LINKAGE DATA FOR GROUP III MARKERS IN NEUROSPORA[1]

DAVID D. PERKINS AND CHIYOKO ISHITANI[2]

Department of Biological Sciences, Stanford University, Stanford, California

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THIS paper presents data from crosses with markers in linkage group III of *Neurospora crassa* (group C of HOULAHAN, BEADLE, and CALHOUN 1949). Participation of the second author in this study was prompted by the discovery by DR. P. ST. LAWRENCE of a chromosomal rearrangement involving group III, and the desire for information on markers and linkage relations that might be useful for investigating it. Three new loci have been placed in the group, and additional information has been obtained on the relations of ten previously mapped genes. All the gene loci now known to be linked in group III are listed alphabetically in Table 1.

MATERIALS AND METHODS

General experimental materials and methods were as described in PERKINS 1959. The new morphological mutants B54 (*com* : compact), B20 (*ro-2* : ropy-2) and B18 (*vel* : velvet) originated in experiments of DR. V. W. WOODWARD (see Table 1 of PERKINS 1959).

TABLE 1

Loci of linkage group III

Symbol and name	Standard mutant	References*
ad-2 : adenine-2	70004t	B, PITTENGER 1954
ad-4 : adenine-4	44206t	B, GILES *et al.*, 1957; WOODWARD *et al.*, 1958
com : compact	B54	PERKINS 1959
leu-1 : leucine-1	33757	B
prol-1 : proline-1	21863	B
ro-2 : ropy-2	B20	PERKINS 1959
sc : scumbo	5801	B
ser : serine	H605	B
thi-2 : thiamine-2	9185	B, EBERHART 1956
thi-4 : thiamine-4	85902	B, EBERHART 1956; EBERHART *et al.*, 1959
thi-lo : low-thiamine†	....	EBERHART 1956; EBERHART *et al.*, 1959
tryp-1 : tryptophan-1	10575	B, PITTENGER 1954
tyr : tyrosine	Y6994	B
vel : velvet	B18	PERKINS 1959

* B: Documented in BARRATT *et al.*, 1954 compilation. Additional references are cited only if they provide new information on linkage, scoring, or gene structure.
† Probable allele of *thi-4*.

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[2] Present address: Institute of Applied Microbiology, University of Tokyo, Bunkyo-ku, Tokyo, Japan.

TABLE 2

Crosses with group III markers

Zygote genotype and recombination percent	Parental combinations		Recombinations: Singles region 1		Singles region 2		Doubles regions 1 and 2		Total and percent germination	Marker isolation numbers
+ *b* *c* / *a* + +	+*bc*	*a*++	+++	*abc*	+*b*+	*a*+*c*	++*c*	*ab*+	...	(a) (b) (c)
+ *thi-4* / *sc* + 0.8	65	61	1	0	..	..	..	..	127 83%	5801 85902
+ *prol-1* *tryp-1* / *sc* + + 7.2 29.9	40	22	5	1	11	17	1 C=0.5	0	97 97%	5801 21863 10575
+ *prol-1* *com* / *thi-4* + + 2.6 7.7	..	35	1	..	3	..	..	0	39 (*com*$^+$ only) 73%	85902 21863 B54
+ *com* *leu-1* / *thi-4* + + 15.4 3.3	34	40	13	1	2	1	0	0	91* 91%	85902 B54 33757
+ *tryp-1* + / *thi-4* + *ro-2* 21.7 14.5	23	23	9	4	5	3	1 C=0.9	1	69 86%	85902 10575 B20
+ *com* *leu-1* / *ser* + + 2.4 2.4	41	39	2	0	2	0	0	0	84* 84%	H605 B54 33757
+ *com* + / *prol-1* + *tryp-1* 6.1 6.1	..	29	2	..	..	2	0	..	33 (*com*$^+$ only) 63%	21863 B54 10575
+ + *vel* / *prol-1* *tryp-1* + 23.8 33.3	12	9	3	4	4	7	1 C=0.9	2	42 72%	21863 10575 B18
+ *ad-4* + / *com* + *leu-1* 0 2.3	95	74	0	0	4	0	0	0	173* 84%	B54 44206t 33757
+ *ad-4* *tryp-1* / *com* + + 5.4 15.5	61	72	5	4	19	7	0	0	168* 84%	B54 44206t 10575
+ *leu-1* / *com* + 4.6	114	92	8	2	..	..	..	..	216* 83%	B54 33757
+ + *thi-2* / *com* *leu-1* + 3.4 3.8	90	104	1	6	6	2	0	0	209* 82%	B54 33757 9185
+ *tryp-1* / *ad-4* + 9.0	83	68	12	3	..	..	..	..	166* 87%	44206t 10575

