J. Phytol. Res. 2 (1), 1989

POSITIVE AND NEGATIVE MUTANT GENES

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Mutant genes are foreign elements in the genome and cytoplasm and are usually of negative selection value to the survival, propogation and perpetuation of an organism. Therefore, such genes are termed as "negative genes". However, a few mutant genes are useful and add positively to the selection, breeding and economical values of an organism. These represent "positive genes". For crop improvement, plant breeder has to select the positive genes for use in breeding. Such mutant genes were selected from M_{2-3} generation of rice and pea populations obtained after Y-rays, EMS, DES treatments, given singly and in combinations. In rice these mutant genes in addition of inducing earliness, increase grain fineness, tiller number and seed protein content. In pea, protein rich genotypes were developed but they are susceptible to diseases and viruses. Rate and fixation of mutant genes is high for quantitatively inherited than for qualitatively inherited traits.

Keywords : Positive gene; Negative gene; Mutant gene; Pea; Rice.

Introduction

Under conditions of stable habitat and inelastic requirements of adaptations, genotypic alterations, whether major or minor, are mostly of negative selection value. This is because a mutant gene represents a foreign element within a genome and creates disturbances in the genic harmony of an otherwise well balanced genotype. Accumulation of mutant genes in the same genome causes even more negative effects resulting in a general decrease of the physiological efficiency, reproductive potential and population fitness, mainly because most of the mutations are usually deleterious and result in repression of normal functioning of an organism. Such mutations are conditioned by the genes termed presently as "negative genes". They usually reduce population fitness and breeding value of a genotype. On the other hand, a few mutant genes are useful and add to the selection, breeding or economic value of an organism. Such mutant genes are presently termed as "positive genes" are to be selected

for use in breeding. Usually a genome lodges a number of positive and negative genes. Judicious selection of positive genes and elimination of negative genes through recombination and selection are the main aims of a breeder. Where certain desired positive genes are absent they are created through induced mutation. But such mutations are associated with certain negative genes whose elimination becomes arduous either due to close linkage or pleiotrophy. This is evidenced by the following two examples using a cereal and a legume genome.

Induced mutation in rice

With a view to remove some of the genetic defects present in three locally cultivated rice varieties, Basmati-370, Jhona-349 and IR-8, mutations were induced using physical (γ-rays) and chemical (DES and EMS) mutagens singly and in combination (Kaul, 1978a). Basmati-370, though a fine grained and a major export crop of our country, is a tall, poor yielder with semi-compact panicles and matures very late. But it has a very good cooking quality, table preference and market value. Jhona-349 is a tall thin and weak culmed variety having coarse grains than Basmati and lodges at maturity. However, it yields better than Basmati and is marketed in the name of Basmati. IR-8 is a dwarf, high yielding variety but has coarse, bold and broad grains with a 'white belly'. It matures very late and needs heavy manuring and irrigation.

Out of 396 mutants selected from 2264300 M_2 plants, 5 mutant each of Basmati and of Jhona and 10 of IR-8 were found to be useful (Kaul, 1978 a). They were cultivated on a large scale and studied for their agrononic performance in M_3-M_8 generations. Progeny performance on plant and plot basis revealed two Basmati mutants Bm_3 and Bm_4 as the promising ones, since their grain yield is much higher and the maturity period and shoot height are lesser than their respective parental lines (Table 1). But their grain fineness is deteriorated. On the other hand, of 5 Jhona mutants and 10 IR-8 mutants, only two mutants, each of Jhona and IR-8, are most promising because of their overall improved agronomic performance and high stability indices of various metric traits. These mutant possess higher grain-yield, better grain fineness, higher total seed-protein productlon (Fig. 4). Unlike Jm_2, whose height equals the initial line, Jm_3 is slightly taller but does not lodge (Table 1).

