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Induced Polygenic Mutation in Ragi* (*Eleusine coracana* (L.) Gaertn.)

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Two ragi genotypes MS 2698 (Bihar) and Sarada (Andhra Pradesh) were treated with N-methyl-N-nitroso N'-nitroguanidine. The mean, genetic variance, heritability and genetic advance were estimated in the M_2 and M_3 generation of these treated genotypes for seven metrical traits. In general, the mean values of most of the treatments in M_2 and M_3 did not substantially deviate from the control. There was, an increase in the genetic variance both in the M_2 and M_3. The M_3 variance of plant height was higher than that of M_2. For all the other characters studied, the M_3 variance was less than the M_2 variance. The heritability and genetic advance values were higher in the treatments than in the Control. Short duration mutants in Sarada and bold-seeded mutants in MS 2698 were obtained as a result of these investigations.

Ragi or finger millet is one of the most important millet crops grown in India. It is a highly self-pollinated crop and the variability in this crop is not as in the cross-fertilized crops. There fore, for enlarging the variability and to increase the scope of selection for yield potential in this crop, induced mutagenesis has been resorted to. The consequent changes in the polygene system measured in terms of mean and genotypic variance of chosen quantitative characters are presented in this paper.

MATERIAL AND METHODS

Two ragi genotypes MS 2698 (Bihar) with a duration of 75 days and Sarada (Andhra Pradesh) maturing in 110 days were treated with N methyl-N nitroso-*N* guanidine, a chemical mutagen in solid form. Based on LD_{50} values on survival of seedlings (Raveendran *et al.*, 1980) the chemical was used at 0, 5.0 and 10.0 m*M* concentrations each for two and four hours on both the varieties. Well filled seeds with a moisture content of 10.5 per cent were pre-soaked in distilled water for eight hours prior to the chemical treatment. All the surviving plants were advanced to M . There were a total number of 249 M_2 families in MS 2698 and 212 in Sarada. The treated families of both the genotypes along with respective controls were raised in two separate trials in randomised block design with two replications. The crop was provided with recommended package of practices. Five random plants were flag labelled at flowering in each row in each replication and observations were recorded on plant height at maturity, days to 50 per cent bloom, number of productive tillers, number of fingers per spike, mean length of fin-

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gers, grain yield per plant and hundred grain weight. The phenotypic variance was partitioned following the method suggested by Allard (1960) and genotypic variance and heritability were estimated. The genetic advance was calculated at five per cent selection intensity (Johnson *et al.*, 1955).

Seventy two plants from the M_2 families of MS 2698 and 55 from Sarada which did not segregate for visible mutations were advanced to M_3. Ten control progenies in each variety were also raised. The M_1 families from each of the two genotypes were raised in two separate trials laid out in randomised block design with three replications. The same characters that were studied in M_2 were measured in M_3 also for ten sample plants per row per replication. The statistical analysis was also similar to that adopted for M_2.

RESULTS AND DISCUSSION

The mean genotypic variance, heritability and genetic advance for all the characters are presented in tables 1 a to 1 d.

In general, the mean values of most of the treatments in M_2 and M_3 for the characters plant height, finger number, finger length and grain yield did not deviate substantially from that of the respective control populations. Although the general observarions on quantitative characters by most of the investigators indicated a slight negative shift in mean values, the choice of the optimum LD_{30} values for survival for raising M_2 and M_3 generations in the present study might have resulted in a substantial reduction of deleterious changes thereby maintaining the original mean values. However, in respect of days to 50 per cent bloom, the mean values of the treatments in Sarada were shifted towards the negative direction in M_2 while it fluctuated on either side in M_3. This reduction in mean value may be attributed to the presence of a larger number of mutants with negative effect than those with positive effect. In this genotype, several early maturing mutants and dwarf variants were obtained in the M_2. Effects such as appearance of early mutants in a late genotype and dwarf mutants in tall genotype through mutagenesis has been hypothesised by Brock (1965) to be due to random mutations shifting the mean away from the direction of the previous selection pressure on the parental genotype. Early mutants in late maturing strain ragi CO 1 were earlier identified by Thangavelu (1973). A positive shift in the mean value was also observed in the case of productive tillers in the M_2 generation of MS 2698 indicating that high tillering mutants have out-numbered those with few tillers. A positive shift in the mean productive tillers in ragi was reported by Goud *et al.*, (1971).

