

GENETICS OF TEST WEIGHT AND OIL CONTENT IN *CUPHEA PROCUMBENS*

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Cuphea is an important genus of medium chain triglycerides and *Cuphea procumbens* is rich in capric acid (C10:0), which is main plant source of petrochemicals. A detailed study was conducted on different genetic systems involved in the inheritance of test weight and oil content in *Cuphea procumbens* following 6 parents diallel. The high value of dominance (H_1) and (δ^2s) and over-dominance obtained by $(H_1/D)^{0.5}$ and graphical analysis indicated the prevalence of non-additive gene action for test weight and oil content. Parent 'NBC-30' in F_1 and 'NBC-03' in F_2 for test weight and 'NBC-30' for both the generation for oil content were best combiners. The crosses 'NBC-12' x 'NBC-30', 'NBC-01' x 'NBC-03' and 'NBC-12' x 'NBC-20' for test weight and 'NBC-01' x 'NBC-03' and 'NBC-25' x 'NBC-30' for oil content were best specific cross combinations in both the generations. The genetic combination of these crosses were additive x additive, additive x dominance and dominance x dominance type interaction due to involvement of high x high, high x low and low x low combiners. A breeding plan to develop bold seeded genotypes to increase oil content has been discussed.

Key words: *Cuphea procumbens*, test weight, oil content, genetics

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INTRODUCTION

Cuphea genus (Fam: Lythraceae) is an important newly tapped oil seed crop of American origin, subtropical Brazil and Mexico being primary and secondary centre of diversity. The seed oil has remarkable pattern of fatty acid diversity ranging C8:0-C18:0 with domination of medium chain triglycerides (MCT) (GRAHAM *et al.*, 1981; ROBBELEN and HIRSINGER 1982; KHANNA and SINGH, 1991, SINGH *et al.* 1998) - an unique in plant kingdom. The medium chain fatty acid comprises caprylic acid (C8:0), capric acid (C10:0) and lauric acid (12:0) which have considerable application in chemical industry, medicines, nutrition and dieties (KAUNITZ *et al.* 1958; ROBBELEN and HIRSINGER, 1982; GRAHAM and KNAPP, 1989; KHANNA and SINGLY, 1991; PANDEY *et al.*, 2000; NEBELLING *et al.*, 1995; DEHESH, 2001). Besides its importance as a renewable oil source, very little work on its genetic improvement to use *Cuphea* as commercial crop has been made. Keeping the uniqueness of the crop, the research work on genetic improvement has been initiated in India since 1998. *Cuphea procumbens*, which contain up to 30% oil in seed and above 90% capric acid (C10:0, PANDEY *et al.*, 2000) as renewable oil source of petrochemical has been undertaken to study the genetics and inheritance pattern of test weight (1000 seed) and oil content following 6 parent diallel.

MATERIALS AND METHODS

Six pure genotypes viz: 'NBC-01', 'NBC-03', 'NBC-12', 'NBC-20', 'NBC-25' and 'NBC-30', selected from breeding stock of different exotic origins (SINGH *et al.*, 1998) maintained at National Botanical Research Institute Lucknow, India, were crossed in half diallel fashion during 1996-97. All the F₁'s were raised to get F₂ seeds and fresh F₁'s were also made in following year. An experiment including 15 each F₁'s and F₂'s along with 6 parents were laid out in randomized block design with 3 replications at experimental plot of Genetics and plant breeding division of the institute during 1998-99. Each plot of parents and F₁'s had single row while F₂'s had 2 rows each. Non-experimental rows were sown to check border effect and last row of each replication was treated as non-experimental. Each row was 3m long with 50cm between rows and 20cm within row. Normal cultural practices were followed throughout the crop season (November - April). Five plants from parents and F₁'s and 10 plants from F₂'s were selected before flowering for detailed observations on test weight (1000 seed) and oil content. The seeds harvested were analyzed separately for oil content according to PANDEY *et al.* (2000).

