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NON-METRIC VARIATION IN SMALL WOOD MOUSE (APODEMUS URALENSIS PALL.) POPULATIONS WITHIN THE EAST URAL RADIOACTIVE TRACK (EURT) ZONE

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Ecological monitoring of small wood mouse (*Apodemus uralensis* Pall) populations carried out in the Sverdlovsk region near Kamensk-Uralski for ten years' period (1992-2002) and in the Chelyabinsk region near Kyshtym for two years (2000-2001), has revealed an increase of morphological diversity in terms of non-metric skull traits on the impact territories along the axis of the East-Ural radioactive track (EURT). It was revealed that both in the southern part of EURT at a site with a density of radioactive contamination about 500 Ki/km² (near Kyshtym) and in it's less contaminated northern part (near Kamensk-Uralski), the impact samples are deviated from the control ones, located outside EURT, on frequencies of non-metric skull traits. The impact populations manifested also the higher level of developmental instability as measured by individual average index of fluctuating asymmetry of bilateral non-metric traits. We suppose that the observed increase of phenotypic malformations within the EURT zone has been caused by the chronic influence of low doses radiation, leading to an accumulation of minor mutations and to disturbances in regular ontogenetic development of the small wood mouse.

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POSTER, S I

CHROMOSOMAL RADIATION OF THE AFRICAN PYGMY MICE, SUBGENUS NANNOMYS (RODENTIA; MURIDAE): KARYOTYPIC AND PHYLOGENETIC ANALYSIS

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The African pygmy mice are a group of small-sized rodents widespread throughout sub-Saharan Africa belonging to the genus Mus (subgenus Nannomys). Owing to their highly conserved morphology, diagnostic characters are scarce leading to ambiguous discrimination of the currently recognized 19 species. On the contrary, cytogenetic studies have uncovered extensive karyotypic evolution within this group mainly involving centric fusions. An analysis of molecular (cytochrome b sequences) and chromosomal markers (2N, NF, G-banding) was performed on 34 specimens from two extremes of the distribution area (Western and South Africa) to assess the role of chromosomal rearrangements in the evolutionary history of this species complex. The molecular phylogeny supported the monophyly of this group within the genus Mus, and resolved four clades, each characterized by diagnostic chromosomal rearrangements or karyotypes. In addition, substantial genetic differentiation between species and/or populations within each clade was uncovered, suggesting the existence of cryptic taxa yet to be described. One of the clades clustered taxa carrying different sex-autosome fusions, associated in some cases with partial deletions of the X or Y chromosomes. As these fusions are expected to be highly deleterious, they are rarely observed in mammals and when present, are considered as efficient reproductive isolating mechanisms. The clustering of these taxa into one clade, if confirmed by additional sampling, would support the occurrence of shared genomic traits allowing the formation and/or fixation of such rearrangements in the taxa within this clade. The diversity of this type of rearrangement within the Nannomys offers the unique opportunity to investigate the molecular basis of sex-autosome fusions as well as the evolutionary consequences on speciation rates and sex determination mechanisms.

ORAL, SY 2