

IOWA STATE UNIVERSITY  
Ames, Iowa  
Department of Genetics

1. A possible locus on chromosome 10 responsible for a high mutation rate.

In last year's News Letter (MGCNL 44:81-84, 1970), I reported on the genetics of a new white endosperm mutant ( $y_9$ ). Since homozygous  $y_9$  plants are sometimes not very vigorous, linkage tests were made by crossing  $F_1$  plants heterozygous for  $y_9$  and the marker genes as males to stocks homozygous for the marker (in the case of  $E_1$  and  $r$ ) or to standard lines (M14/W22) (in the case of  $bf_2$  and T9-10b). These crosses were then self-pollinated to check for the presence of  $y_9$  (and  $bf_2$ , in crosses involving this gene). All selfed ears were seedling tested. In the seedling tests an unusually large number of new seedling mutants was observed. We test seeds from thousands of self-pollinated ears each year and have observed occasional ears that will segregate for a different mutant than the one under test. Such ears are probably the result of spontaneous mutations or contamination during outcrossing. In the  $y_9$  crosses these "new mutants" seemed to be occurring at an unexpectedly high frequency. To determine if this were so, all of the seedling tests of self-pollinated ears from outcrossed heterozygous  $y_9$  plants for the years 1965 to 1968 were checked. The number and types of "new mutants" observed in these crosses are shown in Table 1. Table 2 shows the number of "new mutants" observed in the selfs of outcrosses in linkage studies for several other genes tested in 1968. In Tables 1 and 2 families grouped together by the + sign are replicated plantings from the same outcross ear. It is obvious that stocks carrying  $y_9$  are relatively mutagenic. The crosses recorded in Table 1 represent many different  $F_1$  genotypes (7) and outcrosses (15). Thus the high mutation rate is not the result of the non- $y_9$   $F_1$  parents or the outcross parents but must be the result of the presence of the chromosome 10 which carries  $y_9$ . In all the crosses listed in Table 1, the  $F_1$  parents did not segregate for any of the mutants observed in the outcross.



Table 1 (Continued)

Family	Total No. of Plants Selfed	Seedling Mutants						Total No. of Mutants	No. of Diff. Mutants					
		Yellow- green		Luteus		Pale Yellow				Necrotic	Albino		Pale Green	
		homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>			homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	homo seg + Y <sub>9</sub>	
67-1003	7			1								1	1	
67-1004	10											0	0	
67-1005	7											0	0	
67-1006	6											0	0	
66-7005+8001	41											0	0	
66-7006+8002	44					2						2	1	
66-7007+8003	35	1		1	2	(1)						5	3	
65-1001	9											0	0	
65-1002	3								1			1	1	
65-1003	4											0	0	
65-1004	9				1			2*	3*			6	2	
65-5003	9										1	0	0	
65-5004	7											1	1	
65-5006	7	1+(1)										2	1	
65-5007	7										1	1	1	
65-5008	10	2	2									4	1	
65-5009	9	3			1							4	2	
65-5010	9	2	1									3	1	
65-5011	10											0	0	
65-5012	10								5*			5	1	

Table 1 (Continued)

Family	Total No. of Plants Selfed	Seedling Mutants										Total No. of Mutants	No. of Diff. Mutants		
		Yellow- green		Luteus		Pale Yellow		Necrotic		Albino				Pale Green	
		homo +	seg Y <sub>9</sub>	homo +	seg Y <sub>9</sub>	homo +	seg Y <sub>9</sub>	homo +	seg Y <sub>9</sub>	homo +	seg Y <sub>9</sub>			homo +	seg Y <sub>9</sub>
65-5013	8									1			1	0	0
65-5014	39						1							3	3
65-5015	39						1							1	1
65-5016	43	1	1				1							3	2
65-5017	42			1			1							2	2
65-5018	41	1	2										1	4	2
65-5019	44													0	0
65-5020	41		1	1		2	2							6	3
Total	1663	64	56	49	33	15	15	1	0	26	35	2	3	299	59
Total - *		25	12	25	14	15	15	1	0	7	6	2	3	125	53

\*Mutant possibly contributed by female parent.

\*\*2 mutable.

\*\*\*mutable.

