Fungal Genetics Reports

Volume 45 Article 17

DNA sequence of histidine-3 from two Neurospora wild-types.

P J. Yeadon
Flinders University

A PETERSEN
Flinders University

David E A CATCHESIDE
Flinders University

Recommended Citation

Yeadon, P. J., A. PETERSEN, and D.E. CATCHESIDE (1998) "DNA sequence of histidine-3 from two Neurospora wild-types.," *Fungal Genetics Reports*: Vol. 45, Article 17. https://doi.org/10.4148/1941-4765.1264

DNA sequence of histidine-3 from two Neurospora wild-types.

Abstract

We report sequence differences between laboratory strains of Neurospora within *his-3*,and corrections to published sequence for this locus for ST74A strains, of possible significance to experiments using histidine mutants for gene replacement and gene targeting.

DNA sequence of *histidine-3* from two Neurospora wild-types.

P.J. Yeadon, Arnis Petersen and David E.A. Catcheside - School of Biological Sciences, Flinders University, GPO Box 2100, Adelaide, SA 5001, Australia.

We report sequence differences between laboratory strains of Neurospora within *his-3*, and corrections to published sequence for this locus for ST74*A* strains, of possible significance to experiments using histidine mutants for gene replacement and gene targeting.

In order to investigate polymorphism within the *his-3* gene, PCR primers were designed using *his-3* sequence for the St. Lawrence strain ST74-OR23-IV*A* (Legerton and Yanofsky 1985 Gene **39**:129-140). The complete sequence was obtained from T391, a *his-3* K26 mutant derived in Lindegren Y8743 (Angel *et al.* 1970 Aust. J. Biol. Sci. **23**:1229-1240), and partial sequence from Lindegren *a* (FGSC 541). A single base-pair difference between sequences of the two Lindegren strains defined the position of the K26 mutant site. There was substantial difference between the St. Lawrence and Lindegren sequences, with the latter showing greater similarity to the *HIS4* sequence of *Saccharomyces cerevisiae* (Donahue *et al.* 1982 Gene **18**:47-59). We therefore also obtained sequence from G3:6F, a cosmid from the Orbach/Sachs pMOcosX library (Orbach 1994 Gene **150**:159-162) made from strain ST74-OR23-IV*A*. The newly determined *his-3* sequence for St. Lawrence 74*A* was a closer match to that from Lindegren *a* than was the published sequence and predicted restriction enzyme sites absent in the published sequence but present in the gene. The intron position in *his-3* was determined by comparison of sequence from the ST74-OR23-IV*A* cDNA library (Orbach *et al.* 1990 J. Biol. Chem. **265**:10981-10987) and those from St. Lawrence 74*A* and T391. Neurospora intron consensus sequences (Bruchez *et al.* 1993 Fungal Genet. Newsl. **40**:85-96) did not conflict with this intron position.

Since *his-3* sequences are frequently used in targeting and gene replacement vectors (for example: Legerton and Yanofsky 1985 Gene **39**:129-140, Ebole 1990 Fungal Genet. Newsl. **37**:15-16, Sachs and Ebole 1990 Fungal Genet. Newsl. **37**:35-36, Aramayo and Metzenberg 1996 Fungal Genet. Newsl. **43**:9-13, Margolin *et al.* 1997 Fungal Genet. Newsl. **44**:34-36), we thought it appropriate to make available corrections to the sequence for 74A strains, and note the fact that this gene is substantially polymorphic in Neurospora laboratory strains of different wild-type provenance. There are 14 single base-pair differences between the *his-3* sequences of St. Lawrence and Lindegren. Eight of the single base-pair variations are in the third base position including the stop codon which is TA**G** in St Lawrence but TA**A** in Lindegren. The gene sequence is 2676 bp in total in both wild types, including a single invariant intron of 63 bp. We have not yet investigated the influence of this degree of heterology on the integration of DNA during gene replacement.

his-3 sequences for St. Lawrence 74*A* and Lindegren *a* laboratory wild-types are available from GenBank and have accession numbers of AF045455 and AF045456 respectively.