In both the genotypes under study, in the M_2 and M_3 generations, there was an increase in the genetic variance for most of the traits in the treated population as compared to the control. This is evidently due to the genetic segregation in the M_2 progenies of M_1 individuals heterozygous for the mutations. Previous reports on the increased variance as compared to the control in

this crop were made by Sreekantaradhya (1971), Goud *et. al.*, (1971) and Thangavelu (1973). The M_2 variance in respect of plant height was higher than that of the M_3 suggesting that the segregation of genes for this character persisted in M_3 generation also. However, with regard to other characters studied, the M_3 variance was less than that of M_2 in most of the treatments.

The heritability and genetic advance values of most of the treatments in the M_2 and M_3 generations of both the genotypes were higher than that of the respective control populations which may be due to the increased genetic variance. Previous reports of high heritabliity estimates were made by Thangavelu (1973) in ragi. In respect of 100 grain weight, the heritability and genetic advance estimates higher in the M_2 than in the M_3. The genotype MS 2698, in particular, showed this trend of higher genetic advance for seed size in M_3, indicating that there is good scope for obtaining mutants with bold seeds in small-seeded varieties. In other characters studied, there was a general decline in the values of these parameters in M_3 as compared to M_2. Aastveit and Gaul (1967), working in barley obtained higher values of heritability and genetic advance in the earlier generations of mutagen treated material. However, it was observad that these high values were not maintained in the ater generations. This phenomen on was attributed to the non-additive gene action, genotype environment interaction or a combination to both. while such hypothesis may hold good in the present investigation, the rapid attainment of homozygosity in such a highly self-fertilized crop plant may also result in the quick exhaustion of variability.

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TABLE 1a Mean and Genotypic variance in M_2 and M_3 generations.

Treatments	Mean ± SE		Genotypic variance		Heritability %		Genetic Advance	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
(a) Plant height (cm.)								
MS. 2698								
Control	100.0±2.4	100.0±1.4	1.13	18.52	17.6	29.8	1.58	7.44
NG 5 m*M* (2h)	100.4±3.2	100.0±0.9	33.20	29.73	10.6	52.6	6.51	11.49
NG 10 m*M* (2h	100.5±4.0	97.1±1.4	43.39	30.62	14.0	30.1	8.56	9.89
NG 5 m*M* (4h)	101.0±3.3	99.7±1.3	13.04	100.44	8.6	42.1	3.67	15.68
NG 10 m*M* (4h)	100.2±3.3	92.1±2.3	15.97	119.03	47.2	45.2	9.58	23.54
Sarada								
Control	100.0±1.5	100.0±1.7	15.20	20.22	14.4	6.3	3.63	2.37
NG 5 m*M* (2h)	98.6±0.9	98.8±2.2	28.68	38.66	40.4	7.4	8.41	3.62
NG 10 m*M* (2h)	97.3±0.8	110.2±2.3	133.21	133.90	66.3	32.9	23.68	12.75
NG 5 m*M* (4h)	100.0±1.2	99.9±2.3	89.43	71.15	77.0	40.8	20.35	11.40
NG 10 m*M* (4h)	99.0±0.8	108.1±1.0	132.70	220.85	55.2	33.6	21.20	16.87
(b) Days to 50 percent bloom								
MS. 2698								
Control	100.0±1.8	100.0±0.8	0.40	2.03	0.5	8.0	0.15	1.98
NG 5 m*M* (2h)	99.7±1.3	100.0±0.8	14.04	4.58	23.3	24.3	6.92	4.32
NG 10 m*M* (2h)	100.6±1.4	96.3±1.4	9.10	4.78	26.8	13.5	5.44	4.06
NG 5 m*M* (4h)	100.2±1.4	96.7±1.3	6.25	3.60	19.8	12.6	3.85	3.39
NG 10 m*M* (4h)	100.2±1.4	98.0±1.9	4.09	1.56	19.1	3.5	3.08	1.15
Sarada								
Control	100.0±0.6	100.0±1.1	2.40	12.30	19.7	19.0	1.69	4.89
NG 5 m*M* (2h)	98.2±0.4	105.7±1.2	3.74	25.03	32.9	31.2	2.74	8.46
NG 10 m*M* (2h)	96.5±0.6	95.4±1.8	3.93	10.98	24.4	13.5	2.46	4.09
NG 5 m*M* (4h)	100.0±0.4	96.4±1.2	2.68	3.27	28.2	4.6	2.13	1.29
NG 10 mM (4h)	98.7±0.6	95.4±1.2	8.19	12.69	50.9	35.3	5.05	7.10