+ + *ad-2* *tryp-1* *thi-2* + 0 0.6	81	96	0	0	0	1	0	0	178* 89%	10575 9185 27663
+ *thi-2* *vel* *tryp-1* + + 1.2 20.7	64	..	..	1	..	17	0	..	82 (*vel*- only) 90%	10575 9185 B18
+ *ad-2* + *tryp-1* + *vel* 0.5 13.6	75	101	0	1	11	17	0	0	205* 82%	10575 27663 B18
+ + *tyr* *tryp-1* *ro-2* + 2.3 22.6	56	44	1	2	14	16	0	0	133 93%	10575 B20 Y6994
+ + + *tryp-1* *ro-2* *tyr* 8.0 15.9	52	53	7	4	12	10	0	0	138 55%	10575 B20 Y6994
+ + *tyr* *tryp-1* *vel* + 17.4 3.3	71	75	15	17	4	2	0	0	184* 92%	10575 B18 Y6994
+ *tyr* *vel* + 5.1	70	97	6	3	..	..	..	..	176* 88%	Y6994 B18

Numbers of progeny are given in the body of the table. Progeny genotypes are not designated explicitly, but the genotype of each class can be determined from the order of presentation. The left-hand number of each pair of complementary classes represents the genotype that contains the plus allele of the leftmost marker. Classes of segregants where dashes replace numbers were not scored or recorded. Regions are numbered from left to right, and isolation numbers in the last column are listed in the same order. Crosses are tabulated in a sequence corresponding to the position of their leftmost markers in the linkage group. Where gene order is uncertain, one arbitrarily chosen order has been used consistently. C = coincidence.
* Data of the second author.

Segregants from crosses involving *tryp-1* were grown on supplemented minimal medium containing 10 μg/ml indole and scored at three days (34°) by fluorescence under ultraviolet light. (A 4-watt Blak-Ray lamp is inexpensive and effective. Ultra-violet Products, Inc., San Gabriel, Calif.: Model X4, wavelength 3660.)

EXPERIMENTAL RESULTS

Data from two- and three-point crosses are presented in Table 2, and the results are summarized in the form of a map in Figure 1. These data provide new information on the map relations of several genes. *com* is probably located just proximal to *ad-4*. *ro-2* is between *tryp-1* and *tyr*, and nearest to the former. *vel* is located a short distance from the terminal marker, *tyr*.

Extensive information on sequences in group III was first obtained by HUNGATE (1946), who established the order centromere *sc ser prol-1 leu-1 tryp-1* (or *thi-2*). Subsequent work established the sequences centromere *tryp-1 tyr* (BARRATT, NEWMEYER, PERKINS and GARNJOBST 1954) and *prol-1 ad-4 leu-1* (GILES, PARTRIDGE and NELSON 1957). The data reported here are consistent with the results of these authors.

A number of Group III sequences are still in doubt, notably those of closely linked genes. The seriation shown for *thi-2* and *ad-2* with respect to *tryp-1*

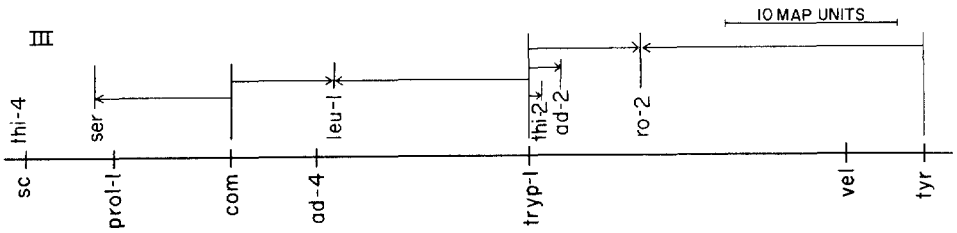

FIGURE 1.—Partial map of group III, summarizing the data from Table 2. The sequence of loci written below the heavy line is based directly on 3-point data for all the genes involved. Above the heavy line, only the relationships indicated by arrows are based on 3-point data. Two opposing arrows indicate that the marker was situated medially in the 3-point cross; each unopposed arrow originates from a medial marker and leads to a marker that was not medial. Interval lengths are imprecise owing to the variability of crossing over. The map is based solely on data from the present paper, except that the position shown for genes above the line may reflect the results of other workers in cases where our own data would require order to be decided arbitrarily or to be based only on quantitative 2-point data from different crosses. See text for sequences established by other workers. The centromere is located just left of *sc*.

depends in each case on a single isolate. It would be desirable to have further 3-point data clarifying the sequence of these loci, and of *thi-4* with respect to *sc* and the centromere.

scumbo, which is near the centromere, was used in tests for linkage in Group III. This should be equally effective in detecting linkage of new markers in either arm of the chromosome. However, the three new markers reported here all proved to be located in the same arm with the ten previously known loci.

A general discussion of these results, in conjunction with comparable data from the other linkage groups, will be found in PERKINS 1959, where such aspects as interference and the variability of crossing over are considered.

SUMMARY

Linkage data on 13 gene loci in linkage group III of *Neurospora crassa* have been obtained by nonselective techniques using random segregants, mostly from 3-point crosses. Three of the loci have not been known previously. All mapped genes are located in the same chromosome arm (with the possible exception of one which is close to the centromere). Interference is apparently orthodox.

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