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relic *L. raddei* carries stable $2n=36$ ($FN_a=52$) without Bs; the G-banded karyotype is presented for the first time.

Intra-population karyotype variation of *L. gregalis* is mainly due to various number of Bs. Besides $2n=36$ ($FN_a=50$) karyotypes, the *L. gregalis* lineages carried 1-5 heterochromatic small acrocentric Bs. Karyotypes of the two species also differ in localisation of C-heterochromatic blocks and distribution patterns of rDNA in A chromosome sets and on Bs, whereas telomeric sequences show stable localisation across all examined karyotype variants.

Immunodetection of several meiotic proteins indicates that the meiotic Bs are transcriptionally inactive, located generally within the sex body and manifest a pattern of meiotic behaviour similar to that of sex chromosomes. These data allow us to suppose some homology of Bs to the sex chromosomes.

Conclusions

The increasing number of Bs can point to an evolutionary series from the older forms of *L. raddei* and *L. gregalis* lineage A (with almost stable $2n=36$) to evolutionarily younger lineages B and C carrying one to five Bs, with complete loss of the initial chromosome set in lineage C.

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S2-O2

Variation in the frequency of B chromosomes in small isolated populations of *Apodemus flavicollis*

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Background

Long-term studies on B chromosome (Bs) dynamics in natural populations of yellow-necked mice, *Apodemus flavicollis*, have unveiled intriguing seasonal variations influenced by environmental factors. On average, one third of animals possessed Bs in large natural populations. Urbanization, a potent catalyst for genetic diversity alterations, brings about habitat fragmentation and degradation, producing patches of small forested areas within urban landscapes. These fragmented habitats pose significant challenges for small mammal populations as migration and gene flow are severely restricted. To comprehensively grasp the repercussions of urbanization on B chromosome frequency, we embarked on a study within the Belgrade region.

Materials and Methods

The frequency of individuals with B chromosomes in five urban isolated forests populations of *A. flavicollis* has been studied. Employing live animal traps, we collected samples, and chromosome preparation was done directly from the bone marrow. Each animal's karyotype was analysed through examination of twenty metaphase figures.

Results

A total of 246 animals were sampled across five forest sites within the Belgrade territory and underwent karyotyping. The prevalence of animals with Bs exhibited remarkable variability, ranging from 3% to 50%. Intriguingly, at four of the sites, the incidence of Bs was significantly lower (ranging from 3% to 13%) compared to the average frequencies observed in natural populations. Conversely, at one site, the frequency soared to an exceptionally high 50%. Since all studied localities are at short distances from each other, climatic factors could be considered as the same. However, the studied sites differ in size and the level of adaptation to people's urban life. In a bid to elucidate the driving factors behind frequency variation, we developed a model simulating the

influence of genetic drift, the predominant evolutionary force in small, isolated populations.

Conclusions

Beyond investigations focused on the molecular structure and origin of B chromosomes, it becomes evident that a comprehensive understanding necessitates population-level research, shedding light on the intricate mechanisms governing their persistence across diverse environments.

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S2-P1

B chromosomes of the bat species *Nyctalus leisleri* from Serbia

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Background

B chromosomes (Bs) are infrequent in bat species, with only four known so far, including Lesser Noctule, *Nyctalus leisleri* (Kuhl, 1817). This western Palearctic species is widely distributed, though seldom captured, due to its late emergence from roosts or the fact they are tree dwellers, thus difficult to track. As a known long-distance migrant, it covers substantial distances between summer and winter roosts. Previously, a cytogenetical study investigated chromosome sets of two males from two Serbian locations, revealing karyotypes with two to five micro Bs. Notably, studies on female *N. leisleri* are scarce.

Materials and Methods

Recently, karyotypes and B's presence of additional specimens from southwestern Serbia (two males), and Belgrade (one female) were examined. Chromosome slides were made from the primary fibroblast cell cultures established from a piece of skin from the wing membrane. At least 20 metaphase plates per individual were assessed.

Results

The species' standard chromosome complement counts 44 (42 autosomes and a sex chromosome pair), with extra chromosomes classified as Bs. In two males, counts were $2n=44+1B$ and $2n=44+2B$, while the Belgrade female had $2n=44+2B$. Notably, the X chromosome was a medium-sized metacentric and the Y chromosome was a small acrocentric, while all Bs were microchromosomes. A previous study from Poland from 1970 reported a female *N. leisleri* karyotype of $2n=46$, but Bs were not mentioned due to the analysis of a single individual. Our findings of a female with $2n=44$ and two additional Bs suggest that the Polish study likely shared the same scenario.

Conclusions

The paucity of B chromosomes in bats might be attributed to their small genome size, possibly linked to the energy demands of flight. Additionally, bats' low reproductive rates could hinder Bs establishment and maintenance, as opposed to rodents, which exhibit the highest occurrence of Bs among mammals. This research marks the first confirmation of Bs in female *N. leisleri*, and supplements the limited understanding of additional chromosomes in bats with two more male karyotypes.

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