

Evolution of vertebrate chromosomal sperm proteins: implications for fertility and sperm competition

Juan Ausi¹, José María Eirín-López^{1,2} and Lindsay J. Frehlick¹

¹Department of Biochemistry and Microbiology, University of Victoria, Victoria, British Columbia, Canada V8W 3P6; ²Departamento de Biología Celular y Molecular, Universidade da Coruña, Campus de A Zapateira s/n, 15071-A Coruña, Spain

The three major types of sperm nuclear basic proteins (SNBPs), histone (H type), protamine-like (PL type) and protamine (P type), are well represented in vertebrates. The three groups are evolutionarily related through a vertical evolutionary process (H → PL → P) that involves a transition from lysine to arginine-rich proteins and results in a sporadic but non-random distribution that can be phylogenetically traced. The arginine-rich P type has been selected in the course of evolution of the vertebrates, probably due to constraints imposed by internal fertilisation. Protamines are subject to a positive Darwinian selection process that results in the characteristic fast evolutionary rate shown by these proteins. This makes their use very suitable for the reconstruction of phylogenies of the different vertebrate groups. In mammals, two different types of protamines (P1 and P2) are present which, in the course of the evolution of this vertebrate group, have undergone a further transition to cysteine-rich proteins which further enhanced their DNA packing efficiency. From a functional perspective, protamines provide the most efficient packaging of sperm chromatin and can probably influence the shape of the sperm nucleus and chromatin stability, both of which have direct implications for fertility. In mammals, alterations of the ratio between P1 and P2 protamines as well as the ratio between histones and protamines are important determinants of sperm fertility. All of this suggests a potential involvement of protamines in sperm competition which is discussed in this paper.

"[Ramon y Cajal] would envisage the sperm-cells as activated by a sort of passionate urge in their rivalry for penetration into the ovum cell."
(Sherrington, 1949)

Evolution of vertebrate sperm nuclear basic proteins

Chromatin, the complex of histones, non-histone proteins and DNA, is a dynamic structure. The core subunit of chromatin, known as the nucleosome core particle, is composed of 146 base pairs of DNA wrapped around an octamer of core histones (H3, H4, H2A and H2B). A linker histone (H1) protects an additional 20 base pairs to form the chromatosome (van Holde, 1988). Altering or remodeling of this structure is important for regulation of many nuclear metabolic events such as, regulation of gene expression, DNA replication and DNA repair. One of the most dramatic examples of chromatin remodeling occurs within male germ cells, where changes in both the protein composition and compaction level of the chromatin take place (Caron *et al.*, 2005). During the postmeiotic maturation of sperm (spermiogenesis), chromatin becomes supercondensed and transcriptionally inert. High compaction of the sperm haploid genome is needed to allow for a more hydrodynamic sperm head and may also protect the DNA from physical and chemical damage (Braun, 2001).

The chromosomal proteins involved in the organization of the mature sperm chromatin are generically known with the name of sperm nuclear basic proteins (SNBPs). They can be grouped into three categories: protamine (P type), protamine-like (PL type) and histones (H type) (Ausi3, 1995, 1999). All three types of SNBPs are structurally analogous and condense DNA into chromatin fibers of 300-500 Å (Casas *et al.*, 1993), regardless of the structure of the individual nucleoprotein complexes (Eir3n-L3pez *et al.*, 2006a).

Organisms containing SNBPs of the P type are well represented amongst vertebrates and have been found in all classes with the exception of Agnatha (see Fig. 1). In these organisms the histones from the progenitor germ cells at the onset of spermatogenesis are replaced by protamine in the late stages of spermiogenesis (Oliva and Dixon, 1991). In mammals, somatic histones undergo post-translational modifications as well as replacement with specialised histone variants during meiotic prophase [reviewed in Lewis *et al.* (2003a); Govin *et al.* (2004); Kimmins and Sassone-Corsi (2005)]. Immediately after meiosis, histones are replaced by transition proteins (TNPs) (Meistrich *et al.*, 1978, 2003), which are unique to mammals. During spermiogenesis, the transition proteins are replaced by protamines, which vary greatly in amino acid sequence, but are all small and have a very high arginine content, which is often much greater than 30%. The high charge density of these arginine-rich proteins allows them to bind DNA with high affinity and to more efficiently shield the charges on the DNA phosphate backbone, compared to somatic histones, resulting in maximal compaction of the genome. Many mammalian protamines have cysteine residues which are involved in disulfide crosslinking that further contributes to the compaction of chromatin fibers (Lewis *et al.*, 2003b).

Some amphibians and fish have structurally intermediate protamine-like proteins in their sperm (PL type) (Fig. 1). These are highly heterogeneous but generally have a high combined arginine + lysine content (35-50%) and are closely related to histone H1 (Ausi3, 1995, 1999). Alternatively, some amphibians and fish retain histones in their mature sperm (H type). Often sperm-specific histone variants of either linker histones or core histones or both are present in these instances. For example, frogs of the genus *Rana* have sperm containing sperm-specific histone H1s, which have higher lysine contents than the *Rana* somatic H1s, as well as a full somatic type histone complement (Itoh, Ausi3 and Katagiri, 1997).

From the examination of SNBPs from many invertebrates and vertebrates it was proposed that SNBPs had undergone a vertical evolution H → PL → P (Saperas *et al.*, 1994; Ausi3, 1995, 1999). Although a link between PL proteins and linker histone H1 had been proposed (Ausi3, 1995, 1999), it remained unclear how a high lysine content, which is characteristic of the members of the histone H1 family, could have given rise to arginine rich PL and P proteins.