Two Basmati mutants are high yielding and early but their grain quality, which is of prime importance to this race, is deteriorated. Two IR-8 mutants and one Jhona mutant are taller and exhibit a high degree of

Table 1. Performance of some promising rice mutants (Mean value of 360 plants, M_5–M_7 generations)

Genotype/ Traits	Shoot height (cm)	Tiller number	Maturity in days	Grain number	1000 grain weight (g)	Grain yield (g)	Grain fineness (L:B)	Protein content (%)	Seed protein production
Basmati-370	147.08 ±0.67	6.23 ±0.16	148.98 ±0.91	155.37 ±2 17	21.11 ±0.20	16.08 ±0 36	3.61 ±0.02	7.58 ±.08	1.22
Bm_3	122.06 ±0.90	5.97 ±0.15	132.15 ±0.95	188 68 ±2 65	24.16 ±0.24	21 37 ±0.55	2 82 ±0.01	7.41 ±0.05	1.58
Bm_4	116.66 ±0.59	5.92 ±0.14	130.69 ±0.88	180.13 ±2.19	24 58 ±0.26	21.34 ±0.52	2.76 ±0.02	7.72 ±0.04	1.65
CD at 5P level*	4.79	0.38	6.34	5.64	0.18	1.25	0.05	0.05	
Jhona-349	131.50 ±0.54	6.27 ±0.17	125.16 ±0.71	197.70 ±3.78	21 20 ±0.30	20.45 ±0.59	3.00 ±0.02	7.33 ±0.04	1.50
Jm_2	128.66 ±0.69	5.43 ±0.15	124.72 ±0.82	193.93 ±2.90	29.37 ±0.37	22 82 ±0 61	3.51 ±0.02	7.66 ±0.09	1.75
Jm_3	137.24 ±0.70	6.17 ±0.15	123.20 ±0.75	224.49 ±2.84	20 36 ±0.19	20.67 ±0.61	3.52 ±0.02	7.56 ±0.08	1.57
CD at 5P level*	4.69	0.35	5.78	7.37	1.84	1.25	0 05	0.06	
IR_8	87.76 ±0.40	6.24 ±0.11	150.90 ±1.38	137.96 ±2.44	28.14 ±0.17	20.59 ±0 36	2.38 ±0.01	7.12 ±0.04	1.47
IRm_1	118 23 ±0.80	6.13 ±0.16	124.19 ±1.85	180.82 ±2.19	25.06 ±0.36	22.55 ±0.36	2.82 ±0 02	8.22 ±0.06	1 85
IRm_6	85 68 ±0.40	6.81 ±0.14	131.68 ±1.48	170.83 ±2.65	21.53 ±0.08	20.70 ±0.36	2.62 ±0 01	8.67 ±0.05	1.80
CD at 5P level*	5.43	0 35	7.42	6.05	0.13	1.03	0.04	0.07	

± Represents the standard error values.

* Computed after analysis of variance.

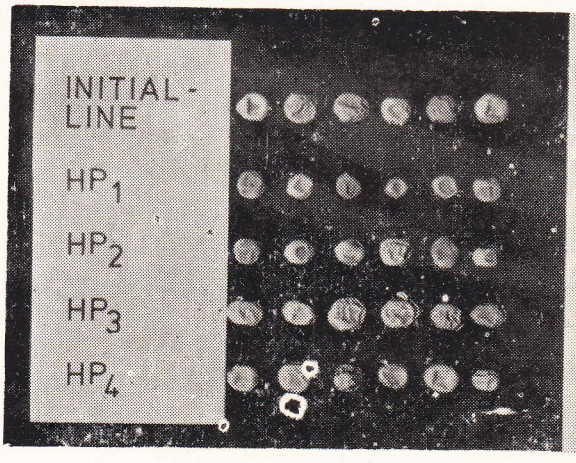

Fig. 1

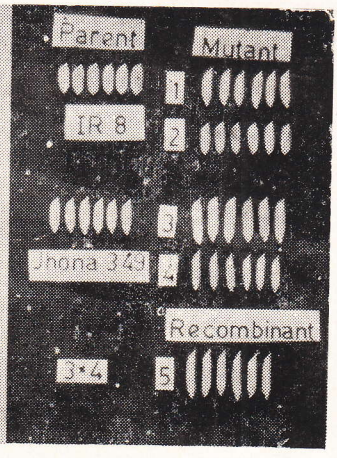

Fig. 2

Fig. 1 Ripe, dried seeds of the initial line Bonneville and the four protein rich genotypes (HP_1-HP_4).

Fig. 2 Seeds of IR-8, its mutants IRm_1 (1) and IRm_6 (2), of Jhona, its mutants Jm_2 (3) and Jm_3 (4) and of a long grained fine recombinant of the cross Jm_2 x Jm_4.

