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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*.

Inversion in the published genetic map of linkage group VII

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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*un-10* showed that *for* is proximal to *wc-1* followed by *frq*, *oli*, *dim-2* and *un-10* (Kouzminova and Selker, unpublished).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.

Cross	Zygote genotype	Genotype and number of recombinant progeny analyzed for *dim-2*	Genotype and number of *dim-2* recombinant progeny	
1 [a]	+ + *un-10* *wc-1* *dim-2* +	*wc-1*⁺ *un-10*⁻ 36	*wc-1*⁻ *dim-2*⁺ *un-10*⁻ *wc-1*⁺ *dim-2 un-10*⁻	21 15
2 [b]	+ *for* (+) *wc-1* ÷ (*dim-2*)[d]	random progeny 100	*wc-1 for dim-2*⁺ *wc-1*⁺ *for*⁻ *dim-2*	4 2
3 [c]	+ *frq::hph* (+) *wc-1* + (*dim-2*)[d]	*wc-1 frq::hph* 10	*wc-1 frq::hph dim-2*⁺ *wc-1 frq::hph dim-2*	10 0

[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.

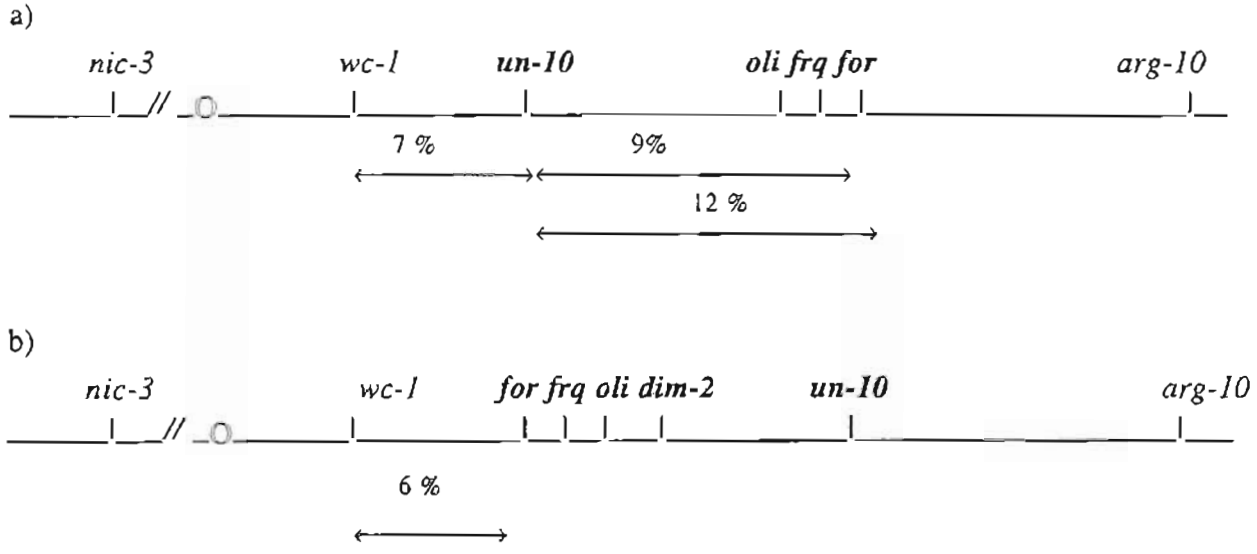

Figure 1. (a) Previous map and percentages of recombination between some genetic markers on LGVII (Perkins *et al.* 1982 Microbiol Reviews, 46:426-570). (b) Revised genetic map based on our findings. Genetic distance between *wc-1* and *for* was calculated from the cross 2 data (Table 1). the centromeric region is indicated by the circle on the left and genes in the disputed region are in bold.

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