GENETIC MAPPING OF THE *pho2*, *PHO82–pho4* AND *pho85* LOCI OF YEAST

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Manuscript received October 25, 1979
Revised copy received March 11, 1980

ABSTRACT

The *PHO82-pho4* (*PHOO-phoD*) locus was mapped on the right arm of chromosome *VI*, 6.5 cM centromere-distal to *met10*. A *pho85* (*phoU*) mutant was newly isolated, and its map location was determined on the left arm of chromosome *XVI*, 15 cM centromere-distal to *rad1*. A mutant gene that causes temperature-sensitive growth on nutrient medium was found very near (or at) the *pho85* locus. The supertriploid method was successfully applied to locate the *pho2* (*phoB*) locus on chromosome *IV*. The *pho2* locus was 40 cM from *rna11* on the left arm of chromosome *IV*.

GENETIC analyses of the production of repressible acid phosphatase of *Saccharomyces cerevisiae* (SCHURR and YAGIL 1971; TOH-E *et al.* 1973; TOH-E and OSHIMA 1974; UEDA, TOH-E and OSHIMA 1975; UEDA and OSHIMA 1975) revealed that at least six chromosomal genes, *pho2* (*phoB*)* *PHO82–pho4* (*PHOO–phoD*), *pho81* (*phoS*), *pho80* (*phoR*), *pho85* (*phoU*) and *pho84* (*phoT*), regulate the synthesis of the repressible acid phosphatase coded for by *pho5* (*phoE*). Among the *pho* genes described above, *pho5* and *pho80* have been mapped. HANSCHE, BERES and LANGE (1978) mapped *pho5* between *tsm134* and *lys2* on chromosome *II*. The *pho80* gene was mapped on the right arm of chromosome *XV* (BERES, personal communication). This report describes the location on the yeast chromosome map of the *pho2*, *PHO82–pho4* and *pho85* loci that were mapped by using the supertriploid method (WICKNER 1979), as well as by standard tetrad analysis. Map distances were calculated by PERKINS (1949) equation, $x = 100\,\frac{\mathrm{T} + 6\mathrm{NPD}}{2(\mathrm{PD} + \mathrm{NPD} + \mathrm{T})}$, and shown as centimorgans (cM).

The *PHO82* strain OC–6A (*αpho3 PHO82*) was crossed with the multiply labelled strain, AT201. The segregation of markers in cross W221 indicated the linkage between *PHO82* and *his2* (Table 1). To determine the location of *PHO82* with respect to the other markers on the right arm of chromosome *VI*, two more crosses (W275 and W424) were carried out. Data shown in Table 1 locate the position of *PHO82* at 6.5 cM centromere-distal to *met10*.

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* The nomenclature system of yeast genetic markers recommended by PLISCHKE *et al.* (1975) is used throughout this work and the conventional name is shown in parenthesis as appropriate.

TABLE 1

Mapping of pho *genes*

Interval tested	Cross*	No. of asci PD	NPD	T	cM
his2–PHO82	W221	13	0	6	
	W275	52	0	13	
	W424	37	0	19	
	Total	102	0	38	13.6
cdc14–PHO82	W275	55	0	11	
	W424	43	0	12	
	Total	98	0	23	9.5
met10–PHO82	W424	47	0	7	6.5
cdc14–met10	W424	56	0	6	4.8
his2–met10	W424	48	0	15	11.9
his2–cdc14	W424	55	0	8	7.3
rad1–pho85	W465	29	0	14	
	W480	52	0	18	
	W486	31	0	16	
	Total	112	0	48	15.0
trp1–pho2	W320**	33	6	81	
	W382	1	8	1	
	W425	3	0	6	
	W458	27	3	61	
	W471	10	5	37	
	Total	74	15	193	49.8
mak21–pho2	W382	2	0	9	
	W425	3	0	6	
	W458	17	5	50	
	W471	12	4	40	
	Total	34	9	105	53.7
rna11–pho2	W425	4	0	5	
	W458	31	3	53	
	Total	35	3	58	39.6
rna11–trp1	W425	7	0	2	
	W458	57	0	31	
	Total	64	0	33	17.0
mak21–trp1	W425	7	0	5	
	W458	45	2	39	
	Total	52	2	44	28.6
rna11–mak21	W425	5	0	6	
	W458	32	3	41	
	Total	37	3	47	37.4

*W221 $\frac{\alpha \; + \; + \; + \; + \; + \; + \; + \; + \; + \; pho3 \; PHO82}{\mathbf{a} \; ade1 \; ura3 \; his2 \; leu1 \; trp5 \; ura1 \; aro7 \; met2 \; pho3 \; +}$

