

Summary of markers at extremes of the known linkage groups

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Abstract

Markers at extremes of linkage groups

Perkins, D. D. Summary of markers at extremes of the known linkage groups.

Genes that defy mapping by showing no linkage to alcoy markers or to other commonly used test loci, may in fact be situated well beyond those portions of the linkage groups that are already marked. A series of crosses testing such mutants for linkage with genes marking the present extremes of each linkage group would in all likelihood extend the mops. Genes useful or markers in such tests are summarized in the table. It will be noted that the left arms of III, IV and V are virtually unmarked, except for loci near the centromere.

Recommended marker gene	To check linkage group	Approximate distance from centromere	Comments
<u>fr</u> : frosty (B110)	I L	60	<u>un</u> (b39) is the leftmost marker that functions as protoperithecial parent. <u>leu-3</u> is leftmost auxotroph. (Use <u>leu-3</u> (R156) (tight) in preference to 47313, which adapts on minimal).
<u>os</u> : osmotic (B135 or E11200)	IR	90	Alternative: <u>so</u> : soft (slightly distal to <u>os</u>). Not good as protoperithecial parent (<u>os</u> is only fair), and not as easy to score.
<u>cys-3</u> (P22)	II L	4 0	<u>cys</u> shows poor recovery from crosses. Therefore, isolate to minimal, and work among <u>cys</u> classes only. 18 units left of <u>pyr-4</u> (Murray 1965).
<u>fl</u> : fluffy	II R	50	<u>tryp-3</u> (td) is slightly more distal, but <u>fl</u> is easier to use. Heterocaryon compatibility gene <u>d</u> has been mopped 23 units right of <u>tryp-3</u> , but can be used only if all compatibility genes are controlled.
<u>acr-2</u> (KH2)	III L	3	Scorable on minimal agar + 50 µg acriflavin per ml.
<u>tyr-1</u> (Y6994)	III R	50	Alternative: <u>vel</u> : velvet, a morphological, a few units proximal.
<u>pdx-1</u> (37803) or <u>pyr-1</u> (H263)	IV L	8	<u>pyr-1</u> is slightly left of <u>pdx-1</u> . Both are in right arm. <u>fi</u> : fissure, is left of centromere, but is difficult to score in some isolates; best scored on 6-inch slants (E. Berry).
<u>cyc-4</u> (K7)	IV R	40	10 units beyond <u>mat</u> (Murray 1965).
<u>lys-1</u> (33933)	V L	3	
<u>hist-6</u> (Y152M105)	V R	60	16 units right of <u>plug</u> and <u>gmn</u> .
<u>chol-2</u> (47904)	VI L	50	
<u>tryp-2</u> (75001)	VI R	30	T (IV;VI) 45502 breakpoint has been mopped well right of <u>tryp-2</u> by N. Murray. T (IV;VI), <u>pyr-3</u> could thus be used for checking VI R linkage.
<u>nit-3</u> (Y31881)	VII L	21	Heterokaryon compatibility locus <u>e</u> is 28 units distal to <u>nit-3</u> (Garnjobst and Wilson 1966). <u>do</u> : doily is slightly distal, but is a small colonial not as convenient as <u>nic-3</u> .
<u>rk</u> : skin (B106) or <u>nt</u> (65001)	VII R	35	Not a good protoperithecial parent. Rightmost nutritional marker is <u>nt</u> , B units proximal to <u>sk</u> . (Score <u>nt</u> as a nicotinamide mutant.)