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# Gene action and combining ability analysis for seed yield components of *Jatropha curcas* L.

**Yogendra K. Tripathi, R. V. Kumar*, Parul Shukla, V. K. Gupta and A.K. Handa**
National Research Centre for Agroforestry, Jhansi-284003, India
*Indian Grassland & Fodder Research Institute, Jhansi, India
Corresponding author email: ygene2005@yahoo.co.in

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## Abstract

Forty five cross combinations were produced by a half diallel-mating system using ten germplasm for gene action and combining ability analysis in *Jatropha curcas* L. The results showed presence of genetic diversity among the parents for all the characters. Moreover, the estimates of ó$^{2}$ GCA and ó$^{2}$ SCA revealed involvement of both additive and non-additive gene action in the inheritance of all the traits under investigation but the magnitude of non-additive gene effects was very high for all the traits. Amongst parental lines, NRCJ-1and NRCJ-2 were best general combiners for plant height, collar diameter, number of branches, branch length, seed yield, number of female flowers and oil content. The most promising specific combiners for seed yield were NRCJ-2 x NRCJ-8, NRCJ-3 x NRCJ-9 and NRCJ-6 x NRCJ-7 and for oil content were NRCJ-3 x NRCJ-9, NRCJ-2 x NRCJ-5 and NRCJ-2 x NRCJ-4. These crosses were found to involve at least one parent with high GCA (General Combining Ability) effect and other parents having either high, average or low GCA effect indicating the involvement of additive as well as non-additive gene action operating in these crosses. In this study, the non-additive gene action played an important role in the inheritance of all seed yield traits, which justifies the role of heterosis breeding for rapid improvement of *Jatropha curcas* L.

**Key words:** Additive and non-additive effects, Biofuel, GCA, Half diallel analysis, *Jatropha curcas* L., SCA

## Introduction

*Jatropha curcas* L., a drought hardy tropical, subtropical small tree (3-4m height), is found through out India under wild natural habitats. It is propagated easily by seed or cuttings. The kernel forms 60-68% w/w of seed and the oil content is 50-60% in kernel and around 30-40% in seed (Kumar *et al*., 2007, 2008). Presently, *Jatropha curcas* is widely known as plant with vast industrial importance for production of bio-fuel in India. In order to reduce the risk of future unsustainable practices and to improve future crop performance, further selection, breeding and domestication of *Jatropha* is primordial. However, substantial prebreeding knowledge is important to facilitate and guide an effective and robust route towards its domestication (Namkoong *et al*., 2004). Knowledge about the degree of genetic diversity among and within natural populations in and outside the center of origin is required to gain the first ideas about where to find potentially valuable genetic material (Kumar *et al*., 2009). Parental selection for creating genetic variability for crop improvement requires knowledge of the likelihood of improving traits of interest. Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis (Sarker *et al.,* 2002; Rashid *et al.,* 2007). The work on genetic improvement of this species is still at the stage of infancy. Thus, our study represents part of wider investigation on gene action and combining ability for seed yield components of *Jatropha curcas*.

## Materials and Methods

**Plant material**: Twenty seven germplasm collected from different geographical locations of India were planted at Experimental farm of National Research center for Agroforestry, Jhansi, India in 2004 and evaluated for the potential accessions of *Jatropha curcas*. Out of twenty seven accessions, ten best performing parent's *viz*., NRCJ-1, NRCJ-2, NRCJ-3, NRCJ-4, NRCJ-5, NRCJ-6, NRCJ-7, NRCJ-8, NRCJ-9 and NRCJ-10 were selected as desirable ideotype and utilized for development of crosses (Table 1).

