Nucleotide sequence of a mouse testis poly(A) binding protein cDNA

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The vast majority of eukaryotic mRNAs possess a poly(A) tract at their 3' termini. Although the function of the poly(A) tail is controversial, most workers agree that it promotes mRNA translation and stability (reviewed in 1, 2). The effects of poly(A) on mRNA metabolism are thought to be mediated by a protein which binds preferentially to poly(A), the poly(A) binding protein (PABP) (reviewed in 1, 2). The sequences of PABP cDNAs from yeast (3, 4), human (5), Xenopus (6) and Drosophila (7) indicate that PABPs have a conserved structure consisting of 4 repeated RNA binding domains near the amino terminus and a less conserved domain of unknown function at the carboxy terminus.

The present study was undertaken to search for testis-specific PABP mRNAs in mice for two reasons. First, haploid spermatogenic cells are an unusual developing system because some translationally active mRNAs have shorter poly(A) tracts than translationally repressed mRNAs (8). Second, there are numerous testis-specific variants of mRNAs which are expressed in somatic cells (reviewed in 9). Two mouse testis cDNA libraries (10, 11) were screened with the 5' proximal EcoRI fragment of human liver PABP cDNA (5) isolating two groups of cDNAs with different sequences.

One of these mouse testis PABP cDNAs encodes a 636 amino acid protein which is respectively 98.9% and 94% identical to human and Xenopus PABPs (5, 6) as shown in Figure 1, and 54.9% and 49.5% identical to Drosophila and yeast PABPs (3, 4, 7) (not shown). The slow rate of evolution of mammalian PABPs is noteworthy. Assuming that mice and humans diverged 80 million years ago, the rate of evolution of non-synonymous sites in the mouse and human PABP coding regions can be estimated as 0.035—0.061 substitutions/10^9 years depending on whether the gap between amino acids 210 and 211 in human is excluded or included (12). The rate of evolution of non-synonymous sites in mouse and human PABP is the fifth slowest among 36 rodent and human proteins analyzed by Li and Grauer (13). Work is in progress comparing the function and expression of the two PABP mRNAs.

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REFERENCES