
Taxonomy Genetics

Genetic analysis of type material brings logical order in geographic distribution and taxonomy. Case study of Central Asian vole genera *Neodon*, *Blanfordimus*, *Lasiopodomys*

Nataliya Abramson, Tatyana Petrova

Zoological Institute RAS, Sankt-Petersburg, Russia, natalia_abr@mail.ru

The systematics and nomenclature of central Asian vole species from genera *Neodon*, *Blanfordimus* and *Lasiopodomys* raised many questions. The dramatic discordance may be discovered in comparison of species distribution and taxonomy. Thus, the range of *Lasiopodomys fuscus* is very narrow and is in the very center of distribution ranges of voles from the genus *Neodon*. It is on the other hand very isolated from two other congeneric species. The range of *Neodon jildaschi* in turn lays in the center of distribution of voles from the genus *Blanfordimus* and is strongly isolated from the distribution of congeneric voles. It should be kept in mind that the proper use of species names depends entirely on the process of verifying whether additional specimens are conspecific with the specimen with which the species name is associated. Related to this the genetic studies of type material are of paramount importance in elucidating taxonomic issues. We successfully extracted DNA and obtained fragments of mitochondrial cytb from lectotype and paralectotypes of *Lasiopodomys fuscus* (collected by Przhevalskii) and the holotype of *Neodon jildaschi* (collected by Severtzov) from the collection of the Zoological Institute RAS. The results of phylogenetic analysis bring back the logic correspondence between zoogeography and systematics. Thus, *Lasiopodomys fuscus* should be without any doubt assigned to the genus *Neodon* and *Neodon jildaschi* to the genus *Blanfordimus*. Both species with a high support find their places within corresponding monophyletic clusters at the phylogenetic tree. Funding: research theme № AAAA-17-1170 424 10 167-2, RFBR grant № 15-04-04602, Program of Presidium RAS "Dynamics of gene pools in natural populations" and "Development of vital and biosphere processes".

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Editors:

Jens Jacob¹ and Jana Eccard²

¹Julius Kuehn Institute, Federal Research Centre for Cultivated Plants,
Institute for Plant Protection in Horticulture and Forests, Vertebrate Research,
Toppheideweg 88, 48161 Münster, Germany

²University of Potsdam, Institute of Biochemistry and Biology,
Animal Ecology Group, Maulbeerallee 1,
14469 Potsdam, Germany

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