**Table 1**: Source of parents and special (high in value) characters

| Name of parents | Source | Characters | Latitude | Longitude |
|---|---|---|---|---|
| NRCJ-1 | Dhodar, Ratlam (Madhya Pradesh) | PH, CD, NB, BL, SY, SL, ST, SW, FL, FW, NS, MF, FF, L, C, PPO, P, NDF, ADF, Lig.,CP, Cellu and hemi. | 23$^{0}$46' 29.86''N | 75$^{0}$06' 23.47''E |
| NRCJ-2 | Dhodar, Ratlam (Madhya Pradesh) | PH, CD, NB, BL, SY, FL, FW, NS, MF, FF, L, C, PPO, P, NDF, ADF, Lig.,CP, Cellu and hemi. | 23$^{0}$46' 34.31''N | 75$^{0}$06' 23.75''E |
| NRCJ-3 | Dhodar, Ratlam (Madhya Pradesh) | PH, CD, FW, NS, SL, ST, SW, MF, FF, L, NDF, ADF, Cellu and hemi. | 23$^{0}$46' 29.77''N | 75$^{0}$06' 38.20''E |
| NRCJ-4 | Jaura, Ratlam (Madhya Pradesh) | PH, NB, BL, SL, ST, SW, FF, L, C, ADF, Lig. and hemi. | 23$^{0}$38' 18.47''N | 75$^{0}$06' 54.50''E |
| NRCJ-5 | Mundari, Ratlam (Madhya Pradesh) | FF, NB, P and Lig. | 23$^{0}$20' 31.43''N | 75$^{0}$02' 75.05''E |
| NRCJ-6 | Palash, Ratlam (Madhya Pradesh) | PH, BL, SL, ST, SW, FL, FF, P, CP, ADF and Cellu. | 23$^{0}$19' 15.73''N | 75$^{0}$06' 25.80''E |
| NRCJ-7 | Karwar, Jhabua (Madhya Pradesh) | SW, ST, FF, FL and FW | 23$^{0}$06' 03.00''N | 74$^{0}$51' 46.45''E |
| NRCJ-8 | Godaria, Jhabua (Madhya Pradesh) | PH, BL and MF | 22$^{0}$46' 45.99''N | 74$^{0}$35' 12.16''E |
| NRCJ-9 | Thandla, Jhabua (Madhya Pradesh) | FE, NS, Cellu. and ADF | 23$^{0}$00' 36.29''N | 74$^{0}$34' 59.02''E |
| NRCJ-10 | Meghnagar, Jhabua (Madhya Pradesh) | SL, SW, ST, FL, FW and NS | 22$^{0}$54' 19.16''N | 74$^{0}$31' 35.59''E |

**PH**: Plant height, **CD**: Collar diameter, **NB**: Number of branch, **BL**: Branch length, **MF**: Male flower, **FF**: Female flower, **SL**: Seed length, **SW**: Seed width, **ST**: Seed thickness, **NS**: Number of seeds **FL**: Fruit length, **FW**: Fruit width, **SY**: Seed yield, **L**: Laccase, **P**: Peroxidase, **PPO**: Polyphenol oxidase, **C**: Cellulase, **ADF**: Acidic detergent fiber, **NDF**: Neutral detergent fiber, **CP**: Crude Protein, **Lig**. Lignin, **Cellu**.: Cellulose and **Hemi**. : Hemicellulose

Ten accessions were used as parents in half diallel fashion making a total of 45 crosses during the flowering stage (July-Aug 2005). A set of fifty-five entries consisting of ten parents and their forty-five resultant $F_1$ hybrids were sown in a randomized block design with three replication in July, 2006. The spacing between plant-to-plant and row-to-row was kept 4m x 4m. All the recommended agronomic practices and plant protection measures were adopted for raising crop. The observations were recorded on five randomly selected plants in each replication for all characters in 2006-2008.

**Statistical procedures:** The data recorded on 55 entries (10 parents and 45 $F_1$'s) were subjected to analysis of variance as per Panse and Sukhatme (1967) using linear model, second-degree heredity parameter by Griffing (1956a) and Gardner and Eberhart (1966). Variance due to gca effects and sca effects were made free from environmental variation. The characters showing significant variance components were subjected to further partition into general and specific combining ability following Griffing (1956b) Method-2, Model-1 (fixed model).

