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# X Chromosome Evolution in Cetartiodactyla

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Numerous Carnivora karyotype evolution investigations have been performed by classical and molecular cytogenetics and were supplemented by reconstructions of the Ancestral Carnivora Karyotype (ACK). However, the group of Pinnipedia was not studied in detail. Here we reconstruct pinniped karyotype evolution and refine ACK using published and our new painting data for 10 pinniped species. The combination of human (HSA) and domestic dog (CFA) whole-chromosome painting probes was used for the construction of the comparative chromosome maps for species from all three pinniped families: Odobenidae – *Odobenus rosmarus* Linnaeus, 1758, Phocidae – *Phoca vitulina* Linnaeus, 1758, *Pusa sibirica* Gmelin, 1788, *Erignathus barbatus* Erxleben, 1777, *Phoca largha* Pallas, 1811, *Phoca hispida* Schreber, 1775 and Otariidae – *Eumetopias jubatus* Schreber, 1775, *Callorhinus ursinus* Linnaeus, 1758, *Phocarcos hookeri* Gray, 1844, *Arctocephalus forsteri* Lesson, 1828. HSA and CFA autosome painting probes have delineated 32 and 68 conservative autosome segments in the studied genomes. The comparative painting in Pinnipedia supports monophyletic origin of pinnipeds, shows that pinniped karyotype evolution was characterized by slow rate of genome rearrangements (less than one rearrangement per 10 million years), provides strong support for refined structure of ACK with  $2n = 38$  and specifies plausible order of dog chromosome syntenic segments on ancestral Carnivora chromosomes. The heterochromatin, telomere and ribosomal DNA distribution was studied in all 10 species.

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## O3

### X chromosome evolution in Cetartiodactyla

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The mammalian X chromosome is characterized by high level of conservation. On the contrary the Cetartiodactyl X chromosome displays variation in morphology and G-banding pattern. It is hypothesized that X chromosome has undergone multiple rearrangements during Cetartiodactyla speciation. To investigate the evolution of this sex chromosome we have selected 26 BAC clones from cattle CHORI-240 library evenly distributed along the cattle X chromosome. High-resolution maps were obtained by fluorescence *in situ* hybridisation in a representative range of cetartiodactyl species from different families: pig (Suidae), gray whale (Eschrichtiidae), pilot whale (Delphinidae), hippopotamus (Hippopotamidae), Java mouse deer (Tragulidae), pronghorn (Antilocapridae), Siberian musk deer (Moschidae), giraffe (Giraffidae). To trace the X chromosome evolution during fast radiation in speciose families, we mapped more than one species in Cervidae (moose, Siberian roe deer, fallow deer and Pere David's deer) and Bovidae (musk ox, goat, sheep, sable antelope, nilgau, gaur, saola, and cattle). We have identified three major conserved synteny blocks and based on this data reconstructed the structure of putative ancestral cetartiodactyl X chromosome. We demonstrate that intrachromosomal rearrangements such as inversions and centromere reposition are main drivers of cetartiodactyl's chromosome X evolution.

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## Cytogenetics and genomics of domestic animals

### L8

### Copy number variations in cattle and pigs: aging and reproduction

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Variability in genomes (including single nucleotide polymorphisms (SNP), copy number variations (CNV) and chromosomal rearrangements (CA)) is responsible for a significant proportion of the diverse phenotypes associated with many important traits including fertility and ageing. We have investigated copy number variation in Canadian Holstein bulls and Yorkshire, Landrace and Duroc boars. In bulls we studied *de novo* CNVs from two perspectives: somatic variability and ageing. In boars we