

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:

$$\text{centromere}/\text{trp-4}/\text{pan-1}/\text{cot-1}/\text{his-4}/\text{met-5}/\text{bd}/\text{nit-3}$$

Table 1. Results of genetic crosses

Zygote genotype and recombination percentage	Parentals	Singles Region 1	Singles Region 2	Doubles	Total
$\frac{+ \quad 8.5 \quad + \quad 1.5 \quad bd}{trp-4 \quad \quad \quad pan-1 \quad \quad \quad +}$	87 92	11 6	2 1	0 0	199 ^a
$\frac{pan-1 \quad 4.0 \quad + \quad 12.1 \quad +}{+ \quad \quad \quad cot-1 \quad \quad \quad bd}$	59 68	3 1	5 11	1 1	149
$\frac{cot-1 \quad 3.7 \quad his-4 \quad 18.3 \quad +}{+ \quad \quad \quad + \quad \quad \quad bd}$	52 99	1 4	11 22	1 1	191
$\frac{cot-1 \quad 4.1 \quad + \quad 8.9 \quad bd}{- \quad \quad \quad met-5 \quad \quad \quad +}$	67 60	6 0	10 3	0 0	138
$\frac{cot-1 \quad 16.6 \quad bd \quad 18.8 \quad +}{+ \quad \quad \quad + \quad \quad \quad nit-3}$	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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