## Results and Discussion

The mean sum of squares revealed highly significant differences among genotypes for all the characters. The partitioning of mean squares due to genotypes indicated that mean squares due to parents as well as hybrids were highly significant for all the traits under study expect for seed width, seed thickness and number of seed. It suggested presence of considerable genetic variability among parents and hybrids for plant height, collar diameter, number of branch, branch length, number of male flower, number of female flower, fruit length, fruit width, seed length, seed yield per plant, oil content and also suggested that the selection of the parents was quite worthy. The magnitude of mean square due to parents *vs* hybrids were relatively high for plant height, collar diameter, number of branch, branch length, fruit length, fruit width and number of seed, seed yield per plant, oil content, which stated presence of high amount of useful heterosis for these traits. Both the general and specific combining ability variance was highly significant for all the characters, which suggested the presence of sufficient genetic variability among the parents utilized under the investigation. The magnitude of SCA variance was very high as compared to GCA for all the characters. Additionally, the ratio of ó$^2$gca/ ó$^2$sca being less than unity, suggest the importance of non-additive/dominance gene action.

The high and positive estimates of GCA effects were recorded for plant height (NRCJ-1 and NRCJ-2), collar diameter (NRCJ-1 and NRCJ-2), number of branches (NRCJ-1, NRCJ-2 and NRCJ-4), branch length (NRCJ-1and NRCJ-2), male flower/inflorescence (NRCJ-1), female flower/inflorescence (NRCJ-1 and NRCJ-2), number of seeds (NRCJ-3), seed width (NRCJ-10), seed thickness (NRCJ-4), fruit length (NRCJ-1 and NRCJ-10), seed yield (NRCJ-2 and NRCJ-1), oil content (NRCJ-1and NRCJ-2) (Table 2).

Both significant positive as well as significant negative SCA effects were observed for plant height. Out of 45 hybrids, eleven hybrids had significant positive SCA effects for the plant height. Twenty three crosses expressed the positive combination for collar diameter. Only eight hybrids showed the positive and significant SCA effects for number of branches. Eight hybrids recorded positive and significant SCA effects for branch length. The hybrid NRCJ-6 x NRCJ-10 recorded the highest and positive significant SCA effects for branch length and thus was observed to be good specific combination. Number of flowers per inflorescence is one of the most important attributes related to seed yield per plant and the hybrid NRCJ-9 x NRCJ-10 registered very high and positively significant SCA effects for female flower/inflorescence. Fifteen hybrids showed the positive and significant SCA effects out of the total hybrids. Twenty eight hybrids marked the desirable positively SCA effects for number of seeds per fruit. The hybrids combination, NRCJ-2 x NRCJ-10 exhibited highly positive SCA effects for seed length. High significant SCA effects for seed width were registered with NRCJ-2 x NRCJ-5. NRCJ-6 x NRCJ-10 estimated highly significant positive SCA effects for seed thickness. The cross NRCJ-5 x NRCJ-9 recorded highly significant positive SCA effects and considered as the best specific combinations for the fruit length trait. The crosses NRCJ-9 x NRCJ-10 expressed highly significant positive SCA effects for fruit width and thus may be considered as very good specific combination for the trait. The hybrid combinations NRCJ-2 x NRCJ-8, NRCJ-3 x NRCJ-9 and NRCJ-6 x NRCJ-7 exhibited highly significant positive SCA effects for seed yield per plant. Thirteen cross recorded highly significant positive SCA effects for oil percent, the most important economic trait. The crosses *viz.,* NRCJ-1 x NRCJ-2 and NRCJ-1 x NRCJ-3 involving good x good combining parents did not record highest SCA effects. While NRCJ-2 x NRCJ-8 and NRCJ-2 x NRCJ-9 recorded high significant SCA effects results from good x poor and good x average. This indicated the inconsistent expression of SCA in the specific hybrids irrespective of the GCA effects of the parents. However, a comparative study of the hybrids based on SCA effects and *per se* performance revealed that the majority of hybrids which have higher yield had either one or both the parent as good/average general combiner for seed yield. The hybrid NRCJ-2 x NRCJ-8 with good x poor general combiners registered the highest SCA effect for seed yield per plant. This indicated that the parents with higher GCA effects are desirable for a hybrid having high SCA effects for realization of the maximum heterosis. The examination of data revealed that the hybrids having higher estimates of SCA resulted from good x good, good x poor, poor x average and poor x poor general combiners. Better performance of hybrids involving poor x poor or average x poor general combiners indicated dominance x dominance (epistasis) type of gene action. Such hybrids could be utilized in the production of high yielding homozygous lines (Darah and Hallauer, 1972). The hybrids showing high SCA effects involving one good general combiner indicated additive x dominance type of gene interaction, which could produce desirable type of transgressive segregants in subsequent generation. However, looking the *per se* performance, it was obvious that the hybrids resulted from good x poor general combiners ranked first for seed yield and other yield contributing characters. This showed that the additive gene action has contributed towards the better expression of these traits. It was also noted that at least one good general combiner was necessary for better expression of these traits in the hybrids. Study reveals importance of both additive and non-additive gene effects in governing yield and most of the yield attributes with predominance of non-additive gene action for most of the yield attributes. In this situation, where both non-additive and additive components were important for the expression of characters, especially when the former component is predominant, simple pedigree method of selection would be ineffective for its improvement. At the same time population improvement programme like reciprocal recurrent selection which may allow to accumulate the fixable gene effects as well as to maintain considerable variability and heterozygosity for exploiting non-fixable gene effects will prove to be the most effective method (Joshi, 1979).

