A full-length cDNA encoding a mitochondrial DNA-specific single-stranded DNA binding protein from *Xenopus laevis*

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We have isolated a full-length cDNA specifying the precursor of one of the two known single-stranded mitochondrial DNA (mtDNA) binding proteins of *Xenopus laevis*. The protein is called mtSSB-1 (1). The putative function of these proteins is to stabilize the displaced single strand of normal and expanded displacement loop (D-loop) during mtDNA replication (1, 2).

We identified a single hybridizing clone, called XL31, from the screening of about $3 \times 10^5$ pfu of a library of *Xenopus laevis* ovary cell cDNA inserted into phage lambda UniZAP XR. The full-length 753-bp cDNA from XL31 includes: 1) a 158-nt GC-rich (58%) 5' untranslated region; 2) a 51-nt region encoding a deduced 17-aa N-terminal presequence rich in basic amino acids (4/17, or 23%), and containing no acidic residues; 3) a 390-nt region encoding the deduced 129 aa-long mature polypeptide, plus a TGA stop codon; the deduced amino-terminal sequence of the mature protein is identical to the published N-terminus of mtSSB-1 (1); 4) a 154-nt 3' untranslated region, containing an AATAAA polyadenylation signal, located 20 bp upstream from a poly(A) tail. We assume that the polypeptide encoded by the cDNA starts at the ATG at nt 159, because: (i) it is the first ATG encountered in the cDNA, (ii) it is in a moderately favorable context for translation initiation (3), with a purine at position −3 relative to the A of ATG, and (iii) there are two in-frame potential stop codons upstream from the ATG at nt 159. Based on available data on the polypeptide sequences for the *Xenopus laevis* mtSSBs (1), the mature protein is assumed to start at the +18 serine residue.

The mature protein (MW of 14627 Da) is a basic polypeptide (calculated pI = 10.17), with an amino acid composition essentially in agreement with previously reported data (1). The two known prokaryotic single-stranded DNA binding proteins (*E.coli* SSB and *E.coli* F sex factor SSB) (4) show significant levels of similarity, due to both identical amino acid residues and conservative substitutions, with mtSSB-1. Thirty-three out of 109 aa are identical between mtSSB-1 and the two prokaryotic SSBs (30% identity). A 43% similarity is found when the conservative substitutions are taken into consideration. These results indicate the existence of a broad class of DNA binding proteins with structural and functional similarities both in prokaryotes and in prokaryote-derived organelles of higher organisms.

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