

GENERATION MEAN ANALYSIS IN FINGER MILLET

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ABSTRACT

Five generation mean analysis was undertaken in finger millet (*Eleusine coracana* Gaertn.) involving six parents, Co 7, Co 9, Co 13, Indaf 9, MS 2655 and MS 2863 and F₁, F₂ and F₃ generations of four crosses Co9 x Co13, Co9 x Indaf 9, Co9 x Co7 and MS 2863 x MS 2655 for eight quantitative characters. The study revealed the importance of both additive and non-additive types of gene action for all the characters studied. Predominance of additive gene action was noted for days to 50 per cent flowering, plant height and 100 grain weight while non-additive gene action played a major role in the inheritance of the other five characters, viz., number of productive tillers per plant, number of fingers per ear, finger length, ear weight per plant and grain yield per plant. Breeding methods such as biparental mating, recurrent selection and reciprocal recurrent selection techniques were suggested for the improvement of the characters studied.

KEY WORDS : Finger millet, generation mean, gene action

The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population (Singh and Singh, 1990). Generation mean analysis, which provides the estimates of the main gene action (additive (d) and dominance (h) and their digenic interactions (additive x additive (i) additive x dominance (j) and dominance x dominance (l) help in understanding the performance of parents used in the crosses and in determining various breeding methods for improvement of the character in question.

MATERIALS AND METHODS

The experiment was conducted at the Regional Research Station, Paiyur, Dharmapuri district. During May 1992, the material comprising of 18 entries viz. 6 parents, 4 F₁s, 4 F₂s and 4 F₃s of the crosses Co9 x Co13, Co9 x Indaf 9, Co9 x Co7 and MS 2863 x MS 2655 were raised in a randomised block design with three replications. Each parent and F₁ was planted in two rows of 3 m length. Each F₂ was planted in 6 rows while 10 rows of F₃ lines from each cross were raised utilising the seeds of 10 F₂ plants selected during the previous season. Each row had 30 plants adopting a spacing of 22.5 x 10 cm. In each replication, 20 plants from each parent, 5 plants from each F₁ population and 100 plants from each F₂ and F₃ population were labelled. The data were collected on single plant basis in the above five generations viz., P₁, P₂, F₁, F₂ and F₃ of the 4 cross combinations for 8

quantitative characters: days to 50 per cent flowering, number of fingers per ear, finger length, ear weight per plant, 100 grain weight and grain yield per plant. Mean, standard deviation, standard error and coefficient of variability were computed from the entire data ignoring replications (panse and Sukhatme, 1967).

Mather's scaling tests C and D were applied to detect the presence of epistasis for the eight characters (1949). Five parameter model was used to estimate the gene effects m(F₂ mean), d, h, i and l following the method of Hayman (1958). Significance of scales and gene effects were tested by 't' test (Singh and Chaudhary, 1985). The type of gene actions (complementary or duplicate) was assessed based on the sign of 'h' and 'l' gene effects (complementary same sign and duplicate - opposite sign).

RESULTS AND DISCUSSION

In the present study, the parents Co7 and Co9 were earlier in flowering and lesser in plant height. Co13 besides short duration was found superior for number of productive tillers, number of fingers and grain yield per plant than other parent while Indaf 9 ranked first for mean finger length, ear weight and 100 grain weight. MS 2863 was almost equal to Indaf 9 with regard to finger length and ear weight. F₁ generations of Co9 x Indaf 9 showed high mean expression for productive tillers, ear weight, 100 grain weight and grain yield while Co9 x Co13 was found to be superior for number of fingers and