Plot means were used for statistical analysis. The data were subjected to W_r-V_r graph and numerical parameters following JINKS and HAYMAN (1953), HAYMAN (1954) and ASKEL and JOHSON (1963). The t² test and test of heterogeneity (W_r+ V_r and W_r- V_r) were estimated according to ALLARD (1956) to determine the adequacy of the model with respect to non-allelic interaction. Combining ability analysis was done according to GRIFFING (1956) model II and method II.

RESULTS AND DISCUSSION

Analysis of variance of plot means for test weight and oil content showed significant differences among parents and crosses suggesting the detailed analysis of gene action based on diallel was warranted.

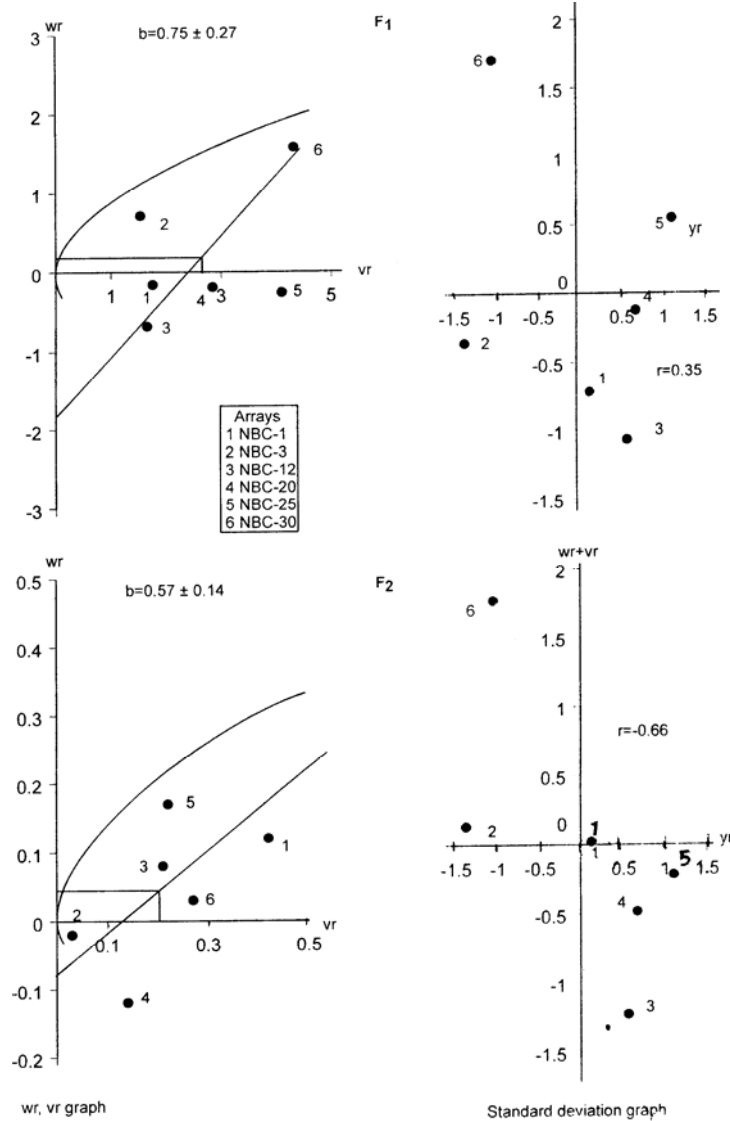


Fig.1. Wr / vr and standard deviation graph of test weight

Graphical analysis - The linear regression of wr against vr, limiting parabola (wr^2), scatter of parental points along with regression line and standard de-