**Table 2**: Estimates of general combining ability (GCA) effects of parents for various characters in *Jatropha curcas*.

| Parents | Plant height | Collar diameter | Branch length | Number of branch | Number of Male flower | Number of Female flower | Seed yield / plant |
|---|---|---|---|---|---|---|---|
| NRCJ-1 | 25.3683** | 1.5514** | 13.4306* | 2.0759** | 24.3011** | 4.2389** | 93.1555* |
| NRCJ-2 | 8.1711 | 0.3858* | 13.8450** | 0.3690 | 12.5233* | 0.7667 | 149.6278** |
| NRCJ-3 | -2.4178 | 0.0039 | 7.8071 | -0.1514 | 2.3733 | 0.1556 | 74.4888 |
| NRCJ-4 | -3.9983 | -0.0572 | -4.0046 | -0.4690* | 1.1011 | 0.0722 | 60.4055 |
| NRCJ-5 | -0.9706 | -0.3056 | -3.7132 | -0.4144* | -9.9489 | -0.8722 | -57.3444 |
| NRCJ-6 | -5.8428 | -0.2310 | -2.7343 | -0.4102 | -10.3433 | -1.2333 | 49.1000 |
| NRCJ-7 | -7.1706 | -0.2398 | -8.8450 | -0.4046 | -5.2822 | -1.5111 | -188.344 |
| NRCJ-8 | -0.1372 | -0.4507** | -7.2276 | -0.4597* | -2.4878 | -0.5944 | -98.7333 |
| NRCJ-9 | -8.1872 | -0.3956* | -6.2568 | 0.1815 | -8.0489 | -1.7889* | -104.594 |
| NRCJ-10 | -4.8150 | -0.2614 | -2.3012 | -0.3171 | -4.1878 | 0.7667 | 22.2388 |
| **S.E. ($g_i$)** | **2.9535** | **0.1079** | **3.0076** | **0.0915** | **3.3613** | **0.5149** | **23.8629** |
| **S.E.($g_i$-$g_j$)** | **4.4029** | **0.1608** | **4.4834** | **0.1364** | **5.0107** | **0.7676** | **35.5728** |
| **CD (5%)** | **8.6296** | **0.3151** | **8.7875** | **0.2674** | **9.8209** | **1.5045** | **69.7227** |
| **CD (1%)** | **11.3418** | **0.4142** | **11.5493** | **0.3515** | **12.9075** | **1.9773** | **91.6356** |

