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1. Linkage relationships for two mutants detected in Italian populations.

Further investigations have been accomplished on linkage relationships of two mutants, described in 1967 MNL, with known genetic markers.

For the ij-type mutant,  $F_2$  segregations (repulsion phase) presented the following data (inclusive of 1966 results):

|                       |                       |                       |                       |                       |                       |                       |                       |
|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| <u>G</u> <sub>1</sub> | <u>I</u> <sub>j</sub> | <u>g</u> <sub>1</sub> | <u>I</u> <sub>j</sub> | <u>G</u> <sub>1</sub> | <u>i</u> <sub>j</sub> | <u>g</u> <sub>1</sub> | <u>i</u> <sub>j</sub> |
| 3882                  |                       | 2037                  |                       | 1889                  |                       | 8                     |                       |

(c.o. 6.5%  $\pm$  1.5 st. error).

The data previously reported about close linkage between a shrunken type (bt) mutant and su<sub>1</sub>, have been confirmed by the scoring of ears obtained from backcrossing, to the triple recessive, plants of the constitution Su<sub>1</sub> bt G<sub>1</sub><sub>3</sub> / su<sub>1</sub> Bt g<sub>1</sub><sub>3</sub>, as follows:

|                        |           |                        |           |                        |           |                        |           |
|------------------------|-----------|------------------------|-----------|------------------------|-----------|------------------------|-----------|
| <u>Su</u> <sub>1</sub> | <u>Bt</u> | <u>su</u> <sub>1</sub> | <u>Bt</u> | <u>Su</u> <sub>1</sub> | <u>bt</u> | <u>su</u> <sub>1</sub> | <u>bt</u> |
| 113                    |           | 4124                   |           | 4157                   |           | 20                     |           |

All the seedlings from the su<sub>1</sub> bt kernels had the G<sub>1</sub> phenotype, while only 26 plants from Su<sub>1</sub> Bt seeds turned out to be g<sub>1</sub>, indicating that part of them derived from contamination. Consequently, considering the bt phenotypes only, the su-bt recombination is 0.5%  $\pm$  0.1.

The bt mutant, then, has to be placed on chromosome 4 (probably allelic to bt<sub>2</sub>), between su<sub>1</sub> and g<sub>1</sub><sub>3</sub> and very close to su<sub>1</sub>.

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2. Abnormal segregations (significantly different from a 1:3 ratio) of genetic markers in the  $F_2$  of lines derived from Italian populations.

In the analysis of a number of  $F_2$  progenies derived from crossing lines from Italian populations to some genetic testers bearing recessive mutants, the following abnormal segregations have been observed:

| Marker                 | Chromosome | Number of<br>examined F <sub>2</sub><br>progenies | Number of<br>Italian<br>populations | Segregations |      |
|------------------------|------------|---|-------------------------------------|--------------|------|
|                        |            |   |                                     | >3:1         | <3:1 |
| <u>lg</u> <sub>1</sub> | 2          | 80  | 74                                  | 4            | 1    |
| <u>sh</u> <sub>2</sub> | 3          | 8   | 8                                   | 0            | 0    |
| <u>su</u> <sub>1</sub> | 4          | 91  | 85                                  | 4            | 1    |
| <u>bt</u> <sub>1</sub> | 5          | 9   | 8                                   | 9            | 0    |
| <u>y</u>               | 6          | 75  | 71                                  | 4            | 0    |
| <u>su</u> <sub>2</sub> | 6          | 2   | 2                                   | 0            | 0    |
| <u>gl</u> <sub>1</sub> | 7          | 67  | 63                                  | 2            | 0    |
| <u>wx</u>              | 9          | 88  | 82                                  | 2            | 4    |

The mean number of ears examined per F<sub>2</sub> is about 7 for kernel markers and 4 for seedling characters.

Abnormal segregations can be, at least partially, interpreted as a consequence of the presence of gametophyte factors. The deviations for the markers of chromosomes 4, 5 and 9 could be attributed to the ga factors known for such chromosomes.

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### 3. Somatic segregation in plants from X-ray and Ethyl-methane-sulphonate (EMS) seed treatments.

In plants derived from seed of a multi-ear popcorn variety treated with X-rays and EMS, the number and relative position of ears segregating mutants have been reported: