Location of ser-4 near arg-2 on linkage group IV.

J. Maxwell
R. Bleeck
S. Growther
M Neal
T Parker

See next page for additional authors

Follow this and additional works at: http://newprairiepress.org/fgr

Recommended Citation
Maxwell, J., R. Bleeck, S. Growther, M. Neal, T. Parker, and L. Winikur (1980) "Location of ser-4 near arg-2 on linkage group IV,"

This Linkage Data is brought to you for free and open access by New Prairie Press. It has been accepted for inclusion in Fungal Genetics Reports by an authorized administrator of New Prairie Press. For more information, please contact cads@k-state.edu.
Location of ser-4 near arg-2 on linkage group IV.

Abstract
Location of ser-4 near arg-2 on linkage group IV.

Creative Commons License
This work is licensed under a Creative Commons Attribution-Share Alike 4.0 License.

Authors
J. Maxwell, R. Bleeck, S. Growther, M Neal, T Parker, and L Winikur
Maxwell, J. R., Bleeck, S., Growther, M. Neal, T. Parker, and L. Winikur.

Location of ser-4 near arg-2 on linkage group IV

Dow Woodward isolated ser-4 (DW110), initially designated P110, by UV irradiation of ST 74 A. The mutant was first described by Urey (1966 Ph. D. Thesis, Caltech) and further characterized by Maxwell (1970 Ph. D. Thesis, Caltech) who tentatively mapped the locus near centromere on linkage group IV. The results reported here place ser-4 0.7 centimorgans to the right of arg-2 on IV.

pyr-1, arg-2 A (FGSC 394) was crossed with ser-4, cot-1 a on solid Westergaard-Mitchell medium supplemented with 1 mg/ml yeast extract and 2% sucrose. Random ascospores were isolated onto small slants of appropriately supplemented Vogel's medium containing 2% sucrose (Horowitz complete medium did not improve the recovery of the ser-4, cot-1 parental type progeny).

<table>
<thead>
<tr>
<th>TABLE 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linkage data obtained from random ascospore isolates from the cross pyr-1, arg-2 x ser-4, cot-1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Zygote genotype and percent recombination</th>
<th>Parental types</th>
<th>Recombinations</th>
<th>Total and percent germination numbers</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Parental region 1</td>
<td>Parental region 2</td>
<td>Parental region 3</td>
</tr>
<tr>
<td></td>
<td>Parental region 1</td>
<td>Parental region 2</td>
<td>Parental region 3</td>
</tr>
<tr>
<td>pyr-1 + at-g-2 +</td>
<td>+</td>
<td>252</td>
<td>1 0 36</td>
</tr>
<tr>
<td>+ + ser-4 cot-1 (2.2) (0) (14.8)</td>
<td>128</td>
<td>9 0 32</td>
<td>458 70-82%</td>
</tr>
</tbody>
</table>

Because the results shown in Table 1 did not indicate whether ser-4 was located proximal or distal to arg-2, prototrophic recombinants were selected from random spores plated onto Vogel's minimal medium supplemented with 1.5% sorbose and 0.5% sucrose. Ten prototrophic colonies were isolated from 2880 spores germinated at 250°C. All prototrophs were cot+, suggesting that ser-4 lies distal to arg-2, and that prototrophs arise from a single crossover between these two loci. The map distance between arg-2 and ser-4 based on the frequency of prototrophs is estimated to be 10/2880 x 2 x 100 = 0.7 centimorgans. Biology Department, California State University, Northridge, Northridge, California 91330.