The New GGBN Data Portal and GGBN Stable Identifiers

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Abstract

The Global Genome Biodiversity Network (GGBN) Data Portal plays an important role in the global biodiversity informatics infrastructure by providing standardized access to 3.8 million DNA, tissue, and environmental samples as well as 2.4 million associated vouchers and cultures from 39 repositories. In addition, more than 3.5 million references to sequence data can be derived from these records and are accessible through the GGBN Data Portal. By making all these resources available in one portal, GGBN is bridging the gap between sequences, samples and vouchers based on well curated physical collections.

In order to increase the usability and interoperability of GGBN data, stable identifiers have been developed based on the Consortium of European Taxonomic Facilities (CETAF) stable identifiers (Güntsch et al. 2017). Each GGBN stable identifier represents a physical object in our member collections, e.g., a sample or voucher.

The landing pages for these identifiers will be embedded in a new version of the GGBN Data Portal, which will be launched by the end of 2024. The portal underwent a complete redesign of the user interface, especially the search and members pages. In addition to the stable identifiers, it will then also be possible to search across all four major GGBN resources (data portal, registry, document library, and wiki). This, in particular, will facilitate the access to information on biobank management, Access and Benefit Sharing, tutorials as well as GGBN conference presentations (Figs 1, 2, 3).
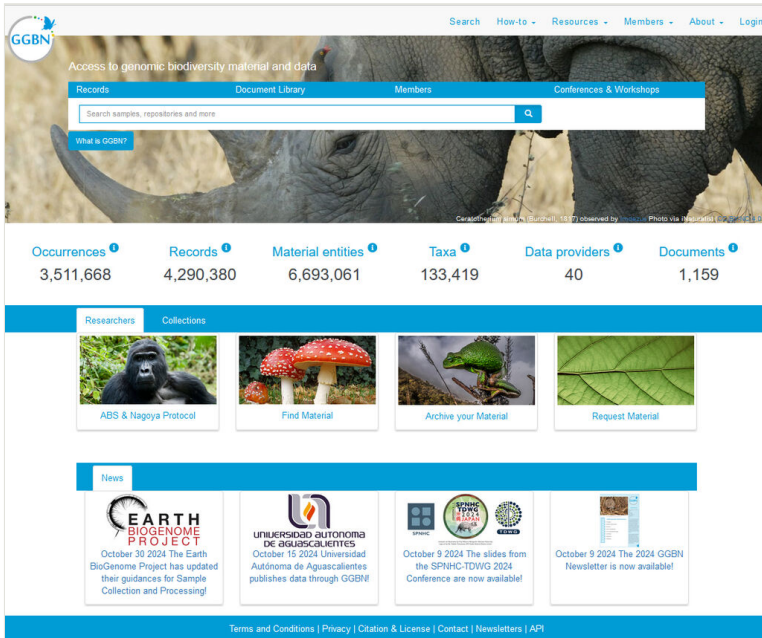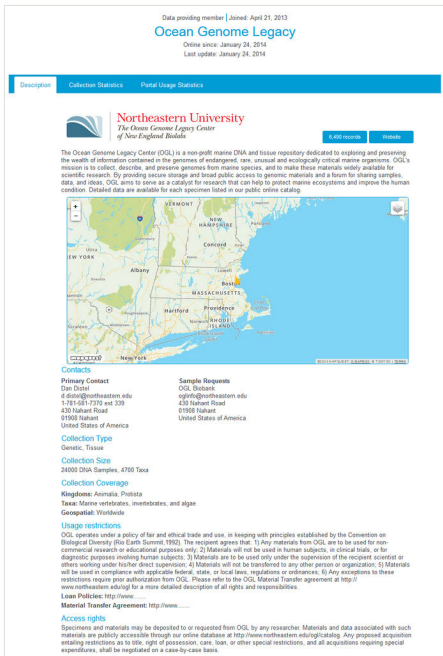
Figure 1.

Landing page of the new GGBN Data Portal.

Figure 2.

Example of the new GGBN members pages.

Figure 3.

Example how the GGBN Stable Identifiers will be displayed and used in the European Nucleotide Archive (ENA) portal.

In this presentation we shared information on the new GGBN Data Portal as well as how the GGBN stable identifiers are structured and their future potential use to enrich data in other infrastructures such as the European Nucleotide Archive (ENA).

Keywords

cross-references, genetic samples, data infrastructure

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Conflicts of interest

The authors have declared that no competing interests exist.

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