

GENOME SEQUENCING

The Complete Genome Sequence of *Desmana moschata*, the Russian desman

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Biodiversity Genomes

The Russian desman (*Desmana moschata*) is a rare member of the Desmaninae subfamily, displaying a semi-aquatic lifestyle. We assembled the whole genome of this species using Illumina, a short-read sequencing approach. The whole genome sequencing outputs were assembled using the Abyss2 *de novo* approach. The raw data and assembled genome are publicly available via European Nucleotide Archive: (ERR13337211 and GCA_965120235, respectively).

Introduction

The Russian desman (*Desmana moschata*) is a poorly known member of the family Talpidae. Together with the Iberian desman (*Galemys pyrenaicus*), they constitute the two extant species of the tribe Desmanini. The current geographic range of the Russian desman comprises the Volga, Don and Ural River basins in western Russia, Kazakhstan and European Russia, and it is currently listed as critically endangered (M. Rutovskaya, Gazzard, and Turvey 2023).

Despite the shared evolutionary history between both desmans, they occupy different ecological niches. The Russian desman inhabits oxbow lakes and slow-moving rivers with a depth of 2-6 m with rich water-marsh vegetation, bushes and primary forests along the banks, and with high macroinvertebrate abundance (M. Rutovskaya, Gazzard, and Turvey 2023; M. V. Rutovskaya et al. 2020). In contrast, the Iberian desman is restricted to fast-flowing, shallow and well-oxygenated waters in mountainous regions of the Iberian Peninsula (Nores 2007; Quaglietta et al. 2024).

Unlike most Talpidae species, which are fossorial or semi-fossorial, desmans exhibit a semi-aquatic lifestyle. Accordingly, they present several convergently adaptive traits to this ecological niche, including large webbed hindfeet, a laterally compressed tail, double-layered fur, and a mobile prehensile snout (Wilson and Mittermeier 2018), and, consequently, modifications in thermoregulation and olfactory physiology (Martinez et al. 2020).



Picture of *D. moschata* taken in captivity at Chernogolovka by Y. F. Ivlev.

Methods

A muscle sample was collected from a male individual of a Russian desman, from the Spassky district of the Ryazan region (Russia) captured in 2008 and maintained in captivity until its death in July 2015. The tissue was used for total DNA extraction using the Qiagen MagAttract HMW DNA extraction kit (Dobra). Whole genome sequencing was conducted at Macrogen Inc (Korea), using a Truseq Nano DNA Illumina library preparation kit, followed by sequencing of paired-end (2×150 bp) reads using a NovaSeq6000 Illumina machine. The raw sequencing outputs were quality filtered and trimmed of adapters using Trimmomatic v.0.38 (Bolger, Lohse, and Usadel 2014). Whole genome *de novo* assembly was produced using Abyss2 (Jackman et al. 2017) specifying a 105 k-mer length, estimated using KmerGenie v.1.7051 (Chikhi and Medvedev 2014).

Results

The genome assembly yielded a total sequence length of 2.09Gbp over 1,670,778 scaffolds, and an N50 length of 64,508bp.

Data availability

Raw and assembled data is publicly available via European Nucleotide Archive (ENA):

Raw genome data

<https://www.ebi.ac.uk/ena/browser/view/ERR13337211>

Assembled genome

https://www.ebi.ac.uk/ena/browser/view/GCA_965120235

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REFERENCES

- Bolger, A. M., M. Lohse, and B. Usadel. 2014. “Trimmomatic: A Flexible Trimmer for Illumina Sequence Data.” *Bioinformatics* 30 (15): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
- Chikhi, R., and P. Medvedev. 2014. “Informed and Automated k -Mer Size Selection for Genome Assembly.” *Bioinformatics* 30 (1): 31–37. <https://doi.org/10.1093/bioinformatics/btt310>.
- Jackman, S. D., B. P. Vandervalk, H. Mohamadi, J. Chu, S. Yeo, S. A. Hammond, G. Jahesh, et al. 2017. “ABYSS 2.0: Resource-Efficient Assembly of Large Genomes Using a Bloom Filter.” *Genome Research* 27 (5): 768–77. <https://doi.org/10.1101/gr.214346.116>.
- Martinez, Q., J. Clavel, J. A. Esselstyn, A. S. Achmadi, C. Grohé, N. Pirot, and P.-H. Fabre. 2020. “Convergent Evolution of Olfactory and Thermoregulatory Capacities in Small Amphibious Mammals.” *Proceedings of the National Academy of Sciences* 117 (16): 8958–65. <https://doi.org/10.1073/pnas.1917836117>.
- Nores, C. 2007. “Desmán ibérico – *Galemys pyrenaicus*.” In *Enciclopedia Virtual de los Vertebrados Españoles*, edited by A. Salvador and I. Barja. Museo Nacional de Ciencias Naturales.
- Quaglietta, L., J. Gisbert, R. García-Perea, and A. Fernández-González. 2024. “*Galemys Pyrenaicus*.” *The IUCN Red List of Threatened Species 2024*.
- Rutovskaya, M., A. Gazzard, and S. T. Turvey. 2023. “*Desmana Moschata*.” *The IUCN Red List of Threatened Species 2023*.
- Rutovskaya, M. V., A. N. Aleksandrov, V. N. Podshivalina, A. S. Soboleva, and O. V. Glushenkov. 2020. “Habitat Conditions of *Desmana Moschata* (Talpidae, Eulipotyphla, Mammalia) in the Buffer Zone of the Prisurskiy State Nature Reserve (Russia).” *Nature Conservation Research* 5 (2): 36–46. <https://doi.org/10.24189/ncr.2020.011>.
- Wilson, D. E., and R. A. Mittermeier. 2018. “Insectivores, Sloths and Colugos.” In *Handbook of the Mammals of the World*, 8:709. Lynx Editions.