3. Gene frequencies in a strain of Reid Yellow Dent

A long term experiment was started in 1948 with the objective of obtaining information on the validity of certain assumptions in population genetics. Population size, randomness of mating, equilibrium, mutation rate, gene frequency, etc. are some of the commonly used terms in the mathematical-statistical treatment of genetic problems. Actual experimental data, though, are rather limited, with the possible exception of Drosophila. The first phase of this study has been completed and will be briefly reported below.

A strain of open pollinated Reid Yellow Dent served as source. 801 selfed ears were obtained in 1948, representing a random sample of the variety. Approximately 50 seeds per ear were germinated in the greenhouse and classified for recessive seedling mutants; 70 kernels were checked for 'germless seed.' The results are set out in Table 1. In previously reported experiments in corn of this sort the frequency of the character but not of the alleles were recorded. Since a number of different loci might be responsible for the expression of a character, it was thought desirable to actually determine the frequency of each recessive allele by intercrossing all progenies which segregated for the same character. This test for allelism among viable types was made by plant to plant intercrosses. For the lethal types, however, it was necessary to grow the material in paired rows. The results are set out in Table 2.

Table 1. Frequency of Occurrence of Segregation for Various Characters in a Sample of Selfed Ears from the Variety Reid Yellow Dent.

		Frequency expressed as	
Character	No. of ears segregating	% of total	% of segregates
Germless	87	10.86	36.56
Yellow-green	44	5.49	18.49
Virescent	25	3.12	10.50
White	28	3.49	11.77
Luteus	15	1.87	6.30
Pale green	10	1.24	4.20
Glossy	7	.87	2.94
Dwarf	8	1.00	3.36
Stripe	6	.75	2.52
Miscellaneous	8	1.00	3.36
	238	29.69	100.00

Table 2. Estimated Gene Frequencies and Mutation Rates for the Various Mutant Alleles.

Character	Allele	Frequency of occurrence	Observed gene frequency	Estimated mutation rate
Yellow-green	yg a	2	.00126	
(viable)	b	1	.00062	
	c	1	.00062	
	d	1	.00062	

(lethal)		e	20	.01248	155.7×10^{-6}
		f	10	.00624	38.9×10^{-6}
		g	3	.00187	3.5×10^{-6}
		h	2	.00125	1.5×10^{-6}
		i	2	.00125	1.5×10^{-6}
		j	1	.00062	$.38 \times 10^{-6}$
		k	1	.00062	$.38 \times 10^{-6}$
		l	1	.00062	$.38 \times 10^{-6}$
		m	1	.00062	$.38 \times 10^{-6}$
Luteus	l	a	7	.00437	19.1×10^{-6}
		b	2	.00126	1.5×10^{-6}
		c	1	.00062	$.38 \times 10^{-6}$
		d	1	.00062	$.38 \times 10^{-6}$
		e	1	.00062	$.38 \times 10^{-6}$
Stripe	str	a	3	.00187	
		b	1	.00062	
White	w	a	21	.01310	171.6×10^{-6}
		b	1	.00062	$.38 \times 10^{-6}$
Glossy	gl	3	4	.00249	
		a	1	.00062	
		b	1	.00062	
		c	1	.00062	
Dwarf	d	a	6	.00375	
		b	1	.00062	
Miscellaneous			1	.00062	
			1	.00062	
			1	.00062	

It should be noted that the number of progenies tested for allelism is usually smaller than the number originally classified. This loss is due to improper sampling, non-heritable cause of the expression, poor stand, etc.

During the course of the study one new seedling character was found. It is tentatively designated as 'mottled albino green.' The seedling leaves are characterized by small normal green spots on an albino background. Only the first 3-5 leaves are affected. Greening occurs rapidly.

The mutation rates for the lethals in Table 2 are estimated by the use of the relationship $q^2 = u$, where q is the frequency of the recessive lethal and the u the mutation rate from the dominant to the recessive condition. Under a certain mutation rate and gene frequency one can calculate the number of generations required to reach the equilibrium level. A number of assumptions, however, are involved in such a calculation.

In a continuation of this experiment an attempt will be made to find out how rapidly the equilibrium values are approached. Ears of the original sample which did not segregate in the S_1 were thought to be free of defectives. A composite of these ears was grown under isolation and a sample saved from each crop harvested. If these samples are analyzed in the same manner as the material reported above, then it should be possible to obtain some estimates on the speed with which equilibrium is approached by the different alleles.

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