Parental		Reg. 1		Reg. 2		Doub.		T
56	59	13	13	7	9	0	1	161
118		26		16		1		

$\underline{Tu} - \underline{Gl}_3 = 16.8 \pm 2.9$ $\underline{Gl}_3 - \underline{C}_2 = 10.6 \pm 2.4$ c = 0.35

Two-point data from the cross of $\underline{+}\ \underline{+}/\underline{gl}_3\ \underline{c}_2$ x $\underline{gl}_3\ \underline{c}_2$ give a better estimate of the map distance:

		+ +	+ c	gl +	gl c	T	%
$\underline{Gl}_3\ \underline{C}_2$	CB	468	22	28	440	958	5.2 ± 0.7

E. H. Coe, Jr.

2. Selective enrichment experiments with pollen.

Tests parallel to those outlined last year (News Letter 41: 139) show some encouraging results. Tests with pollen from a multiple heterozygote for $\underline{bz}_2$, $\underline{a}_1$, $\underline{c}_2$, $\underline{a}_2$ $\underline{pr}$, $\underline{c}_1$ $\underline{bz}_1$, and $\underline{r}$ (8 markers, 5 chromosomes) have been analyzed. Tests with other markers are in progress.

Pollen from the multiple heterozygote (1 ml) was mixed with 4 ml of aqueous medium (modified according to work of Y. H. Chang; 0.35M sucrose plus 1,200 ppm Ca Cl_2) and applied with a # 8 or # 9 brush to the silks. Each mixture was used on all 8 recessive testers, one ear each. The medium contained one of two concentration levels of one of 28 different agents. The list below gives the class, identity, and concentration of each agent tested. Ratios are given only for tests in which one or more of the ratios for that marked chromosome were significantly deviant (**1%, *5%, + or - 10%). Three hundred and eight of the 450-odd pollinations yielded sufficient seed for statistical test of the ratio; the 10 highly-significant ratios should include several true enriched samples.

The flavonoid relatives appear to be the most promising agents, as might be expected since the markers are flavonoid factors.

Agent	Ppm	Ratio	Locus	Dev.	Chrom.
Acridine orange	1000	0:1	$\underline{c}_1$	+*	9
	1000	10:2	$\underline{c}_1$		9
	500	11:8	$\underline{c}_1$		9
Carbohydrate metabolism					
2, 4-dinitrophenol	100				
	50				
Oligomycin	50				
	25				
turanose	5000				
	2500				

Agent	Ppm	Ratio	Locus	Dev.	Chrom.
Flavonoid relatives					
p-methoxy cinnamic acid	5000	58:92	c_1	-**	9
	2500	21:27	c_1		9
p-nitro cinnamic acid	100	14:84	a_1	-**	3
	50	37:30	a_1		3
	100	6:153	a_2	-**	5
	50	10:7	a_2		5
	100	4:4	pr		5
	100	2:0	bz_1		9
	50	12:9	bz_1		9
	100	23:11	c_1	+	9
	50	11:11	c_1		9
	50	51:70	bz_2	-	1
	1000	2:2	r		10
esculin	500	40:25	r	+	10
	1000	0:5	bz_2	-	1
hesperidin	500	82:119	bz_2	-**	1
	1000	3:1	c_2		4
	500	48:30	c_2	+*	4
	1000	1:0	bz_1		9
	500	33:21	bz_1		9
	1000	13:7	c_1		9
	500	46:65	c_1	-	9
	100	5:0	r	+	10
naringin	50	50:49	r		10
	1000	4:5	a_2		5
phloridzin	500	77:28	a_2	+**	5
	1000	6:1	pr		5
	500	34:17	pr	+	5
	500	9:4	bz_1		9
quercitrin	500	1:1	bz_1		9
	250	1:0	bz_1		9
	500	1:3	c_1		9
	500	0:6	c_1	-*	9
	250	12:6	c_1		9
	1000	18:6	a_2	+	5
rutin	1000	2:0	pr		5
Hormones					
gibberellic acid	2500				10
	1250				10
indole-3-acetic acid	500	20:14	r	-	
	250	89:114	r		
Lysine relatives					
arginine	10000	7:0	a_2	+*	5
	10000	2:0	a_2		5
	5000	20:29	a_2	-*	5

