

Chromosome evolution in Ruminantia

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In the order of Cetartiodactyla the suborder Ruminantia is represented by mammals that typically possess horns, reduced incisors, and a multi-chambered stomach. It includes a lot of domestic livestock and rare hoofed animals. Within the ruminants there are two infraorders: Pecora and the Tragulina. Pecora includes pronghorns, bovids, deers, giraffes and musk deers, while Tragulina represented nowadays entirely by the chevrotains.

Genome evolution in Ruminantia is characterized by two features: the wide among mammals spans of diploid chromosome numbers ranging from 7 to 70 and non-standard X-chromosome morphology. We have comprehensively studied genomes of representatives from each family in Ruminantia by a wide range of complex approaches: classical and banding cytogenetics, BAC clone's and comparative chromosome mapping, genome sequencing. Major trends in genome evolution of each ruminant family were identified. By dense BAC mapping of the X chromosome across Ruminantia we have identified three major conserved syntenic blocks and reconstructed the structure of putative ancestral cetartiodactyl X chromosome. We have demonstrated that intrachromosomal rearrangements such as inversions and centromere repositions are main drivers of remarkably sped up cetartiodactyl's chromosome X evolution. Localization of ribosomal DNA on a range of species allowed us to illustrate dynamics of the distribution of these repeats on ruminant chromosomes. Comprehensive mapping data allowed improving Ruminantian and Pecoran ancestral karyotype reconstructions: to identify the order of conservative segments and positions of evolutionary breakpoints. Overall, we have characterized major trends in the genome evolution of Cetartiodactyla that can now be deeply studied by genome sequence analysis.

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