



# DSMZ - the German GBIF node for prokaryotes and viruses: linking data on living biological material to GBIF



Kracht, M. and Naumovs, A.

HOME | GBIF | BROWSE TAXONOMY | SEARCH | DATA PROVIDERS | COUNTRIES | DATA USE | BACK

**GBIF**  
Prototype data portal  
Global Biodiversity Information Facility

**Data provider: DSMZ**

Description: <http://www.dsmz.de/>  
E-mail: [contact@dsmz.de](mailto:contact@dsmz.de)

**Service: German collection of microorganisms and cell cultures (DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen)/microorganisms (www2.dsmz.de)**

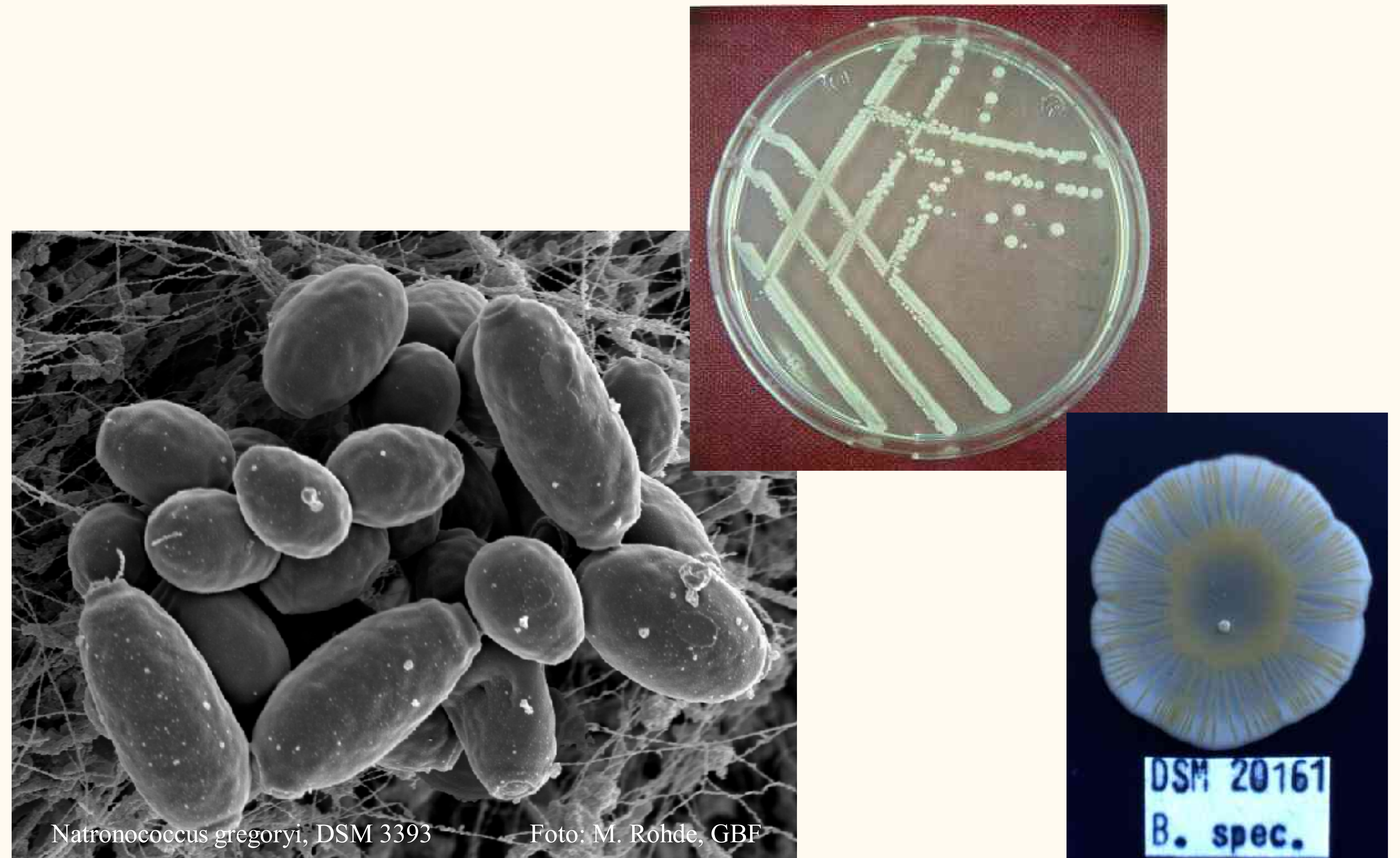
Type of data: Specimen/observation  
Description: ABCD provider of German collection of microorganisms and cell cultures (DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen)/microorganisms  
Access point (BioCAsE): <http://www2.dsmz.de/biocase/databases/microorganisms/dbwrapper.py>

