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# Pinniped Karyotype Evolution Substantiated by Comparative Chromosome Painting of 10 Pinniped Species (Pinnipedia, Carnivora)

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homology between species (for genome mapping, phylogenomics and genome organization studies) and the ability to anchor genomic sequence data to chromosomes (for chromosome assembly) is therefore restricted.

To overcome these difficulties, we developed a set of universal avian BAC probes, selected through the identification of evolutionary conserved regions. This BAC set was then used to upgrade the genomes of 5 avian species to a chromosome-level. Successful hybridisation of these probes to a further ~30 avian species revealed genome-wide patterns of chromosome stability and rearrangement between species. In addition, the probes successfully hybridized on non-avian reptile species (turtles and anole lizard) revealing a level of genome conservation extending far beyond birds.

Further, we applied the approach developed for avian probes to the selection of BACs from the cattle and human genome with the aim of generating a universal mammalian BAC set. Selection criteria were validated by testing probes on species at key nodes of the phylogenetic tree. Hybridisations were achieved on species as diverse as horse *Equus ferus* Boddaert, 1785, dolphin *Tursiops aduncus* Ehrenberg, 1833, bat *Lophostoma silvicolium* D'Orbigny, 1836 and lemur *Eulemur macaco* Linnaeus, 1766.

These preliminary results illustrate that our combined FISH-bioinformatics approach is also applicable to mammals. Development of a universal BAC set therefore permits cross-species sequence anchoring and comparative genomic research at a higher resolution than previously possible, providing new insight into the nature of genomic evolution and genomic stability.

## O2

### **Pinniped karyotype evolution substantiated by comparative chromosome painting of 10 pinniped species (Pinnipedia, Carnivora)**

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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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