Table 1. Scaling tests and estimation of gene effects in finger millet

Para meter	Days to 50% flowering				Plant height				No. of productive tillers/plant				No. of fingers/ear			
	C ₁	C ₂	C ₃	C ₄	C ₁	C ₂	C ₃	C ₄	C ₁	C ₂	C ₃	C ₄	C ₁	C ₂	C ₃	C ₄
Scaling test																
C	4.89*	-2.51	-5.06*	19.65*	31.84*	45.56*	-55.46*	22.19*	-4.22*	-9.07*	-2.40*	-7.56*	-4.42*	0.76	3.32*	2.53*
D	6.77*	4.63*	24.76*	22.19*	8.14	-5.08	75.04*	33.77*	-2.06*	-2.47*	-0.56	-0.82*	1.26*	1.54*	1.80*	-1.15*
Gene effects																
m	69.49*	70.48*	65.71*	75.85*	112.53*	119.85	86.72*	115.16*	3.52*	3.28*	3.60*	2.59*	7.50*	7.43*	7.74*	8.80*
d	1.03*	-3.93*	1.45*	0.88*	-4.76*	-10.75*	1.14	4.31*	-0.25*	0.03	0.16*	0.14*	-1.69*	-0.94*	0.04	0.82*
h	-2.45*	-14.28*	-13.74*	-8.95*	9.22*	16.12*	-46.10*	-21.70*	1.08	3.04*	0.45*	0.77*	-0.35	-2.39*	0.65	1.41*
i	62.92*	57.17*	49.27*	59.01*	95.02*	106.12*	35.87*	96.55*	4.79*	4.26*	4.09*	3.17	4.73*	3.15*	5.65*	9.34*
l	2.51	9.52	39.76*	3.39	-31.60*	-67.52*	174.00*	15.44	2.88*	8.80*	2.45*	8.99*	7.57*	7.07*	-2.03	-4.91
Type of epistasis																
	Dup	Dup	Dup	Dup	Dup	Dup	Dup	Dup	Com	Com	Com	Com	Dup	Dup	Dup	Dup
Scaling tests																
C	4.19*	7.62*	-1.34*	3.07*	-22.81*	-42.08*	-21.87*	-21.44*	0.03	0.06	0.36*	0.14*	-21.65*	-33.19*	-16.53*	-21.29*
D	6.39	-5.26*	5.96*	2.33*	-8.39*	12.40*	15.29*	-7.04*	0.45*	0.32*	0.40*	0.06*	-7.75*	11.47*	9.57*	-6.39*
Gene effects																
m	7.73*	9.82*	6.02*	9.25*	16.36*	14.19*	14.13*	14.19*	0.28*	0.34*	0.36*	0.30*	12.67*	11.53*	11.45*	10.53*
d	-0.97*	-2.56*	-0.05	0.40*	-1.35*	-1.60*	0.37*	0.75*	-0.01*	-0.03*	0.01*	0.01*	-1.20*	-0.75*	0.21	-0.16
h	-2.15	5.47*	-2.50*	-1.77*	6.89*	-5.40*	-10.25*	1.12	-0.22*	-0.07*	-0.11*	-0.03	6.26*	-4.11*	-6.62*	1.05
i	1.45	9.79*	1.26*	8.20*	19.96*	1.89	4.33*	22.35*	-0.07*	0.03	0.02	0.26*	16.10*	1.35	5.40*	16.24*
l	2.93	-17.17	16.16*	-0.99*	19.23*	76.64*	49.55*	21.87*	0.56*	0.35*	0.05	-0.11	18.48*	59.55*	34.80*	19.87*
Type of epistasis																
	Dup	Dup	Dup	Com	Com	Dup	Dup	Com	Dup	Dup	Dup	Dup	Com	Dup	Dup	Com

C₁ = Co9 x Co13; C₂ = Co9 x Indaf 9; C₃ = Co9 x Co7; C₄ = MS 2863 x MS 2655; * = Significant at 5% level; Com = Complementary; Dup = Duplicate

finger length than their parents. The other two crosses Co9 x Co7 and Ms 2863 x MS 2655 were mid way to their parents for all the characters. However, all these F₁s recorded increased means over their mid parental values.

