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Restriction polymorphism maps of *Neurospora crassa*: update.

When a gene or other fragment of DNA is cloned. it is often useful to identify the chromosomal region from which it arose. This is conveniently done with a set of progeny from one or more reference crosses in which many polymorphic differences are segregating. Data which allow the mapping of cloned genes have been published (Metzenberg et al. 1984, Neurospora Newsl. 31:35-39; ibid. Proc. Nat. Acad. Sci. U.S. 1985, 82:2067-2071, Metzenberg and Grotelueshen, 1988, Fungal Genetics Newsl. 35:30-35). The following is an update of the 1988 article. As noted previously, 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 "O" 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 (0) in Isolate 1 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 O and M by definition. Loci which were previously identified in the 1988 article, or are in the Compendium (Perkins et al. 1982, Microbiol. Reviews 46:426-570) are not further identified. All loci corresponding to 5S RNA-coding regions, previously given only as Arabic numerals starting with 1, are now identified as Fsr-1, etc. All of the telomeres (Tel) which have been included are due to the efforts of Michael Schechtman, whose article in this issue should be consulted. A number of loci whose identities were being kept confidential are now shown with informative names, instead of coded numbers beginning with a string of zeroes. COXVIII is subunit VIII of cytochrome oxidase, and is coded by a cloned, but unnamed, gene (M. Suarez/U.L. RajBhandary, in preparation). The following are newly named or unpublished loci, with the name(s) of the person or persons who should be consulted about them: cyt-21 (M. Kuiper/A. Lambowitz); sod-1 superoxide dismutase (D. Natvig); pma-1, plasma membrane ATPase (K. Hager/C.W. Slayman/B. Bowman); lys-6, (Ming Chow/U.L. RajBhandary); cyt-2, (A. Kubelik/A. Lambowitz); cyt-8 and cya-2, (M. David/U.L. RajBhandary); cat-3, (D. Natvig); ccg-1 and ccg-2, (J. Lores/J. Dunlap); SPIAE, an anonymous DNA fragment, (M. Schechtman); frq and for, (J. Dunlap). pho-4 was formerly called van (B. Bowman). Finally, the scoring of rDNA (LG V) of isolate C4 has been changed from M to O. The previous result may have been in error, but inspection of the original blots suggests it may not have been. Initially, C4 was an exceptional strain having both M and O types of rDNA, with a large preponderance of M, but subsequent preparations have been pure O. The preponderant rDNA form of the strain may thus have changed during mitotic events, and should be considered questionable. The other genes of this strain seem to behave conventionally.

If you have found these data useful, please pass on the favor by pencilling in any results of your own onto a copy of this table and sending it to RLM. You may ask that it be assigned a number which preserves confidentiality.

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