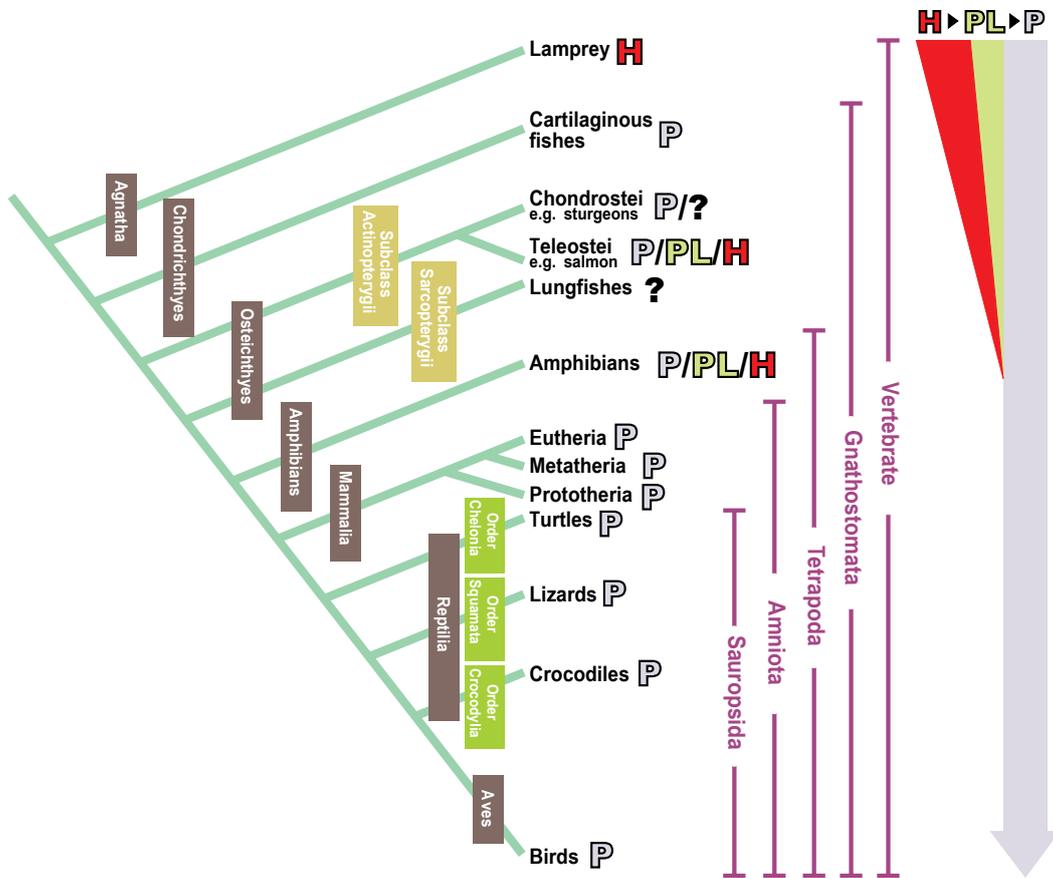


Figure 1. Cladogram of the subphylum Vertebrata showing the currently accepted relationships of monophyletic groups making up the subphylum. Each branch represents a monophyletic group. The arrow shown on the right hand side depicts the direction and approximate distribution of the three main types of SNBPs (in different colours) during the course of evolution of this group. H: histone type; PL: protamine-like type; P: protamine type. It has been proposed that protamines (P type) may have evolved from a histone H1-related protein as indicated at the base of the large arrow (Ausió, 1999; Lewis *et al.*, 2004; Eirin-Lopez *et al.*, 2006).

Two recent studies have shed light on the possible mechanisms underlying this change, lending direct support for a link between H1s, PLs, and protamines (Lewis *et al.*, 2004; Eirín-López *et al.*, 2006b). In the first study, examination of the SNBPs of two closely related species of tunicates, *Styela montereyensis* and *Ciona intestinalis*, revealed the presence of proteins of the PL type in their sperm (Lewis *et al.*, 2004). However, while in *S. montereyensis* the PLs were arginine rich, in *C. intestinalis* the PLs were lysine-rich. Detailed analyses of the coding nucleotide sequences suggested that a single frameshift mutation may have allowed lysine-rich clusters in the C-terminal tail of *C. intestinalis* to convert to arginine-rich clusters in *S. montereyensis*, establishing the evolutionary link between PL and protamine type SNBPs (Lewis *et al.*, 2004). A second report, focused on the evolutionary relationships shown by members of

the histone H1 family and the SNBPs of the PL type, revealed the presence of a common origin for both groups of proteins (Eir6n-L6pez et al., 2006b). In this regard, it now seems clear that H1 histones and PLs are descendants of an ancient group of 'orphon' H1 replication-dependent histones, which were excluded to solitary genomic regions of the genome as early in metazoan evolution as before the differentiation of bilaterians. This 'orphon' lineage was ultimately responsible for the origin of the replication-independent somatic H1 lineage (as histone H5 and H1^o), as well as SNBP lineage. Both of these lineages were subject to a purifying process, that shifted towards adaptive selection in the case of the SNBP lineage at the time of the lysine to arginine transition (Eir6n-L6pez et al., 2006b). Due to the more efficient DNA condensation properties of arginine (Puigdom6nech et al., 1976; H6l6ne and Lancelot, 1982; Ausi6 et al., 1984), proteins with a high global content of this amino acid would have been positively selected for during the course of evolution.

The evolution of SNBPs through a H → PL → P process involving a primordial replication independent histone H1 (Ausi6, 1995, 1999; Eir6n-L6pez et al., 2006a; Eir6n-L6pez et al., 2006b) lends support to the old concept of a potential relationship between ontogeny and phylogeny (Bloch, 1976; Ausi6, 1995, 1999). Indeed, during mammalian spermiogenesis a gradual transition in the composition of chromosomal proteins is observed that involves highly specialized H1 histones [H1t (Seyedin and Kistler, 1980), HILS1 (Iguchi et al., 2003; Yan et al., 2003), Hanp1/H1T2 (Martianov et al., 2005; Tanaka et al., 2005)] that precede and/or coexist with TNPs (Meistrich, 1989; Meistrich et al., 2003) which are ultimately replaced by protamines (Lewis et al., 2003b) in the mature spermatozoa.

