REARRANGEMENT OF THE GENETIC MAP OF CHROMOSOME *VII* OF *SACCHAROMYCES CEREVISIAE*

JOHN L. CELENZA AND MARIAN CARLSON

Department of Human Genetics and Development, College of Physicians and Surgeons, Columbia University, New York, New York 10032

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ABSTRACT

The genetic map of the right arm of chromosome *VII* of *Saccharomyces cerevisiae* includes markers on a distal segment for which meiotic linkage to the centromere-proximal marker *cly8* has not previously been demonstrated. According to the currently accepted map, *SUF4* is the most distal marker on the right arm. We have shown by tetrad analysis that *SUF4* is linked to *cly8* and *ade6*. The genetic distance between *SUF4* and *cly8* is 29 cM. These data indicate that the genetic map of the right arm of chromosome *VII* should be revised by inverting the orientation of the distal segment so that *SUF4* is located near *cly8*, and *SUC1* and *MAL1* are the most distal markers. With this revision, all of the polymeric fermentation markers that have been mapped are located at the ends of chromosomes.

THE current genetic map of the right arm of chromosome *VII* of *S. cerevisiae* (Figure 1A) includes a distal segment for which linkage to proximal markers was established by mitotic analysis. ROMAN showed that *ade3* and *MAL1* are linked mitotically to *ade6* (1956a,b) and that *SUC1* is linked mitotically to *cly8* (cited in MORTIMER and SCHILD 1980). No meiotic linkage was detected between *SUC1* and *cly8*, and the tetrad data showed that the interval between these markers is greater than 100 cM (H. ROMAN, cited in MORTIMER and SCHILD 1980). We have recently cloned the *SUC1* gene and flanking DNA sequences. We discovered that the 14-kilobase pair region located 3′ to the *SUC1* structural gene contains sequence components found adjacent to telomeres; homology was detected to the *Y* and 131 elements that CHAN and TYE (1983) have identified near telomeres (M. CARLSON, J. CELENZA and F. ENG, unpublished results). These findings suggested that *SUC1* is near the telomere and, therefore, that the genetic map of the right arm is incorrect. If the orientation of the distal segment was inverted, *SUC1* would be the most distal marker, and *SUF4*, which was mapped by GABER *et al.* (1983) to a position 53 cM from *ade3*, would then be located immediately distal to *cly8* (Figure 1B). To verify this hypothesis, we tested for meiotic linkage of *SUF4* to *cly8* and *ade6*.

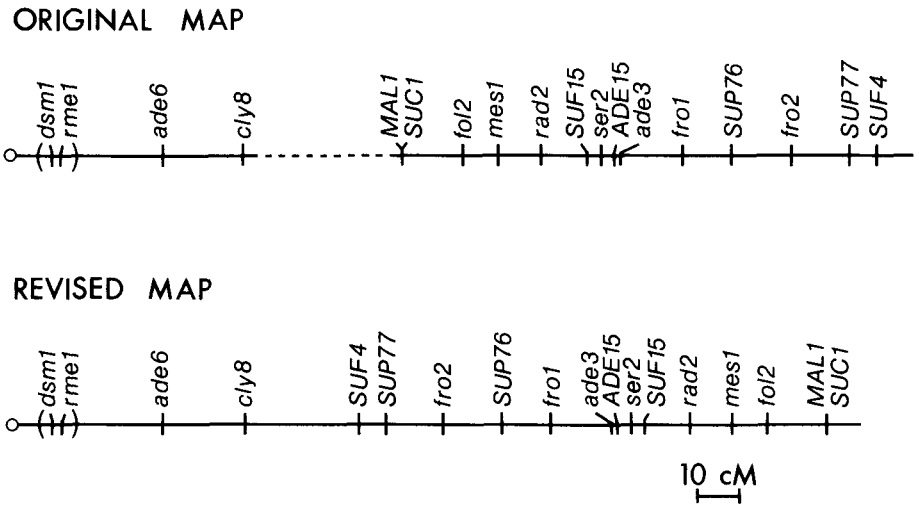

FIGURE 1.—Original and revised genetic maps of the right arm of chromosome *VII*. A, Original genetic map taken from MORTIMER and SCHILD (1982). B, Genetic map revised in accord with the data presented here. The centromere is represented as a circle. Solid lines represent linkages established by tetrad analysis. The dashed line represents linkage established by mitotic analysis, which was arbitrarily assigned a distance of 100 cM.

