Reciprocal translocation AR30 has a breakpoint distal to all known IIL markers.

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Abstract
Reciprocal translocation AR30 has a breakpoint distal to all known IIL markers.

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Reciprocal translocation AR30 has a breakpoint distal to all known IIIL markers.

Three crosses were used to map the IIIL breakpoint. Data from the cross T AR30 x Normal pi pyr-4 (Table 1, cross A) place the AR30 breakpoint outside and a considerable distance from the pi pyr-4 region although the direction is not certain. The off-ratios in the first two classes can be attributed to decreased germination and/or growth of pi progeny.

**TABLE 1**

Crosses mapping AR30 breakpoint

<table>
<thead>
<tr>
<th>Crossovers</th>
<th>Parentals</th>
<th>I &amp; II</th>
<th>III</th>
<th>II &amp; I, II</th>
</tr>
</thead>
<tbody>
<tr>
<td>A. pi pyr-4</td>
<td>AR30 + +</td>
<td>23</td>
<td>29</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>84</td>
<td>7</td>
<td>2</td>
</tr>
<tr>
<td>B. pyr-4 +</td>
<td>AR30 + +</td>
<td>28</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>30</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>C. ure-3 fl</td>
<td>AR30 arg-5 + + rip</td>
<td>29</td>
<td>26</td>
<td>16</td>
</tr>
<tr>
<td>D. caf-1 at</td>
<td>AR30 + +</td>
<td>17</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>19</td>
<td>5</td>
<td>2</td>
</tr>
</tbody>
</table>

A. The number of normal (N) progeny for each class is given in the upper line.
B. The number of AR30 progeny in the reciprocal classes is given in the lower line.
C. The number of arg-5 progeny for each class is given in the upper line.
D. The number of AR30 progeny far each class is given in the lower line.

Data from crosses homozygous for AR30 are also shown in Table I. In heterozygous translocation crosses, markers distal to the IIIL breakpoint will segregate independently of markers proximal to the IIIL breakpoint. Markers on VL behave similarly. Cross B in Table I (AR30 pyr-4 x AR30 arg-5) indicates that pyr-4 and arg-5 remain linked so the AR30 breakpoint is not between pyr-4 and arg-5. Similarly, cross C shows that arg-5 is linked to ure-3, ure-3 is linked to fl, and fl is linked to rip: P < 0.001 from Chi-square tests for independence, for all four intervals. Thus, the IIIL breakpoint of AR30 is on IIIL distal to the known genetic markers but not terminal.

Data from the cross T AR30 x Normal at caf-1 Table I, cross D) show that the VL breakpoint is distal to caf-1. Perkins, Raju and Barry (1980 Chromosoma 76: 255-275) have shown cytologically that the AR30 breakpoint is proximal to the nucleolus organizer. Thus, the VL breakpoint of AR30 is between caf-1 and the nucleolus organizer.

A word of caution regarding this rearrangement is necessary. In heterozygous crosses (AR30 x normal sequence) many defective ascospores turn black. Instead of the 50% black spores expected from a reciprocal rearrangement crossed with normal sequence, about 85% of the shot spores from AR30 x Normal are black (the percentage of black spores increases with age). Consequently, the viability of the black spores from such a cross can be as low as 25 to 30% in crosses homozygous for AR30 a normal situation prevails - 90 to 95% black spores are shot and 90 to 95% of the spores are viable. Thus, scoring AR30 visually by percent of shot black spores can be done only with practice, preferably by making comparisons of the tested stock when crossed with a known rearrangement tester and when crossed with a known normal-sequence tester. AR30 stocks containing fluffy are useful for such tests, and both TIII; VL AR30 fla (FGSC #3948 and TIII; VL AR30 fla (FGSC #3949) have been deposited with FGSC. I have also deposited TIII;VL AR30 caf-1 at (FGSC #3950) and TIII;VL AR30 caf-1 at (FGSC #3951) which should be useful in detecting extremely distal IIIL markers by linkage to caf-1 and at. (Supported by Public Health Service Grant AI-01462.) - - Department of Biological Sciences, Stanford University, Stanford, California 94305.

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TABLE 1

Rates of growth and fungicide resistance of osmotic mutants of Neurospora crassa

<table>
<thead>
<tr>
<th>Locus</th>
<th>Allele or isolation number</th>
<th>PGSC stock number</th>
<th>Rate of growth</th>
<th>Resistance to fungicides</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>MM</td>
<td>CH</td>
</tr>
<tr>
<td>os-1</td>
<td>M16</td>
<td>812</td>
<td>50</td>
<td>19</td>
</tr>
<tr>
<td></td>
<td>M155-1</td>
<td>824</td>
<td>61</td>
<td>23</td>
</tr>
<tr>
<td></td>
<td>B135</td>
<td>951</td>
<td>49</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>P668</td>
<td>973</td>
<td>50</td>
<td>44</td>
</tr>
<tr>
<td></td>
<td>MM233(t)</td>
<td>1287</td>
<td>92</td>
<td>80</td>
</tr>
<tr>
<td></td>
<td>P3282</td>
<td>1508</td>
<td>46</td>
<td>23</td>
</tr>
<tr>
<td></td>
<td>MM204(t)</td>
<td>1637</td>
<td>80</td>
<td>60</td>
</tr>
<tr>
<td></td>
<td>P3282</td>
<td>1644</td>
<td>49</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td>AR2</td>
<td>1675</td>
<td>63</td>
<td>21</td>
</tr>
<tr>
<td></td>
<td>P5990</td>
<td>2432</td>
<td>51</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td>P6549</td>
<td>2584</td>
<td>64</td>
<td>23</td>
</tr>
<tr>
<td>os-2</td>
<td>UCLA80</td>
<td>2238</td>
<td>106</td>
<td>109</td>
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<tr>
<td></td>
<td>UCLA93</td>
<td>2240</td>
<td>98</td>
<td>95</td>
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<td>os-4</td>
<td>MM2010</td>
<td>2429</td>
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<td>112</td>
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<td>os-5</td>
<td>MM2160</td>
<td>1638</td>
<td>98</td>
<td>98</td>
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<tr>
<td>flm-1</td>
<td>Y256M209</td>
<td>3624</td>
<td>94</td>
<td>76</td>
</tr>
<tr>
<td>flm-2</td>
<td>Y256M223</td>
<td>2668</td>
<td>98</td>
<td>93</td>
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<tr>
<td>cut</td>
<td>LLM1</td>
<td>2385</td>
<td>96</td>
<td>102</td>
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<td>gla</td>
<td>T9M150</td>
<td>3428</td>
<td>58</td>
<td>58</td>
</tr>
<tr>
<td></td>
<td>T9N150</td>
<td>3429</td>
<td>108</td>
<td>116</td>
</tr>
</tbody>
</table>

a Increase in colony diameter, mm/24 hr, at 26°C; mean of 3 replicates.  
CH = MM supplemented with 0.5% casamino acids and 0.5% yeast extract.  
b0 = sensitive (ED95 < 10ug fungicide/ml); ++ = low resistance (ED95 = 2-10ug/ml);  
+++ = high resistance (ED95 >50ug/ml); ED95 >100ug/ml); ++ = intermediate levels  
of resistance.  ED values are the concentrations of fungicide in agar media that  
reduce radial growth by 50% or 95%.