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Restriction polymorphism maps of Neurospora crassa: updates

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Abstract

When a gene or an unidentified fragment of DNA from an organism has been cloned, it is often useful to map its site of chromosomal origin with respect to known markers.

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When a gene or an unidentified fragment of DNA from an organism has been cloned, it is often useful to map its site of chromosomal origin with respect to known markers. The methods and materials for doing this, and some data on segregation of markers, has been published (Metzenberg *et al.* 1984. Neurospora Newsl. 31:35-39; ibid. Proc. Natl. Acad. Sci. U.S. 1985. 82:2067-2071; Metzenberg and Grotelueschen, 1987. Fungal Genetics Newsl. 34:39-44). The following data include the previous scorings of two crosses from the 1987 article and contains new data on the same two crosses from our own lab, and from others.

As noted in the 1987 article, 38 segregants from the first cross were taken from ordered asci, and provide somewhat more information than can be obtained from the 18 segregants which represent random spores from the second cross. Both crosses, however, have been used in a number of laboratories, and data from both are presented. The scoring of segregants is coded in the same way as before: "M" or "0" indicate segregants that are like the Mauriceville parent or like the Oak-Ridge-derived parent, respectively: "-" indicates that the scoring was not done or was equivocal for technical reasons; and (O) in Isolate I and (M) in Isolate 6 for all lanes of the second cross means that these are not progeny but are the parental strains of the cross, and are 0 and M by definition. The notation for genes or DNA fragments mapped in these crosses is a mixed one. As before, some are obvious gene symbols (e.g. *thi-4*) and are indexed in the compendium of loci (Perkins *et al.* 1982. Microbiol. Rev. 46:426-570). Those with simple numbers like 33 or 1 or 18, unprefaced by zeros, are the loci of 5S rDNAs, as in the 1984 article. Those containing a colon (e.g. 12:8B) are loci identified by probing blots with the corresponding cosmid from the Vollmer-Yanofsky clonal library (Vollmer and Yanofsky 1986. Proc. Natl. Acad Sci. U.S. 83:4869-4873). H3H4 is histone H3 + H4 (Woudt *et al.* 1983. Nucleic Acids Res. 11:5347-5360). *con* loci are associated with conidiation (Berlin and Yanofsky 1985. Molec. Cell. Biol. 5:839-848; ibid. 849-855). Loci with names starting with LZ and DB are arbitrary DNA fragments of unknown function, studied in our laboratory by Ludwika Zagorska and David Butler, respectively. *hbs* is "homebase", studied in J. Kinsey's laboratory. *cat-2* (Simmons *et al.* 1987. Fungal Genetics Newsl. 34:55-56) is a catalase-encoding gene scored by protein polymorphism rather than DNA polymorphism; note that its segregation in Ascus E suggests the occurrence of a gene conversion. Finally, the substantial number of loci whose numbers begin with one or more zeros are data that have been reported to us, but whose authors would like the loci to remain unidentified and themselves to be anonymous until publication or five years have elapsed, whichever is first. Even without identification, the results enrich the map and help others map their clones to a chromosome.

If you have found these data useful please pass on the favor by pencilling any results of your own, including those from random fragments and from "mistakes" in cloning onto a copy of the appropriate page from this article and sending it to RLM. You may ask that a number which preserves confidentiality be assigned to it, or if you are willing for the gene and yourself to be identified, that will be done. If we cooperate on this, we can hope to see this map become more densely and increasingly useful. Supported by NIH Grant GM 08995. - - - Department of Physiological Chemistry, University of Wisconsin, Madison, WI 53706