The different SNBP types display a heterogeneous distribution across the different vertebrate groups (Fig. 1). Nevertheless, as it was shown in fish, the sporadic appearance of the different types is not random and follows the vertical evolutionary phylogeny of the groups where these proteins are present (Saperas et al., 1994). As can be seen from Figure 1, the occurrence of protamines is seen in vertebrates as ancient as sharks and other cartilaginous fishes. Agnatha, which are a superclass of primitive jawless fish (lamprey and hagfish) have sperm that only contain histones and thus are of the H type (Saperas et al., 1994, 1997). In contrast, all the species examined within the class Chondrichthyes (cartilaginous fish), which includes the sharks, skates and rays, are of the P type. Within the subclass Actinopterygii, or ray-finned fish, representatives from all SNBP types are present (Chiva, 1995). The examined sturgeons and paddle fish which are within the subclass Chondrostei contain protamines, whereas the teleost fish or bony fish (the largest group of living fish) are more diverse containing organisms of the H, PL and P types, even though they are all within the subclass Sarcopterygii. A similar sporadic SNBP distribution is seen within the class Amphibia (Kasinsky, 1989). It is apparent from the analysis of the SNBP composition of both fishes and amphibians that a lysine to arginine transition (or divergence from H type to PL type to P type) likely occurred multiple times in the course of their evolution. It has been suggested that the driving force behind this evolution in fish and amphibians may be differing constraints placed on the sperm by internal versus external fertilisation (Kasinsky, 1989, 1995). There is a correlation that suggests that the harsh and viscous environment that sperm are subjected to within female reproductive tracts during internal fertilisation may select for protamines (Mann et al., 1982; Kasinsky et al., 1985; Kasinsky, 1989, 1995).

Following the appearance of Amniota, all organisms contain protamines in their sperm (P type) (Fig. 1). This may suggest an evolutionary trend towards the use of protamines to package sperm DNA in 'higher' vertebrate organisms. The replacement of histones with protamines is typical of taxa located at the uppermost tips of evolutionary branches (Ausi6, 1999). In mammals, two types of protamines have been identified: protamine P1 and the protamine P2 family. For the P2 family, proteolytic cleavage of the N-terminus of the P2 precursor protein yields

the form of the protein that is present in the mature sperm (Sautiere *et al.*, 1988; Hecht, 1989; Lewis *et al.*, 2003b). Although P1 has been found in all species studied, P2 is exclusively expressed in only a few eutherian organisms, including human and mouse (Oliva, 2006; and references therein). An additional compositional transition in the course of vertebrate SNBP evolution took place in mammals where some of their protamines became rich in cysteine (Oliva and Dixon, 1991; Lewis *et al.*, 2003b). This residue is absent from metatherian protamines and is uncommon in other chromosomal proteins (van Holde, 1988). Cysteine first appears in the protamines of placental (eutherian) mammals and it is well established in both the P1 and P2 protamine lineages. Cysteine also appeared later in the marsupial P1 protamines of the genus *Planigales* through a process of convergent evolution (Retief *et al.*, 1995a). The acquisition of cysteine, which can form inter- and intramolecular disulfide bonds (Vilfan *et al.*, 2004), adds stability and increases the compaction of the nucleoprotamine complexes. The lysine to arginine conversion in the transition from H to PL SNBPs and the acquisition of cysteine by the P type during the course of evolution of vertebrate SNBPs is highly reminiscent of the similar compositional transitions that have been observed in the equivalent invertebrate SNBP types (Lewis *et al.*, 2003b).

The importance of being a protamine and the evolution of vertebrate protamines

Despite the continued effort to characterise protamines from different representative groups of vertebrates, there is still an important lack of information on these proteins. Although protamines appear to be compositionally simple proteins (small and arginine rich), the amino acid distribution in the primary structure of protamines does not seem to be random. In fact, as it will be described in the following sections, the amino acid sequences of these proteins appear to be critical for their function and can be used to trace their evolution.

Protamines exhibit a large structural heterogeneity, as can be seen from the large extent of variation observed in their electrophoretic mobility and primary structure (Fig. 2). Despite this diversity, their amino acid sequence stores very valuable phylogenetic information (Oliva, 1995; Lewis *et al.*, 2003b). Figure 2A provides an electrophoretic analysis of protamines of representative organisms from different vertebrate groups (see Fig. 1) and Figure 2B outlines their corresponding amino acid sequences. We have shown in the past that it is possible to use this kind of sequence information to produce phylogenetic trees that closely resemble those obtained using other molecular markers and/or those based on paleontological/anatomical traits (Lewis *et al.*, 2003b). For instance, we were able to generate a phylogeny for the closely related species of sticklebacks that was indistinguishable from that generated from morphological and behavioural analysis of this group of Gasterosteidae fish (Giménez-Bonafé *et al.*, 2000). Using a broader range of teleost fish species, for which there is a relatively abundant amount of sequence information for protamines, it was possible to reconstruct a phylogenetic tree which was almost identical to that currently available from the use of conventional markers (Frehlick *et al.*, 2006b). The protamine sequence information has also been useful in confirming the close relationship between birds and reptiles (Sauropsida) (Hunt *et al.*, 1996; Ausiό *et al.*, 1999) and has additionally provided support to the monophyletic origin of Paleognathae birds (ostriches, emus, tinamou) (Ausiό *et al.*, 1999). Similar phylogenetic results have been obtained with different groups of mammals (also see below) (Retief *et al.*, 1993; Queralt *et al.*, 1995; Retief *et al.*, 1995c).

