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micro-dissected B chromosomes and flow-sorted B chromosome-containing micronuclei. To identify differentially expressed genes that might drive B chromosome elimination in *S. purpureosericeum* tissues, an extensive RNA-Seq analysis of embryonic tissues was performed. Comparative transcriptome analysis of embryos at various developmental stages was carried out together with RNA-Seq analysis of laser-microdissected (LM) embryonic regions supposed to actively undergo B chromosome elimination. Preliminary results show a significant group of upregulated genes in B+ samples and indicate a potential role of B chromosomes in gene expression regulation, mainly during early embryo development.

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S1-P2

Transcriptome atlas of the maize B chromosome

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Maize (*Zea mays* L.) is one of the most important crops. It serves as a well established model for biological research and the maize B chromosome has been studied for many decades. However, the gene expression of the maize B chromosome across different plant tissues has not been thoroughly described. Here we present the first results of a comprehensive gene expression analysis of 15 maize tissues. We identified B-chromosome specific genes expressed in various developmental stages and plant organs. Roughly, one third of B-chromosome-localized genes are expressed in at least one of the tissues. Further, the effect of the B chromosome on the expression of A-chromosomal complement was investigated. This effect is most pronounced in reproductive organs. The transcriptome analysis of developing pollen indicated candidates for key B-chromosome accumulation mechanism, non-disjunction in the second pollen mitosis.

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Session 2 - Dynamics of the B chromosomes in the population

S2-PL1

B chromosomes in populations of *Apodemus flavicollis* – never ending story

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B chromosomes (Bs) are uncommon in mammals, featuring less than 2% of species, but six out of 22 species possess them in the genus *Apodemus*. In Serbia, over 40 populations of yellow-necked mice (*Apodemus flavicollis*) with varying habitat quality were studied. The frequency of B carriers (range: 0.09 to 0.67) increased with elevation,

correlated with sub-zero days, and inversely with average temperature. B carrier frequency remained stable over eight years despite population density fluctuations, while seasonal variations linked to population size were observed. Overcrowding stress reduced B carriers among pre-reproductive individuals but enhanced survival in sub-optimal conditions.

Phenotypic traits and B frequency were correlated, influencing cranial morphometric development. B carriers showed distinct developmental pathways for cranial traits, suggesting environment-specific benefits. Bs' presence did not affect carrier fecundity or fertility and was evenly distributed across age groups. B chromosomes (up to five) displayed common structures across populations in Serbia and Eastern Europe, possibly originating from sex chromosome pericentromeric regions. B-specific chromatin spatially resembled pericentromeric sex chromosomes, suggesting a similar mechanism to bypass meiotic checkpoints.

Current data support a heterotic model in *A. flavicollis*. Bs likely contribute to species adaptability by increasing genetic variability, potentially expanding their distribution.

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S2-O1

Supernumerary chromosomes contribute to karyotypic diversity within cryptic species of the subgenus *Stenocranius* (Cricetidae, Rodentia)

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Background

The subgenus *Stenocranius* includes two cryptic species, *Lasiopodomys raddei*, which occurs in South-Eastern Transbaikalia and widespread *L. gregalis*; the latter has three allopatric and genetically well-isolated lineages A, B and C having unclear taxonomic rank. Previous literature data published in the last century showed that most of the studied narrow-headed vole populations are characterised by a stable $2n=36$, while in populations from Central Mongolia $2n$ has varied between 36 and 40 owing to the presence of one to four B chromosomes (Bs).

Materials and Methods

To identify speciation mechanisms within the subgenus *Stenocranius*, we analysed karyotypic variation of narrow-headed voles from previously unexplored regions of South Siberia, including the Altai-Sayan region and Transbaikal Region – the major centres of diversity within the subgenus. In total, 49 individuals from 15 new localities were karyotyped; a total sample of 121 individuals from 37 localities was analysed. To determine karyotypic differences we used both classic differential bandings as well as fluorescent *in situ* hybridisation with ribosomal and telomeric DNA probes. In addition, we examine the structure and meiotic silencing of Bs using immunocytochemical analysis of synaptonemal complexes (SCs) in *Stenocranius* pachytene spermatocytes.

Results

Two cryptic species differ in several chromosomal characteristics although initially they shared the same $2n=36$. The Early Pleistocene