generations. The array point scattered around the regression line in F_1 while in F_2 it clustered in two groups. The parents 'NBC-12', NBC-20', 'NBC-25', 'NBC-1' and 'NBC-3' possessed more of the dominant alleles and parents P6 maximum recessive alleles in F_1 and F_2 generations. The standardized deviation graph confirms the result of Wr-Vr graph regarding the description of dominant and recessive alleles among parents.

3. Fruits/plant: The regression line cut the Wr axis much below the origin in both the generation indicating the prevalence of over-dominance. The regression coefficient (b) of Wr on Vr differed significantly from zero (B-0) but not from unity (1-B) and thus absence of epitasis or non- allelic interaction was noticed in both the generations. The array are scattered all along the regression line below limiting parabola in F_1 indicated genetic diversity among parents. While in F_2 arrays are diversed in two clusters. Three parents ('NBC-1, 'NBC-12', 'NBC-25') and two parents ('NBC-3', NBC-30') clustered together reflecting low diversity. Parental orders of dominance on standardized deviation graph are in order of 'NBC-20', NBC-12','NBC-3', NBC-30', 'NBC-25'in F_1 and 'NBC-25', 'NBC-20', 'NBC-13', 'NBC-30', 'NBC-3' in F_2 generation.

4. Seeds/fruit: The regression coefficient differed significantly from zero and approaching unity indicating the absence of non-allelic interaction. Regression line passed below the origin indicating the over dominance in both the generations. High genetic diversity among parents was observed in both the generation by wide scattering of arrays all along the regression line. The parental order of dominance was almost similar from Wr-Vr and standard deviation graph. Parents 'NBC-20', NBC-3', NBC-25', 'NBC-1' in F_1 and 'NBC-20', 'NBC-3', in F_2 possessed maximum dominant alleles while 'NBC-12' in F_1 and 'NBC-1' in F_2 had maximum recessive alleles being too far from origin.

5. Seed yield/plant: The Y intercept of regression line was much below the origin indicating over dominance in F_1 and F_2 generations. However, magnitude of dominance was higher in F_1 than F_2. The estimates of regression coefficient (b) was significantly different from zero but not from unity indicating the absence of non-allelic interaction. All the arrays distributed wide along the regression line in Wr-Vr graph indicating much diversity among parents for seed yield/plant. However, all the 6 parents clustered in 3 groups in each generation viz. I ('NBC-20', 'NBC-25'), II ('NBC-25, 'NBC-12', NBC-1') and III ('NBC-3') in F_1 and I ('NBC-12', NBC-20'), II ('NBC-25', 'NBC-3', 'NBC-1') and III ('NBC-30') in F_2.The standard deviation graph confirms the result of Wr-Vr graph regarding the description of dominant and recessive alleles among parents.

Table 1. - Components of diallel variance and their estimates for diffeent quantitative traits in Cuphea procumbens

