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Abstract

As an initial step toward cloning the band (bd) gene, we sought to pinpoint its genetic location relative to known flanking markers on LGIV prior to initiating a chromosome walk.

Genetic mapping of the *bd* locus

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As an initial step toward cloning the *band (bd)* gene, we sought to pinpoint its genetic location relative to known flanking markers on LGIV prior to initiating a chromosome walk.

Previous data (Table 1) from Sargent & Woodward (1969 J. Bacteriol. **97**:861-866) showed the *bd* gene distal to *pan-1* by 1.5 map units. Our follow-up crosses (Table I) show *bd* to be far more distal than anticipated. By two and three point crosses, we now place *bd* 8.9 map units distal to *met-5* and 18.8 map units proximal to *nit-3*. The gene order is therefore:

centromere/trp-4/pan-1/cot-1/his-4/met-5/bd/nit-3

Table 1. Results of genetic crosses

Zygote genotype and recombinaton percentage	Parentals	Singles Region 1	Singles Region 2	Doubles	Total
+ 8.5 + 1.5 *bd* *trp-4* *pan-1* +	87 92	11 6	2 1	0 0	199[a]
pan-1 4.0 + 12.1 + + *cot-1* *bd*	59 68	3 1	5 11	1 1	149
cot-1 3.7 *his-4* 18.3 + + + *bd*	52 99	1 4	11 22	1 1	191
cot-1 4.1 + 8.9 *bd* - *met-5* +	67 60	6 0	10 3	0 0	138
cot-1 16.6 *bd* 18.8 + + + *nit-3*	63 90	12 21	33 5	2 3	229

[a] From Sargent and Woodward (1969) J. Bact. 97:861-866.

These data, once again, highlight the variability sometimes observed in *Neurospora* genetic crosses as well as the importance of establishing flanking genetic markers prior to initiating a chromosome walk.

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