**Resource: German collection of microorganisms and cell cultures (DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen)**

Description: German collection of microorganisms and cell cultures (DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen)

Contact: Dr. Manfred Kracht  
E-mail: [contact@dsmz.de](mailto:contact@dsmz.de)  
Number of records indexed: 10030  
Taxon count: 3854 - [Browse taxonomy](#) - [List taxa](#)

[Contact info](#) | [Webmaster](#)



## ABCD version 1.49d (excerpt for microbial culture collections)

```

CultureCollectionUnit 0/1 cml-type [CultureCollectionUnit]
  OrganismType 0/1 smpl-type [String]
  InfraspecificName 0/1 smpl-type [String]
  CultureNames 0/1
    CultureName 0/∞ cml-type [StringL]
      language [optional]
  Serovar 0/1 smpl-type [String]
  Mutant 0/1 smpl-type [String]
  Genotype 0/1 smpl-type [String]
  GrowthConditions 0/1 cml-type [StringL]
    language [optional]
  GrowthConditionAtomised 0/1
    CultureMedium 0/1 cml-type [StringL]
      language [optional]
    Aerobicity 0/1 cml-type [StringL]
      language [optional]
    Temperature 0/1 xtnd-W3C [xs:string]
    TemperatureType
  References 0/1
    Reference 0/∞ cml-type [Reference]
  FormOfSupply 0/1 cml-type [StringL]
    language [optional]
  Applications 0/1 cml-type [StringL]
    language [optional]
  Hazard 0/1 cml-type [StringL]
    language [optional]

```

## Extract of the DSMZ wrapper

```

<Concept>
/DataSets/DataSet/Units/Unit/Identifications/Identification/TaxonIdentified/ScientificNameAtomized/Bacterial/SpeciesEpithet
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/Identifications/Identification/TaxonIdentified/ScientificNameAtomized/Bacterial/Subgenus
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitCollectionDomain/CultureCollectionUnit/Aerobicity
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitCollectionDomain/CultureCollectionUnit/CultureMedium
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitCollectionDomain/CultureCollectionUnit/Temperature
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitDigitalImages/UnitDigitalImage/ImageIPR/LegalOwner/Organisation/OrganisationCodes/OrganisationCode
</Concept>
<Concept>/DataSets/DataSet/Units/Unit/UnitID/</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitStateDomain/SpecimenUnit/Accessions/AccessionDate
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitStateDomain/SpecimenUnit/Accessions/AccessionNumber
</Concept>
<Concept>
/DataSets/DataSet/Units/Unit/UnitStateDomain/SpecimenUnit/NomenclaturalTypeDesignations/NomenclaturalTypeDesignation/TypeStatus
</Concept>
<SupportedSchemas>
</SupportedSchemas>
</content>

```

## Providing DSMZ data for the BioCAsE protocol

The BioCAsE protocol is used for the DSMZ data together with the ABCD schema as the data bearing schema.

Based on the XML technology, standards have been developed to exchange structured data and to present it to the users.

The wrapper software (XML/CGI interface to heterogeneous databases) needs a mapping of the database schema to the XML concept.

The DSMZ database is based on the MINE (Microbial Information Network Europe) format which was developed about 15 years ago.

The original database definition comprises about 160 fields which cover all aspects of taxonomy, strain administration, culture conditions, morphology, physiology, and applications. This format has been used by the EU project CABRI (Common Access to Biotechnological Resources and Information, [www.cabri.org](http://www.cabri.org)) to define the minimum standards of culture collections with respect to agreed data input rules and authentication procedures. The so called Minimum Data Set (MDS) is the set of data which is required for each culture from each collection. The Recommended Data Set (RDS) contains additional fields for which data should be delivered. Collection centres are free to provide data for other fields, which are part of the Full Data Set (FDS).

The current ABCD schema (version 1.2) is not able to provide definitions for all MDS fields; but the draft version 1.49 has been extended with regard to collections holding living material. Consequently, together with already existing fields, it is possible to provide data of the MDS for the GBIF project.

It would be highly recommended to supplement further ABCD versions with at least 20 fields of the FDS, mainly information on growth conditions, physiology, applications, and biological interactions.