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Detailed analysis of distribution of repetitive sequences across genomes of *Martes* (Mustelidae, Carnivora, Mammalia)

Beklemisheva V.R.*, Lemskaya N.A., Prokopov D.Yu., Romanenko S.A., Serdyukova N.A., Utkin Ya.A., Graphodatsky A.S.
Institute of Molecular and Cellular Biology, SB RAS, Novosibirsk, Russia
** bekl@mcb.nsc.ru*

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Motivation and Aim: Recently more attention is paid to the significant role that repetitive elements may play in the genome functioning. Mustelidae (martens, otters, weasels, minks, badgers, wolverine and others) is a diverse family that diverged from other Carnivora about 17 million years ago [1], that is characterized by evolutionary conserved karyotypes [2, 3] and diploid number close to the ordinal ancestral ($2n = 38$). The genus *Martes* (martens and sables) has a more basal position on the tree of Mustelidae. While evolutionary younger mustelids possess additional entirely heterochromatic chromosome arms, *Martes* autosomes possess moderate amounts of pericentromeric heterochromatin. Here we used an array of modern molecular cytogenetic methods and bioinformatic genome analysis to describe distribution of constitutive heterochromatin and tandem repeats (such as telomeric sequences, macrosatellites and ribosomal genes) on chromosomes of four species from the genus *Martes*: stone marten (*M. foina,* $2n = 38$), sable (*M. zibellina,* $2n = 38$), pine marten (*M. martes,* $2n = 38$), and yellow-throated marten (*M. flavigula,* $2n = 40$).
Methods and Algorithms: Interest in the increased amount of the constitutive heterochromatin in mustelids launched the studies of satellite repetitive sequences content and distribution on the chromosomes in the 1980s [4]. Here most abundant tandem repeats (TR) were mined using graph-based sequence clustering with TAREAN pipeline based on stone marten whole-genome sequencing data. Eleven probes were designed from high-confidence TR clusters for FISH investigation of their distribution. Constitutive heterochromatin was characterized by C-banding staining, the AT/GC-content was characterized by CDAG staining (Chromomycin A3-DAPI-after G-banding). The distribution of telomeric repeats and ribosomal genes was shown by FISH.
Results: Overall, eight satellite probes out of 11 produced distinct unique patterns of chromosome signals. Satellite signals were detected in pericentromeric areas on ⅔ of stone marten chromosomes as well as in heterochromatic regions of sex chromosomes. Interestingly, the S46 probe had non-centromeric interstitial localization on the q-arm of X chromosome. We have identified an X-specific centromeric S40 satellite. Some of the satellites had Martes-wide distribution. While other satellites were stone marten specific and provided only faint signals in other species.
Constitutive heterochromatin in *Martes* was mostly centromeric on autosomes and on the X with large heterochromatin block on the Yq. We describe AT/GC-rich repetitive areas on chromosomes of four *Martes* species. The heterochromatin in *Martes* is mostly GC-rich: centromeric areas, additional heterochromatin blocks, Y-chromosome heterochromatin. Nucleolar organizing regions are represented by a single site in all four

species and are also GC-rich (as in other mammalian species). Telomeric regions were CDAG-stained as light green indicating mixed AT/GC content, while some telomeric heterochromatin blocks were GC-rich and stained bright green.

Conclusion: We deeply characterized repetitive fractions of the genome in four *Martes* species and revealed patterns of satellite localization and clustering. Our findings are summarized on repeat chromosomal maps.

There is apparent heterochromatin variation among species displayed in the amount and the distribution of the heterochromatin and satellite repeat representation. The array of molecular-cytogenetic methods applied here clearly displays variation of the repetitive genome component in species with conserved syntenic groups.

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