

constitution: oocytes are X;A and sperm are 2X;A. This is so because meiosis is orthodox in females but highly specialised in males, showing elimination of the paternally derived genome (1st division), and the non-disjunction of the two X chromatids and elimination of one chromatid of each autosome during the 2nd division. When the zygotic nuclei reach the egg cortex, one paternal X chromosome is eliminated in the somatic cells of embryos destined to be females (2X;2A) and two are eliminated in those destined to become males (X;2A). In the formation of the X/A chromosomal signal in sciarids an imprinting process occurs in one of the parents, which determines that the chromosomes to be eliminated are of paternal origin [2]. A maternal factor controls the number of X chromosomes eliminated by the zygote [3, 1, 4]. Therefore, the formation of the primary, chromosomal signal (2X;2A versus X0;2A) determining gender in sciarids is the consequence of four processes: lethality of non-X bearing sperm, non-disjunction of maternal-derived X chromatids during spermatogenesis, elimination (controlled by a maternal factor) of X paternal-derived X chromosomes in the embryo and chromosome imprinting. This work focuses on the putative evolutionary pathways that gave rise to sciarid sex determination system from the more ancient XX/X0 system, where the primary, chromosomal signal (2X;2A versus X0;2A) is a direct consequence of the chromosomal constitution of the gametes: oocytes are X;A and sperm are 0;A.

Acknowledgements: this work was financed by grants BFU2005-03000 awarded to L. Sánchez by the D.G.I.C.Y.T., Ministerio de Educación y Ciencia, España.

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Evolutionary process of a tetranucleotide microsatellite locus in Acipenseriforms

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The tetranucleotide microsatellite locus Spl-106 has been widely used as a molecular marker in sturgeon studies. To investigate the evolutionary process of this highly variable locus in Acipenseriforms, cross-species amplifications were performed in 130 individuals from 15 species and successful in 13 species. All PCR products were sequenced. According to the flanking sequences, a total of 94 alleles at locus Spl-106 were found in 11 out of 13 species. Twenty-three haplotypic flanking sequences were detected and four of them are dominant types present in 70 out of 94 alleles. Two of the dominant types are species-specific types, and the other two are composed of alleles from species of the Pacific and Atlantic lineages, respectively. The repeat region evolved synchronously with the flanking region. The Atlantic clade was also found in the genealogy tree of the repeat region constructed using the MS_Align method. Although the basic repeat structure was variable, several alleles were highly conserved among species and evolved independently. The evolutionary process of this locus in Acipenseriforms was reconstituted from a single repeat (TAGA)_n to compound repeats (TAGA)_n(TAAA)_m, then to another single repeat (TAAA)_n, and finally to a totally new compound repeat structure (TAAA)_m(GAAA)_n. Reciprocally, for the sturgeon phylogeny, our results suggest that *Acipenser sturio* diverged earlier than *Schphirhynchus platorynchus*, and infirm the *Huso* genus, since the two *Huso* species are classified within the *Acipenser* species of the Pacific and Atlantic lineages, respectively. Moreover, the sequence information also supports the close relationship between *A. sinensis* and *A. dabryanus*, and the relationships among *A. transmontanus*, *A. schrenckii*, and *H. dauricus*.

Application of Matlab in population genetics and molecular evolution

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