

MUTATION GENETIC STUDIES IN RICE-DEVELOPMENT OF PROTEIN RICH MUTANTS*

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Oryza sativa, the richest source of calorie intake, has amongst the cereals, the highest biological value, digestibility and protein efficiency ratio as well as a high lysine content. But its seed protein content is low. Though this could be increased through nitrogenous fertilizer and chemical applications and through agronomic management, influence of environmental factors upon protein quality is profound (Kaul, 1980). Developing protein rich genotype through conventional breeding procedures has not been successful, mainly because of the negative correlation existing between grain yield and seed protein content (Kaul, 1980). Since artificial mutagenesis offers a possibility for induction of desired attributes and perhaps some of those that either cannot be found naturally or have been lost (Kaul, 1978), induction of mutations in three rice varieties was attempted

Materials and Methods

Husked seeds of IR-8, Jhona-349 and Basmati-370 with moisture content stabilized at 13% were irradiated with 20, 30, 40 and 50 Kr *gamma* rays at a dose rate of 1250 rads/minute with Co 60 source at the I. A. R., New Delhi. EMS and DES were obtained from Eastman Kodak Ltd. (U. S. A.) and B. D. H. (India), respectively.

Seeds pre-soaked in distilled water for 12 hrs were treated at 30°C with 0.5, 1.0 and 1.5% aqueous solutions of EMS or DES for 6 or 2 hrs, respectively. DES solutions were changed after every half an hour, because of its quick half life period. To facilitate uniform solubility and absorption, flasks containing the seeds and mutagen were continuously shaken in a mechanical shaker and volume of the mutagens used was three times the volume of seeds treated. For sequential administration of mutagens, 20 Kr *gamma* ray irradiation either preceded or followed 1.00 percent solution of EMS for 6 hrs or DES for 2 hrs. After the treatments, the seeds were washed thoroughly for 30 minutes in running tap water.

Out of 296 mutants isolated in M_1 generation, 40 were selected and carried through M_2 generation in a split plot design with 100 plants each in four replications. Ten plants per treatment per genotype were selected randomly from each of the four replications and utilised for computing the data tabulated in Tables 1 and 2. Grains per panicle were recorded from the first emerging panicle of each plant. Grain length and breadth were measured by Vernier calipers and L : B ratio recorded as the index of grain fineness. Semi-micro kjeldahl method was followed for estimating the total nitrogen

of the brown rice. The value obtained thereof was multiplied by 5.95 to give the crude protein content of the seeds.

Genetic coefficients of variation was estimated by the formula suggested by **Burton (1952)** by dividing the square root of the genotypic variance by the population mean and multiplying it by 100. Heritability was calculated in the broad sense by the formula suggested by **Hanson *et al.* (1956)**. Expected genetic advance was estimated by the formula given by **Johnson *et al.* (1955)**.

Results and Discussion

Six mutants of IR 8 (Table 1) were high yielding and matured about 30 days earlier than the initial line. Grains of all the mutants were finer than those of the initial line. The crude protein content of the mutants ranged from 10.49% to 12.88%. This represents a remarkable improvement as the initial line has only 8.68% of crude protein content. Though 1000 grain weight of mutants decreased, a few of them are higher yielding than the initial line (Fig. 1). But all the mutants except IRm-7 which is the only dwarf mutant recorded with finer grains, better protein and enhanced seed protein production, besides being early had somewhat lesser grain yield. Amongst the mutants, IRm-1 exhibits the highest seed protein production (Fig. 1).

Six Jhona mutants (Table 2) exhibited both an increased crude protein content (11.49–13.34%) and seed protein production (2.45–3.50 g) though a slight degree of lodging occurred in them. Grains per panicle, grain yield per plant and seed protein production registered a significant increase in Jm-13 (Fig. 2). But it matured a few days later than the initial line and lodged due to more plant height. Of the fine grained mutants, JM-4, Jm-7, and Jm-4 have the longest grains (L: B 10.23 : 2.50 : 4.09) and the highest 1000 grain weight (28.8 g).

In contrast to IR 8 and Jhona-349, Basmati-370 yielded only two improved mutants (Table 2). Bm-2 and Bm-5 are superior in being early and in having, better crude protein content and overall seed protein production per plant (Fig. 2). Therefore, both the mutants are well on the scale and could reliably be used in hybridization programme and through backcrossing fine grain genes could be incorporated in them.

In order to assess the breeding value of these high protein mutants, genetic parameters of a few yield contributing traits were computed (Table 3). Heritability values are high for culm length, grain shape, 1000 grain weight and grains per panicle. Naturally, these traits will be subjected to a very low non-heritable or environmental variability. The expected genetic advance expressed as the percentage of mean had the highest value for the number of fertile grains per panicle (68.56). However, 42.48 percent expected genetic advance for yield is also quite significant.