The fidelity with which protamines work as phylogenetic markers is primarily due to the rapid evolution of these proteins (Oliva and Dixon, 1991; Oliva, 1995; Lewis *et al.*, 2003b), a trait they share with other reproductive proteins (Swanson and Vacquier, 2002). This fast evolu-

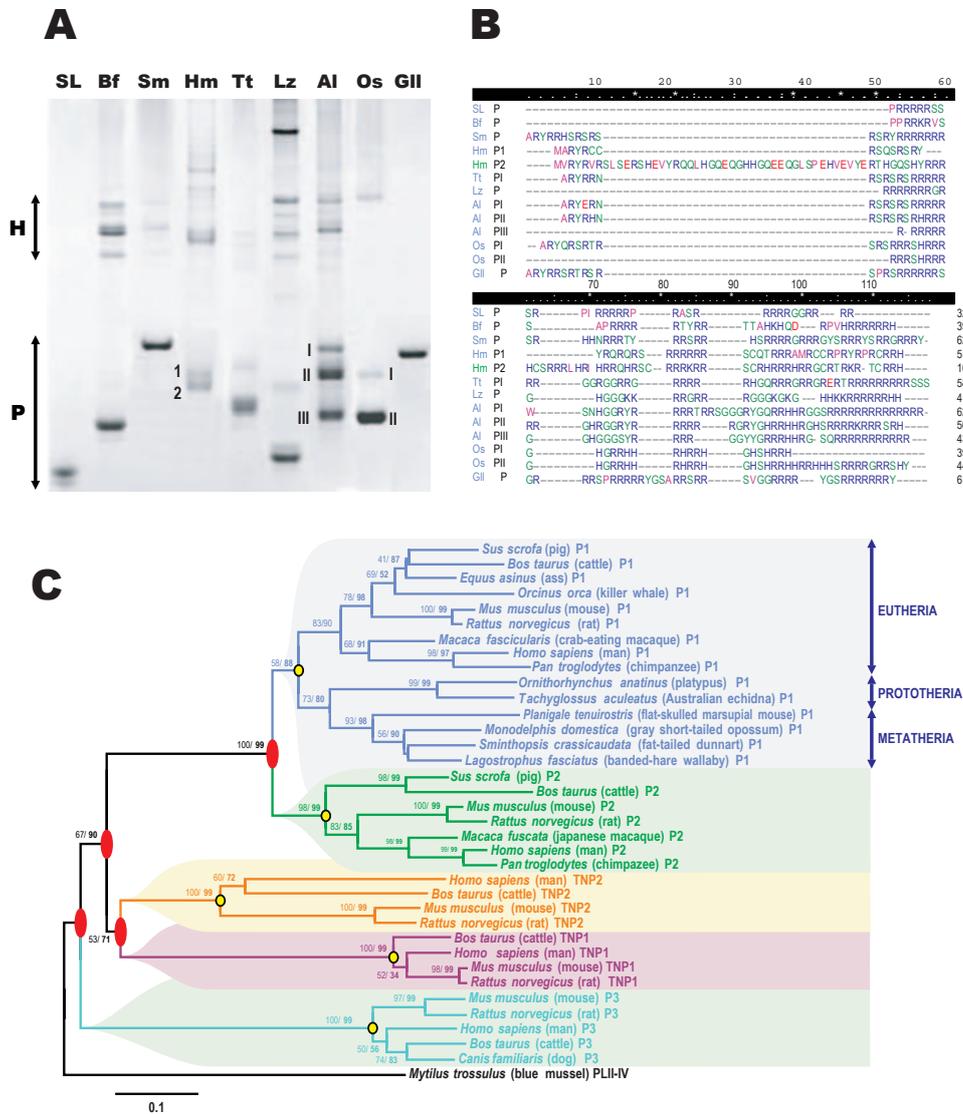


Figure 2. (A) Acetic acid-urea polyacrylamide gel electrophoresis (AU-PAGE) of protamines from several representative species of the main monophyletic groups of the subphylum Vertebrata shown in Figure 1. Al: *Alligator mississippiensis* (alligator); Bm: *Bufo marinus* (cane toad); Gll: *Gallus gallus* (rooster); Hm: *Homo sapiens* (human); Lz: *Anolis carolinensis* (green anole, lizard); Os: *Struthio camelus* (ostrich); SL: *Oncorhynchus keta* (chum salmon, salmine); Sm: *Sminthopsis crassicaudata* (fat-tailed dunnart); Tt: *Chrysemys picta* (painted turtle). H: histones; P: protamines. Amino acids are colour-coded according to their side-chain properties: Blue, basic; green, polar uncharged; pink, non-polar hydrophobic; red, acid. (B) Amino acid sequences of the protamines from the species shown in (A). The sequences have been aligned using the BIOEDIT (Hall, 1999) and CLUSTAL_X (Thompson et al., 1997) programs. (C) Phylogenetic relationships between different mammalian chromosomal sperm proteins (P: protamines; TNP: transition proteins; PL: protamine-like proteins). The amino acid sequences were aligned as in B and the phylogenetic tree derived from this alignment was constructed as described elsewhere (Eirin-Lopez et al., 2006). Numbers for the interior branches represent the BS (bootstrap probability) values followed by the CP (confidence probability, internal-branch test) values based on 1000 replications and are only shown when their value is higher than 50% (Eirin-Lopez et al., 2006).

tion has been ascribed to positive Darwinian selection (Rooney and Zhang, 1999; Clark and Civetta, 2000; Wyckoff *et al.*, 2000; Swanson and Vacquier, 2002) and involves an unusual form of purifying selection that is responsible for maintaining the overall high arginine composition of these proteins regardless of the specific position of the residues in the molecule (Rooney *et al.*, 2000).