viation graphs are depicted in Fig. 1. The non-significant of t^2 values showed that the assumptions of diallel analysis are fulfilled and additive-dominance model is an adequate description of data for both the characters. The regression coefficient (b) differs significantly from zero (b-0) but not from unity (1-b) in both F_1 and F_2 generations of test weight and only in F_2 of oil content indicating the absence of non-allelic interaction. In F_1 estimate of regression coefficient was not significant from zero (b-0) indicating the presence of epistasis but non-significant of regression from unity confirmed the validity of assumption and thus the absence of epistasis was also confirmed in F_1 hybrids for oil content. The regression line intersected the wr axis much below the origin revealing the presence of over-dominance in both F_1 and F_2 generations of test weight and oil content. Array points fell below the theoretical line of unit slope and distributed wide inside the limiting parabola all along the regression line suggesting the prevalence of complementary epistasis and considerable genetic diversity among parents. The parents 'NBC-01', 'NBC-12', and 'NBC-20' possessed maximum number of dominant and 'NBC-30' maximum number of recessive genes in F_1 while in F_2 'NBC-03' and 'NBC-20' had maximum dominant and 'NBC-25' had maximum recessive alleles for test weight. For oil content parents clustered in two distinct groups where parents 'NBC-01', 'NBC-03' and 'NBC-20' were very close to origin in both the generations and therefore had maximum dominant alleles. Where as 'NBC-25' and 'NBC-30' in F_1 and 'NBC-12' and 'NBC-30' in F_2 were far from origin indicating excess of recessive alleles. The remaining arrays possessed almost equal proportion of dominant and recessive alleles. The pattern of parental order of dominance was almost same from wr-vr graph and standard deviation graph for both the characters in both the generations.

Genetic components and gene action - The estimates of components of variances and their estimates are presented in Table 1. The estimate of additive component (D) was non-significant for both the characters except test weight in F_2 , while two measures of dominance viz: \hat{H}_1 and \hat{H}_2 were highly significant in both the generations for both traits and also higher than additive component (D). Similarly the estimate of δ^2_s was also higher than δ^2_g , though gca and sca variances were significant. The mean degree of dominance $(\hat{H}_1/D)^{0.5}$ and $(\delta^2_s/\delta^2_g)^{0.5}$ were more than unity in F_1 and F_2 for both the characters indicating the presence of over-dominance which is in close agreement of graphical analysis. The proportion of dominance $(\hat{H}_2/4\hat{H}_1)$ was much below the theoretical value ($U=V=0.5$) in both generations except oil content in F_2 suggesting asymmetrical distribution of positive and negative alleles among parents. The differences of $\hat{H}_1 - \hat{H}_2$ also supported above finding as estimates of $\hat{H}_1 - \hat{H}_2$ were far from zero for test weight in F_1 and F_2 and oil content in F_1 . The higher proportion of dominant and recessive alleles ($Kd/Kr > 1$) and positive F for test weight in F_1 and F_2 and oil content in F_1 demonstrated the excess of dominant genes involved in the inheritance. The negative F and low magnitude of $Kd/KR (< 1)$ revealed the excess of recessive alleles. The effective factors which control the dominance (\hat{h}^2 / \hat{H}_2) was most likely controlled by one group of genes for both the characters except oil content in F_2 .

However, numbers of gene groups are under estimated in present study due to unequal distribution of dominant alleles among parents. The significant positive correlation in F_1 (0.64*) and F_2 (0.96**) for oil content suggests the recessive alleles controlling the oil content, while low positive in F_1 (0.35) and significant negative (-0.75**) in F_2 indicating recessive and dominant alleles contributing towards the expression of test weight.

Table 1: Components of diallel variances for test weight and oil content in *Cuphea procumbens*

