

## Genetic mapping of the bd locus

M T. Lewis  
*University of California*

J F. FELDMAN  
*University of California*

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



This work is licensed under a [Creative Commons Attribution-Share Alike 4.0 License](https://creativecommons.org/licenses/by-sa/4.0/).

---

### Recommended Citation

Lewis, M. T., and J.F. FELDMAN (1998) "Genetic mapping of the bd locus," *Fungal Genetics Reports*: Vol. 45, Article 8. <https://doi.org/10.4148/1941-4765.1255>

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](mailto:cads@k-state.edu).

---

## Genetic mapping of the bd locus

### 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

Michael T. Lewis and Jerry F. Feldman - Department of Biology, 337 Sinsheimer Labs, University of California, Santa Cruz, CA 95064.

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 recombinaton percentage	Parentals	Singles Region 1	Singles Region 2	Doubles	Total
$\begin{array}{ccc} + & 8.5 & + & 1.5 & \text{bd} \\ \text{trp-4} & & \text{pan-1} & & + \end{array}$	87 92	11 6	2 1	0 0	199 <sup>a</sup>
$\begin{array}{ccc} \text{pan-1} & 4.0 & + & 12.1 & + \\ + & & \text{cot-1} & & \text{bd} \end{array}$	59 68	3 1	5 11	1 1	149
$\begin{array}{ccc} \text{cot-1} & 3.7 & \text{his-4} & 18.3 & + \\ + & & + & & \text{bd} \end{array}$	52 99	1 4	11 22	1 1	191
$\begin{array}{ccc} \text{cot-1} & 4.1 & + & 8.9 & \text{bd} \\ - & & \text{met-5} & & + \end{array}$	67 60	6 0	10 3	0 0	138
$\begin{array}{ccc} \text{cot-1} & 16.6 & \text{bd} & 18.8 & + \\ + & & + & & \text{nit-3} \end{array}$	63 90	12 21	33 5	2 3	229

<sup>a</sup> 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.

#### Acknowledgements

We wish to thank Mignon Fogarty and Katie Wymore for technical assistance.