We have taken advantage of all this and revisited here (Fig. 2C) the phylogenetic analysis of mammals using the SNBP sequence information available to date for this vertebrate group. The phylogenetic relationships between mammalian protamines and transition proteins bear an enormous resemblance to those obtained for these proteins when analysed within a broader phylogenetic tree that included SNBPs from all types belonging to both deuterostome and protostome organisms (Eirín-López *et al.*, 2006c). Accordingly, mammalian protamine P3 encoded by the *PRM3/GENE4* gene of the human protamine locus (Nelson and Krawetz, 1994; Kramer and Krawetz, 1998) appears to be more closely related to invertebrate PL proteins than to any other protamines (including mammalian P1 and P2 protamines encoded by *PRM1/PRM2* genes) (Eirín-López *et al.*, 2006b), a fact that could be taken as indicative of the more primitive origin of this mammalian protamine type. As pointed out by Oliva (2006) the name protamine for the protein encoded by *PRM3* may be misleading as it contains a large amount of glutamic acid which is uncharacteristic of a DNA binding protein. Interestingly however, the phylogenetic analysis suggests that a P3 ancestor may have been the precursor of mammalian TNP and P1 and P2 protamines (see Fig. 2C), in contrast to earlier propositions which suggested that *PRM3* was derived from *PRM1* (Kramer and Krawetz, 1998). It is then not surprising that, *PRM3* (Schluter and Engel, 1995; Schluter *et al.*, 1996; Kramer and Krawetz, 1998) and the *PRM1*, *PRM2* and *TNP2* genes are found in the same vicinity within the same protamine locus (Nelson and Krawetz, 1993).

As can be seen in Figure 2C, the analysis not only provides useful information about the potential evolutionary links between the SNBPs of mammals but their protamines (Oliva, 1995), in particular protamine P1, accurately define the phylogeny of the group. The Metatheria (Marsupialia) (Retief *et al.*, 1995a,b), Prototheria (Monotremata) (Retief *et al.*, 1993) and Eutheria (Oliva, 1995; Queralt *et al.*, 1995) appear well defined, thus providing yet another example of the usefulness of protamines as highly reliable phylogenetic markers.

In addition to all this, the tree shown in Figure 2C also suggests that transition proteins arose earlier in evolution than mammalian P1/P2 protamines and that P1 and P2 are closely related, with the slightly more recent appearance of the P2 type likely arising by gene duplication of a P1 precursor (Krawetz and Dixon, 1988). The evolutionary path followed by these mammalian SNBPs is reminiscent of the sequential order in which these proteins appear during spermatogenesis. Together with the close relation of TNPs to invertebrate PLs (Eirín-López *et al.*, 2006c) all this lends additional support to the notion of a relationship between the ontogeny and phylogeny of the three main SNBP types (Bloch, 1976; Ausiό, 1995, 1999).

Do SNBPs affect sperm shape?

Amphibians provide an excellent system for a first approximation to the answer of this question as this vertebrate group contain species that are representative of each of the three main SNBP types (Frehlick *et al.*, 2006a) (Fig. 3).

A few preliminary considerations about chromatin organization need to be introduced here before further discussion on the topic. The association of histones, PL proteins and protamines with DNA results in nucleoprotein complexes with a fiber-like organization of 300-500 Å (van Holde, 1988; Casas *et al.*, 1993; Saperas *et al.*, 2006) that is ultimately determined by an

overall energy minimization of the complex and not by the specific nature of the protein–DNA interactions described next (Subirana, 1992). In the H type, such as in *Rana*, the chromatin is organised in a 300 Å fiber consisting of approximately six nucleosomes per turn (see Fig. 3D, H). In contrast, the invertebrate (Ausi3 and Subirana, 1982) and vertebrate (Saperas *et al.*, 2006) PL type chromatin consists of irregular parallel DNA bundles. In mammalian protamines, chromatin loops are organised in toroidal structures containing similar parallel nucleoprotamine bundles (Hud *et al.*, 1995; Ward and Zalensky, 1996; Balhorn, 1999; Brewer *et al.*, 1999) (see Fig. 3D PL/P).