| Components | Test weight | | Oil Content | |
|---------------------------|-----------------|-----------------|-----------------|------------------|
| | F_1 | F_2 | F_1 | F_2 |
| D | 0.17 ±0.17 | 0.18 ±0.09 | 0.44 ±0.22 | 0.23 ±0.20 |
| \hat{H}_1 | 1.21* ±0.43 | 3.08** ±0.88 | 2.46** ±0.56 | 16.67** ±2.04 |
| \hat{H}_2 | 0.84** ±0.38 | 2.67** ±0.79 | 2.03** ±0.50 | 16.72** ±1.82 |
| \hat{h}^2 | 0.03 ±0.26 | 0.45** ±0.13 | -0.18 ±0.38 | 16.17** ±0.31 |
| F | 0.42 ±0.41 | 0.42 ±0.43 | 0.13 ±0.54 | -1.96 ±0.98 |
| E | 0.05 ±0.06 | 0.05 ±0.03 | 0.33 ±0.08 | 0.64 ±0.08 |
| Proportions of components | | | | |
| $(\hat{H}_1/D)^{0.5}$ | 2.64 | 4.17 | 2.37 | 8.53 |
| $\hat{H}_2/4\hat{H}_1$ | 0.17 | 0.22 | 0.20 | 0.25 |
| Kd/Kr | 2.69 | 1.81 | 1.13 | 0.33 |
| \hat{h}^2/\hat{H}_2 | 0.04 | 0.19 | 1.07 | 0.97 |
| r | 0.35 | -0.75** | 0.64** | 0.96** |
| t2 | 0.42 | 0.33 | 0.43 | 0.08 |
| b | 0.75 ±0.27 | 0.57 ±0.14 | 0.79 ±0.29 | 0.82 ±0.21 |

**, * $p > 0.05, 0.01$ respectively

Considering the gene actions involved in the inheritance, over-dominance was observed for test weight and oil content in both the generations. *Cuphea procumbens* is cross-pollinated crop and according to reproductive mechanism additive as well as nonadditive genetic variances should be exploited. The high value of \hat{H}_1 and δ^2_s and overdominance obtained by $(\hat{H}_1/D)^{0.5}$, $(\delta^2_s/\delta^2_g)^{0.5}$ and graphical analysis exhibited nonadditive type gene action in F_1 and F_2 . Thus it is desirable

and important to maintain heterozygosity in population for improvement purposes (SINGH and SINGH, 1981). Recurrent selection followed by bi-parental mating would be more suitable to breed and select bold seeded genotype with high oil content.

Table 2: Analysis of variance for combining ability for test weight and oil content in *Cuphea procumbens*

| Sources | d.f. | Test weight | | Oil content | |
|--|------|----------------|----------------|----------------|----------------|
| | | F ₁ | F ₂ | F ₁ | F ₂ |
| g.c.a | 5 | 0.196** | 0.115 | 1.430** | 2.320** |
| s.c.a | 15 | 0.228** | 0.206* | 0.745** | 1.122** |
| Error | 40 | 0.043 | 0.061 | 0.048 | 0.370 |
| Components of combining ability variance | | | | | |
| δ^2g | | -0.004 | -0.011 | 0.085 | 0.150 |
| δ^2s | | 0.185 | 0.145 | 0.697 | 0.750 |
| δ^2A | | -0.008 | -0.022 | 0.170 | 0.300 |
| δ^2D | | 0.185 | 0.145 | 0.697 | 0.750 |
| δ^2s / δ^2g | | -0.021 | -0.075 | 0.122 | 0.200 |
| $(\delta^2s / \delta^2g)^{0.5}$ | | --- | --- | 2.860 | 2.236 |

** , * p>0.05, 0.01 respectively

Combining ability - Mean squares due to gca and sca, were significant for both the traits except test weight in F₁ (Table 2). The high value of δ^2s and po-tence ratio $(\delta^2s / \delta^2g)^{0.5}$ indicates the presence of non-additive gene action and con-

Table 3: General combining ability effect for test weight and oil content in *Cuphea procumbens*

| Parents | Test weight | | | Oil content | | |
|---------|-------------|--------------------|--------------------|-------------|--------------------|--------------------|
| | Mean | gca F ₁ | gca F ₂ | Mean | gca F ₁ | gca F ₂ |
| NBC01 | 3.1 | 0.55 | -0.114 | 27.60 | -0.530** | -0.820 |
| NBC03 | 4.3 | 0.52 | 0.227** | 27.93 | 0.052 | 0.450 |
| NBC12 | 3.3 | 0.036 | -0.004 | 29.20 | 0.386** | 0.108 |
| NBC20 | 3.8 | -0.132* | -0.051 | 28.90 | -0.359 | 0.120 |
| NBC25 | 3.6 | -0.223** | -0.068 | 28.93 | -0.113 | 0.454 |
| NBC30 | 4.1 | 0.221** | 0.010 | 30.00 | 0.565** | 0.587 |
| SE (gi) | | 0.067 | 0.061 | | 0.071 | 0.312 |
| CD (5%) | | 0.131 | 0.120 | | 0.139 | 0.611 |
| (1%) | | 0.172 | 0.156 | | 0.182 | 0.801 |