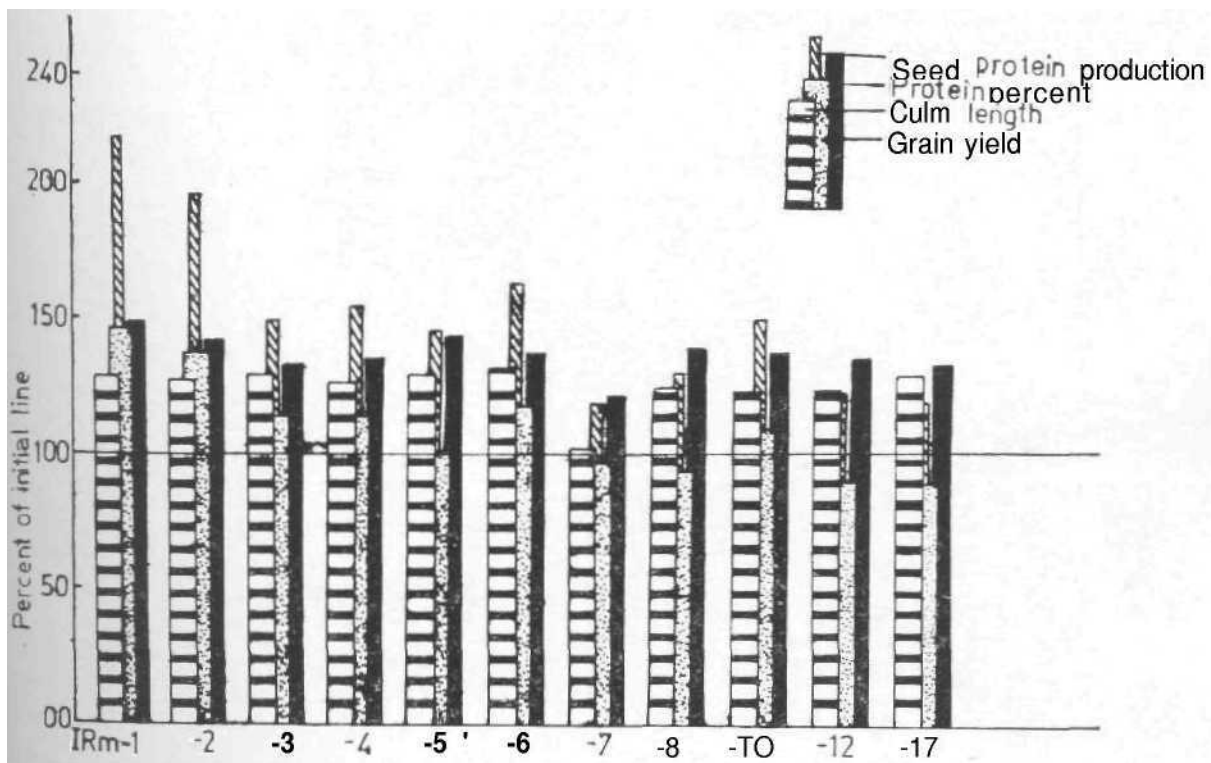


Fig.1: Performance of 'IR-8' mutants .