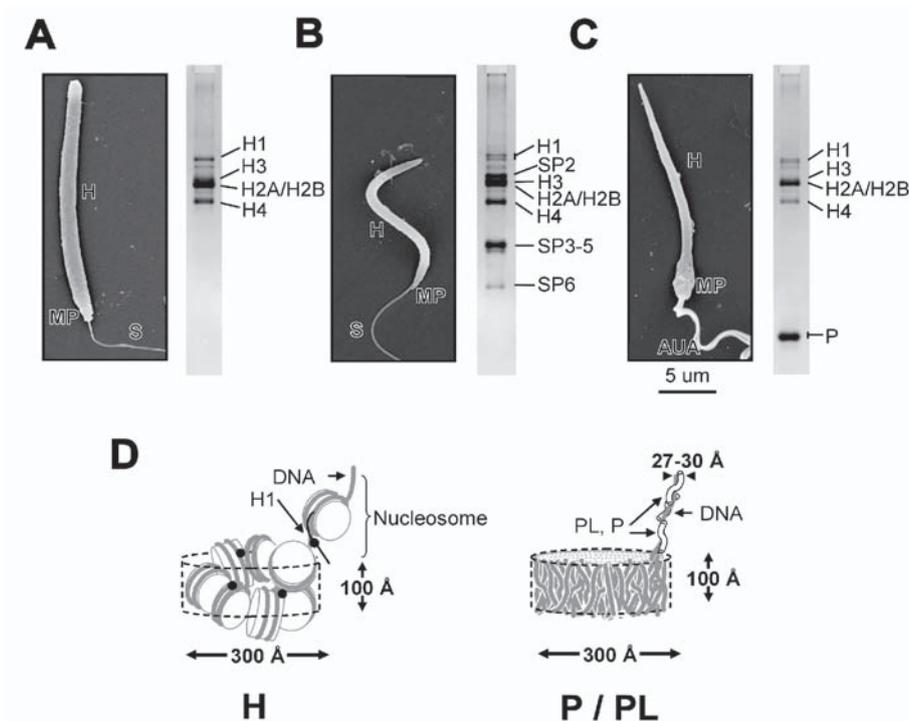


Figure 3. Scanning electron microscopy micrographs of the sperm heads (lanes 1) and AU-PAGE analysis of the SNBPs (lanes 2) of three different species of amphibians: (A) *R. catesbeiana* (bullfrog); (B) *X. laevis* (African clawed frog); (C) *B. marinus* (Cane toad). AUA: axoneme-undulating membrane-axial rod; H: head, MP: midpiece and S: single flagellum only with axoneme. (D) Schematic representation of a 100 Å cross-section of a 300 Å fiber of a histone-containing (H) or a P/PL-containing sperm chromatin fiber (see text for more details).

With the structural information currently available for these different types of chromatin organizations, it is possible to theoretically calculate the extent of DNA compaction achieved by each of them (see Fig. 3D). If we consider a 110 Å thick section and the DNA retains its B conformation (Ausi3 and Subirana, 1982; van Holde, 1988) with an average raise of 3.4 Å per base pair, it is possible to fit 100 nucleoprotein (P/PL) bundles (of approximately 30 Å in diameter) into a PL/P chromatin fiber with a 300 Å diameter. If the DNA was fully stretched this would amount to approximately $(100 / 3.4) \times 100$ (complexes) = 2900 base pairs of DNA compacted within this cross section. In the H type, chromatin is organized in discrete subunits (nucleosomes) each consisting of approximately 210 base pairs of DNA. In the presence of histone H1, the nucleosome

arrays can fold into a higher order structure consisting of approximately 6 nucleosomes per turn and a 300 Å diameter. Since the nucleosome is approximately 100 Å tall, this implies that about 1300 base pairs of DNA are compacted within a 100 Å by 300 Å section. Thus, the PL/P– DNA complexes can compact DNA about twice (2.2) as densely as the complexes of the H type.

We have used several scanning electron microscopy (SEM) pictures of *Rana catesbeiana* (H type), *Xenopus laevis* (PL type) and *Bufo marinus* (P type) sperm whose haploid C-value ranges are: 6.63-9.00, 3.00-3.85 and 3.98-5.65 picograms respectively (Gregory, 2006) to calculate the approximate sperm head volume/C-value ratios (v/C) and in doing so we observed that both *X. laevis* and *B. marinus* apparently exhibit the same v/C ratio, whereas the v/C ratio is approximately 1.7 times larger in *R. catesbeiana* (Fig. 3A-C). This higher value for the H type chromatin is in good agreement with the value theoretically calculated from the corresponding chromatin conformations, although it is a bit lower (1.7 vs. 2.2). The lower than expected compaction value could be attributed to the fact that the 300 Å nucleosomally organised chromatin fibers (Fig. 3 D, H) can interdigitate to some extent (Daban, 2003; Robinson *et al.*, 2006) increasing the theoretically calculated value.

While all this does not answer completely the question raised at the beginning of this section, it does demonstrate that, in general, histones are less efficient in packaging sperm chromatin than P and PL proteins. In addition to better compacting the sperm chromatin P and PL proteins erase the epigenetic contribution of histones (Caron *et al.*, 2005; Rousseaux *et al.*, 2005). These are most likely two of the important reasons why these protein types, especially protamines, have been selected throughout evolution (see Fig.1). In terms of sperm head shape it is difficult from just the three amphibian examples shown in Figure 3 to make any predictions other than the observation that while PL/P types seem to lead to more conical streamlined head shapes (Fig. 3 B,C), histones appear to result in rounder shapes (Fig. 3A). The morphology of the sperm head for those organisms containing exclusively protamines can be extremely heterogeneous across different taxa (Baccetti and Afzelius, 1976; Oliva and Dixon, 1991) and no SNBP-related rule appears to exist other than the previous generalization for H versus PL/P type.

It is very likely that SNBPs are not the sole determinants of the sperm nuclear shape. Mouse sperm co-expressing different amounts of a heterologous rooster protamine does not exhibit significant changes in its gross morphology (Maleszewski *et al.*, 1998). It has been shown that SNBP composition and regulation of the contraction of the perinuclear microtubule matrix may have co-evolved to produce the highly unique structural characteristics of the sperm nucleus and head, such as occurs with the cysteine-rich protamines of the nucleus of the sperm of the marine octopod *Eledone cirrhosa* (Giménez-Bonafé *et al.*, 2002). A synergistic effect between multiple protein components would explain the enormous sperm head shape diversity, when compared to the three main groups of SNBPs. However, at the level of closely related species or taxa is possible that protamines and their relative composition (when several molecular species are present, as is the case in mammals) may result in alterations of the overall sperm architecture, as has been observed in protamine deficient human spermatozoa (Blanchard *et al.*, 1990) and in protamine 2 deficient mice (Cho *et al.*, 2003). As the shape of the head may play an important role in sperm competition (Roldan, Gomendio and Vitullo, 1992) it would be worth analyzing the protamine composition of closely related species in relation to the sperm head morphology to determine the existence of any potential correlation.

Mammalian SNBPs and infertility

The multiplicity of SNBPs involved in mammalian spermiogenesis [H1t (Seyedin and Kistler, 1980), HILS1 (Iguchi *et al.*, 2003; Yan *et al.*, 2003), Hanp1/H1T2 (Martianov *et al.*, 2005;

Tanaka *et al.*, 2005), TNPs (Meistrich, 1989; Meistrich *et al.*, 2003) and P1/P2 protamines (Lewis *et al.*, 2003b)] suggests that alterations in any of these proteins could affect male fertility. In this regard, homozygous *Hanp1/H1T2* disrupted male mice are infertile (Tanaka *et al.*, 2005), *Tnp1/Tnp2* deficient mice exhibit an altered chromatin structure and reduced fertility (Yu *et al.*, 2000; Zhao *et al.*, 2001; Zhao *et al.*, 2004) and haplo-insufficiency of P1 or P2 causes infertility in the same organism (Cho *et al.*, 2001, 2003). In the last example, the effect is system-dependent as bull and boar lack protamine P2 as a result of mutations on this gene (Maier *et al.*, 1990) and, in contrast to mice, P2 expression is suppressed in rats (Bunick *et al.*, 1990).

