stage itself as insensitive or responsive following external application of GA. Using this technique, *Gai/Rht* 1 allele was located on chromosome 4A[7] and *Gai/Rht* 2 on chromosome 4D[8]. In the present study, the euploid F_2 of the cross Kalyansona × Chinese Spring as well as monosomic F_2s from hybrids between Chinese Spring monsomics 4A, 4B, 4D and Kalyansona were studied for their response to GA treatment.

Cytologically identified monosomic plants of Chinese Spring monosomes 4A, 4B and 4D were crossed as female parents to the semi-dwarf wheat variety Kalyansona which is one of the most widely grown cultivars in the country at present. Monosomic F_1 plants were identified cytologically in each of the three crosses and selfed. Euploid F_1 between disomic Chinese Spring and Kalyansona was also selfed. F_2 progeny from both monosomic F_1s and euploid F_1 was grown in soil in wooden flats and 7-day-old seedlings were sprayed with 10^{-6} M concentration of GA_3 solution after measuring their height. Seedling height was measured again 7 days after the GA treatment.

TABLE I

Segregations for GA-response in monosomic and euploid F_2 progenies to determine the location of Gai/Rht 1 *in Kalyansona*

Cross	GA-response		X^2 (3 : 1)	P
	Insensitive	Responsive		
Chinese Spring × Kalyansona	83	33	0·74	0·50–0·25
Mono-4A × Kalyansona	33	3	5·33	0·025–0·010
Mono-4B × Kalyansona	21	8	0·10	0·75 ..
Mono-4D × Kalyansona	23	10	0·49	0·50–0·25
Mexipak × Kalyansona	67	0	..	..

The euploid F_2 of hybrids between Chinese Spring and Kalyansona segregated into 3 insensitive : 1 responsive (Table I). Monosomic F_2s of the crosses Kalyansona × Mono-4B and Mono-4D also segregated like the euploid F_2. The F_2 segregation in the cross between Kalyansona and Mono-4A was found to be distorted from the 3 : 1 ratio. The three responsive F_2 plants appeared to be nullisomic for 4A showing narrow leaves and slow seedling growth. The F_2 monosomic analysis indicated location of *Gai/Rht* 1 on chromosome 4A of Kalyansona.

According to the varietal classification of Gale and Law[5] for the presence of *Gai/Rht* alleles, the wheat variety Mexipak carries the *Gai/Rht* 1 allele on chromosome 4A. Kalyansona was crossed to its sister selection Mexipak to test for allelism. The F_2 of this cross was also treated with GA and seedling height measured. All the 67 F_2 plants were insensitive to GA (Table I). This indicates that *Gai/Rht* genes in these two varieties are allelic.

Jain and Kulshrestha[9] described three different dwarf height groups D_1, D_2 and D_3 an different spring wheat varieties. In Indian wheat breeding programmes, dwarf wheats have been commonly classified as one-gene, two-gene and three-gene dwarfs. However, no genetic studies appear to have been reported to establish the presence of three recessive genes for dwarfing. Allan, Vogel and Peterson[3] showed that Norin 10 carried only two independent recessive genes for semi-dwarfism. Consequently, all Norin 10-derived semi-dwarf wheats carry either one or both the height reducing genes, *Rht* 1 and *Rht* 2. Allan[10] showed that *Rht* 2 produces a shorter straw than *Rht* 1. This probably explains the three different dwarf height groups D_1, D_2 and D_3 with D_1 corresponding to *Rht* 1 dwarf, D_2 to *Rht* 2 dwarf and D_3 to *Rht* 1 + 2.

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INFLORESCENCE MUTANT IN BARLEY

BARLEY has been an ideal material for fundamentnl research in plant genetics[1]. Very often radiations have been used for the improvement of this crop[2–5]. Several floral mutants which could interest cell biologists, physiologists and plant breeders have been reported[6–9]. C138 a cultivar of rainfed area suffers from poor tillering, lodging, susceptibility to yellow

rust and poor yield. To improve upon these characters gamma radiation treatments were tried on this variety.

Experimental results revealed that in M_1, most of the visible mutants were chlorophyll mutants. The lowest and highest frequency of these mutants were in 10 kR (2%) and 30 kR (36%) respectively. In M_2, one mutant with modified floral structure was obtained from 10 kR treatment. It was found to be true breeding mutant in M_3 and subsequent generations. In M_3 reciprocal crosses were made between mutant and C138. In F_1 earheads were of C138 type (normal) in both the cases. In F_2 and F_3 generations a ratio of 3 (normal) : 1 (mutant) was observed as indicated by X^2 test ($p = 0{\cdot}2$ and $0{\cdot}28$ respectively). Therefore, the expression of mutant character was found to be controlled by single recessive gene. This locus is hereby designated as egl 1.

Ten competitive plants were selected randomly for recording observations on mutant (M_7 generation) and parental variety C138. Simple 't' test revealed that the differences were real for all the morphological characters except 1,000 grain weight.