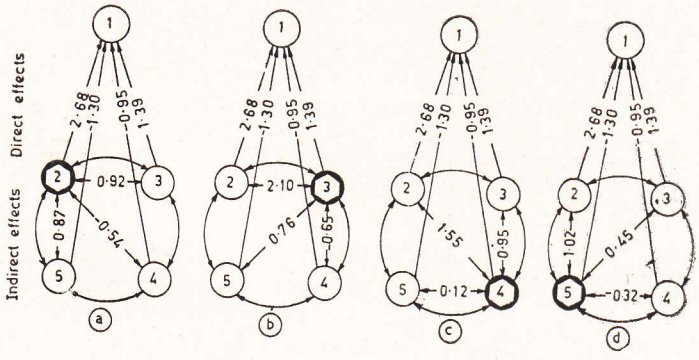

Fig 3

Fig. 3 Path coefficient analysis. Direct and indirect effects of shoot height (2a), fruit (3, b), and grain number (4, c) and seed protein (5, d) over grain yield (1).

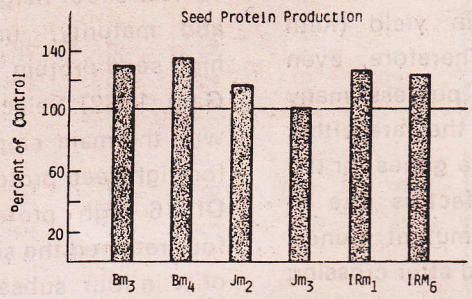

Fig. 4 Seed protein production of Basmati mutants Bm_3, Bm_4, Jhona mutants Jm_2, Jm_3 and IR-8 mutants IRm_1 and IRm_6.

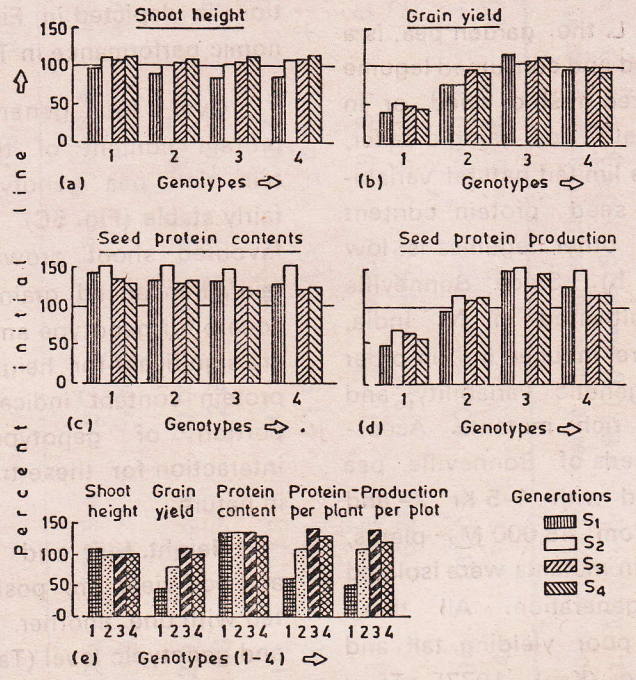

Fig.5. Progeny performance of protein rich genotypes.

Fig. 5 Progeny performance of protein-rich pea genotypes. Shoot height (a), grain yield (b), seed protein content (c), and seed protein production (d) of high-protein genotypes in four subsequent generations (S_1–S_4); mean performance over four generations (e).

lodging primarily due to weak, thin culms and heavy grain yield (Kaul and Kumar, 1982). Therefore, even though these mutants possess many positive mutant genes, they are either linked to some negative genes or the observed negative effect is due to pleiotropy of the mutant genes. Recombinants obtained after crossing these mutants with other induced mutants and parents have been obtained and they are being stabilized through selection and selfing.

