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**Nucleotide sequence of a cDNA for  $\phi$ , a histone to protamine transition protein from sea cucumber spermatozoa**


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Chromatin from spermatozoa of the echinoderm *Holothuria tubulosa* contains a highly basic protein called  $\phi$ . (1) and a specific arginine-rich H1 subtype (2), in addition to the other main histones. Protein  $\phi$ . has an amino acid composition in between that of the C-terminal half of echinoderm H1-S and that of protamines, provided that Arg is considered equivalent to Lys, with an average  $M_r$  of 8640 Da (3). Accumulation of  $\phi$ . occurs during spermiogenesis and represents about 4% of the histone moiety of the mature spermatozoa (1). Moreover, the nucleosomal organization of chromatin is not altered by the presence of  $\phi$ . (4).

Cell-free translation of oligo(dT)-fractionated RNA has suggested that  $\phi$ -mRNA is polyadenylated. A gonad-specific  $\lambda$ gt11 cDNA library (5) has been constructed and screened with polyclonal anti- $\phi$ . antibodies (6). Several positive clones have been characterized and the longest insert sequenced on both strands (7). The cDNA sequence, shown below, spans an open reading frame for a basic protein of 77 residues (8550 Da), flanked by leader and trailer tracts. The deduced protein sequence conforms to the partial amino acid sequence of  $\phi$ . previously established. Poly(A)<sup>+</sup> RNA and DNA blot hybridizations with the cloned cDNA indicate that the  $\phi$ -mRNA is about 600 nt long and suggest that the  $\phi$ . gene is present as a single copy in the *H. tubulosa* genome.

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tccccctgtgtcggaaattccaactacaatcaataatc ATG GTA GCC AGA CGA CAA ACA AAG   63
          M   V   A   R   R   Q   T   K

AAA GCT AGG AAG CCT GCA GCC AGG AGA CGC AGC GCA GCC AAA CGC GCA GCC CCA  117
  K   A   R   K   P   A   A   R   R   R   S   A   A   K   R   A   A   P

GCT GCG AAG AAA GCG GCG AGT CGC CGT CGT CCA AAG AGT GCT AAG AAG GCT AAG  171
  A   A   K   K   A   A   S   R   R   R   P   K   S   A   K   K   A   K

CCC GCA GCA AGG AGA CGC AGC AGC GTC AAA CCT AAA GCA AAA GCA GCC GCC  225
  P   A   A   R   R   R   S   S   V   K   P   K   A   A   K   A   A   A

CAA GTC CGT CGC AGG AGC CGA CGA ATT CGC CGT GCG TCC GTG TCA AAG TAA tcc  279
  Q   V   R   R   R   S   R   R   I   R   R   A   S   V   S   K   end

aatggaagactgatcattaaatcgtaacccttcaaaagactaaatttattattttagttttgtagaact  350
gtccaaatcttctagaatattgcagaactgaacattttaaacacatccaattcgtaagcgaacaagcaag  421
caacgatgacctacaaaaaa                                     441

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