The role of vertebrate SNBPs and protamines in male infertility has been the subject of two recent extensive reviews (Nishimune and Tanaka, 2006; Oliva, 2006). In humans, which retain some (ca. 15%) sperm-specific residual histones in the mature sperm (Gatewood *et al.*, 1987; Wykes and Krawetz, 2003; Churikov *et al.*, 2004), three main types of alterations that have been described so far which can affect fertility are: altered histone/protamine ratio, altered P1/P2 ratio and mutated P1 or P2 (Fig. 4 A, B).

Alterations in the relative amount of histones with respect to the protamine content can alter the sperm morphology (Blanchard *et al.*, 1990) and have been described in infertile men (Hofmann and Hilscher, 1991; Foresta *et al.*, 1992; de Yebra *et al.*, 1993; Carrell and Liu, 2001; Zhang *et al.*, 2006). Although this type of protein imbalance is usually related to protamine deficiency (Zhang *et al.*, 2006), in some instances it may alternatively be the result of an incomplete replacement of histones during spermiogenesis (Oliva, 2006), as is observed in males with antecedents of cryptorchidism (Fernandez Valades *et al.*, 2001).

An increase in the P1/P2 ratios as a source of infertility has long been recognized (Chevaillier *et al.*, 1987; Balhorn *et al.*, 1988; Bach *et al.*, 1990; Blanchard *et al.*, 1990; Belokopytova *et al.*, 1993; de Yebra *et al.*, 1993; Bench *et al.*, 1998; de Yebra *et al.*, 1998; Mengual *et al.*, 2003; Aoki *et al.*, 2005). Interestingly, an increased level of P2 precursors has also been described, suggesting a potential role of protamine processing in infertility (Bench *et al.*, 1998; de Yebra *et al.*, 1998; Torregrosa *et al.*, 2006).

The potential role of SNBP mutations in infertility has been recently reviewed (Nishimune and Tanaka, 2006). Although this does not appear to be a common source of the problem, a few mutations have been described in both the *PRM1* and *PRM2* genes of infertile males. A single nucleotide polymorphism (SNP) (c248t) in the *PRM2* gene that results in early mRNA termination has been detected in an infertile patient that presumably results in haplo-insufficiency of P2 and is responsible for infertility (Tanaka *et al.*, 2003). More recently, an amino acid transition from R to S at position 34 of human P1 (see Fig. 4B) in a group of infertile patients has been described (Iguchi *et al.*, 2006). This mutation was shown to be the result of a heterozygous single nucleotide polymorphism and there are reasons to believe that it may be involved in infertility. The replacement of arginine by a serine in the context of the region of P1 where the transition takes place is interesting as it generates an RSR motif amenable to phosphorylation by SR-protein-specific kinase 1 (Papoutsopoulou *et al.*, 1999). Phosphorylation of the repetitive N-terminal "RS" domains and of protamine serine residues in general has been shown to play a critical role in the proper interaction and deposition of these proteins onto DNA (Bode *et al.*, 1977; also see Oliva and Dixon, 1991, and Raukas and Mikelsaar, 1999, for reviews) and hence are important for the proper organization of sperm chromatin. Thus, the appearance of a new internal serine in P1 could potentially have a very disruptive effect. In this regard, and as shown in Figure 4B, phosphorylation of S(34) introduces two negative charges that have the potential to neutralise the adjacent positive charge of the surrounding R(33)/R(35) leading to a significant modification of the protamine-DNA interaction and/or to changes in the local secondary

structure of the protein, both of which can result in an anomalous chromatin organization. Alterations of sperm chromatin structure have the potential to lead to infertility and altered binding of protamines to DNA may affect the proper formation of a male pronucleus after fertilisation.