Components	Plant height F_1	F_2	Branches/plant F_1	F_2	Fruits/plant F_1	F_2	Seeds/fruit F_1	F_2	Seed yield/plant F_1	F_2
$\hat{D}$	0.70 ±4.80	0.60 ±2.30	4055.66** ±248.93	3059.10** ±133.87	9270.70** ±395.17	520.98 ±311.24	5.90 ±3.53	5.40* ±2.74	0.63 ±0.93	0.59 ±0.27
$\hat{H}_1$	48.30** ±12.20	147.30** ±24.00	2142.80** ±631.93	6950.85** ±1359.41	22083.68** ±1003.16	10690.80** ±790.12	31.35** ±8.96	53.94** ±25.77	10.42 ±2.29	15.56** ±2.76
$\hat{H}_2$	46.50** ±10.90	139.10** ±21.40	1392.37** ±564.52	3252.45 ±1214.39	5983.93** ±896.15	9666.06** ±705.83	24.37* ±8.01	42.13 ±24.81	9.10 ±2.04	13.06 ±2.45
$\hat{h}^2$	11.40 ±7.30	74.80** ±3.60	92.78 ±379.86	15.19 ±204.39	1090.16 ±603.17	-94.01 ±475.07	8.46 ±5.39	2.54 ±4.17	9.74 ±1.38	0.04 ±0.41
$\hat{F}$	-1.90 ±11.80	-4.80 ±11.50	284.14 ±94.09	480.70 ±30.60	-12783.55** ±965.39	1060.14 ±790.12	1.86 ±8.63	11.17 ±13.36	0.73 ±2.20	1.53 ±1.32
$\hat{E}$	1.50 ±1.80	1.50 ±0.90	3543.08** ±608.14	7955.54 ±654.11	192.89 ±149.36	92.44 ±117.63	1.35 ±1.33	1.85 ±1.03	0.20 ±0.34	0.24 ±0.10
PROPORTION OF COMPONENTS OF VARIANCES										
$(\hat{H}_1/\hat{D}_1)^{0.5}$	8.31	15.00	0.73	1.34	1.54	3.13	2.30	3.16	4.07	5.15
$\hat{H}_2/4\hat{H}_1$	0.24	0.24	0.16	0.12	0.18	0.25	0.19	0.20	0.22	0.21
$\hat{K}_D/\hat{K}_r$	0.00	0.00	4.01	7.62	0.38	1.57	2.54	2.02	1.33	1.67
$\hat{h}^2/\hat{H}_2$	0.25	0.54	0.06	0.01	0.18	0.37	0.35	0.01	1.07	0.00
r	0.65**	0.36	0.88**	0.94**	-0.71**	-0.80**	-0.67**	-0.26	0.29	0.66**
t^2	0.84	3.46	1.95	3.73	2.49	2.56	0.06	1.88	0.94	0.79
b	0.63	0.69	1.15	1.17	0.70	0.85	1.33	0.90	1.01	0.73
SE	0.14	0.19	0.15	0.16	0.22	0.16	0.41	0.28	0.36	0.22

**, * significant at p=0.01 and p=0.05 respectively

Table 2. - Per-se performance, breeding value (Yr), and rank index in Cuphea procumbens

Parents Traits	NBC-01	NBC-03	NBC-12	NBC-20	NBC-25	NBC-30
Plant height						
Per-se	40.2	38.9	38.9	39.6	40.9	40.9
Rank	2	4	4	3	1	1
Breeding value	0.112	-1.046	-1.046	-1.336	1.158	1.159
Rank	3	4	4	5	1	1
Branches/plant						
Per-se	96.3	79.3	115.6	72.1	101.8	149.6
Rank	4	5	2	6	3	1
Breeding value	-0.336	-0.609	-0.057	-0.718	-0.262	1.982
Rank	4	5	2	6	3	1
Fruits/plant						
Per-se	222.6	155.4	188.6	185.6	187.0	187.3
Rank	1	5	2	4	3	3
Breeding value	1.661	-1.230	0.206	0.061	0.126	-0.819
Rank	1	6	3	4	2	5
Seeds/fruit						
Per-se	30.6	30.5	26.5	30.7	27.5	27.2
Rank	2	3	6	1	4	5
Breeding value	1.306	0.526	-1.442	0.613	-0.328	-0.680
Rank	1	3	6	2	4	5
Seed yield/plant						
Per-se.	10.0	8.63	10.40	10.50	10.90	8.90
Rank	4	6	3	2	1	5
Breeding value	0.116	-1.383	0.554	0.664	1.103	-1.054
Rank	4	6	3	2	1	5
RANKS OVER ALL THE CHARACTERS						
Per-se						
Index value	13	23	17	16	12	15
Rank	II	VI	V	IV	I	III
Breeding value						
Index value	13	24	18	19	11	17
Rank	II	VI	IV	V	I	III

