Nucleic Acids Research, 1993, Vol. 21, No. 10 **2523**

Identification of a Drosophila protein similar to rat S13 and archaebacterial S11 ribosomal proteins

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Received March 12, 1993; Revised and Accepted April 6, 1993

EMBL accession no. Z19052

We have characterized a *Drosophila melanogaster* cDNA which encodes a protein similar to rat S13, nematode S17 and archaebacterial S11 ribosomal proteins. Based on this similarity and a predicted protein molecular weight of 17 kD, we refer to the Drosophila gene as *Rpl7*. Archaebacterial S11 is similar in sequence and function to *E.coli* S15, which is important in the assembly of the 15S rRNA into the small ribosomal subunit and in interactions between large and small ribosomal subunits (1, 2).

The *Rp17* cDNA, hybridizes a 740 nucleotide RNA which is expressed abundantly in all life stages and appears to be complete. *Rp17* is a single copy gene. It maps to 29A on the polytene chromosome map.

Computer searches for proteins similar to Rpl7 (PROSRCH; 3) recovered S13 ribosomal protein from rat (4), a 17.4 kD protein from the nematode *Brugia pahangi* (5), and S11 ribosomal protein from the archaebacterium *Halobacterium marismortui* (6, 7; Figure 3). Rpl7 and rat S13 are the most similar, with 83% identity. Rat and nematode sequences are significantly more similar to each other than are fly and nematode sequences. Homologs of Rpl7 possess strikingly different charges. The calculated pI for Rp17 is 10.8, for rat S13, 11.0, for Brugia S17, 11.3 and for Halobacterium S11, 4.8. This difference is consistent with the adaptation of archaebacterium to a high salt environment (1).

Halobacterium S11 appears related to eubacterial S15; within its carboxy half they are 64% conserved (6). *E.coli* S15 binds with archaebacterial rRNA (6), consistent with conservation of its role in the assembly of ribosomes and suggesting a role for homologs of S11 such as Rpl7.

Eukaryotic and archaebacterial Rp17 homologs are very similar in sequence and in length and appear to be more closely related to each other than to the eubacterial protein, consistent with previous reports (9). However, RNAs for *H.marismortui* S11 and bacterial S15 appear to encode at least one additional product (8, 10) thus transcriptional organization of the archaebacterial gene may more closely resemble that of prokaryotes than of eukaryotes.

ACKNOWLEDGEMENTS

We gratefully acknowlege the gift of the Drosophila head cDNA library from Dr Paul Salvaterra, City of Hope Medical Center, Duarte, California, in situ hybridizations performed by Ms Jenny Trenear and Mrs Tamsin Majerus at the Department of Genetics, University of Cambridge, assistance in processing sequence data by Mr David Judge of the DNA Sequencing Computing Facility, University of Cambridge, SEQNET (SERC, Daresbury) and the Edinburgh University Biocomputing Centre, and calculation of the pI values by Dr Jefferson Foote. This work was supported by an MRC Programme Grant to M.A.

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DROS          MGRMHAPGKGISQSALPYRRTVPSWLKLNADDVKEQIKKA
RAT           MGRMHAPGKGLSQSALPYRRSVPTWLKLTSDDVKEQIYKL
BRUGIA        MGRMHNPGKGISQSALPYRRSVPTWLKLTSEEVQEQVTRL
HALO          MARMHTRRRGSSDSDKPAADEPPEWSDVDEDAIEARVVEL
              *.***   .* *.*  *     * *  .  . .  ..
                                                     80
DROS          GQEGSDSLQIGIILRD----SHGVAQVRFVNGNKILRIMK
RAT           AKKGLTPSQIGVILRD----SHGVAQVRFVTGNKILRILK
BRUGIA        AKKGLRPSQIGVILRD----SHGVAQVRRVTGNKIVRILK
HALO          AEQGHSPSEIGLKLRDEGVQGTPIPDVSLATGKKVTEILE
              .     . .**. ***          *.*. *.*. .*
                                                    120
DROS          SVGLKPDIPEDLYHMIKKAVAIRKHLERNRKDKDGKFRLI
RAT           SKGLAPDLPEDLYHLIKKAVAVRKHLERNRKDKDAKFRLI
BRUGIA        AKGMAPEIPEDLYHLIKKAVNIRKHLERNRQDKDSKYRLI
HALO          ENEAEPDLPEDLRNLLERAVRLRDHMDENPGDYQNKRALQ
                   *..**** ... .** .* *.. *  * . *  *

DROS          LVESRIHRLARYYKTKSVLPP-NWKYESSTASALVA-
RAT           LIESRIHRLARYYKTKRVLPP-NWKYESSTASALVA-
BRUGIA        LVQSRIHRLARYYKTKRQLPA-TWKYESSTASALVS-
HALO          NTQSKIRRLIDYYRGDEVDENFTYSYDNAVE-ALGLE
                .*.*.**  **.           *...   **
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Figure 1. Alignment of the conceptual translation of Drosophila *rp17*, rat S13 (4), *B.pahangi* S17 (5), and *H.marismortui* S11 (8). Asterisks indicate identities; periods, similarities.

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