** , * p>0.05, 0.01 respectively

firmed the conclusions of graphical and components of diallel analysis (Table 1). On the basis gca effect, parent 'NBC-30' in F_1 and 'NBC-03' in F_2 were significantly superior combiners for test weight. For oil content parent 'NBC-30', 'NBC-12' and 'NBC-03' in F_1 and 'NBC-30', 'NBC-25' and 'NBC12' in F_2 were good general combiners. However, 'NBC-30' and 'NBC-12' in F_1 were only significantly superior. The significant gca effect of 'NBC-30', and 'NBC-12', was closely associated with high *per-se* performance of parents (Table 3). This corroborates that the major part of variability resulted from additive gene action. Thus the performance of genotypes might be useful for predicting the combining ability in early generation of breeding programme.

Table 4: Specific combining ability effects for test weight and oil content in *Cuphea procumbens*

| Crosses | Test weight | | | | Oil content | | | |
|-------------|-------------|---------|-------|-------|-------------|---------|-------|---------|
| | Mean | sca | Mean | sca | Mean | sca | Mean | sca |
| | F_1 | F_1 | F_2 | F_2 | F_1 | F_1 | F_2 | F_2 |
| NBC01xNBC03 | 4.4 | 0.47* | 4.4 | 0.27 | 29.8 | 1.57** | 24.9 | 1.16** |
| NBC01xNBC12 | 4.1 | 0.22 | 4.4 | 0.47 | 27.7 | -0.89** | 25.3 | 0.02 |
| NBC01xNBC20 | 3.7 | -0.04 | 4.5 | -0.65 | 28.4 | 0.55* | 25.5 | 0.32 |
| NBC01xNBC25 | 3.9 | 0.25 | 3.3 | -0.53 | 27.9 | -0.19 | 26.2 | -0.28 |
| NBC01xNBC30 | 3.8 | 0.29 | 3.4 | -0.51 | 27.9 | -0.90** | 25.3 | -1.60** |
| NBC03xNBC12 | 3.8 | -0.06 | 4.2 | -0.07 | 29.3 | 0.09 | 26.2 | 0.98** |
| NBC03xNBC20 | 2.9 | -0.83** | 4.0 | -0.15 | 28.3 | -0.13 | 26.4 | 0.08 |
| NBC03xNBC25 | 2.7 | -0.91** | 4.5 | 0.29 | 28.3 | -0.41 | 26.0 | -0.55 |
| NBC03xNBC30 | 4.5 | 0.41 | 4.2 | 0.08 | 30.1 | 0.25 | 27.4 | 0.04 |
| NBC12xNBC20 | 4.2 | 0.47* | 4.2 | 0.21 | 29.1 | 0.31 | 25.8 | -1.39** |
| NBC12xNBC25 | 4.4 | 0.09 | 4.2 | 0.23 | 29.7 | 0.69* | 28.7 | -1.23** |
| NBC12xNBC30 | 4.5 | 0.45 | 4.6 | 0.61 | 30.2 | 0.48 | 26.9 | -0.24 |
| NBC20xNBC25 | 3.5 | 0.07 | 4.0 | 0.08 | 26.9 | -1.39** | 27.9 | 0.33 |
| NBC20xNBC30 | 3.7 | 0.21 | 3.4 | -0.57 | 27.9 | -1.04** | 26.5 | -1.78** |
| NBC25xNBC30 | 3.8 | 0.02 | 4.4 | 0.47 | 29.7 | 0.51 | 27.6 | 1.01** |
| SE (sij) | | 0.21 | | 0.35 | | 0.34 | | 0.38 |
| CD (5%) | | 0.42 | | 0.68 | | 0.66 | | 0.77 |
| (1%) | | 0.55 | | 0.92 | | 0.87 | | 0.97 |