r– 0.83**

Genetic components

The estimate of additive component ($\hat{D}$) was non significant for all the characters except fruits/plant in F_1 and seeds/fruit in F_2 (Table 1). The two measures of dominance viz $\hat{H}_1$ (dominance effect) and $\hat{H}_2$ (proportion of dominance due to positive (U) and negative (V) effect of a gene) were highly significant for all the traits in F_1 and F_2 except seeds/fruit in F_2. However, the magnitude of $\hat{H}_1$ was higher than $\hat{H}_2$ component indicating that positive and negative alleles at loci governing these characters were not equally proportional among the parents. The difference $\hat{H}_1$-$\hat{H}_2$ supported the above conclusion as the estimates $\hat{H}_1$-$\hat{H}_2$ were far from zero. Positive F value for seed yield/plant, seeds/fruit, branches/plant in both the generations indicated greater frequency of dominant alleles among parents for these traits and negative for fruits/pant and plant height exhibited greater value of recessive alleles among parents. The mean degree of dominance $(\hat{H}/D)^{1/2}$ was more than unity for all the traits except branches/plant in F_1 suggesting the presence of over-dominance. Partial dominance was noticed for branches/plant in F_1. The magnitude of $\hat{H}_2/4\hat{H}_1$ was close to 0.25 for plant height in F_1 and F_2 and fruits/plant in F_2 suggesting the symmetrical distribution of positive and negative alleles among the parents while for other characters asymmetry was noticed. The proportion of dominant and recessive alleles (Kd/Kr) was more than unity for branches/plant, seeds/fruits and seed yield/plant in F_1 and F_2 and plant height in F_2 demonstrated the excess of dominant alleles in parents while excess of recessive alleles was noticed for plant height in F_1 and fruits/plant in F_2. The number of gene group differentiating the parents ($\hat{h}_2/\hat{H}_2$) was less than unity for all the characters in both the generations suggesting the control of one gene group.

DISCUSSION

Diallel analysis based on certain assumptions (JINKS 1954, 1956), DICKINSON and JINKS (1956), MATHER and JINKS (1971), was fulfilled in present set of material where parents were diploid and homozygous pure lines obtained through selfing of several generations. KEARSEY and JINKS (1968), JANA (1975), SINGH and SRIVASTAVA (1992) pointed out that validity of all the assumptions is unlikely. However, the assumptions with regard to parent failed, the arrays well of the line of unit slope of Wr-Vr graph may be deleted from diallel set until the remaining crosses satisfied the test. However, this may be resulted in loss of randomness of sample (KEMPTHORNE 1956). The removal of arrays is undesirable when interest of breeder is to study the particular set of parents selected for desirable characters. JANA (1975) and SINGH and SRIVASTAVA (1992) reported that the assumption of non-allelic interaction has been very difficult to satisfy in most of the studies wherever diallel analysis has been used. The analysis may therefore be partially fulfilled. The absence of epitasis was noticed for all the characters over generation. However, Non-significant of t^2 test (HAYMAN 1954) supported the over all validity of the assumptions. The conclusions drawn from present study are

expected to be realistic and should form a guideline for improvement of populations under study.

The analysis of Wr-Vr graph and components indicated over dominance for all the characters except branches/plant in F_1. Branches/plant in F_1 exhibited partial dominance where the regression line cut the ordinate above origin (Fig 2). This was also revealed by potence ratio $(\hat{H}/D)^{1/2}$ which is less than unity in F1 and indicates the presence of partial dominance. The mean degree of dominance $(\hat{H}/D)^{1/2}$ was more than unity for other characters suggesting apparently that over dominance plays an important role, which confirms the finding of Wr-Vr graph. The array scattered all along the regression line below limiting parabola in two groups viz. dominance and recessive. However, the accumulation of arrays in dominance and recessive groups were different for different characters (Fig 1-5). The Wr-Vr graph was confirmed by standardized deviation graph regarding the distribution of dominant and recessive alleles. To demonstrate more clearly the positive and negative effects of an accumulation of dominant and recessive alleles, the parental measurement (Yr) was correlated with parental order of dominance (Wr+Vr). This correlation has found negative for fruits/plant, seed/fruit in both F_1 and F_2 generations and for Seed yield in F_2 and days to flowering in F_1 indicating that dominant genes contributed towards positive direction while plant height, branches/plant in F_1 and F_2 and seed yield in F_1 and days to flowering in F_2 were under the control of recessive genes. The ranking of parents based on their standardized breeding value (Yr) and *per-se* performance are closely associated (Table 2) .The rank correlation was highly significant (r=0.83**).

