

Neurospora crassa chromosome walks

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Abstract

Chromosome walks have been executed for all seven chromosomes of *N. crassa*, but the amount of coverage varies greatly, from less than 3% (LG V) to about 25% (LG VII). Overall, about 10% of the genome has been covered by chromosome walks (Table 1). All chromosome walks are shown with respect to the position on the chromosome, oriented from the left telomere to the right. The standard nomenclature for these genomic libraries is followed: pSV50 (Vollmer and Yanofsky 1986 Proc. Natl. Acad. Sci. USA 83:4869-4873), pMOcosX (Orbach 1994 Gene 150:159-162), EMBL3 (Yeadon and Catchside 1995 Curr. Genet. 28:155-163), pCRD103 (Davis et al. 1994 Genetics 136:1297-1306), CBM1 (Cabibbo et al. 1991 Fungal Genet. Newsl. 38:68-70), CBM2 (Ballario et al. 1996 EMBO J. 15:1650-1657) and yeast artificial chromosome (YAC; Centola et al. 1994 Fungal Genet. Newsl. 41:23-33). For precise map positions of the cited alleles, refer to Perkins et al. (1982 Microbiol. Rev. 46:426-570) and Perkins (1992 Fungal Genet. Newsl. 39:61-70).

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A comparison of genetic and physical distances has been published recently (Radford and Parish 1997 Fungal Genet. Biol. 21:258-266). On average, 1 map unit (MU) corresponds to about 43 kb, but this value varies from about 20 to 80 kb per MU. In centromere-proximal regions, the crossover-suppressing effect of the centromere contributes to even larger distances per MU (Centola and Carbon 1994 Mol. Cell. Biol. 14:1510-1519). Regions corresponding to nearly 100 MU (of the ~1010 MU total for *N. crassa*) have been covered in the chromosome walks reported here.

Updated versions of chromosome walks will be available through the *Neurospora* Genome Project HomePage (<http://biology.unm.edu/~ngp/home.html>). Please share your chromosome walk information with Mary Anne Nelson (manelson@unm.edu) or Don Natvig (dnatvig@unm.edu), so that this important resource will be available to the whole community.

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Table 1. Chromosome walks

| Position | Markers spanned | Cosmids, plasmids, lambda clones and YACs ^a | Length ^b | Reference ^c |
|----------|--------------------------------------|--|---------------------|------------------------|
| LG II | <i>eth-1</i> , <i>arg-3</i> | X22:H2, L2, G19:G4, G13:C4, X17:D9, G6:F6, X1:F3, G4:G5, 28:12D, 26:11B, X10:H6, G3:E9, G9:C4, G17:E10, X8:D4, X17:B1, G15:B10, X9:C6, G8:D5, G1:A11 | 230 kb | 1 |
| LG II | <i>mei-3</i> , T39311 | G3:B5, X11:H2, G1:A7, 9:7G, 9:1H, X10:C2, X10:D3, G10:H5, X5:D9, X14:G3, G11:B1 | 100 kb | 1 |
| LG IR | <i>un-2</i> , <i>his-2</i> , TAR173, | 5:F10*, 22:F5*, 12:B6*, 14:D7*, 17:E2*, 22:G2*, 5:A10*, 5:D1*, 13:F7*, 12:C6* | 500 kb | 1 |
| LG IR | <i>his-2</i> , TAR173 | X20:D8, X7:H7, G2:B2, G13:B4, 10:6F, G19:B11, G13:H11, X11:B4, X21:G12 | 125 kb | 1 |
| LG IR | <i>his-3</i> | λJY25, λJY29, G3:6F, 23:3H | 60 kb | 2 |
| LG IR | <i>hom</i> , <i>al-1</i> | X1:7G, X9:3H, 3:11H, X24:3E, G2:8G, G10:10B, G16:11C, G8:7G, G16:8A | 270 kb | 3 |
| LG III | <i>un-24</i> , <i>het-6</i> , TAR18 | X19:F1, G25:F11, X18:H11, X24:G9, G8:F7, G12:E3, G8:G1, X14:C1, X5:F11, X7:G5 | 270 kb | 4 |

