Complementation of un-16 and the development of a selectable marker for transformation of Neurospora crassa

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Abstract
Although nearly sixty temperature-sensitive lesions have been mapped in Neurospora crassa, most of their functions have not been identified. These loci are called unknown (un). As part of an effort to identify the open reading frame associated with one of these, we undertook to walk to un-16 using the complementation of temperature-sensitivity as a selection. Cosmids complementing un-16 were identified and the un-16 gene was subcloned. DNA sequence analysis of un-16 revealed that it encodes the highly conserved S9 protein of the 40S ribosomal subunit. This gene has proven useful as a selectable marker and may provide a simple mechanism for the controlled alteration of protein synthesis in N. crassa.

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Complementation of \textit{un-16} and the development of a selectable marker for transformation of \textit{Neurospora crassa}

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Although nearly sixty temperature-sensitive lesions have been mapped in \textit{Neurospora crassa}, most of their functions have not been identified. These loci are called \textit{unknown (un)}. As part of an effort to identify the open reading frame associated with one of these, we undertook to walk to \textit{un-16} using the complementation of temperature-sensitivity as a selection. Cosmids complementing \textit{un-16} were identified and the \textit{un-16} gene was subcloned. DNA sequence analysis of \textit{un-16} revealed that it encodes the highly conserved S9 protein of the 40S ribosomal subunit. This gene has proven useful as a selectable marker and may provide a simple mechanism for the controlled alteration of protein synthesis in \textit{N. crassa}.

Temperature-sensitive mutants can be very useful tools for various studies, because they allow temperature-controlled inactivation of essential cellular processes such as DNA, RNA and protein syntheses. An extensive set of temperature-sensitive \textit{N. crassa} mutants is available from the Fungal Genetics Stock Center (FGSC); however, only a few of these mutants have been studied in depth (Perkins et. al., 2001). To enhance the usefulness of this potentially valuable collection of mutants, we have begun to clone and define the respective mutations in some of these strains. Direct selection of complementing cosmids offers a straightforward approach to identifying the underlying lesion associated with temperature-sensitive mutants in a number of organisms (for example, see Osherov et al, 2000). This is made simpler when the mutation being studied has been mapped on the genome. We have undertaken to complement temperature-sensitive mutants using cosmids mapped on the genome by the Neurospora genome program (Galagan et al. 2003).

\textit{un-16} was known to be near mating type on linkage group I (Inoue and Ishikawa, 1970, Ishikawa and Perkins, 1983); therefore, we endeavored to walk to \textit{un-16} from the \textit{mat} locus. Strain 4306 (\textit{un-16 A}) was transformed using the protoplast protocol described by Vollmer and Yanofsky (1986) using cosmid DNA prepared by the Qiagen midi prep procedure. Selection was carried out by holding the plates at room temperature for several hours prior to incubating plates at 37°C. Because the recipient strain does not have any secondary markers, we included a negative, no-DNA control. In eight transformation experiments, no revertants were seen on these controls. Cosmid pLorist6Xh 54B6 (Kelkar, et al. 2001) was one of the first chosen for the walk as it includes the mating type locus on its right end. This cosmid was found to complement \textit{un-16}. Additional cosmids that contain genomic inserts overlapping the insert contained in cosmid 54B6 were used in transformation experiments to define the region of the genome containing the complementing gene (Table 1).

\begin{table}[h]
\centering
\begin{tabular}{|l|c|c|}
\hline
\textbf{Cosmid} & \textbf{total transformants} & \textbf{Replicates} \\
\hline
pLorist6Xh 54B6 & 465 & 5 \\
pLorist6Xh 67D4 & 131 & 6 \\
pMOcosX* X5D12 & 1 & 2 \\
pMOcosX X9B4* & 0 & 1 \\
pMOcosX X14D1 & 0 & 1 \\
pLorist6Xh 63H10* & 1 & 1 \\
\hline
\end{tabular}
\caption{Cosmids assayed for complementation of \textit{un-16}}
\end{table}

*Orbach and Sachs, 1991

The high efficiency of complementation by cosmids 67D4 and 54B6 encouraged us to look carefully at the 29 Kb overlap between these two cosmids (Figure 1). This area included five open reading frames, NCU01948.3, NCU01949.3, NCU01950.3, NCU01951.3 and NCU01952.3. Sakai et al. (2002) had previously complemented \textit{un-16} with NCU01949.3 as part of their investigation of \textit{upr-1}. Our results, plus those of Sakai \textit{et al.} lead to the conclusion that NCU01949.3 encodes the \textit{un-16} phenotype.
Based upon its homology to other identified genes including one in *Podospora*, *un-16* encodes the 40S ribosomal protein S9 (Dequard-Chablat, 1985). This protein is highly conserved among eukaryotes and archaea (Figure 2). The 40S ribosomal S9 protein is distantly related to the bacterial S4 ribosomal protein and has been found to function in maintaining the accuracy of protein synthesis (Vincent and Liebman, 1992). *Saccharomyces cerevisiae* is unusual in that it has two genes encoding the S9 proteins, S9-A and S9-B. Two mutations have been identified in yeast S9-B (*SUP46-1* and *SUP46-2*) that result in increased misreading of mRNA by translating ribosomes (Vincent and Liebman, 1992). The respective positions of these mutations are listed in Figure 2.

![Figure 1](https://newprairiepress.org/fgr/vol54/iss1/3)

**Figure 1.** Overlapping cosmids complement *un-16*. Cosmids shown as solid arrows complement the *un-16* mutation while those shown as open arrows do not.