Genetic Improvement of Pea

Pisum sativum L. the garden pea, is a widely relished and consumed legume which is utilized fresh or dried or in the canned state. Pea, being a selfer, accumulates a limited natural variability and its seed protein content compared to other legumes is low (Kaul, 1978 b). Since Bonneville variety is cultivated in N. India, mutations were induced in it in order to enhance genetic variability, and select protein rich mutants. Accordingly the seeds of Bonneville pea were irradiated with 1-5 Kr X- and γ-rays and from 48,000 M_3 plants, 37 high protein mutants were isolated in the M_3 generation. All these mutants were poor yielding, tall and later maturing (Kaul, 1977). They were intercrossed, backcrossed to the initial line up to BC_4 and were also crossed with two dwarf early flowering and ripening mutants in order to recover the lines with traits for low shoot height early flowering and maturity, improved yield and high seed protein content (Kaul and Garg, 1982). Selection was done in F_5 with the main emphasis on selecting for high seed protein content (<24%). Of 16 high protein lines selected, four retained the seed protein superiority in four subsequent generations of testing (F_7-F_{10}). They are termed presently as protein rich genotype (Fig. 1). They are abbreviated as PR_1, PR_2, PR_3 and PR_4. Their progeny performance over 4 generations is depicted in Fig. 5 and agronomic performance in Table 2.

Over four generations, seed protein content of the fonr protein rich pea genotypes remained fairly stable (Fig. 5C) Higher rainfall favoured shoot growth, but lower rainfall enhanced grain yield Mean square for genotype and environment are significant for height, yield and protein content indicating a major portion of genotype-environment interaction for these traits as linear in nature.

Height, fruit and grain number and pod yield are positively correlated with one another at both total and genotypic level (Table 3). These correlations remain unaltered when the influence of other traits (except that of grain number on yield and protein content and of protein production on yield and fruit number) were partialled out (Table 3B), but the total

Table 2. Agronomic performance of high protein pea (S_1–S_4 generations).

Genotype	Shoot height (cm)	Days to maturity	Fruit/ plant	Grains/ plant	1,000 grain weight (g)	Grain yield plant (g)	Seed protein content (%)	Protein production/ plant*	Protein yield/ plot*
Bonneville	87.2 a ±3.19	156.5 a ±4.22	19.7 a ±4.48	79.9 a ±6.17	185.8 a ±6.17	14.9 a ±2.28	19.1 a ±1.24	2.82	73.33
PR_1	93.2 a ±8.28	168.8 b ±4.64	20.6 a ±2.37	64.0 b ±2.11	99.7 b ±9.84	6.4 b ±2.13	26.1 b ±1.41	1.66	38.31
PR_2	87.1 a ±5.76	173.8 c ±7.1	21.1 a ±1.9	74.7 a ±4.5	149.4 c ±6.6	11.9 c ±1.3	25.7 b ±1.8	3.08	82.53
PR_3	87.9 a ±4.17	169.5 b ±6.25	21.1 a ±2.8	83.6 a ±4.9	192.8 a ±9.2	16.1 a ±2.8	25.1 b ±1.5	4.03	100.5
PR_4	88.6 a ±6.41	167.0 b ±7.7	20.3 a ±3.0	75.6 a ±3.8	193.1 a ±8.7	14.6 a ±1.9	24.9 b ±1.5	3.62	87.5

Mean values not followed by the same letter differ from each other at 5P level, as revealed from Duncan's multiple range rest. *Mean value of 60 (N) plants (5p x 3R x 4Y), for others, N=360 (P=plants, R=replications, Y=years.)

correlation existing between various metric traits and protein content and protein production are insignificant at the genotypic level (Table 3A). Protein content and production appear to depend on these since multiple correlations between them were significant (Table 3C). Thus, whereas 94% of the variance in yield is due to its association with fruit and grain number ($R^2=0.94$), influence of protein content appears to be equally potent ($R^2=0.80$, Table 3C). However, influence of other traits over variance in grain number, protein content and protein production is small, since coefficients of multiple determination (R^2) varied only between 12%–54% (Table 3A, b–d).

Correlations identify related components of a metric trait, but do not indicate the relative importance of direct and indirect influences exerted by these components over the metric traits. Path coefficients partition correlations into unidirectional and alternative pathways and thus represent a special type of multivariate analysis identifying the "causes" and "effects". Direct effects of height and fruit number as well as indirect effects exerted by them on the yield via other traits, (except gain number) are high and positive (Fig. 3). Like these two traits, the grain number is also positively correlated with yield but unlike them its direct effect over grain yield is negative. This effect is compensated by positive indirect effects exerted via other metric traits. Insignificant correlations between yield and seed protein content appear to be due to negative direct plus low positive indirect effects exerted via shoot height and fruit number, and a negative indirect effect via grain number (Fig. 3).

