

## Linkage among melanin biosynthetic mutations in *Cochliobolus heterostrophus*

A Guillen

*Universidad Complutense de Madrid*

B G. Turgeon

*Iowa State University*

P. R. Thorson

*Cornell University*

C. R. Bronson

O. C. Yoder

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

---

### Recommended Citation

Guillen, A., B.G. Turgeon, P.R. Thorson, C.R. Bronson, and O.C. Yoder (1994) "Linkage among melanin biosynthetic mutations in *Cochliobolus heterostrophus*," *Fungal Genetics Reports*: Vol. 41, Article 11. <https://doi.org/10.4148/1941-4765.1373>

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).

---

# Linkage among melanin biosynthetic mutations in *Cochliobolus heterostrophus*

## Abstract

Melanin is synthesized by *C. heterostrophus* from acetate via pentaketide and several dihydroxynaphthalene intermediates (Tanaka et al. 1991 *Mycol. Res.* 95:49-56), as it is for certain other fungi (Bell and Wheeler 1986 *Ann. Rev. Phytopathol.* 24:411-451; Kubo et al. 1989 *Exp. Mycol* 13:77-84; Chumley and Valent 1990 *Mol. Plant-Microbe Int.* 3:135-143). Previously, five melanin deficient mutants of *C. heterostrophus* were analyzed by Tanaka et al. (*Mycol. Res.* 95:49-56), who were unable to establish complete linkage relationships because three of the mutations (*alb1*, *alb3*, and *brn1*) showed no recombination when crossed to each other, and were unlinked to the other two (*sal1* and *pgr1*), which mapped about 12 cM apart. A sixth color mutation, *scr1*, represented a third linkage group, but there was no evidence of its involvement in melanin biosynthesis. Independently, we have recovered six melanin-deficient mutants, one of which (*alb1*, Leach et al. 1982 *J. Gen. Microbiol.* 128:1719-1729) was included in the study of Tanaka et al. and maps to chromosome 1 on the *C. heterostrophus* RFLP map (Tzeng et al. 1992 *Genetics* 130:81-96). We report here that our remaining five melanin-deficient mutants [*crm1* (light cream), *crm2* (dark cream), *brn1* (brown), *rsy1* (rose), and probably *gra3* (gray)] are linked to, but are not allelic with, *alb1* (white) and constitute a gene cluster on chromosome 1

## Creative Commons License



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

# Linkage among melanin biosynthetic mutations in *Cochliobolus heterostrophus*

A. Guillen<sup>1</sup>, B. G. Turgeon, P. R. Thorson<sup>2</sup>, C. R. Bronson<sup>2</sup> and O. C. Yoder - Department of Plant Pathology, Cornell University, Ithaca, NY 14853. <sup>1</sup>Departamento de Microbiología III, Universidad Complutense de Madrid, 28040 Madrid, Spain; <sup>2</sup>Department of Plant Pathology, Iowa State University, Ames IA 50011

Melanin is synthesized by *C. heterostrophus* from acetate via pentaketide and several dihydroxynaphthalene intermediates (Tanaka et al. 1991 Mycol. Res. 95:49-56), as it is for certain other fungi (Bell and Wheeler 1986 Ann. Rev. Phytopathol. 24:411-451; Kubo et al. 1989 Exp. Mycol 13:77-84; Chumley and Valent 1990 Mol. Plant-Microbe Int. 3:135-143). Previously, five melanin deficient mutants of *C. heterostrophus* were analyzed by Tanaka et al. (Mycol. Res. 95:49-56), who were unable to establish complete linkage relationships because three of the mutations (*alb1*, *alb3*, and *brn1*) showed no recombination when crossed to each other, and were unlinked to the other two (*sal1* and *pgr1*), which mapped about 12 cM apart. A sixth color mutation, *scr1*, represented a third linkage group, but there was no evidence of its involvement in melanin biosynthesis. Independently, we have recovered six melanin-deficient mutants, one of which (*alb1*, Leach et al. 1982 J. Gen. Microbiol. 128:1719-1729) was included in the study of Tanaka et al. and maps to chromosome 1 on the *C. heterostrophus* RFLP map (Tzeng et al. 1992 Genetics 130:81-96). We report here that our remaining five melanin-deficient mutants [*crm1* (light cream), *crm2* (dark cream), *brn1* (brown), *rsy1* (rose), and probably *gra3* (gray)] are linked to, but are not allelic with, *alb1* (white) and constitute a gene cluster on chromosome 1 as shown in Figure 1. Since *alb1* is the only mutant common to both our analysis and that of Tanaka et al., we do not know which (if any) of the remaining mutants in our collection correspond to those in the previous study.

