Inversion in the published genetic map of linkage group VII

E Kouzminova
University of Oregon

E U. Selker
University of Oregon

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

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

Recommended Citation

This Regular Paper 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.
Inversion in the published genetic map of linkage group VII

Abstract
In the course of cloning the dim-2 gene of Neurospora crassa we found that the published map of LG VII has an inversion of a segment extending from for to un-10K. Direct physical mapping confirmed that the gene order in this region should be wc-1, for, frq, oli, un-10.
In the course of cloning the dim-2 gene of Neurospora crassa we found that the published map of LG VII has an inversion of a segment extending from for to un-10. Direct physical mapping confirmed that the gene order in this region should be wc-1, for, frq, oli, un-10.

In preparation to clone the dim-2 gene (Foss et al. 1993 Science 262:1737-1741) of Neurospora crassa, we mapped this gene to the right arm of linkage group VII (LGVII) between wc-1 and arg-10. To map the dim-2 gene more precisely, three other crosses were performed (Table 1). We used strains with genetic markers wc-1, frq and for on LGVII and initially relied on a published genetic map (Figure 1a) to interpret our results. Data from the cross between un-10 and wc-1 dim-2 strains suggested that dim-2 is left of un-10 and between wc-1 and un-10; about half of the recombinants (21/36) in the wc-1 to un-10 interval were dim-2 (Table 1, cross 1). In two additional crosses in which one of the parents carried either a for or a frq mutation, however, we could not find dim-2 recombinant progeny of the genotype wc-1 dim-2 for and wc-1 dim-2 frq (Table 1, crosses 2 and 3); other markers in these crosses segregated as expected from the published genetic map (data not shown). Therefore, dim-2 appeared to be tightly linked to both for and frq. This result was unexpected since frq and for were reported to be to the right of un-10 by approximately 9 and 12 map units, respectively (Figure 1a). To explain our genetic data we considered the possibility that the segment including un-10, oli, frq and for is inverted (Figure 1b). This orientation accounted for all our data and was subsequently confirmed by physical mapping (data not shown). Results of chromosomal walks from wc-1 and un-10 showed that for is proximal to wc-1 followed by frq, oli, dim-2 and un-10 (Kouzminova and Selker, unpublished). Thus we suggest that the order of the genes for, frq, oli and un-10 is as shown in Figure 1b.

Table 1. Map data.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Zygote genotype</th>
<th>Genotype and number of recombinant progeny analyzed for dim-2</th>
<th>Genotype and number of dim-2 recombinant progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 a</td>
<td>+ + un-10</td>
<td>wc-1&quot; un-10&quot;</td>
<td>wc-1&quot; dim-2&quot; un-10&quot; 21</td>
</tr>
<tr>
<td></td>
<td>wc-1 dim-2 +</td>
<td>36</td>
<td>wc-1&quot; dim-2&quot; un-10&quot; 15</td>
</tr>
<tr>
<td>2 b</td>
<td>+ for (+)</td>
<td>random progeny</td>
<td>wc-1 for dim-2&quot; 4</td>
</tr>
<tr>
<td></td>
<td>wc-1 + (dim-2)(^d)</td>
<td>100</td>
<td>wc-1 for dim-2 2</td>
</tr>
<tr>
<td>3 c</td>
<td>+ frq::hph (+)</td>
<td>wc-1 frq::hph</td>
<td>wc-1 frq::hph dim-2&quot; 10</td>
</tr>
<tr>
<td></td>
<td>wc-1 + (dim-2)(^d)</td>
<td>10</td>
<td>wc-1 frq::hph dim-2 0</td>
</tr>
</tbody>
</table>

\(^a\)Recombinant progeny were selected on minimal medium at 34°C to select against un-10 progeny. The wc-1 mutation was scored under constant light at 34°C.

\(^b\)Progeny were scored without selection.

\(^c\)Progeny were selected on plates supplemented with hygromycin and scored for wc-1 under constant light at 34°C.

\(^d\)Parentheses indicate that the position of dim-2 relative to either for or frq could not be determined from the cross.
Figure 1. (a) Previous map and percentages of recombination between some genetic markers on LGVII (Perkins et al. 1982 Microbiol Reviews, 46:426-570). (b) Revised genetic map based on our findings. Genetic distance between wc-1 and for was calculated from the cross 2 data (Table 1). The centromeric region is indicated by the circle on the left and genes in the disputed region are in bold.