Table 1. continued.

| <u>Position</u> | <u>Markers spanned</u> | <u>Cosmids, plasmids, lambda clones and YACs^a</u> | <u>Length^b</u> | <u>Reference^c</u> |
|---------------------|--------------------------------|---|---------------------------|------------------------------|
| LG I | <i>het-C, pyr-4</i> | X2:C1, G20:D11, G22:H5, X25:A1, X7:F1, X11:C6 | 150 kb | 5 |
| LG IIIR | <i>ser-1, pro-1, ace-2</i> | 22:4D, 27:10H, 25:3G, 14:1C, 3-30:2B, 24:5G, 2-13:10B, 2-11:12A, 28:5H, 3:11A, 4:9C, 8:1E, 13:7C, 13:10A, 21:6D, 18:2C, 18:12G, 11:1B, 1:6G | 205 kb | 6 |
| LG IVR | <i>tol, np-4</i> | G13:C8, X25:D7, X7:C2, G1:E5, G6:E12, X4:E10, X14:C2, G4:A9, X17:B5, X10:A4, X17:C11, G6:C9 | 350 kb | 7 |
| LG VR | <i>am, gul-1, ace-5, ure-1</i> | G9:A10, G9:D12, X12:D8, G15:A7, X8:H6, X4:A2, X15:D8, G18:D11, X25:B7, G24:H8, G20:D6, X15:H8, X9:C3, G12:G1, X16:F6, X13:F3, G17:B9, G17:H9, X21:D7, X23:F10 | 240 kb | 8 |
| LG VII ^d | <i>Bml</i> | G14:11C, X9:9B, X5:7F, G12:10C | 110 kb | 9 |
| LG VII | <i>ylo-1, un-13, cpc-1</i> | G7:5F, G13:4D, G2:3A, X7:8E, X16:12D, X10:5H, X5:9H, G22:2C, X3:9C, X13:5A, G17:11E, G7:5F, G8:6D, G15:8E, pHL200, 2:5A, 22:11A | 420 kb | 9 |
| LG VII ^e | <i>qa-2, met-7, met-9</i> | 24-1-C*, 12-10-H*, 19-5-B*, 15-6-H*, 24-3-G*, 7-10-D* | 750 kb | 10 |
| LG VIIR | <i>met-7, wc-1</i> | 20:D-7, p550, 2-I, 3:H-3, 22-F, 12:F-8, 31:G-3, 54:E-6, G17:H7, 20:G-9, G7:G3, 56:E-7 | 230 kb | 11 |
| LG VIIR | <i>oli, frq, for</i> | 2:10A, 15:12G, λ3L10, λ2L82, λ19a, λ13a, λ13R, λ7R, 30:1A, 26:2A, 8:3B, 6:5A, 31:5E, 26:1H, 23:9D | 190 kb | 12 |

^a Context for clone references and nomenclature conventions. *N. crassa* YAC clones are indicated with an asterisk, to distinguish them from cosmid clones with similar nomenclature.

^b The approximate extent of the chromosome walk in kilobase pairs (kb) is indicated.

^c References: [1] Rosa *et al.* 1997 Fungal Genet. Biol. 21:315-322. [2] Yeadon and Catcheside 1995 Curr. Genet. 28:155-163. [3] Schmidhauser *et al.* 1997 Fungal Genet. Biol. 21:323-328. [4] Smith *et al.* 1996 Genetics 144:523-531. [5] Saupe *et al.* 1996 Genetics 143:1589-1600. [6] Davis *et al.* 1994 Genetics 136:1297-1306. [7] N.L. Glass, personal communication. [8] Bowring and Catcheside 1995 Curr. Genet. 29:27-33. [9] Wan *et al.* 1997 Fungal Genet. Biol. 21:329-336. [10] Centola and Carbon 1994 Mol. Cell. Biol. 14:1510-1519. [11] Ballario *et al.* 1996 EMBO J. 15:1650-1657. [12] McClung, Fox and Dunlap 1989 Nature 339:558-562.

^d Orientation of this walk is unknown.

^e This chromosome walk spans the LG VII centromere.