MATERIALS AND METHODS

Yeast strains: The genotypes and sources of strains used in this study are listed in Table 1. All genetic designations are those described by MORTIMER and SCHILD (1980, 1982). Strains were constructed by standard genetic procedures. Strains MCY846 and MCY847 carry the *cly8* allele derived from R277, the *ade6* allele derived from DBY543 and the *leu2-3* allele obtained from M. CULBERTSON. The *cly8* mutation in R277 was shown to be allelic to the *cly8-1* mutation in 197 by complementation analysis.

Genetic methods and media: Standard genetic procedures of crossing, sporulation and tetrad analysis were followed (MORTIMER and HAWTHORNE 1969; SHERMAN, FINK and LAWRENCE 1978). Rich media (YPD), minimal media (SD) and sporulation media were prepared as described by SHERMAN, FINK and LAWRENCE (1978). The segregation of *cly8* was scored by testing for temperature sensitivity of growth at 36°; the permissive temperature used was 25°. The segregation of *SUF4* was scored by suppression of the *leu2-3* frameshift mutation, which was homozygous in the relevant crosses. The spore viability in the crosses MCY846 × L203 and MCY847 × L202 was about 75 and 90%, respectively.

RESULTS AND DISCUSSION

Linkage analysis: Tetrad analysis was carried out on the crosses MCY846 × L203 and MCY847 × L202, and data were obtained from tetrads having four viable spores and showing 2:2 segregation for the three markers (Table 2). The tetrad data established a linkage relation between *SUF4* and *cly8*, and a map distance of 29 cM was calculated. The data also provided evidence for linkage of *SUF4* and *ade6*. Although the calculated genetic distance for this marker pair was greater than 60 cM, the ratio of parental ditype to nonparental ditype asci differed significantly from 1:1 at the 2.5% level (20:8, $\chi^2 = 5.14$), indicating that these two markers are linked. In this study the value determined for the genetic distance between *ade6* and *cly8* was 43 cM, whereas

TABLE 1

Yeast strains

Strain	Genotype	Source
MCY846	*MAT***a** *cly8 ade6 leu2-3*	This work
MCY847	*MATα cly8 ade6 leu2-3*	This work
L202	*MAT***a** *leu2-3 SUF4*	M. CULBERTSON
L203	*MATα leu2-3 SUF4*	M. CULBERTSON
DBY543	*MATα ade6*	D. BOTSTEIN
R277	*MATα cly8 ura3 lys2 his7 tyr1 ade2 ade5 ade6 met13 trp5 cyh2*	R. ROTHSTEIN
197	*MAT***a** *cly8-1 ade1 ade2 ura1 his7 lys2 tyr1 gal1 ade6*	Yeast Genetic Stock Center

TABLE 2

Linkage data

Gene pair	No. of tetrads			Map distance (cM)
	PD	NPD	T	
ade6-cly8	28	3	58	43
cly8-SUF4	48	2	39	29
ade6-SUF4	20	8	61	61

PD, parental ditype; NPD, nonparental ditype; T, tetratype. Genetic map distances in centiMorgans (cM) were calculated from the tetrad data by the equation of PERKINS (1949): cM = 100(T + 6NPD)/2(PD + NPD + T).

the value previously established from the compiled data of MORTIMER and SCHILD (1980) was 18.2 cM; we suggest that differences in the genetic background of the mapping crosses were responsible for this discrepancy. Regardless of this discrepancy, the map distances are consistent with the gene order *ade6—cly8—SUF4*. These data indicate that the map of chromosome *VII* should be revised as shown in Figure 1B. With this revision, *SUC1* and *MAL1* are the most centromere-distal markers, and thus, all of the polymeric fermentation markers that have been mapped are located at the ends of chromosomes (MORTIMER and SCHILD 1982). From a historical perspective, it is interesting to note that ROMAN (1956b) originally proposed the correct order, centromere—*ade6—ade3—MAL1*, on the basis of mitotic segregation studies.

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