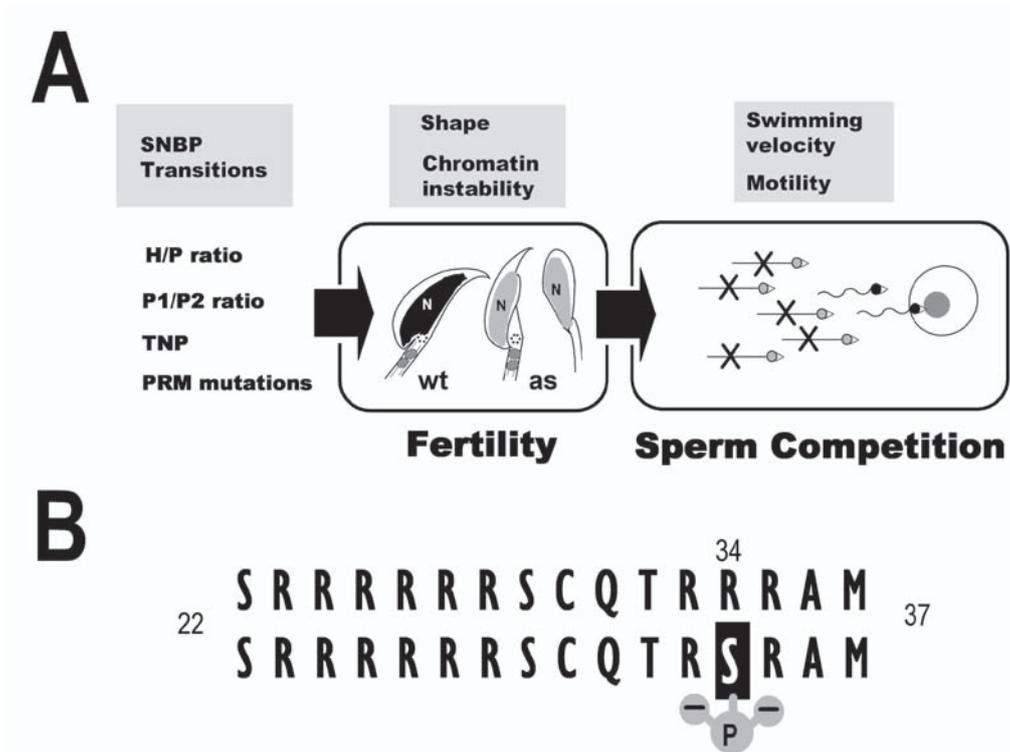


Figure 4. (A) Transitions in SNBPs can affect sperm morphology (shape) and chromatin instability, affecting fertility. Schematically shown is a representation of mouse sperm heads of the wild type (wt) or exhibiting an altered shape (as) resulting from a protamine 2 deficiency (Cho *et al.*, 2003) [redrawn from pictures shown in Fig. 2 from Cho *et al.* (2003)]. In conjunction with other cellular changes it is possible that the SNBP-mediated conformational changes may have a significant effect on sperm mobility (in this representation X indicates reduced mobility) which may play an important role in sperm competition (see text for a detailed discussion). H: histones; N: nucleus; P: protamines; TNP: transition proteins. (B) A recently discovered single nucleotide polymorphism leads to an amino acid transition (R to S) at position 34 of human protamine 1 and may participate in infertility (Iguchi *et al.*, 2006).

Can protamines play a role in sperm competition?

Support for the notion that protamines may have a role in sperm competition comes from evolutionary studies carried out with these proteins. It has been proposed that the positive Darwinian selection of protamine P1 in primates may have been driven by sperm competition (Rooney and Zhang, 1999; Wyckoff *et al.*, 2000; Swanson and Vacquier, 2002). However, the structural determinants involved in the process are not known. If protamines can have some direct or indirect effect on sperm shape and chromatin stability (Fig. 4A), altering the overall mobility

and having implications for infertility (Cho *et al.*, 2003), the exciting possibility exists that protamines may also play a role in sperm competition (Fig. 4A). It has also been shown that expression of a heterologous avian protamine from rooster in transgenic mice (Rhim *et al.*, 1995) resulted in reduced mobility and lower fertility (Maleszewski *et al.*, 1998). Therefore, it appears that protamines may have a significant effect in sperm competition, however further research in this area is still needed.

Recent work with Iberian red deer (*Cervus elaphus hispanicus*) has shown that the hydrodynamic shape of the sperm head in conjunction with the force generated by the flagellum play a critical role in determining sperm swimming velocity (Malo *et al.*, 2006). Also, a unique morphological conformation has been described for the falciform head of the wood mouse (*Apodemus sylvaticus*) sperm which results in sperm cooperation where distinctive aggregations of genetically related sperm results in the increase of the sperm's progressive motility (Moore *et al.*, 2002). As sperm swimming velocity and motility are very important determinants of male fertilisation success (Birkhead *et al.*, 1999; Froman *et al.*, 1999; Levitan, 2000; Gage *et al.*, 2004) the shape of the sperm head may be a component in sperm competition (Roldan *et al.*, 1992). In this hypothetical setting the influence of the protamine P1/P2 composition in the shape of the mice sperm heads is quite revealing and lends further support to the notion that protamines may play a role in sperm competition (Fig. 4A).

It has been pointed out that sperm competition is a potent evolutionary force among mammals (Roldan *et al.*, 1992) which influences sperm morphology (Gomendio and Roldan, 1991). It could be that the selection for protamines in the course of SNBP evolution was not exclusively determined by the transition from external to internal fertilisation but may have also been influenced by sperm competition.

Concluding remarks

The rapid evolution of sperm proteins, in particular protamines, is allowing us to observe the evolution of proteins at its best. The transition from the H type to the P type in the course of evolution may have ultimately been driven by the enhanced ability of these proteins to compact the genome, while efficiently erasing the epigenetic histone component inherited from the stem cells at the onset of spermatogenesis.

In general, the sperm head shape appears to be highly variable and independent of the SNBP composition. However, protamines and PL proteins compact DNA much more efficiently and the possibility exists that protamine variation may affect the shape of the sperm head in relatively closely related species and hence have a role in fertility and even perhaps in sperm competition. Increased chromatin compaction by protamines decreases the volume and streamlines the shape of the sperm head, providing better protection against externally damaging agents and enhancing sperm mobility. Ultimately, differences in sperm swimming velocity in internally fertilising organisms are an important component of sperm competition. Also, there is now a significant amount of accumulated data that indicates that protamines play an important direct role in fertility. This involvement suggests again that the SNBP transitions responsible may also affect sperm competition.

In closing, we would like to go back to Sherrington's quote at the beginning of this chapter on Cajal's anthropomorphic views of cell systems (Sherrington, 1949). Evolution of SNBPs together with other male reproductive proteins appears to have an important role in optimizing the cell parameters that allow sperm to accomplish its "passionate urge" (fertility) and successful "rivalry" (competition). This later issue, sperm competition, is an important selective force whose role in the evolution of SNBPs has yet to be explored.

Acknowledgements

This work was supported by Natural Science and Engineering Research Council of Canada Grant (NSERC) OGP 0046399-02 to J.A. J.M.E-L is a recipient of a Postdoctoral Marie Curie International Fellowship within the 6th European Community Framework Programme. L.J.F. is a recipient of an NSERC postgraduate doctoral scholarship.

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