None of the hybrids was significantly superior for both the traits. For test weight 3 crosses viz: 'NBC-01'x 'NBC-03', 'NBC-12'x 'NBC-20' and 'NBC-12'x 'NBC-30' showed significant positive sca effects in F_1 (Table 4). In F_2 generation no cross was found showing significant sca effect. However, on the basis of magnitude of sca effects the cross 'NBC-01'x 'NBC-20' followed by 'NBC-12'x 'NBC-30', 'NBC-25'x 'NBC30' and 'NBC-01'x 'NBC-12' were good specific combiners. The three crosses viz: 'NBC-01'x 'NBC-03', 'NBC-12'x 'NBC-20' and 'NBC-12'x

'NBC-30' were common in both the generations. Out of 15 crosses 3 in F_1 and 4 in F_2 generation showed significant sca effects for oil content. The maximum was found in cross 'NBC-01' x 'NBC-03' (1.57) followed by 'NBC-03' x 'NBC-30' (0.75) and 'NBC-12' x 'NBC-25' (0.69) in F_1 and 'NBC-20' x 'NBC-30' (1.78), followed by 'NBC-01' x 'NBC-03' (1.12) and 'NBC-25' x 'NBC-30' (1.01) in F_2 . High sca, effects in these crosses are also coupled with high *per-se* performance of parents combinations indicating close association of sca effects and *per-se* performance. It was also noticed that most of the crosses, which did well in F_1 , failed to do so in F_2 and in general magnitude of sca effect was higher in F_2 than in F_1 for both the characters. This difference might be due to large amount of non-allelic interaction operating for the expression of these characters.

The crosses viz: 'NBC-01' x 'NBC-03', 'NBC-25' x 'NBC30', which showed high *per-se* and sca effect for test weight also had high *per-se* and sca effect for oil content showing positive association with each other. Positive correlation of test weight with oil content was also reported by SINGH (2001). Thus to enhance the oil percentage in *Cuphea procumbens*, breeding and selection of genotypes with bold seed should be taken in to consideration.

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GENETIKA HEKTOLITARSKE MASE I SADRŽAJA ULJA U CUPHEA PROCUMBENS

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Izvod

Vrbičica je važan rod srednjeg lanca triglicerida a velika vrbičica (*Cuphea procumbens*) je bogata kaprinskom kiselinom (C10:0), koja je glavni biljni izvor petrohemičija. Detaljno istraživanje je izvedeno na različitim sistemima koji su uključeni u nasleđivanje hektolitarske mase i sadržaja ulja kod *Cuphea procumbens* nakon 6 roditeljskih dijalela. Visoka vrednost dominantnosti (H_1) i (δ^2s) i overdominantnosti dobijenih kod (H_1/D)^{0.5} i grafička analiza pokazuju da geni sa neaditivnim efektima preovladavaju u nasleđivanju hektolitarske mase i sadržaja ulja. Najbolja kombinaciona sposobnost utvrđena je kod roditelja 'NBC-30' u F_1 i 'NBC-03' u F_2 generaciji za hektolitarsku masu i kod 'NBC-30' u obe generacije za sadržaj ulja. Ukrštanja 'NBC-12' x 'NBC-30', 'NBC-01' x 'NBC-03' i 'NBC-12' x 'NBC-20' za hektolitarsku masu i 'NBC-01' x 'NBC-03' i 'NBC-25' x 'NBC-30' za sadržaj ulja su bile najbolje kombinacije ukrštanja sorti u obe generacije. Genetičke kombinacije ovih ukrštanja su bile aditivni x aditivni, aditivni x dominantni i dominantni x dominantni tip interakcije zahvaljujući visoka x visoka, visoka x niska i visoka x niska kombinaciona sposobnost. Izložen je plan oplemenjivanja kojim će se stvoriti genotipovi glatkog semena i povećanog sadržaja ulja.

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