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A Survey of in Silico Analysis and Phylogeny of Some Mammalian Protamine-P1

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ABSTRACT

Both P1 and P2 have been shown to be required for normal sperm function in primates and many rodents. In higher organisms, the chromatin of sperm is organised in a highly condensed protamine-based structure. In premeiotic stages and shortly after meiosis, histones carry multiple modifications. Here, we focus on post-meiotic stages and show that also after meiosis, histone H3 shows a high overall methylation of K9 and K27 and we hypothesise that these modifications ensure maintenance of transcriptional silencing in the haploid genome. Furthermore, we show that histones are lost during the early canoe stage and that just before this stage, hyperacetylation of histone H4 and mono-ubiquitylation of histone H2A occurs. We believe that these histone modifications within the histone-based chromatin architecture may lead to better access of enzymes and chromatin remodellers. This notion is supported by the presence of the architectural protein CTCF, numerous DNA breaks, SUMO, UbcD6 and high content of ubiquitin, as well as testes-specific nuclear proteasomes at this time. Moreover, we report the first transition protein-like chromosomal protein, Tpl94D, to be found in Drosophila. We propose that Tpl94D – an HMG box protein – and the numerous DNA breaks facilitate chromatin unwinding as a prelude to protamine and Mst77F deposition. Finally, we show that histone modifications and removal are independent of protamine synthesis.
Keywords: In sillico analysis and phylogeny, mammals,Protamine P1

I. INTRODUCTION

The protamines are a diverse family of small arginine-rich proteins that are synthesized in the late-stage spermatids of many animals and plants and bind to DNA, condensing the spermatid genome into a genetically inactive state. Vertebrates have from one to 15 protamine genes per haploid genome, which are clustered together on the same chromosome.

Comparison of protamine gene and amino-acid sequences suggests that the family evolved from specialized histones through protamine-like proteins to the true protamines. Structural elements present in all true protamines are a series of arginine-rich DNA-anchoring domains (often containing a mixture of arginine and lysine residues in non-mammalian protamines) and multiple phosphorylation sites. The two protamines found in mammals, P1 and P2, are the most widely studied. P1 packages sperm DNA in all mammals, whereas protamine P2 is present only in the sperm of primates, many rodents and a subset of other placental mammals. P2, but not P1, is synthesized as a precursor that undergoes proteolytic processing after binding to DNA and also binds a zinc atom, the function of which is not known. P1 and P2 are phosphorylated soon after their synthesis, but after binding to DNA most of the phosphate groups are removed and cysteine residues are oxidized, forming disulfide bridges that link the protamines together.

Harold E. Kasinsky et al., 2011 studied Structural Complexity, Evolution and Chromatin Patterning of Protamines despite their relatively simple amino acid composition (protamines exhibit a high extent of diversity at the primary structure level. In addition, their high basic amino acid contents does not prevent

them from adopting under certain conditions, such as in the presence of helico-genic solvents [33] or upon interaction with DNA, a considerable extent of secondary structure organization; hence they fall within the category of intrinsically disordered proteins. The additional presence of cysteine, an amino acid which is otherwise absent in other SNBPs, in certain protamines adds structural complexity to this group of chromosomal proteins. several dozen species with chromatin/nucleoplasmic patterning, showing that a lamellar step in mid-spermiogenesis is widespread in evolution. However, this only occurs during spermiogenesis in a small minority of internally fertilizing species in animals, as well as in several species of algae that show features similar to internal fertilization in animals. Analysis of the histone-to-protamine transition. Chromatin/nucleoplasm inversion may be the case in both an octopus and a relict ciliate José M. Eirín-López et al 2006 studied Common Phylogenetic Origin of Protamine-like (PL) Proteins and Histone H1 The structural similarities between PL and H1 proteins pose very interesting questions regarding the evolutionary mechanisms to which these two groups of proteins are sub- ject. On one hand, it has been shown that the long-term evo- lution of H1 histones is best described by a birth-and-death process under strong purifying selection rather than by con- certed evolution (Eirín-Ló pez et al. 2004a). The differenti- ation between the replication-dependent (RD) and the replication-independent (RI) H1 lineages can be traced back to the transposition of an ‘‘orphon’’ group of H1 genes to a solitary genomic location early in metazoan evolution (Eirín-Ló pez et al. 2004a; Eirín-Ló pez et al. 2005). The subsequent evolution of both lineages led to the diversifi- cation observed inside the H1 family. On the other hand, the differentiation of SNBPs of the PL type must have also occurred early in metazoan evolution as they are present in both diploblastic and triploblastic (bilaterians) animals (Ausió 1999). The lysine to arginine transition leading to the differentiation of protamines from a PL precursor was a critical step in SNBP evolution, resulting in a strong positive selection process favoring the high arginine con- tent of these proteins (Ausió 1999; Eirín-Ló pez, Frehlick, and Ausió 2005), making protamines one of the fastest evolving groups in nature (Oliva and Dixon 1991; Oliva 1995; Lewis et al. 2003).