Since the data in Table 1 are subject to more than one interpretation, there are several possible ways to calculate the mutation rate. For example, in many instances mutants with the same phenotype segregated in several plants from the same outcross family. Are these the result of separate mutational events or did a mutation take place in a somatic cell that gave rise to a cluster of microsporocytes all of which carried the mutation? In some families nearly one half of the plants segregated for a given mutant. Is this due to the mutational event occurring early in the development of the sporophyte so that the whole tassel carried the mutant allele or are these the result of a mutant contributed by the female parent of the outcross? No allele tests have been made between similar mutants in the same family.

If all the segregating ears are counted as resulting from independent mutational events, the mutation rate is 17.98% ( $299 \div 1663$ ). However, if all mutants with the same phenotype from a given family are considered to be the result of a single mutation, the mutation rate is 3.55% ( $59 \div 1663$ ). If those families in which nearly one half of the ears segregated for a mutant of a given phenotype are considered to be the result of a mutation in the female parent and thus are not counted in the totals, the two mutation rates indicated above become 7.52% ( $125 \div 1663$ ) and 3.19% ( $53 \div 1663$ ), respectively. The most conservative estimate of the mutation rate (3.19%) is nearly 15 times the corresponding rate observed for the control population ( $4 \div 1763 = .23\%$ ). This is certainly a minimal figure since it is only the rate of seedling color mutations. Seed and mature plant mutations have also been observed in these outcross families. Sixteen of the families listed in Table 1 were observed to be segregating for defective seeds, one family for shrunken seeds and one for brittle seeds. Families of ten seeds each from the self of four outcross ears were planted. Two families did not segregate for any mature plant traits but one family produced a tassel seed plant with thick tassel branches and a short brachytic-like plant and another family produced several plants with small crinkled leaves. Thus, if seed and mature plant mutations were included the mutation rate would be considerably higher than 3.19%.

Table 2  
Spontaneous mutants observed in crosses not carrying  $\gamma_9$

Family	Total No. of Plants Selfed	Albino	Pale Yellow	Total No. of Mutants	Total No. of Diff. Mutants
68-7026+7027	87				
68-7028+7029	92				
68-7030+7031	91				
68-7037+7038 +7039+7040	131				
68-7041+7042	90				
68-7043+7044	91				
68-7053+7054 +7056 +7057+7058	198				
68-7090	48			2	1
68-7091	44	2			
68-7092	46				
68-7093+7094	94				
68-7095+7096	92				
68-7097+7098	88	1		1	1
68-7099+7100	67				
68-7127+7128	85				
68-7129+7130	85			4	1
68-7131+7132	85			1	1
68-7133+7134	78				
68-7229	44				
68-7230	42				
68-7231	39				
68-7232	46				
Total	1763	3	5	8	4

From Table 1 it can be seen that mutants occur in ears that are not segregating for  $y_9$  and those that segregate for this gene. Thus, the mutations are probably not confined to the chromosome 10 carrying  $y_9$  or the homologous ten. None of the mutants in Table 1 have been located to chromosome although a mutant found in a  $y_9$  line in 1963 turned out to be allelic to  $w_3$  on chromosome 2. This would suggest that the mutants are not necessarily confined to chromosome 10. If the mutator locus on chromosome ten affects any locus and if it functioned in the sporocyte before microsporogenesis, it would explain the presences of possibly more than one outcross ear segregating for the same mutation in an outcross family and the occurrence of the mutations on ears with and without  $y_9$ .

Whether the mutator locus is the same as  $y_9$  or just closely linked to it cannot be determined from the present information. Most of the data considered in this report were obtained incidentally in experiments designed to give information on the location of  $y_9$ . Experiments designed to clarify the apparent mutagenic nature of this stock are planned.

Donald S. Robertson

## 2. Linkage studies involving $o_5$ .

In 1967 (MGNL 41:94-95) I reported on a new opaque mutant  $o_5$ . This mutant has opaque shrunken seeds that produce pale green seedlings which grow into mature plants a little less vigorous than normals. In our previous report, preliminary linkage tests with only 70 plants had indicated this mutant was on chromosome 7, 12.9 units from the breakpoint of 7-9a (7L.63). Additional linkage information involving 7-9a are given in Table 1 which are in close agreement with the previously reported data. The results of linkage tests with  $gl_1$  are given in Table 2.