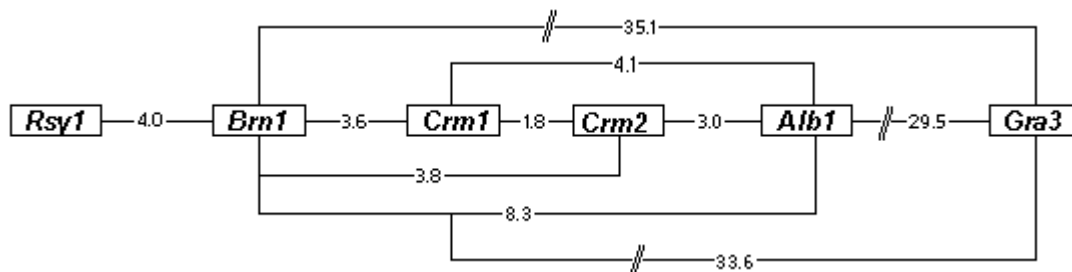


Figure 1. Proposed map of the gene cluster encoding melanin biosynthetic enzymes on chromosome 1 of *C. heterostrophus*, based on the two point cross data in Table 1. The gene order and the map distances must be considered tentative, since two point data may not accurately reflect recombination frequencies and do not prove gene order. Note that *Rsy1* could be on either side of *Brn1* and that linkage of *Gra3* to the cluster is tenuous because of the distance between them. Numbers indicate cM.

In addition to the randomly isolated ascospores reported in Table 1, a few complete tetrads (four sets of twins/ascus) were recovered from each cross; they were predominantly parental ditypes

with at least one tetratype ascus from each pair of parents (nonparental ditypes were not found in any progeny). Color patterns in tetratype asci indicated the following epistatic relationships [evidence for epistasis of *brn1* over *rsy1* is based on the relative high abundance of *brn1* progeny from the *brn1* X *rsy1* cross (Table 1), not on tetratype asci]:

*alb1* > *crm1* > *crm2* > *brn1* > *rsy1* > *gra3*

Table 1. Progeny tests of two point crosses between *C. heterostrophus* color mutants.

| Cross                     |             | Number of progeny |               |    |           |
|---------------------------|-------------|-------------------|---------------|----|-----------|
| Map distance <sup>a</sup> |             |                   |               |    |           |
| Parent 1                  | Parent 2    | Parent 1 type     | Parent 2 type |    | Wild type |
| (cM)                      |             |                   |               |    |           |
| —                         |             |                   |               |    |           |
| <i>brn1</i>               | <i>alb1</i> | 47                |               |    | 45        |
| 8.3                       |             |                   |               |    | 4         |
| <i>brn1</i>               | <i>crm1</i> | 75                |               |    | 86        |
| 3.6                       |             |                   |               |    | 3         |
| <i>brn1</i>               | <i>crm2</i> | 76                | 80            | 3  | 3.8       |
| <i>alb1</i>               | <i>crm1</i> | 74                | 70            | 3  | 4.1       |
| <i>alb1</i>               | <i>crm2</i> | 97                | 97            | 3  | 3.0       |
| <i>crm1</i>               | <i>crm2</i> | 612               | 513           | 10 | 1.8       |
| <i>gra3</i>               | <i>alb1</i> | 58                | 92            | 26 | 29.5      |
| <i>gra3</i>               | <i>brn1</i> | 27                | 34            | 13 | 35.1      |
| <i>gra3</i>               | <i>crm1</i> | 24                | 55            | 16 | 33.6      |
| <i>rsy1</i>               | <i>brn1</i> | 87                | 108           | 4  | 4.0       |

<sup>a</sup> Recombinant progeny included wild types (recognizable by their dark brown-green color) and double mutants (which could not be recognized because they expressed the color of the epistatic parent). The number of double mutants in each progeny was assumed to equal that of wild types, and the wild type number was doubled to calculate the recombination frequency.

An attempt was made to test the gene order shown in Figure 1 by scoring progeny from the three point cross *alb1;brn1* X *crm2*. Of 945 progeny isolated, 478 were *alb1*, 431 were *crm2*, 24 were *brn1*, and 12 were wild type. These data are not consistent with the gene order *Brn1-Alb1-Crm2*, which would require that the *Brn* phenotype represent double cross overs as the least frequent class, which it is not. However, because epistasis obscured certain recombinant classes of progeny, the data do not distinguish between the other two possible gene orders: *Brn1-Crm2-Alb1* (which the two point data in Table 1 suggest) and *Crm2-Brn1-Alb1*.

Although albino (*alb1*) strains of *C. heterostrophus* cannot survive in the field, they cause lesions qualitatively similar to those of wild type on the host plant (corn) in a growth chamber or greenhouse (Fry et al. 1984 *Phytopathology* 74:175-178). To determine if there are quantitative differences in virulence among color mutants or between color mutants and wild type, lesions on

corn plants (in a greenhouse) caused by strains carrying *alb1*, *crm1*, *crm2*, *brn1*, or *rsy1* were counted and measured, and compared with the sizes and numbers of lesions caused by wild type. No statistically significant differences were detected in any pair-wise comparison, suggesting that melanin plays no significant role in the virulence of *C. heterostrophus* to its host, in contrast to certain other fungi such as *Colletotrichum lagenarium* (Kubo et al. 1991 *Mol. Plant-Microbe Int.* 4:440-445) and *Magnaporthe grisea* (Chumley and Valent 1990 *Mol. Plant-Microbe Int.* 3:135-143), which require melanin for penetration of the host epidermis.