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,

the standard errors were calculated to determine fit, that is, percentage of the time a given recombination frequency higher or lower than the mean would be expected by chance. Finally, coincidence calculations were made on all double exchanges, and the probabilities of these values occurring by chance in a population whose true interference level was zero.

As a result of the statistical analysis several graphs could be constructed. First, fit (P) to a coincidence of one for each sample, separating those with c less than one from those with c greater than one, was plotted against frequency. Such a graph was desirable in order to evaluate whether the population at hand was spread according to theoretical expectations. It is expected that a few samples will have high coincidence, since this is a property of the binomial distribution when q is extremely small as compared to p. What is not expected is any sort of clustering, but this is what has been found.

Of twenty samples carrying a translocation internal to one of the intervals considered, twelve had coincidence in excess of one. Of these, six had P values between zero and twenty per cent, three approaching deviations which might be significant, having P values between five and eight per cent. The eight internal-translocation bearing samples with coincidence less than one had no deviations which even approached significance. When coincidence was considered with respect to immediately adjacent intervals on opposite sides of the translocation cross, all four samples were found to have an interference level in excess of one with P values between zero and twenty per cent. Two of these approached deviations which might be significant, having P values of five and seven per cent. When this observation was extended to include all adjacent intervals involving an internal translocation, seven out of eight were found to have coincidence greater than one.

An examination of those samples involving external translocations also yielded interesting information. Of the twenty samples comprising this population nine had coincidence greater than one, deviations for two samples being significant.

Double exchange in directly adjacent regions free from structural anomalies also merits consideration. Two samples with coincidence less than one were significant. Six out of fourteen samples with coincidence greater than one were significant. Of these six, four were from directly adjacent regions. This may indicate that double exchange within directly adjacent regions is more coincidental than in more widely separated regions.

At this point it became important to determine the effect translocations were having on recombination frequency in this population. Frequency distribution graphs to a fit to $\overline{p}_t$ were made for the six regions. Of the nine translocation-bearing samples involving region 1, seven were below $\overline{p}_t$. In region 2, eight of the ten translocation-bearing samples were found to have recombination frequencies below $\overline{p}_t$. In region 3, three out of four translocation-bearing samples fell below $\overline{p}_t$. The other three regions showed the effect also.

One final figure was plotted which sought to combine the information of the preceding ones. Probability (P) for a given p_i was positioned in the graph according to whether it was higher or lower with respect to its $\overline{p}_t$. This then was related to the associated coincidence for that region with another region in the same sample (involving either whole regions or segments thereof depending on the position of intervening genes or translocations) with respect to a fit to coincidence equal to one. For a given sample, recombination in an interval may be higher or lower than $\overline{p}_t$. This should have direct bearing on the interference levels when the doubles involving such a region are considered. The figure generated was divided into four parts. The first zone designated recombination frequencies lower than their respective $\overline{p}_t$ for intervals which yield coincidence less than one. The second zone designated recombination frequencies higher than their $\overline{p}_t$ for intervals which yield coincidence less than one. The third zone designated recombination frequencies lower than their $\overline{p}_t$ for intervals which yield coincidence values in excess of one. The fourth and last zone designated recombination values higher than their respective $\overline{p}_t$ for intervals which yielded coincidence in excess of one.

One of the most striking features of this graph was the distribution of translocation-bearing samples. Since it was demonstrated that the presence of a translocation reduced recombination frequency, it was expected that reduction of p_i for an interval would also reduce the associated doubles, as interference levels are a function of p. Therefore the great majority of aberration carriers is expected to be found in quadrant one. On the contrary, of twenty-four samples with an internal translocation, where p_i for the interval was less than $\overline{p}_t$ thirteen were in quadrant three (coincidence greater than one). Included in these were two cases where the coincidence was greater than one for immediately adjacent regions on opposite sides of the translocation cross. On the one hand, p_i was low for the interval as a whole, whereas on the other, double exchange was high--being significant in one case at the five per cent level. Considering all adjacent regions in the samples with an internal translocation, where p_i for the interval being studied was lower than $\overline{p}_t$, it was found that of nine samples five were associated with coincidence greater than one. For doubles which were not immediately adjacent and where p_i for the sample was lower than $\overline{p}_t$, out of fifteen samples eight were associated with coincidence greater than one.

When p_i for a given sample was higher than $\overline{p}_t$ and the sample carried a translocation, its position was always external. Samples carrying external translocations occurred in all four quadrants. This variability presumably reflects the differences in the position of the breakpoints.

Reference must also be made to the distribution of samples carrying no aberration. The area of interest here was quadrant four (high p_i, high c). Of sixteen samples twelve involved exchanges between adjacent intervals. Furthermore, four out of five samples in quadrant three (low p_i, high c) involved exchanges between adjacent intervals. This may be taken as another indication that double exchange in general takes place between more closely associated areas, although this effect is reduced by the presence of an intimately associated translocation.

In summary, the presence of translocations reduced overall single exchange, but multiple exchange was not similarly reduced. In fact, high coincidence values were associated with the presence of a translocation. In addition, in normal samples, coincidental exchange seemed to be more closely associated with directly adjacent regions, in contrast to what has previously been observed. Before definitive statements can be made as to what the above means in terms of mechanism, critical comparisons of double exchange in normal and structurally aberrant populations are needed.

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4. A B-type translocation involving the short arm of chromosome 3.

A new B-type translocation involving the short arm of chromosome 3 was reported last year (News Letter 41:139). The translocation has now been further characterized and can be designated TB-3b.

The segment of chromosome 3 distal to the break carries not only $\underline{cr}_1$ and $\underline{d}_1$ but also $\underline{ra}_2$. Maize linkage maps usually place $\underline{ra}_2$ in the long arm of chromosome 3. Since TB-3b uncovers $\underline{ra}_2$ in addition to the 3S markers $\underline{cr}_1$ and $\underline{d}_1$, $\underline{ra}_2$ appears to reside in 3S instead of 3L.

J. B. Beckett

5. A translocation complex involving chromosomes 5, 6, and a supernumerary.

Last year it was reported (News Letter 41:139) that the gene pr on the long arm of chromosome 5 appeared to be uncovered by a new A-B translocation. It is now evident that the genes ae, pr, $\underline{gl}_8$, $\underline{lw}_2$, $\underline{ys}_1$, $\underline{v}_2$, and $\underline{v}_{12}$ are distal to the break and that $\underline{bt}_1$ is proximal. Since the gene order is normally given as $\underline{bt}_1$ $\underline{v}_3$ $\underline{bv}_1$ pr, progenies involving $\underline{v}_3$ and $\underline{bv}_1$ will be tested next summer to locate the breakpoint more precisely.

Preliminary cytological observations indicate the presence of a translocation complex involving chromosomes 5, 6, and a B.

From a cross by pollen from a normal plant, 15 plants were tested for the ability to produce hypoploid sperm (pr test). Eight plants with 60-70% aborted pollen gave about 20% hypoploid endosperms, two plants with 60-70% aborted pollen gave no hypoploid endosperms, and five plants with 10-25% aborted pollen gave no hypoploid endosperms. Therefore, it is still not clear whether the B-type translocation is separable from the remainder of the translocation complex.

J. B. Beckett

6. Duplications from translocations between homologous chromosomes.

A method for the detection of duplications arising from translocations between homologous chromosomes was presented in a previous issue (MNL 38: 101-105). Further work has been done on this problem.