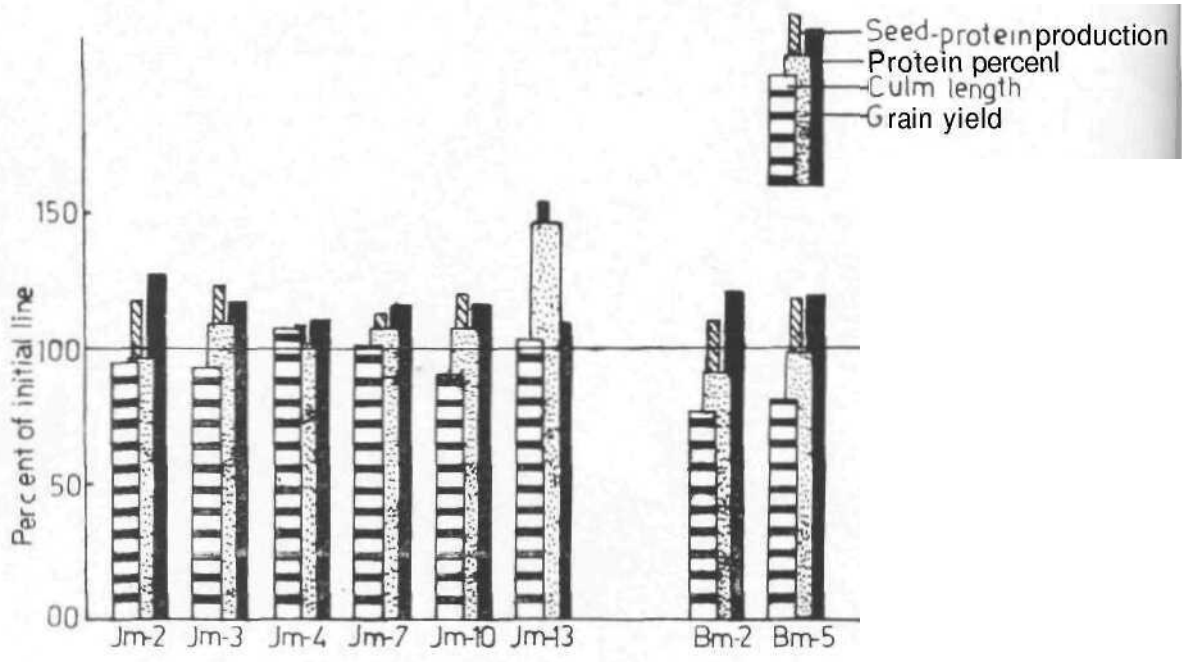


Fig.2: Performance of 'Jhona' and 'Basmati' mutants.

| No | Name | Dose | C | Til e s per plant | p N ² o m u s o | | S s o s | D in | Qain ield Per lant | G s o L.B | d ein | eed p tei o procu ion (%) |
|----|------|----------|------|-------------------------|----------------------------|-------|------------|---------|-----------------------------|--------------|----------|------------------------------------|
| | | | | | St e ff | S s | | | | | | |
| 1 | Rm-1 | 1.5% | 14.8 | 13.2 | 12 | 123.0 | 5.0 | 23.7 | 3.8 | 3.32 | 12.88 | 4.22 |
| 2 | Rm-2 | " | 14.0 | 2.0 | 07 | 113.9 | 6.4 | 22.8 | 3.8 | 3.82 | 12.29 | 3.79 |
| | Rm-3 | " | 15.3 | 0.3 | 08 | 122.7 | 4.0 | 24.7 | 2.0 | 3.97 | 11.55 | 2.89 |
| | Rm-4 | " | 13.0 | 0.4 | 09 | 126.6 | 5.1 | 24.7 | 2.5 | 3.71 | 11.71 | 2.99 |
| | Rm-5 | " | 15.4 | 0.3 | 10 | 107.4 | 0.0 | 25.0 | 2.6 | 3.30 | 2.47 | 2.82 |
| 6 | Rm-6 | " | 17.4 | 0.4 | 08 | 120.1 | 6.2 | 25.5 | 2.2 | 3.77 | 1.86 | 3.11 |
| | Rm-7 | DES 0.5% | 30.7 | 9.1 | 23 | 108.7 | 3.0 | 20.9 | 2.6 | 3.85 | 0.49 | 2.27 |
| | Rm-8 | DES 1.5% | 11.1 | 7.5 | 19 | 117.7 | 2.7 | 23.4 | 2.8 | 3.68 | 2.02 | 2.50 |
| 9 | Rm-1 | EMS + DC | 09.6 | 9.3 | 11 | 19.2 | 0.6 | 23.2 | 2.4 | 3.64 | 1.81 | 2.88 |
| | Rm-1 | " | 10.8 | 9.2 | 11 | 115.8 | 0.8 | 23.6 | 2.3 | 3.72 | 1.71 | 2.38 |
| | Rm-1 | " | 15.5 | 7.9 | 17 | 121.3 | 8.1 | 24.7 | 2.1 | 3.03 | 1.43 | 2.30 |
| | Rm-8 | 0.01 | 89.7 | 7.8 | 42 | 128.7 | 0.8 | 28.9 | 2.4 | 2.42 | 8.68 | 1.94 |

Table—2

Performance of high protein mutants of Jhona—349 and Basmati—370. (Mean values)

