

## A chromosome walk linking the *gatA* and *alcC* genes of *Aspergillus nidulans*

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# A chromosome walk linking the *gatA* and *alcC* genes of *Aspergillus nidulans*

## Abstract

The *amdA* gene of *Aspergillus nidulans* has been mapped to linkage group VII, between the *gatA* and *alcC* genes (Jones and Sealy-Lewis 1990 *Curr. Genet.* 17:81-85). As clones of both of the genes flanking *amdA* were available, they were used as starting points for chromosome walking towards *amdA*. The relative orientation of these genes on linkage group VII was not known at the time. Therefore, both walks extended in both directions until overlapping clones from the different walks were detected. The total distance covered by all walks is approximately 240 kb.

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## A chromosome walk linking the *gatA* and *alcC* genes of *Aspergillus nidulans*

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The *amdA* gene of *Aspergillus nidulans* has been mapped to linkage group VII, between the *gatA* and *alcC* genes (Jones and Sealy-Lewis 1990 Curr. Genet. 17:81-85). As clones of both of the genes flanking *amdA* were available, they were used as starting points for chromosome walking towards *amdA*. The relative orientation of these genes on linkage group VII was not known at the time. Therefore, both walks extended in both directions until overlapping clones from the different walks were detected. The total distance covered by all walks is approximately 240 kb.

The walk from *gatA* (encoding GABA transaminase) was initiated using the cosmid clone pGIT-1 (Richardson et al. 1989 Mol. Gen. Genet. 217:118-125) and the *alcC* (encoding alcohol dehydrogenase III) walk was initiated with the plasmid pANa3 (Jones and Sealy-Lewis 1989 Curr. Genet. 17:81-85). The walks were undertaken using an MH2088 (*wA3*; *cbxA1*; *niiA4*; *facB88*) genomic library in lambdaGEM-11. Lambda clones from all steps were checked against genomic DNA digests to ensure continuity of the walk. In addition, the *alcC*-containing cosmids W28:C03, W15:D05 and W7:G02 from the chromosome VII-specific library (Brody et al. 1991 Nucl. Acid. Res. 19:3105-3109) were mapped relative to the early steps of the *alcC* walk. These cosmid clones and overlapping lambda clones AC-6, -7 and -8 contained a repetitive (~5 copies/genome) element of approximately 2 kb. No other repetitive elements were detected in the region of the *A. nidulans* genome covered by the walk. Overlap of lambda clones was detected when the end fragment of lambda40 (*gatA* walk) hybridised to the same library plaques (lambdaAC-21, -22 and -23) as end fragments of lambdaAC-18 (*alcC* walk). Southern blots confirmed that lambdaAC-21, -22 and -23 clones and lambda40 and AC-18 hybridised to common genomic sequences.

The linking of the *gatA* and *alcC* walks allowed the direction of transcription of these two genes to be orientated relative to each other (see below). The region between the two genes is approximately 130 kb. Complementation studies have shown that the *amdA* gene lies within a 5 kb *Bgl*II fragment of lambdaAC21 (RL, MD and MJH, Mol. Microbiol., in press). Therefore, the known genetic distances between *amdA* and *gatA* and between *amdA* and *alcC* could be compared with the molecular distances as shown below. The overall value of 15 kb/mu is slightly higher than the overall estimate of 11 kb/mu for chromosome VII, but well within the range of 11.0 - 24.6 kb/mu across the *A. nidulans* genome (Brody et al. 1991 Nucl. Acid. Res. 19:3105-3109).

The clones from the chromosome walks are available from this laboratory.

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