Beske, J. L. and R. L. Phillips. Preliminary mapping of nineteen new translocations with the alcoy multiple translocation tester strain.

The nineteen translocation strains listed in Table 1 were generously given to us by D. D. Perkins and are presently available from the Fungal Genetics Stock Center (see Revised Stock List, Neurospora Newsl., this issue). These strains were crossed with the alcoy triple translocation tester strain (T(I;II) al-1; T(IV;V) 2355, cot; T(III;VI) 1, ylo-1) to obtain information on the linkage groups involved. Crosses were made on a 1.7% Difco corn meal agar medium by simultaneously inoculating both parent strains. All crosses were maintained at 25°C. Random ascospores were isolated to a solid Fries minimal or complete medium. For certain crosses, 100 ascospores were isolated on two occasions approximately two weeks apart. The same pattern of re-

Table 1. Linkage data from 19 new translocation strains crossed with the alcoy multiple translocation tester strain [T(I;II) al-1; T(IV;V) 2355, cot; T(III;VI) 1, ylo-1].

Phenotype	Genotype**	NM 131	NM 121	NM 114	NM 112	NM 111	NM 107	P 2640	NM 163	NM 161	NM 141	NM 170	ALS 6	AR 9	AR 12	AR 1,	NM 109	NM 127	NM 150	NM 180
		A. Independence*						B. al-ylo linkage				C. al-cot linkage	D. Complex results							
cot al	cot al ylo / cot al +	3	13	13	13	20	10	18	15	7	16	2,	26	15	42	12	19	31	14	34
cot ylo	cot + ylo	2	7	3	7	7	3	3	0	0	6	2	3	926		1	1		0	0
cot +	cot • +	2	7	6	4	9	0	9	7	8	2	2	6	23	911		2	5	9	0
+ al	+ al ylo / + al +	18	36	19	16	19	10	32	19	26	31	2	33	33	28	7	10	36	22	28
+ ylo	+ + ylo	7	17	8	12	11	9	6	5	2	2	10	10	5	26	10	3	7	6	14
+ +	+ + +	8	13	5	13	15	7	25	20	22	32	32	8	51	17	10	6	20	2	18
Total		40	93	54	65	81	39	93	66	65	89	75	86	136	124	56	41	100	53	94
% Germination		40	47	54	65	81	20	4,	66	65	89	75	43	68	62	56	46	53	53	52
% Recombinants**		Independence						19	15	6	18	8								

* These data were tested for goodness of fit to a ratio of 2 al:1 ylo:1 wild-type in the cot^+ and cot class. A satisfactory fit was obtained in each case.

** The % recombinants for group B translocations was calculated by doubling the frequency of al^+ ylo recombinants.

*** cot is now known as cot-1 and ylo is now known as ylo-1.

sults was obtained from the two isolations in every case.

The mechanics of utilizing the olcoy strain have been described in detail by Perkins (1964 N eurospora Newsl. 6: 22) for mapping new mutants to linkage groups. Perkins (1966 Neurospora News!. 9: 11) stated that tmnslocotions phenotypically indistinguishable from wild type also may be mapped using the alcoy tester stmin. Normally independent alcoy markers will show linkage to each other if the new tmnslocation has breaks close to the breakpoints of two of the marked alcoy tmnslocotions. Therefore, a linkage between al and ylo would indicate that the new tmnslocotion involved linkage groups I or 11 ond 111 or VI. Similarly, a linkage between al and co+ would indicate the involvement of linkage groups I or 11 ond IV or V, while a linkage between cat ond ylo would indicate involvement of IV or V and III or VI. If the olcoy markers remain independent, one of the fallowing situations exists: (1) Linkage group VII is involved in the new tmnslocation; (2) The new tmnslocation involves linkage groups I and II, 111 and VI, or IV and V; or (3) One of the two linkage groups involved in the new tmnslocation is common to one alcoy translocation and the other linkage group is common +a another alcoy tmnslocotion, but with the two breaks widely separated in a+ least one of the common linkage gmups. Independence is indicated by a mtio of 2 al: 1 ylo: 1 wild type in the cot^+ and cot class, since al is epistatic to yla.

The linkage results (Table 1) are grouped into four categories; (A) Independence, (B) Linkage of al and ylo; (C) Linkage of al and cat; and (D) Complex results not expected of simple reciprocal tmnslocations (note the al: non-al ratios). The recombination values calculated from the data in categories Bond C give a measure af the total genetic length of the two differential (between breaks) segments separating the linked alcoy markers and are not extremely valuable in mapping the actual breakpoints of the new translocations.

Fewer cot than cot^+ germinants were obtained from crosses involving all but two of the translocation strains (AR17 and NM109). NM150 and NM161 were "morphs" and NM141 and NM170 were "peach", but progeny with these phenotypes ore considered as wild types for the purposes of Table 1. An interaction of "peach" with some of the alcoy markers is suspected.

The results from NM180 crosses ore particularly intriguing since they indicate independence between the alcoy markers in the cot^+ class but an al-cot linkage in the cot class. This unusual genetic behavior might be expected if NM180 were the result of two translocations involving three linkage groups (IV, V, and I or II) with breaks located such that an association of six chromosomes plus a "pair" carrying only the cot^+ allele would result from a cross with the alcoy stmin instead of an association of eight. This strain will be investigated farther.

In summary, tmnslocations NM107, 111, 112, 114, 121, and 131 are independent of the alcoy translocations, NM141, 161, 163, and P2648 involve linkage groups I or II and III or VI, and NM170 involves linkage groups I or II and IV or V. Translocations ALS6, AR9, 12, 17, NM109, 127, 150 and 180 appear to be more complicated than simple reciprocal tmnslocotions. (Undergraduate Research Problem by the first author under the direction of the second author conducted as part of Special Problems Course No. 25. • • • Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, Minnesota 55101.