A desirable parent for future breeding programme may be one, which combines high *per se* performing dominant alleles over all the characters. To conclude the real breeding behaviour of an individual strain, the parents were ranked firstly on the basis of parental measurement (Yr) and secondly on the basis of *per se* performance (Table 2). In present study parents NBC-01, NBC-25 and NBC-30 possess high *per-se* as well as dominant alleles for most of the characters. It may therefore, be concluded that the breeding value of a parent is closely associated with frequency of dominant alleles in that parent for such trait (Singh and Srivastava 1992). These parents may be utilized in breeding programme to develop desired varieties. A suitable technique, which will increase the frequency of both dominant and recessive alleles with favourable effects, should be practiced. Genotypes involving dominant genes can easily be identified but concerning the recessive alleles there is less chance of getting the best alleles combinations as they remain concealed in heterozygous conditions. Thus selections based on progeny performance with a large population, which increases the frequency of favourable alleles, will be suitable under this situation.

Cuphea procumbens is self-pollinated crop with wide degree of out crossing depending upon the frequency of beetles. According to reproductive mechanism involved additive genetic variance should be exploited for improvement. However, in present study prevalence of non-additive variance was observed for most of the characters. Conventional breeding method exploits only

that part of genetic variance, which is due to additive or additive x additive gene effect. Non-additive genetic variability is not fixable and thus under this situation it is desirable and important to maintain heterozygosity in the population. Simultaneous exploitation of both additive and non-additive components of variances should be emphasized for the improvement of characters. To exploit such type of variability breeding methods such as bi-parental mating followed by recurrent selection are likely to be important. In order to facilitate gene flow in recombination cycle of recurrent selection procedure, the male sterility or other out crossing devices should be searched out (SINGH and SINGH 1981)

REFERENCES

ALLARD, R.W. (1956): The analysis of genetic-environmental interaction by means of diallel crosses. Genetics, 41:305-308.

BABAYAN, V. (1987): Medium chain triglycerides and structured lipids. Lipds. 22:417-420.

BACH, A.C. and V.K. BABAYAN (1982): Medium chain triglycerides: An update. American J. Clinica Nutri. 36: 950-62.

CAMBELL, T.A. (1989): Mutation induction for domestication of Cuphea: Effect of gamma rays. Mutation Breed. News lett. 33:11.

DEHESH, K. (2001): How we can genetically engineer oil seed crops to produce high levels of medium chain fatty acids (MCFA). European J. Lipid Sci.Technol., 103:688- 697

DICKINSON, A. G. and J. L. JINKS (1956): A generalized analysis of diallel crosses. Genetics. 41:65-78.

HAYMAN, B.I. (1954): The theory and analysis of diallel crosses. Genetics 39: 789- 809.

HAYMAN, B.I. (1957): Interaction, heterosis and diallel crosses. Genetics 42: 336-355.

HIRSINGER, F. (1985): Agronomical potential and seed composition of *Cuphea*- an annual crop for lauric and capric seed oil. J. Am. Oil. Chem. Soc. 67: 76-80.

JANA, S. (1975): Genetic analysis by means of diallel graph. Heredity 35: 1

JINKS, J.L. (1954): The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. Genetics 39: 767-788.