In the F₂ generation, the cross Co9 x Co13 recorded low means for days to 50% flowering and plant height. It also showed increase in ear weight and grain yield than the other F₂s. The crosses Co9 x Indaf 9, Co9 x Co7 and MS 2863 x MS 2655 were found to be superior for mean finger length, number of fingers and 100 grain weight respectively. In F₃ generation, the cross Co9 x Co13 recorded less mean for days to 50 per cent flowering and plant height while Co9 x Indaf 9 recorded high mean for number of fingers, ear weight and grain yield followed by the crosses Co9 x Co13 and Co9 x Co7. The crosses MS 2863 x MS 2655 and Co9 x Co7 were found to be superior for mean finger length and 100 grain weight respectively. Decrease in mean for days to flowering in the F₃ generation from F₂ was observed in the crosses Co9 x Co7 and Co9 x Indaf 9 while such decrease in plant height was recorded

in the crosses Co9 x Co13 and Co9 x Indaf 9. In the crosses Co9 x Co13 and Co9 x Indaf 9, there was increase in the mean values of finger length and 100 grain weight from F₂ to F₃. Mean productive tillers was found higher in the F₃s of Co9 x Co7 and MS 2863 x MS 2655 than their F₂s. In the crosses Co9 x Co13, Co9 x Co7 and MS 2863 x MS 2655, mean finger length increased from F₂ to F₃ whereas such an increase was recorded for mean ear weight and grain yield in all the crosses except Co9 x Co13.

The generation mean analysis revealed the role of digenic non- allelic interaction for the inheritance of the yield and its seven components of finger millet as measured by the significance of either scale C or D or both (scaling tests) in the four crosses studied (Table 1).

For days to flowering, the fixable type of gene effects were predominant in most of the crosses with duplicate type of epistasis suggesting biparental mating approach for the improvement of this character. Presence of both fixable and non-fixable gene action with predominance of the

former with mostly duplicate type of epistasis was observed for the characters plant height, number of fingers per ear and finger length. Under such situations, intermating of the selected plants in the early segregating generation (biparental mating) may be employed. For number of productive tillers per plant the fixable and non-fixable types of geneaction with complementary type of epistasis was noted suggesting recurrent selection technique for improving this character. With regard to 100 grain weight, both fixable and non-fixable types of gene action with predominance of the latter and duplicate type of epistasis were recorded. For this case also, recurrent selection procedure may be useful. In respect of ear weight and grain yield, presence of additive, dominance, additive x additive and dominance x dominance gene effects suggested scope of employing reciprocal recurrent selection for the genetic upgradation of these

characters. The method also provides opportunities for breaking up of undesirable linkages and possibilities of throwing high yielding lines under selection pressure.

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INHERITANCE OF DURATION, LEAF COLOUR, STERILITY MOSAIC DISEASE RESISTANCE AND GROWTH HABIT IN PIGEONPEA

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ABSTRACT

Direct and reciprocal crosses were attempted between two contrasting pigeonpea varieties viz., Vamban-1 and Gulbarga-1. The study of parents, hybrids and F₂ segregating population revealed that the characters such as duration, leaf colour, resistance to sterility mosaic disease and growth habit are monogenetically controlled and are inherited as a linkage block or single unit of recombination. The linkage block has been designated as EDgRDt and its allelic block as edgrdt.

KEY WORDS : Pigeonpea, monogenic, linkage block.

Pigeonpea is one of the most important grain legumes widely cultivated in India. Information available on the inheritance of morphological characters is limited. Some of the morphological characters may have linkage with important diseases viz., sterility mosaic, wilt and phytophthora blight. Thus, morphological characters could be used as markers for resistance to diseases. The knowledge of inheritance pattern of these characters is imperative. Therefore, the present study on the inheritance of duration, leaf colour, resistance to sterility mosaic disease and growth habit was conducted.

MATERIALS AND METHODS

Both direct and reciprocal crosses were attempted between two contrasting pigeonpea varieties viz., Vamban-1 and Gulbarga- 1 during March 1994 at the National Pulses Research Centre, Vamban. The well filled crossed seeds were hand picked and sown as F₁ hybrids and studied during *rabi* 1994. The performance of the parents and the hybrids are given in Table 1. High yielding true hybrids from both cross combinations were identified, tagged and forwarded to F₂ as single plant progenies and studied during summer 1995. Observations were made on the following characters at appropriate time of expression. The