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Empirical Equation That Can Be Used to Determine Genetic Map Distances from Tetrad Data

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An empirical equation has been developed that can be used to calculate genetic map distances from tetrad data with good accuracy for distances of up to at least 120 centimorgans.

In organisms amenable to tetrad analysis, genetic map distances between two genes on a chromosome are determined from the relative frequencies of parental ditype (PD), nonparental ditype (NPD), and tetratype (T) asci for those two genes (for review, see reference 1). Perkins (3) derived the standard equation used for determining map distances (x_p) on the assumption that only zero, one, or two exchanges occur in the interval between the two genes and that there is no chromatid interference; i.e.,

$$x_p = \frac{100\ (T + 6NPD)}{2\ (PD + NPD + T)} \quad (1)$$

This equation gives a good estimate of map distances for short intervals (up to about 35 centimorgans [cM]), but because it ignores higher crossover ranks, it underestimates lengths of longer intervals.

Snow (4) has used the maximum likelihood method to derive a set of equations for determining map distances (x') that consider all crossover ranks. Solution of these equations for a given set of PD, NPD, and T values yields, in addition to the x' value, a value for the interference parameter, k, and values for the standard deviations in x' and k. Values of x' and x_p are very close for short intervals but differ greatly for longer intervals (Table 1 and reference 4). Because values of x' more accurately reflect actual map distances, they should be used in preference to x_p values. However, solution of the equations derived by Snow involves iterative steps requiring a computer, and because of this, application of these equations has been limited. We have found empirically using the data summarized in Table 1 that the equation

$$x_e = \frac{80.7x_p - 0.883x_p^2}{83.3 - x_p} \quad (2)$$

gives a very good estimate of x' over the range $x_p = 0$ to $x_p = 75$ cM (Table 1 and Fig. 1). The average deviation of x_e from x' over the full range of values of x_p is only 2.0%, although the individual variations are greater than this for large x_p values. This deviation is due, at least in part, to variations in interference over the yeast genome; the relationship between x' and x_p, in contrast to that between x_e and x_p, depends on interference. For values of x_p of less than 35 to 40 cM, equation 1 yields sufficiently accurate values of map distances; equation 2 should be used for longer distances. The coefficients in equation 2 were chosen to give a best fit to data

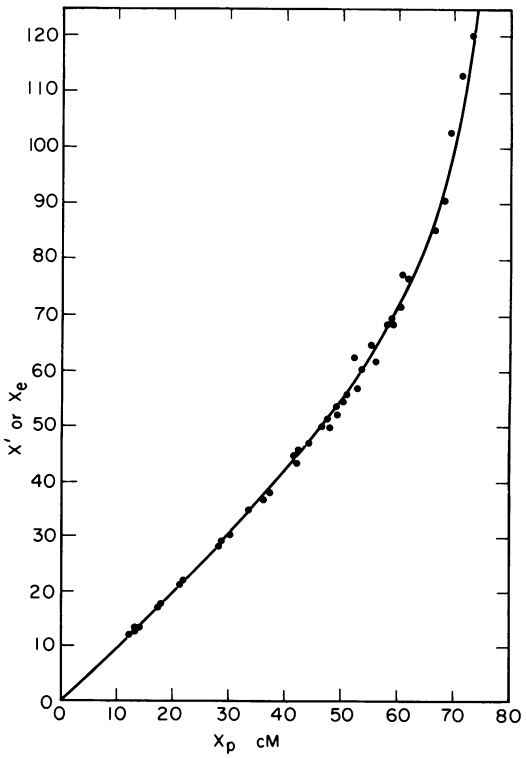

FIG. 1. Plot of x' (●) and x_e (—) versus x_p.

TABLE 1. Genetic map distances for different intervals in *S. cerevisiae* determined by three methods[a]

Interval	Chromosome	PD	NPD	T	k	x_p	x'	x_e
pky1-ade1	I	172	19	262	0.57	41.5	44.5	43.7
gal1-lys2	II	217	44	524	0.48	50.2	54.9	55.2
lys2-cdc28		259	4	296	0.14	28.6	28.7	29.0
lys2-tyr1		1,560	91	2,704	0.25	37.3	37.9	38.7
lys2-dur1		280	71	944	0.35	52.9	56.9	59.1
lys2-met8		219	82	752	0.48	59.1	68.4	69.6
lys2-his7		275	153	852	0.83	69.1	102.7	95.8
tyr1-his7		469	61	894	0.46	44.2	47.0	47.1
his4-leu2	III	2,818	23	1,290	0.37	17.3	17.4	17.1
his4-MAT		1,659	278	3,519	0.50	47.5	51.5	51.4
leu2-MAT		2,686	150	3,041	0.49	33.5	34.7	34.4
leu2-thr4		419	50	649	0.60	42.4	45.8	44.8
pgk1-MAT		251	1	176	0.09	21.3	21.3	21.3
MAT-thr4		2,434	38	1,489	0.41	21.7	21.9	21.7
cdc2-trp1	IV	42	9	107	0.47	50.9	55.8	56.2
trp1-mak24		123	12	262	0.30	42.1	43.3	44.5
rna11-trp1		208	0	108	0.02	17.2	17.2	17.3
aro1-pet14		116	2	148	0.13	30.1	30.2	30.6
trp4-ade8		85	5	126	0.33	36.1	36.9	37.3
ura3-hom3	V	538	101	1,467	0.37	49.2	52.4	53.8
arg9-hom3		126	24	366	0.34	49.4	52.3	54.0
hom3-arg6		3,841	5	1,172	0.13	12.0	12.0	11.8
rad51-rad4		82	28	244	0.56	58.2	68.4	68.0
lys5-leu1	VII	86	52	270	0.89	71.3	113.5	105.4
aro2-met13		493	2	169	0.32	13.6	13.7	13.4
met13-cyh2		1,365	8	518	0.38	17.6	17.6	17.4
met13-trp5		414	106	1,072	0.54	53.6	60.6	60.2
met13-leu1		297	164	1,136	0.57	66.4	85.4	86.7
trp5-ade6		362	129	1,109	0.55	58.8	69.5	69.1
trp5-cly8		232	141	925	0.57	68.2	90.3	92.5
leu1-cly8		261	85	990	0.37	56.1	61.7	64.3
SUC1-ade15		76	28	197	0.75	60.6	77.4	72.6
SUC2-his5	IX	184	51	450	0.63	55.2	64.6	62.8
SUP17-lys1		259	174	880	0.85	73.3	120.2	117.1
his6-lys1		359	56	744	0.48	46.6	50.2	50.2
ilv3-cyc1	X	485	11	342	0.46	24.3	24.7	24.4
met4-pet8	XIV	48	20	151	0.61	61.9	76.5	75.3
arg8-SUF17	XV	86	34	285	0.54	60.4	71.9	72.2
ade2-his8		194	32	594	0.28	47.9	49.9	52.0

[a] The PD, NPD, and T values for different genetic intervals are from Mortimer and Schild (2). The intervals were selected on the basis of adequate sample size and to cover representative areas of the yeast genome. x_p and x_e values were calculated by using equations 1 and 2. x' and k values were determined by using the program written by Snow (4) and adapted by him for an Apple II computer.

from *Saccharomyces cerevisiae*. In this organism, the interference is positive and has an average value of 0.36 (2, 4). We expect that equation 2 would apply to other tetrad organisms with similar interference values, such as *Neurospora crassa*. By use of equations 1 and 2, long map distances in yeasts and similar tetrad organisms can be determined relatively easily and with good accuracy.

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