TABLE 1b Mean and Variance in M_2 and M_3 generations.

Treatments	Mean±SE		Genotypic variance		Heritability (%)		Genetic Advance.	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
(c) Number of productive tillers/plant								
MS. 2698								
Control	100.0±9.1	100.0±4.9	0.11	0.08	3.8	6.8	3.48	5.73
NG 5 m*M* (2h)	104.4±7.1	124.9±2.4	2.59	0.17	28.9	28.8	41.88	17.60
NG 10 m*M* (2h)	101.5±7.4	122.9±6.8	1.46	0.25	91.6	14.0	18.60	15.08
NG 5 m*M* (4h)	105.2±6.9	122.9±6.4	0.79	0.09	17.4	7.7	17 99	6.74
NG 10 m*M* (4h)	100.5±9.8	127.1±7.8	1.33	0.89	19.1	36.1	26.60	44.24
Sarada								
Control	100.0±3.4	100 0±12.9	0.57	0.02	8.6	1.0	11.04	1.22
NG 5 m*M* (2h)	93.9±4.1	90.5± 4.7	1.99	0.11	34.2	9.2	44.04	10.00
NG 10 m*M* (2h)	96.4±5.1	96.1± 7.3	0.87	0.02	18.1	1.2	20.71	1.39
NG 5 m*M* (4h)	101.9±4.1	95.3±18.1	2 34	0.15	40.5	61.9	47.73	25.98
NG 10 m*M* (4h)	99.5±4.1	96.9±15.5	0.91	0.39	34.9	28.0	28.12	30.19
(d) Number fingers/panicle								
MS. 2698								
Control	100.0±1.9	100.0±4.9	0.71	0.15	14.7	9.9	5.84	3.40
NG 5 m*M* (2h)	102.2±1.4	93.2±1.2	2.42	1.50	54.3	58.1	21.63	28.16
NG 10 m*M* (2h)	101.1±1.4	93.6±2.1	2.91	0.60	70.0	23.0	26.20	11.16
NG 5 m*M* (4h)	98.7±1.8	95.9±3.2	1.04	1.46	35.7	24.2	11.99	17.46
NG 10 m*M* (4h)	101.1±1.8	98.2±2.2	1.67	0.21	52.6	10.9	15 59	4.38
Sarada								
Control	100.0±5·6	100.0±4.1	0.14	0.15	14.4	5.0	8.69	2.54
NG 5 m*M* (2h)	101.6±2.3	97.6±2.4	0.71	0.66	64.4	18.7	19.51	10.56
NG 10 m*M* (2h)	101.4±3.0	95.7±3.0	3 22	0.15	36.3	5.7	31.36	2 82
NG 5 m*M* (4h)	101.1±3.3	95.0±2.9	1.31	0.75	68.9	31.0	28.21	14.96
NG 10 m*M* (4h)	102.7±3.3	97.9±3.7	1.60	1.33	72.6	47.1	30.63	23.83

TABLE 1c Mean and Variance in M_2 and M_3 generations.