| S.No. | Geno type | Mutagen and dose | Culm length (cm) | Tillers per plant | Seed to seed days | Fertile grains per panicle | Sterile grains per panicle | 1000 grain wt. (g) | Grain yield per plant (g) | Grain L:B | Crude protein (%) | Seed protein production (g) |
|-------|-------------|------------------|------------------|-------------------|-------------------|----------------------------|----------------------------|--------------------|---------------------------|-----------|-------------------|-----------------------------|
| 1 | Jm-2 | EMS 15% | 119.1 | 8.7 | 118 | 124.8 | 8.7 | 20.5 | 20.1 | 3.90 | 13.34 | 2.68 |
| 2 | Jm-3 | GR+EMS | 116.8 | 9.1 | 117 | 109.4 | 6-5 | 24.8 | 22.7 | 3.89 | 12.32 | 2.80 |
| 3 | Jm-4 | DES 1.0% | 133.7 | 8.0 | 116 | 139.6 | 9.8 | 28.8 | 21.2 | 4.09 | 11.56 | 2.45 |
| 4 | Jm-7 | | 126.1 | 11.1 | 125 | 136.6 | 8.8 | 19.7 | 21.3 | 4.13 | 12.12 | 2.58 |
| 5 | Jm-10 | DES 0.5% | 112.6 | 8.8 | 109 | 128.4 | 14.7 | 25.0 | 22.4 | 3.73 | 12.17 | 2.73 |
| 6 | Jm-13 | GR+DES | 129.0 | 8.2 | 124 | 175.3 | 17.8 | 21.5 | 30.5 | 3.71 | 11.49 | 3.50 |
| 7 | Jhona-349 | Control | 124.9 | 8.5 | 118 | 122.1 | 11.4 | 21.3 | 20.9 | 3.61 | 10.49 | 2.28 |
| 8 | Bm-2 | EMS 1.0% | 115.5 | 7.0 | 109 | 127.3 | 17.6 | 25.1 | 16.7 | 3.70 | 12.08 | 2.02 |
| 9 | Bm-5 | DES 0.5% | 122.3 | 7.3 | 111 | 101.7 | 17.6 | 25.5 | 18.2 | 3.82 | 11.95 | 2.17 |
| 10 | Basmati 370 | Control | 152.0 | 9.3 | 138 | 101.5 | 7.5 | 21.7 | 18.4 | 4.37 | 9.98 | 1.84 |

Table—3

Estimates of genetic parameters of some phenotypic traits of rice

| | Heritability (h^2) in percent | Genetic advance | Expected genetic advance as percent of mean | Genetic co- efficient of variation | Phenotypic coefficient variation |
|----------------------------------|---|--------------------|---|--|--|
| Culm length | 98.67 | 52.33 | 53.81 | 26.29 | 26.47 |
| Effective tiller number | 60.75 | 5.51 | 56.52 | 37.53 | 48.15 |
| 1 COO grain weight | 12.96 | 12.14 | 50.08 | 26.29 | 29.30 |
| Total grain number per panicle | 73.05 | 76.32 | 67.66 | 38.45 | 44.99 |
| Fertile grain number per panicle | 71.13 | 70.31 | 68.56 | 39.53 | 46.87 |
| Grain L:B | 97.22 | 1.20 | 37.50 | 18.41 | 18.73 |
| Yield per per plant | 46.18 | 11.47 | 42.48 | 30.32 | 44.63 |

A knowledge of genetic advance produced by applying selection pressure to a population is useful in designing an effective breeding programme. It was found that grain number per panicle had a high heritability, coefficient of variation and therefore, high genetic advance. This is a good indication that the variation in this trait is attributable to a high degree of additive genetic effect. 1000 grain weight which has a low genetic advance is also negatively correlated with grain yield (Kaul, 1973). Instead, fertile grain number per panicle is a highly heritable trait with high genetic advance and is also positively correlated with grain yield ($r=0.45$). Therefore, it forms a better and more reliable index for the yielding capacity of a rice plant and has a higher selection index for practical rice breeding.

Hence, amongst these protein rich mutants, Jm-4, -7, -10 and Jm-13 of Jhona and Bm-2 and Bm-5 of Basmati, represent the most reliable genotypes for use in rice breeding. However, while the culm length of IR-8 mutants can be reduced by backcrossing them with the initial line and using the mutants as the recurrent parents, mutants of Jhona can further be improved by intercrossing amongst themselves. Since fineness of the grains of Basmati mutants has deteriorated, improvement in this trait could be achieved by backcrossing them to the initial line using these mutants as the recurrents.

Summary

Three locally grown rice varieties IR-8, Jhona-349 and Basmati-370 were subjected to various doses of *gamma* rays, EMS and DES individually and in combination. In M_4 , 11 mutants of IR-8, 6 of Jhona, and, 2 of Basmati were found to possess higher seed protein content and better seed protein production than their initial lines. Of all the IR-8 mutants which were early and fine grained, six had higher yield, 2 Jhona mutants were high yielding and the Basmati mutants were shorter and good yielding. Fertile grain number possesses high heritability, coefficient of variation and genetic advance and it is positively correlated with total grain yield. Therefore, this represents a trait of high selection index and breeding value. Hybridization between these mutants to secure the most desirable recombinations are suggested.

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IR-8, ജോന-349, ബാസ്മതി-370 എന്നീ നെൽവിത്തു നങ്ങളിൽ ഗാമ്മാ
EMS, DES എന്നീ രാസവസ്തുക്കൾ ഉപയോഗിച്ച്
(മുതലായും) ഗതമാനം

ഈ മൂട്ടേഷനുകൾ രാജാജി ജെ. പരസ്പരം

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