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Mitochondrial large ribosomal RNA: an abundant polyadenylated sequence in *Drosophila*

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We have cloned and sequenced an abundant polyadenylated RNA from *Drosophila melanogaster*. Sequence similarity to the mosquito (1) and *D. yakuba* (2) mitochondrial large subunit ribosomal RNA genes identified the clone as the *D. melanogaster* homolog. The abundance of this sequence was inferred both from the fact that it could be visualized as a distinct band in ethidium bromide-stained gels of poly-A+ RNA, and from the fact that it represents about ten per cent of all the clones in the cDNA libraries. The DNA sequence of one of these clones reveals why this mitochondrial sequence is elevated in poly-A+ RNA preparations: there is an extensive poly-A tail added to the 3' end of the transcript (see Figure). Our results indicate that Drosophila mitochondrial ribosomal RNAs are polyadenylated, as has already been demonstrated for their mammalian counterparts (3). It is of interest that the Drosophila poly-A tail (the clone described here contains a 43 to 47 base poly-A tail remnant) is much longer than that which has been observed in the mammalian transcripts, and is comparable to that observed for cytoplasmic mRNA transcripts. This is consistent with previous observations that the Drosophila large mit rRNA is present exclusively in the poly-A+ fraction of RNA (4). This extensive polyadenylation of rRNA sequences in Drosophila raises several fundamental questions about the function and mechanisms of polyadenylation, for both cytoplasmic and mitochondrial transcripts. Our results also have the practical implication of demonstrating significant levels of "contamination" by mitochondrial ribosomal RNA sequences in cDNA libraries prepared from poly-A+ RNA when oligo dT is used to prime first strand synthesis.

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cDNA:    5'- GGTTGGTTTC TATCTTTAAA AAATTATGAT ATTTTAGTAC
genomic: 5'- ---------- ---------- ---------- ----------

 GAAAGGACCA AATATCAAAA TAATTATATT TTTTATAAGA ATATTATTAA
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 TATAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA - 3'
 ---AAAACTA TTTTGGCAGA TTAGTGCAAT AAATTTAGAA TTATATATGT - 3'
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Figure 1. Comparison of genomic and cDNA sequences for the 3' region of *D. melanogaster* mitochondrial large rRNA gene. The genomic sequence is from Garesse (5). Polyadenylation site is boxed.

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