Treatments	Mean + SE		Genotypic variance		Heritability (%)		Genetic Advance	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
(e) Number of productive tillers/plant (cm.)								
MS. 2698								
Control	100.0±3.7	100.0±4.4	0.51	0.20	10.3	18.2	11.46	9.50
NG 5 m*M* (2h)	104.2±3.2	96.8±1.7	0.50	0.16	30.3	21.7	20.10	9.62
NG 10 m*M* (2h	102.2±4.7	97.1±1.2	4.46	0.16	73.0	90.7	89.88	19.47
NG 5 m*M* (4h)	105.6±3.0	98.8±2.2	3.08	1.32	83.1	64.5	76.69	46.94
NG 10 m*M* (4h)	103.5±6.2	96.1±2.4	0.23	0.27	19.1	29.9	10.28	14.97
Sarada								
Control	100.0±1.4	100.0±3.3	0.26	0.33	5.7	18.2	4.29	9.66
NG 5 m*M* (2h)	97.4±1.0	94.2± 1.9	0.61	0.33	54.7	14.3	21.21	9.06
NG 10 m*M* (2h)	99.7±2.3	99.6± 2.9	0.83	0.71	35.8	37.0	19.52	20.39
NG 5 m*M* (4h)	99.6±0.9	101.3±3.9	1.04	1.07	75.4	28.8	31.71	21.69
NG 10 m*M* (4h)	98.6±1.4	89.4±4.0	0.47	0.07	60.6	33.1	19.37	6.87
(f) Grain weight/plant (g)								
MS. 2698								
Control	100.0±17.3	100.0±5.0	4.66	1.38	12.8	17.5	32.89	20.12
NG 5 m*M* (2h)	90.6±18.1	90.8±2.4	10.84	1.56	17.8	43.4	53.92	37.50
NG 10 m*M* (2h)	90.3±18.2	92.2±7.2	15.59	2.47	22.5	62.8	73.22	55.76
NG 5 m*M* (4h)	93.2±12.8	986±3.4	10.64	3.01	31.4	53.1	68.73	52.97
NG 10 m*M* (4h)	89.2±7.5	105.0±9.2	11.19	6.45	31.4	31.6	73.7	56.02
Sarada								
Control	100.0±2.2	100.0±3.2	0.65	3.25	6.4	14.2	3.59	19.13
NG 5 m*M* (2h)	91.3±2.3	82.9±6.6	2.65	3.74	51.7	13.9	22.47	24.41
NG 10 m*M* (2h)	98.7±3.3	102.1±7.5	3.12	6.00	29.6	49.2	16.82	47.67
NG 5 m*M* (4h)	97.0±2.0	93.8±5.5	1.86	3.93	26.4	14.4	12.80	22.55
NG 10 m*M* (4h)	95.9±4.1	94.8±5.9	2.59	6.38	46.5	19.2	20.00	32.89

TABLE 1d. Mean and genotypic variance in M_2 and M_3 generation

Treatments	Mean ± SE		Genotypic Variance		Heritability %		Genetic Advance	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
	100 grain weight (g)							
MS 2698								
Control	100.0±0.7	100.0±0.7	2.47	3.72	17.5	17.5	0.69	0.85
NG 5 m*M* (2h)	101.5±0.6	99.0±1.4	6.38	6.89	21.3	29.5	1.20	1.47
NG 10 m*M* (2h)	93.3±0.6	91.8±1.6	7.21	13.54	38.7	30.6	1.89	2.34
NG 5 m*M* (4h)	97.4±0.5	92.8±0.7	10.18	15.38	39.7	42.5	2.18	2.92
NG 10 m*M* (4h)	96.9±0.6	97.4±0.5	9.43	13.98	43.5	39.5	2.21	2.56
Sarada								
Control	100.0±0.7	100.0±0.8	1.98	6.58	6.9	3.9	0.25	0.32
NG 5 m*M* (2h)	99.4±0.6	103.6±0.7	4.35	10.65	18.5	23.5	0.60	1.02
NG 10 m*M* (2h)	103.6±0.7	101.0±0.7	3.18	11.37	18.0	40.6	0.69	1.41
NG 5 m*M* (4h)	102.6±0.6	100.0±0.9	9.25	9.51	38.6	52.5	1.20	1.48
NG 10 m*M* (4h)	102.3±0.7	102.6±0.8	10.31	11.28	51.7	49.7	1.49	1.53

Mean and standard error expressed as percentage on control.

Genetic Advance expressed as perecntage on mean.