| Parents | Fruit length | Fruit width | Seed thickness | Seed length | Seed width | Number of seed | Oil content |
|---|---|---|---|---|---|---|---|
| NRCJ-1 | 0.1308** | 0.0203 | 0.0300 | 0.0571 | 0.0061 | 0.0038 | 1.9972** |
| NRCJ-2 | 0.0392 | 0.0453 | -0.0450 | -0.0100 | -0.0330* | -0.0104 | 3.1222** |
| NRCJ-3 | -0.0058 | 0.0204 | 0.1800* | 0.0267 | 0.0225 | 0.0103 | 0.3583 |
| NRCJ-4 | -0.0500* | -0.0130 | -0.1450 | 0.0214 | 0.0204 | 0.0412** | -1.5139** |
| NRCJ-5 | -0.0575* | -0.0222 | -0.0117 | -0.0790 | -0.0329* | -0.0307 | -2.0417** |
| NRCJ-6 | 0.0025 | 0.0128 | -0.1117 | 0.0004 | 0.0008 | 0.0078 | -0.4444 |
| NRCJ-7 | -0.0483* | -0.0672 | -0.0367 | -0.0072 | -0.0061 | -0.0056 | -0.0333 |
| NRCJ-8 | -0.0200 | -0.0230 | -0.0200 | -0.0127 | 0.0019 | -0.0176 | 0.1222 |
| NRCJ-9 | -0.0450 | 0.0978** | 0.1050 | -0.0080 | 0.0020 | -0.0058 | -1.2750** |
| NRCJ-10 | 0.0542* | -0.0713* | 0.0550 | 0.0116 | 0.0183** | 0.0070 | -0.2917 |
| **S.E. ($g_i$)** | **0.0157** | **0.0194** | **0.0510** | **0.0297** | **0.0097** | **0.0093** | **0.1412** |
| **S.E.($g_i$-$g_j$)** | **0.0234** | **0.0290** | **0.0760** | **0.0443** | **0.0145** | **0.0138** | **0.2106** |
| **CD (5%)** | **0.0458** | **0.0568** | **0.1490** | **0.0868** | **0.0284** | **0.0271** | **0.4127** |
| **CD (1%)** | **0.0602** | **0.0746** | **0.1958** | **0.1141** | **0.0373** | **0.0356** | **0.5424** |

** and ** indicated significant at 5% and 1% level of probability, respectively.*

The identification of specific parental combination capable of producing the desired level of $F_1$ heterotic effect is important in improving the yield potential of this crop. Thus, our study on combining ability provides a useful clue for selection of desirable parents for the development of better hybrids.

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## References

Darah, L. L. and A. R. Hallauer 1972. Genetic effect estimates from generation mean in four diallel sets of maize inbreds. *Crop Sci.* 12: 615-621.

Gardner, C. O. and S. A. Eberhart 1966. Analysis and interpretation of the variety cross diallel and related population *Biometrics* 22: 439-452.

Griffing, B. 1956a. A generalized treatment of the use of diallel crosses in quantitative inheritance *Heredity* 10: 31-50.

Griffing, B. 1956b. Concept of general and specific combining ability in relation to diallel crossing system *Austr. J. Bioscience* 9:463-493.

Joshi, A. B. 1979. Breeding methodology for autogamous crops. *Indian J. Genet.* 39: 567-578.

Kumar, R. V., Y. K. Tripathi, V. P. Yadav and S. P. Ahlawat. 2008. Oil percentage in *Jatropha curcas* L germplasm of national agroforestry repository. *Indian J. Genet.* 68 (4): 463-466.

Kumar R. V., Yogendra K. Tripathi, Parul Shukla, S. P. Ahlawat and V. K. Gupta. 2009. Genetic diversity and relationships among germplasm of *Jatropha curcas* L revealed by RAPDs. *Trees - Structure and Function* 23(5): 1075-1079.

Kumar R. V., Y. K. Tripathi, V. P. Yadav and S. P. Ahlawat. 2007. Study on laccase, peroxidase, cellulase and polyphenol oxidase enzyme activities in *Jatropha curcas* L *Indian J Agroforestry* 9 (1): 42-46.

Namkoong, G., R. C. Lewontin and A. D. Yanchuk. 2004. Plant genetic resource management: The next investments in quantitative and qualitative genetics. *Genet. Resour. Crop Evol.* 51: 853-862.

Panse, V. G. and P. V. Sukhatme 1967. *Statistical Methods for Agricultural Workers*, Indian Council of Agricultural Research, New Delhi.

Rashid, M, A. A. Cheema and M. Ashraf, 2007. Line x tester analysis in basmati rice. *Pak. J. Botany* 39 (6): 2035-2042.

Sarker, U. P., S. Biswas, B. Prasad and M. A. Khaleque Mian. 2002. Heterosis and genetic analysis in rice hybrid . *Pak. J. Biological Sciences* 5 (1): 1-5.