W275 $\frac{\mathbf{a} \; his2 \; his7 \; cdc14 \; + \; + \; + \; pho3 \; +}{\alpha \; + \; + \; + \; leu1 \; trp5 \; ura1 \; pho3 \; PHO82}$

TABLE 1—Continued

	Interval tested	Cross*	No. of asci PD	NPD	T	cM
W424	α *his2 cdc14 PHO82* + + + + + *pho3* **a** + + + *met10 his4 leu2 ura1 ade2 pho3*					
W465	**a** *his7* + + + + *pho3 pho85* α + *arg1 rad1 cdc4 gal4 pho3* +					
W480	**a** *his7 cdc4 gal*⁻ + + + + *pho3 pho85* α + + + *arg6 rad1 cyh2 mak3 pho3*					
W486	**a** his7 arg6 cyh2 rad1 + + *pho3 pho85* α + + + + *leu1 arg1 pho3* +					
W320	**a** + + + *arg1 pho3 pho2* α *cdc16 asp5 trp1* + *pho3* +					
W382	**a** + + *trp1 pho3 pho2* [KIL-b]*** α *leu2 mak21* + + + [KIL-0]					
W425	**a** *arg6 pho3 pho2* + + + [KIL-b] α + + + *trp1 rna11 mak21* [KIL-0]					
W458	**a** *arg1 pho3 pho2* + + + [KIL-b] α + + + *trp1 rna11 mak21* [KIL-0]					

** Pooled tetrad data from crosses other than listed in this table are included in this line.
*** [KIL-b] is a mutant killer plasmid showing superkiller phenotype. This mutant plasmid bypasses some *mak* mutations, but not *mak21* (TOH-E and WICKNER, unpublished) .

A new *pho85* mutant (B104) was isolated from AT199 (**a** *pho3 his7*) after ethyl methanesulfonate mutagenesis (LINDEGREN et al. 1965) and mapped. B104 showed two other mutant phenotypes: temperature-sensitive growth on nutrient medium and respiratory deficiency. Both of these phenotypes segregated 2+:2− in the cross of B104 × wild type. The temperature sensitivity co-segregated with the *pho85* character, but the respiratory deficiency of B104 segregated independently of the *pho85* trait. No recombination could be detected between *pho85* and *ts* among 46 asci tested. A temperature-resistant revertant was isolated from the *pho85–ts* strain (AT275). The revertant still had the *pho85* phenotype. However, this reversion was due to an extragenic suppressor.

Since the *pho85* locus was known previously to be centromere-linked, AT275 (**a** *pho3 pho85–ts his7*) was crossed with strains having known centromere markers. Linkage between *pho85* and *rad1* on chromosome *XVI* was found in cross W465. The pooled tetrad ratio collected from the crosses (W465, W480, and W486) was PD : NPD : T = 112 : 0 : 48, and the distance between these two genes was calculated as 15 cM (Table 1). No close linkage between *pho85* and *mak3* could be observed. The sequence, *pho85–rad1*–centromere, was deduced by analyzing individual tetrads of cross W486. This arrangement is consistent with the fact that the frequency of second-division segregation of *pho85* (25.5%) is higher than that of *rad1* (15%).

The linkage group of *pho2* was analyzed by the supertriploid method described by WICKNER (1979). A *pho2* strain W273–14C (**a** *pho3 pho2 arg6*) was mated with spores of supertriploid 1234 *en masse* and protrophs were selected. Resulting

diploids having random trisomes were dissected, and the segregation patterns of *pho2* and that of standard markers were compared. Thus, the possible chromosomal location of *pho2* was narrowed to chromosome *IV*, *VI* or a new chromosome. The tetrad ratio data between *pho2* and *trp1* were collected from crosses in which both of these two markers segregated 2+ :2−. The cumulative ratio was PD : NPD : T = 33 : 6 : 81. Since this ratio indicates loose linkage between *pho2* and *trp1*, the linkage between *pho2* and other markers on chromosome *IV* was tested. Cross W366, containing *aro1D* and *pho2*, gave the ratio PD : NPD : T = 0 : 2 : 3 with respect to these markers, which showed no linkage between *aro1D* and *pho2*. Then, the linkage between *pho2* and *rna11* and *mak21* was tested. The tetrad distribution shown in Table 1 indicates: (1) *pho2* is loosely linked to *trp1* and *mak21*, and (2) the linkage between *pho2* and *rna11* is closer than that between *pho2* and *trp1*. WICKNER and LEIBOWITZ (1979) mapped *mak21* between *trp1* and *aro1D* and explained the inconsistency of map distance between *mak21* and *rna11* by relocating *rna11* on the left arm of chromosome *IV*. The linkage data shown in Table 1 support this revision.

I am grateful to Reed B. WICKNER for helpful discussion and for critically reading the manuscript.

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Corresponding editor: F. SHERMAN