

УДК 57  
ББК 28  
X 942

**Редакционная коллегия**

акад. РАН *И. Ф. Жимулев*, член-корр. РАН *А. С. Графодатский*,  
д-р биол. наук *И. Ю. Баклушинская*, д-р биол. наук *Ю. Ф. Богданов*,  
д-р биол. наук *А. В. Вершинин*, канд. биол. наук *Н. Е. Воробьева*,  
д-р биол. наук *Е. Р. Гагинская*, акад. РАН *П. Г. Георгиев*,  
акад. РАН *С. Г. Георгиева*, д-р биол. наук *А. И. Калмыкова*,  
д-р биол. наук *Т. Д. Колесникова*, акад. РАН *А. В. Кочетов*,  
д-р биол. наук *В. А. Лухтанов*, д-р биол. наук *С. А. Романенко*,  
д-р биол. наук *Н. Б. Рубцов*, д-р биол. наук *В. А. Трифонов*

**X 942** Хромосома – 2023 : материалы Междунар. конф. 5–10 сентября 2023 г. / Ин-т молекулярной и клеточной биологии СО РАН ; Новосиб. гос. ун-т. — Новосибирск : ИПЦ НГУ, 2023. — 226 с.

ISBN 978-5-4437-1514-8

Сборник материалов содержит тезисы докладов и постеров, представленных на Международной конференции «Хромосома – 2023». Основные результаты, представленные на конференции, посвящены организации и эволюции хромосом и геномов, гетерохроматину, генетической организации интерфазных хромосом, структуре ядра и другим темам. Материалы представляют интерес для научных сотрудников, работающих в области генетики и молекулярной биологии.

УДК 57  
ББК 28

ISBN 978-5-4437-1514-8  
DOI 10.25205/978-5-4437-1514-8

© Новосибирский государственный университет, 2023  
© ИМКБ СО РАН, 2023

## **Achievements of mammalian cytogenetics in the development of chromosomal diagnostics and species systems**

**Orlov V.N.**<sup>1</sup>, **Lyapunova E.A.**<sup>2</sup>, **Baskevich M.I.**<sup>1</sup>, **Kartavtseva I.V.**<sup>3</sup>, **Malygin V.M.**<sup>4</sup>,  
**Bulatova N.Sh.**<sup>1\*</sup>

<sup>1</sup> A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, 119071 Russia

\*e-mail: bulatova.nina@gmail.com

<sup>2</sup> N.K. Koltsov Institute of Developmental Biology, Russian Academy of Sciences, Moscow, 113994 Russia

<sup>3</sup> Biology and Soil Institute of Far East Branch, Russian Academy of Sciences, Vladivostok, 690022 Russia

<sup>4</sup> Biology Department, Lomonosov Moscow State University, Moscow, 119234 Russia

The use of cytogenetic methods has largely changed the system of mammalian species, initially based solely on morphological approaches. Since the 1960s, classical cytogenetic analysis and methods of differential chromosome staining - later molecular cytogenetic analysis - have been used in institutions of the Russian Academy of Sciences, SB RAS, FEB RAS to study issues of evolutionary problems and systematics based on progressive levels of analysis of chromosomal rearrangements and the genome. Based on the materials of cytogenetic collections of several laboratories with a long history of chromosome research, for the first time in connection with the 50th anniversary of the Theriological Society at the Russian Academy of Sciences, a taxonomic analysis of most mammalian genera studied, including with the participation of the review authors, on the territory of the country was carried out. It is emphasized that new karyotypes are still being found even within previously studied taxa, and it has often been possible to show that in many cases large polytypic species of traditional taxonomy are complexes of morphologically similar, but genetically well distinguishable and reproductively isolated species. The identification of cryptic taxa (hidden twin species) is a necessary link in the description of biological diversity and at the same time draws attention to the discussion of the concepts of species and speciation at a new level. Modern molecular cytogenetic analysis makes it possible to establish the homology of large segments of the genome – the arms of chromosomes and whole chromosomes, as well as to identify point features that reveal intrachromosomal genetic differentiation of taxa at the DNA level, which qualitatively changes the previously accepted permissive levels of comparative cytogenetics. The support of the State Task IPEE RAS № FFER-2021–0003 is acknowledged.