None of these four genotypes are significantly taller than the initial line, but they are slow growing and late maturing (Table 2). While in PR_1 grain weight and grain number are low, in PR_2 only grain number is low. Total grain yield of these two genotypes is very low in all the four generations of testing (Fig. 5b). On the other hand, in PR_3 and PR_4, grain yield equalled the initial line and their protein production was enhanced due to their higher seed protein content (Fig. 5c, d). Thus these two represent promising protein rich genotypes. They need genes that would decrease their shoot height, increase growth rate, induce earliness in podding and resistance to diseases like virus and *Perenospora*. But when dwarf and early genes were introduced into their genomes, the seed yield and protein content dropped by 35–50% marring their superiority completely. Hence the "PR genome" of pea represents a mixture of positive and negative genes. Rectification of these defects reduces some of their major positive qualities like grain yield and seed protein content.

Table 3. Correlation matrices.

A : Bivariate correlations (total above and genotypic below)

Variable	H	F	G	Y	S	P (protein production)
Height (H)	—	.64**	.53**	.62**	.24	.26*
	—	.66	.58	.58	.21	.29
Fruit number (F)	.64**	—	.68**	.97**	.58**	.51**
	.66*	—	.68*	.94*	.47	.48
Grain number (G)	.53**	.66**	—	.71**	.51	.65**
	.58*	.67*	—	.68*	.34	.49
Grain yield (Y)	.62**	.97**	.71**	—	.48**	.71**
	.58*	.94*	.68*	—	.23	.56
Seed protein(S)	.24	.58**	.51**	.48**	—	.28
	.21	.47	.34	.23	—	.51

B : Partial correlations

(a) YG H=0.57*	(b) YF H=0.95**	(c) YS H=0 43**	(d) YP.H=0 72**
.F=0.28*	.G=0.90**	.F=-0 42**	.F=0.10
.S=0.45**	.S=0.96**	.P=0.41**	.G=0.46*
.P=0.65**	.P=0.99**	.G=0 19	.S=0.68**

C : Multiple correlations

(a)
$R_{Y.GH}=0.76^{**}$ ($R^2=.59$)
$R_{Y.GF}=0\ 96^{**}$ ($R^2=.94$)
$R_{Y.GS}=0.89^{**}$ ($R^2=.80$)
$R_{Y.GP}=0.78^{**}$ ($R^2=.61$)

(b)
$R_{G.SH}=0\ 56^{**}$ ($R^2=.43$)
$R_{G.SF}=0.69^{**}$ ($R^2=.48$)
$R_{G.SY}=0.73^{**}$ ($R^2=.54$)
$R_{G.SP}=0.72^{**}$ ($R^2=.53$)

(c)
$R_{S\ GF}=0.60^{**}$ ($R^2=.36$)
$R_{S.GN}=0.51^{**}$ ($R^2=.26$)
$R_{S.GH}=0.51^{**}$ ($R^2=.26$)
$R_{S.GY}=0.53^{**}$ ($R^2=.29$)
$R_{S.GP}=0.51^{**}$ ($R^2=.26$)

(d)
$R_{P.SY}=0.71^{**}$ ($R^2=.51$)
$R_{P.SG}=0\ 65^{**}$ ($R^2=.43$)
$R_{P.SF}=0.51^{**}$ ($R^2=.26$)
$R_{P.SH}=0.33^{**}$ ($R^2=.12$)

(*$P<0.05$, **$P<0.01$, for S & P, N=60, for rest N=360)

Positive and negative genes obtained after mutagenic treatments are considered at mutant genes. Spontaneously they arise frequently but are either lost or preserved indefinitely depending upon the selection value and breeding system of the population. Mutagens enhance mutation rate and produce traits that have been either lost or are new to the populations (Kaul and Kumar, 1982). The mutation rate and its fixation are much higher for the genes controlling quantitative traits than for those controlling qualitative traits. Of course, they include both + and — genes.

Acknowledgements

The author is grateful to Alexander von Humboldt Foundation, Germany and to Fulbright Foundation, USA for fellowship awards during the tenure of which this work was done.

Accepted March, 1989.

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