**Figure 2.** Alignment of *N. crassa* un-16 with the 40S ribosomal S9 subunit. *Nc*, *Neurospora crassa*; *Sc*, *Saccharomyces cerevisiae* 40S ribosomal protein S9-B (accession number NP_009748); *At*, *Arabidopsis thaliana* 40S ribosomal protein S9 (accession number NP_197024); *Hs*, *Homo sapiens* 40S ribosomal protein S9 (accession number NP_001004); *Mt*, *Methanoseta thermophila* PT, 40S ribosomal protein S4 (accession number YP_844026). Asterisks indicate the positions of the *S. cerevisiae* *SUP46-1* and *SUP46-2* (94N) and *SUP46-2* (L97W) that result in increased misreading of mRNA by translating ribosomes (Vincent and Liebman, 1992). The respective positions of these mutations are listed in Figure 2.

```
\begin{verbatim}
Nc un-16        ----MAPRSYSKTAKVPKRPFEEARLSDELKLVGEMYGLNKRERLVVFLLTSKIRRAARQ 56
Sc 40S rp S9-B  --MPRAPRTYSKTSTTPKRPEYESRDLAELKLAGEFGLNKRARYIFSPQLSKIRRAARD 58
At 40S rp S9    MVHCYCRNYGKTFKPRPYPERKRLDSELKLVGEMYGLNKRERLVVFLLTSKIRRAARD 60
Hs 40S rp S9    --MPVARSWCRKRTYPVRPFERSLDQEKLIGEYGLNKRERLVVFLLTSKIRRAARD 62
Mt 30S rp S4    ----MGYFGKSHTYDRPKPWEADRMANEVELIKTYGLNKRERLWKAESIIYRVRGRM 57

Nc un-16        LLTLDEK-DPKRLFEGLNALRRLVVRGVLDESRMLKDYYVLANAEDFLERLQLTCVYKLQ 115
Sc 40S rp S9-B  LLTRDEK-DPKRLFEGLNALRRLVVRGVLDESRMLKDYYVLANAEDFLERLQLTCVYKLQ 117
At 40S rp S9    LLTLDEK-SPRIFEGEAALRRMNYGLLDESQNKLDYVHALTENFLERLQLTCVYKLQ 119
Hs 40S rp S9    LLTLDEK-DPRIFEGEAALRRMNYGLLDESQNKLDYVHALTENFLERLQLTCVYKLQ 118
Mt 30S rp S4    LLASKARGEARADIEAAVNLRSFPGILKD-ADLADILSKITDILERLQTYRVQG 116

Nc un-16        LAKSIIHRVLQRHIIQRGKVQIYVPSFVRLDSQKHFALTSPFG-GGRPGRFQVRK 174
Sc 40S rp S9-B  LKSVIIHVLQRHIIQRGKVQIYVPSFVRLDSQKHFALTSPFG-GGRPGRFQVRK 176
At 40S rp S9    LKSIIHRVLQRHIIQRGKVQIYVPSFVRLDSQKHFALTSPFG-GGRPGRFQVRK 178
Hs 40S rp S9    LKSIIHRVLQRHIIQRGKVQIYVPSFVRLDSQKHFALTSPFG-GGRPGRFQVRK 177
Mt 30S rp S4    LANTIRQAPQFIMHTIQVAGQVRPSYLVKRGDEMFTIDYAGSPLAREGHPPRSSKIV 176

Nc un-16        A---KAAEGGAAEED--- 190
Sc 40S rp S9-B  AA-RKAEQGAAEAEDEE--- 195
At 40S rp S9    EKSAASKGSGGADGDEDEE--- 198
Hs 40S rp S9    AK---QGQGGAGGDEDEE--- 193
Mt 30S rp S4    AR---TGSSA-------- 183
\end{verbatim}
```
To further characterize *N. crassa* un-16, DNA sequence analysis was used to define the respective mutations in two independent un-16 mutants, allele T42M38(t) in strain FGSC#4306 and allele T42M69 in strain FGSC#7558. Allele T42M38(t) of un-16 was found to contain a single nucleotide difference changing leucine codon 34 to an arginine codon, and the un-16 allele T42M69 contained a single nucleotide difference changing leucine codon 103 to an arginine codon (Figure 2). The L34R mutation is located in the N-terminal domain of the S4/S9 protein, whereas the L103R mutation is located within the S4 domain.

*N. crassa* un-16 mutants were easily complemented by the wild-type allele suggesting that the un-16 mutations are recessive. However, because un-16 encodes a mutant ribosomal protein S9, it is possible that it could disrupt protein synthesis in heterokaryons with strains carrying a wild type un-16 gene. To address this issue, we attempted to make heterokaryons of un-16 and a strain with a wild type un-16 locus. Strains FGSC#4306 and FGSC#7558 were paired individually with strain FGSC#8964 (a⁢a₃3 arg-3 ad-3A) and with each other on minimal medium and incubated at 37°C. In two separate replicates, both un-16 strains grew vigorously with FGSC#8964 at 37°C while they did not grow at 37°C when paired with each other or when alone. Strain FGSC#8964 did not grow alone on minimal medium.

The ease of use of un-16 as a selectable marker led us to clone the un-16 fragment by amplifying a DNA fragment containing the un-16 gene. Primers were selected to amplify a 1.5 Kb fragment and the fragment was cloned into the pSC-A cloning vector using topoisomerase I-mediated ligation followed by Cre-mediated recombination (Stratagene). DNA from eight of the resulting clones were prepared using a Wizard prep (Promega) and transformed into prepared un-16 protoplasts. Seven of the resulting clones complemented the un-16 lesion. One clone, pUN16-6, gave the best transformation and it is available through the FGSC.

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