



Conference Abstract

# Building a genome reference database for Bulgarian biodiversity - highlights from the GenBul project

Stefaniya Kamenova<sup>‡,§</sup>, Salza Palpurina<sup>§</sup>, Todor Karakiev<sup>§</sup>, Georgi Kunev<sup>l</sup>, Nadejda Apostolova<sup>§</sup>, Snežina Popova<sup>§</sup>, Albena Gjonova<sup>l</sup>, Ilija Gjonov<sup>l</sup>, Radost Angelova<sup>l</sup>, Monica Pramatarova<sup>l</sup>, Stanimira Deleva<sup>§</sup>, Vladimir Vladimirov<sup>¶</sup>, Stoyan Beshkov<sup>§</sup>, Rostislav Bekchiev<sup>§</sup>, Rumyana Kostova<sup>l</sup>, Ana Nahirić<sup>§</sup>

<sup>‡</sup> BG Bol, Sofia, Bulgaria

<sup>§</sup> National Museum of Natural History, Bulgarian Academy of Sciences, Sofia, Bulgaria

<sup>l</sup> Sofia University, Sofia, Bulgaria

<sup>¶</sup> Institute of Biodiversity and Ecosystem Research Bulgarian Academy of Sciences, Sofia, Bulgaria

Corresponding author: Stefaniya Kamenova ([stefaniya.kamenova@gmail.com](mailto:stefaniya.kamenova@gmail.com))

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## Abstract

With the advancement of high-throughput, cost-effective sequencing, the application of genomic approaches to biodiversity research is becoming increasingly accessible and inclusive. As the availability of a reference genomes database is indispensable for genomics research, a recent pan-European effort - the European Reference Genome Atlas (ERGA) - was established to scale up the generation of high-quality reference genomes for European eukaryotic biodiversity. Here, we report the results from the GENBUL project, funded by the EU Horizon Europe BGE-ERGA Consortium to support the sampling of reference genomes from biodiversity hotspots in Bulgaria. Focusing on two key biodiversity areas, Slavyanka and Southern Pirin mountains (including the Nature Reserve "Alibotush") and the Strandzha Nature Park, we successfully sampled 190 plant and insect species, including several Bulgarian and Balkan endemics. This effort represents the first major effort for broader-scale genome referencing from Bulgaria

and makes an important contribution towards local capacity-building in biodiversity genomics. However, considering the complexity of the genome sampling workflows, standards and metadata management, the GENBUL project also enabled to pinpoint major challenges, currently hindering the deployment of large-scale reference genome sampling in Bulgaria. Based on this experience, we outline key capacity, knowledge and research culture barriers faced by Bulgarian scientists and make recommendations to the international genomics research community for mitigation actions, also applicable to other Southeast European countries.

## **Keywords**

Genomics, biodiversity hotspots, reference genome, European Reference Genome Atlas, Bulgaria

## **Presenting author**

Stefaniya Kamenova

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## **Conflicts of interest**

The authors have declared that no competing interests exist.