JINKS, J.L (1956): The F2 and back cross generations from set of diallel crosses. Heredity 10: 1-30.

JINKS, J.L. and B.I. HAYMAN (1953): The analysis of diallel crosses. Maize Genetics Co-op. News 23:48-54.

JOHNSON, L.P.V. and R. ASKEL. (1959): Inheritance of yielding capacity in a fifteen-parent diallel cross of barley. Canadian J. Genet. Cytol., 1:208-265.

KABARA, J.J. (2000): Health oils from the tree of life (Nutritional and Health Aspect of Coconut Oil.). Indian Coconut J., 31(8): 2-8.

KEARSEY, and J.L. JINKS (1968). A generalized method of detecting additive, dominance and epistatic variation for metric traits. Heredity 23: 403-409.

KEMPTHORNE , O. (1956): The theory of diallel cross. Genetics 1:451-459.

KHANNA, K.R. and S.P. SINGH (1991): Genetics of fatty acid composition and breeding for modified seed oil . In *Biochemical Aspect of Crop Improvement* (Ed. K.R. Khanna). Pp 255-281. CRC press, Boston.

MATHER, K. and J.L. JINKS (1971): Biometrical genetics. Chapman and Hall Ltd. London.

RAMESHKUMAR, R. and S.P. SINGH (2004): Breeding for designer oil seed crops. Appl. Bot. Abst. 24(1): 58-77.

ROBBELIN, G. and F. HIRSINGER (1982): Cuphea- the first annual oil seed crop for the production of medium chain triglycerides (MCT). In *Improvement of oil seed and industrial crops by induced mutation.* pp161-170. International Atomic Agency, Vienna.

SINGH, S.P. and H. N. SINGH (1981): Gene systems involved and their implication in breeding of lablab bean. Z. *Pflanzenzuchtg.* 87: 240-247.

SINGH, S.P. and J.P. SRIVASTAVA (1992): Diallel analysis in lablab bean (*Dolichos lablab* L.). Genetika 24(1): 57-68.

SINGH, S.P. and R. RAMESHKUMAR (2003): *Cuphea*: Importance and bibliography. Appl. Bot. Abstr. **23**: 60-75.

SINGH, S.P. and MEENAKSHI SINGH (2004): Heterosis in Cuphea (*Cuphea procumbens* Orteg.). Indian J. Agric. Sci., 74:639-543.

THOMPSON, A. F. (1984): *Cuphea*: A potential new crop. Hort. Sci., 19(3): 352-354.

DIALELNA ANALIZA PRINOSA
I KOMPONENATA PRINOSA ZRNA *CUPHEA PROCUMBENS*

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I z v o d

Cupea procumbens Ortega je značajna jednogodišnja biljka izvor viših masnih kiselina srednje dužine lanca. U ovim istraživanjima su dati rezultati istraživanja različitih sistema gena uključenih u kontrolu nasleđivanja važnih kvantativnih osobina kao što su visina biljaka, grančica po biljci, plodova po biljci, semena po plodu i prinos semena po biljci. Istraživnja su vršena u F1i F2 generaciji polu dialela 6 roditeljskih linija. Grafički prikaz Wr - Vr i analiza komponenata prinosa su potvrdili glavni uticaj overdominantnosti u kontroli svih osobina izuzev broja grančica po biljci u F1 generaciji. Raspored podataka duž linije regresije se približava paraboli u dve grupe, dominantnosti i recesivnosti i potvrđena je grafikonom standardne devijacije. Rang značajnosti na osnovu vrednosti oplemenjivanja (Yr) roditelja i osobine *per se* su usko povezani (r= 0,83**). Na bazi ranga, roditelji 'NBC-01', 'NBC-25' i NBC-30' su odabrani kao najbolji jer nose dominantne allele za većinu osobina. U radu je na osnovu aktivnosti uključenih gena diskutovan plan oplemenjivanja.