Mutant was characterized by extended glumes and lemma, bigger earheads (Fig. 1), higher tiller number, low plant height, slightly lesser 1,000 kernel weight, more number of grains per spike, late in flowering, field resistance to yellow rust and higher grain yield per plant than C138. Special feature of this mutant was that, because of extended glumes and lemma these structures were loosely attached to the grain, thus flowers were relatively more open than in C138 normal plant. During the threshing operations most of the husk was removed leaving behind some husk adhered to the grain. This gave a semi-husked appearance to the grain (Fig. 2) and as a result bran percentage in flour was reduced significantly, *i.e.*, from 6·8 to 4·6%.

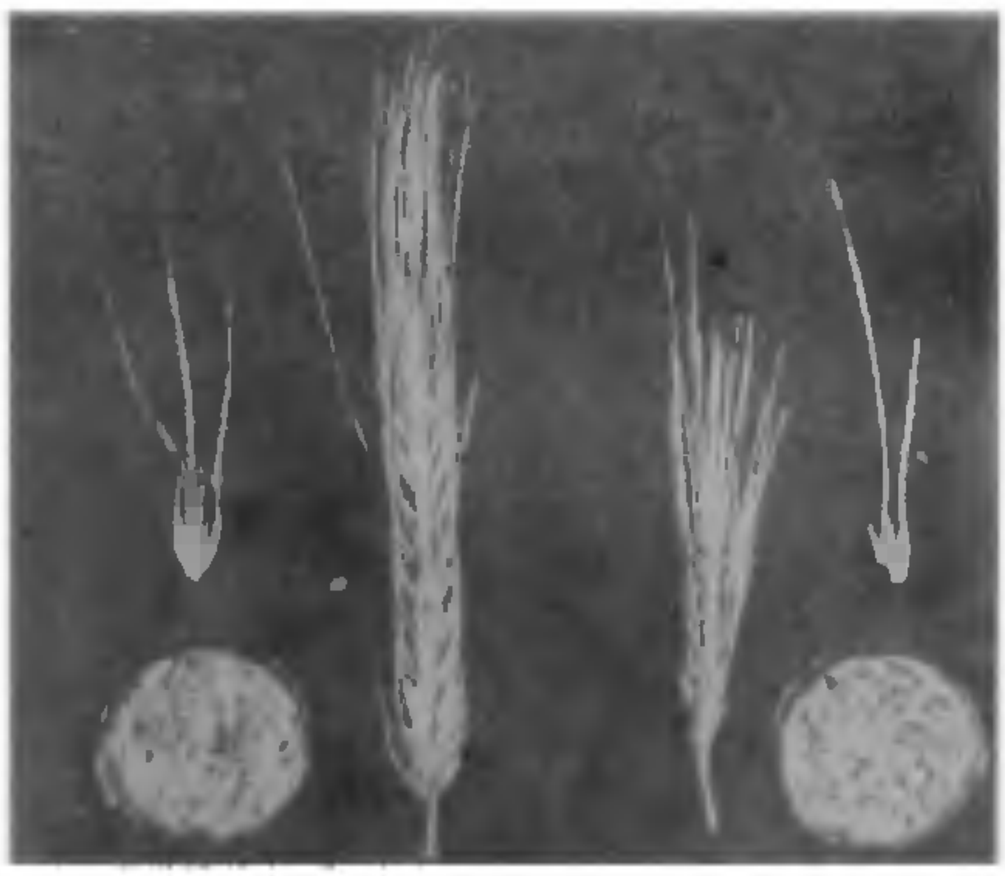

FIG. 1

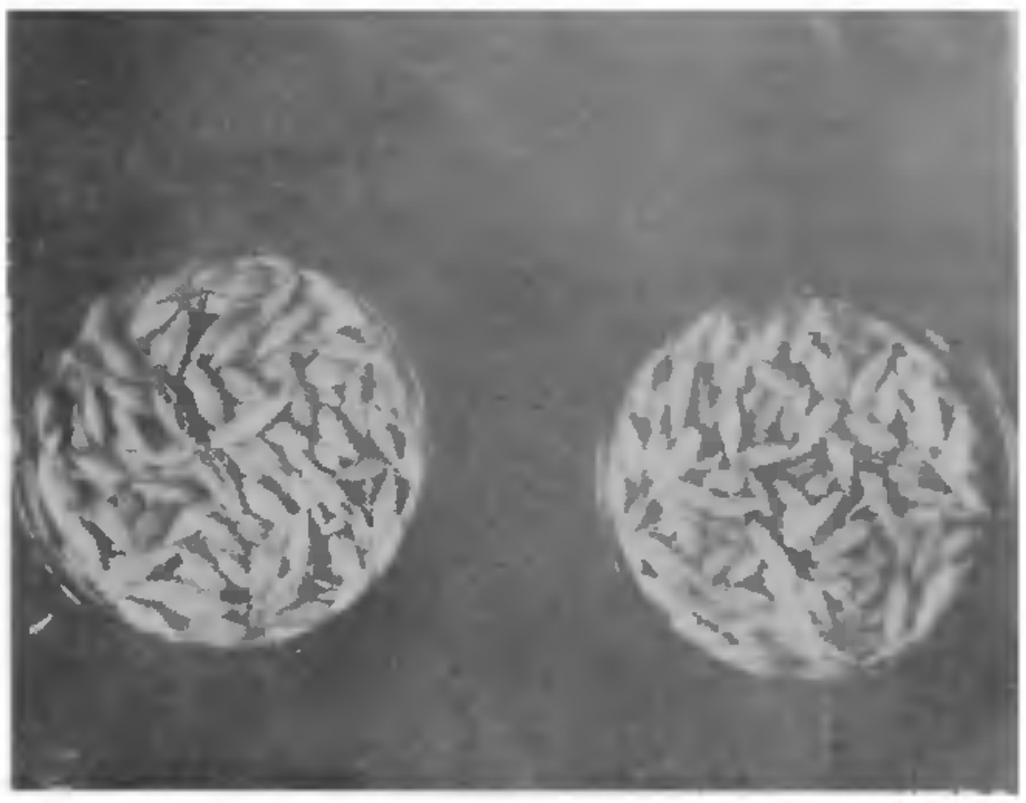

FIG. 2

Biochemical studies indicated that the mutant was superior to its parent in protein (26·7% increase) and starch content (9·4% increase). Low lysine content was recorded in the mutant. However, because of high grain yield per plant, higher protein percentage and a narrow gap between mutant and C138 for lysine content, it is expected that recovery of both lysine and protein per unit area and time would be higher in mutant than C138.

TABLE I

Comparison of average performance of mutant with C138 for various characters

Sl. No.	Character	Mutant	C138	t.cal.
	Morphological characters :			
1.	Days to ear emergence	98·6	92·3	3·98
2.	Plant height (in cm)	85·1	101·0	8·48
3.	Tiller number	17·77	11·0	4·59
4.	Ear length (cm)	9·64	5·90	9·21
5.	Number of grains/ear	64·67	55·11	4·69
6.	1000 grain weight (gm)	43·2	44·6	N.S.
7.	Grain yield/plant (gm)	43·77	31·11	3·11
	Quality characters :		% increase or decrease over C138	
8.	Protein (%)	12·25	9·52	26·68
9.	Total minerals (%)	1·53	1·58	3·17
10.	Starch (%)	76·0	67·8	9·44
11.	Lysine (%)	0·31	0·37	16·22
12.	Bran (%)	4·63	6·77	31·61

No cytological abnormality was encountered in root tip studies (motosis) and cytoplasmic effects were absent.