II. MATERIALS AND METHODS

To analyse the protein rhodopsin the amino acid sequence of human rhodopsin was retrieved from NCBI site and was used for analysis in PepTool 2.0 demo version.

Method For Obtaining Protein Sequences in FASTA Format:

Google window of internet explorer was opened. Wrote NCBI, pressed enter, NCBI home page was displayed. On home page, wrote protein name, got list of animal in display box. Clicked one by one on names of animals, sequences of protein were displayed. Copied required information of animals. Then clicked on FASTA. Amino acid sequence of a protein in FASTA format was displayed. Copied the sequence and pasted into MS word. Copied as many as larger number of sequences as possible.

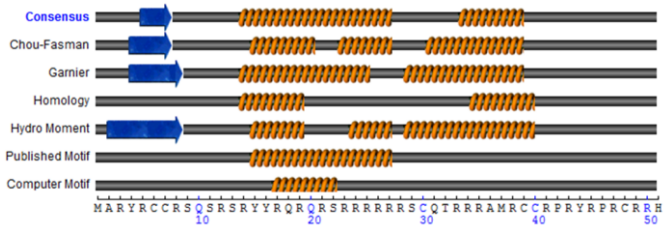
Method for Phylogenetic Tree Reconstruction:

The amino acid sequences downloaded from the NCBI site were subjected to alignment and for the construction of phylogenetic tree using MEGA6. A phylogenetic tree was saved and analysed.

III. OBSERVATIONS AND RESULTS

Protein Analysis:

Amino Acid Sequence of Protamine P1in Human: Total amino acids- 51



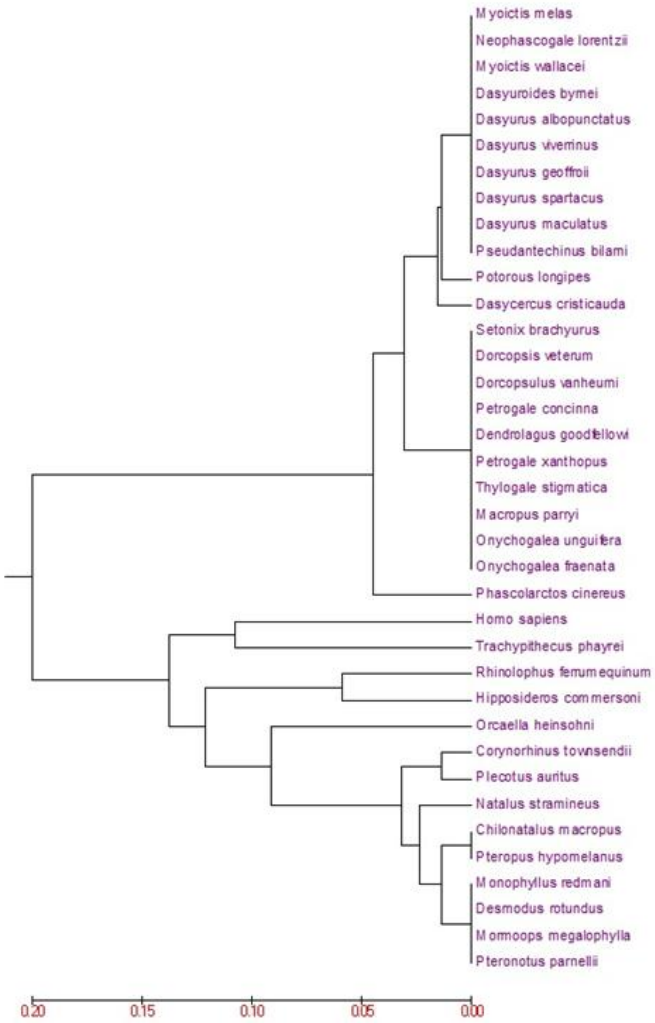


Figure 1. Phylogenetic tree of Protamine P1 In some Mammalian species

IV. CONCLUSION AND SUMMARY

From the result and discussion of present in silico protein analysis study of vertebrate Protamine P1 it can be concluded that the amino acid sequences among different mammalian species show slight to moderate differences without affecting its function in the late-stage spermatids of many animals and bind to DNA. It also can be concluded from the phylogenetic tree analysis that the Protamine P1 in different vertebrate also have strong to moderate sequence similarities among studied vertebrates.

V. REFERENCES

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