Agent	Ppm	Ratio	Locus	Dev.	Chromo.
Lysine relatives (cont'd)					
arginine	10000	2:7	pr	-	5
	10000	0:1	pr		5
	10000	1:1	bz_1		9
	5000	2:1	bz_1		9
	10000	17:10	c_1		9
	10000	8:11	c_1		9
	5000	9:1	c_1		9
lysine	10000	7:0	a_2	+*	5
	10000	1:1	a_2		5
	5000	6:5	a_2		5
	10000	0:1	pr		5
	10000	3:3	pr		5
	5000	15:15	pr		5
Methionine relatives					
ethionine	1000	11:4	bz_2	+**	1
	500	27:6	bz_2	+	1
	1000	9:2	a_1		3
	500	15:11	a_1	-	3
	1000	5:14	c_2		4
	500	33:22	c_2		4
methionine	10000	3:4	bz_2	-**	1
	5000	146:221	bz_2		1
	10000	1:0	a_1	+**	3
	5000	9:0	a_1		3
Tryptophan-niacin relatives					
3-acetyl pyridine	1000				
	500				
anthranilic acid	500				
	250				
5-fluorotryptophan	500				
	250				
5-hydroxy tryptophan	2500				
	1250				
indole	1000				
	500				3
kynurenine	500	4:3	a_1	+**	3
	250	42:21	a_1		5
	500	1:2	a_2	+*	5
	250	110:65	a_2		5
	500	9:2	pr		5
	250	20:18	pr	+**	4
	500	83:12	c_2		4
	250	37:33	c_2		

Agent	Ppm	Ratio	Locus	Dev.	Chromo.
Tryptophan-niacin relatives (cont'd)					
nicotinamide	500				4
	250			-	4
alpha-picolinic acid	500	0:5	$\underline{c}_2$		
	250	0:1	$\underline{c}_2$		
pyridine-3-sulfonic acid	10000	8:11	$\underline{bz}_1$		9
	5000	33:30	$\underline{bz}_1$		9
	10000	17:7	$\underline{c}_1$	+	9
	5000	32:38	$\underline{c}_1$		9
tryptophan	5000	29:22	$\underline{bz}_1$		9
	10000	24:25	$\underline{c}_1$	+	9
	5000	19:8	$\underline{c}_1$		

Deviations in opposite directions for the same chromosome do not necessarily negate each other, nor do insignificant deviations necessarily negate significant ones. The anthocyanin markers themselves may be responsible for physiological differences that are subject to selection, but they may also be linked with unknown factors that were heterozygous in either parent of the hybrid plants that were used as males. Of course possible contaminations and other errors require that the above tests be repeated extensively.

E. H. Coe, Jr.

3. Recombination frequency and coincidence in maize.

The aim of the present study was to examine the effects of translocations on recombination, using coincidence and recombination percentage together as a measure of these phenomena. The backcross data studied, which were compiled by D. R. Knott (1963, Maize News Letter 37:164-172), represent largely the work reported by R. A. Emerson in 1940 and 1941.

Statistical analysis was done on backcross material which was either structurally normal or translocation-bearing in the F_1 generation. The translocations all involved chromosome 1 and differed from one another with respect to their individual breakpoints; not all were located precisely. For convenience the long arm of chromosome 1 was divided into four regions: $\underline{br}$-$\underline{f}$, designated as region 1; $\underline{f}$-$\underline{an}_1$, region 2; $\underline{an}_1$-$\underline{gs}_1$, region 3; and $\underline{gs}_1$-$\underline{bm}_2$, region 4. Regions covering more than one of these were designated by 1-2, 1-3, etc. For all samples containing one or more of the intervals 1, 2, 3, 1-2, 1-4, and 3-4, average recombination values were calculated from the raw data by dividing the total number of recombinations for the region, regardless of structural constitution, by the grand total of individuals for the region. These values, which may be symbolized as $\overline{p}_t$, were used as the means to which individual recombination frequencies were compared to indicate those values which were higher than the average and those which were lower. In addition,