The increase in grain yield in mutant can be attributed to higher tiller numbers more number of grains per spike, field resistance to yellow rust and reduction in plant height which avoids losses due to lodging. Further high protein coupled with high starch content in the mutant indicated it to be biologically more efficient genotypes than C138. Therefore, it may furnish good material for physiological studies such as sink-source relationship and bioenergetic considerations. Also, its open flower structure may permit its incorporation in hybrid breeding programme, if male sterility is induced in it.

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ASPERGILLUS CLAVATUS DESM. MUT. *ALBINO* RAPER AND FENNELL—A NEW RECORD FROM INDIA

MUTATION is quite common in Aspergilli both under natural and artificial conditions. Several mutants haye been isolated and used by earlier workers[1–6] as basis for species/varieties. *Aspergillus clavatus* mut. *albino* has been isolated repeatedly and in abundance from Kasaragod (Kerala) soil. This is reported for the first time from India.

Aspergillus clavatus Desm. mut. *albino* Raper and Fennell

Colonies on Czapek-Dox agar growing more rapidly at 28°C, attaining a diameter of 4·5 to 5·0 cm in 10 days with conspicuous radial furrows, white in color (R. Plate LIII), later turn to seashell pink (R. Plate XIV). Reverse colorless to pale ochraceous salmon (R. Plate XV). Exudate abundant. Odor strongly foetid. Conidial heads white, clavate, large, 150·6–380·0 × 50·0–95·6 μm. Conidiophores thin walled, smooth, hyaline, 1453·6–2410·6 × 15·0–35·0 μm, gradually enlarge to form a clavate vesicle. The fertile area of vesicle is 120·0–330·6 × 50·2–75·8 μm. Phialides in a single series, 3·5–14·5 × 2·0–3·0 μm. Conidia smooth, heavy walled, subglobose to elliptical, 2·0–6·0 × 2·6–3·0 μm. No sclerotia and cleistothecia observed. Hülle cells absent.

The description of the present isolate is in conformity with Raper and Fennell[6] but it differs in the larger size of phialides and predominantly in the albino color of the colony.

Culture deposited as I.T.C.C. 2598, Division of Mycology and Plant Pathology, IARI, New Delhi, J. L. Varshney.

Culture examined : I.T.C.C. 1443.

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