

Fields Specifications for Aggregate BRC Information Standard

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The present work outlines the initial version a standard reflecting strain data for different groups of microorganisms (fungi, bacteria, microalgae, etc.) and focuses on the arrangement and grouping of information pertinent to isolation source, growth conditions, biological interactions, enzyme production, practical application, etc.

In arranging the information we tried to use the experience accumulated in development of such standards as ABCD, Darwin Core, MINE, OECD/CABRI Minimum Dataset / Recommended Dataset / Full Dataset.

It is to be hoped that the proposed standard may facilitate the creation of catalogues for BRCs and culture collections and assist the construction of aggregated data bases to be employed in WEB request system such as GBRCN, WDCM or BRIO, being able to answer a wide spectrum of reasonable questions in areas such as microbiology, biotechnology, agriculture, medicine, etc.

The success of operation of such a system heavily depends on maximal clarity in the description of content in all the standard's fields. Following the general trend of preexisting microbiological standards, we expect the titles and content of the recognized fields to be thematically focused as follows:

1. Field's name.
2. Short description of the content.
3. Specification of the content.
 - 3.1. Detailed description of the content, difference from the other fields that may look similar.
 - 3.2. List of subfields and their descriptions.
 - 3.3. Specification of the coding for the field and subfields.
 - 3.4. The list of possible values related to the field (if short) or a reference to a file with long list, reference to thesaurus, or reference to ontology.
 - 3.5. Reference to a manual which describes this field content.
 - 3.6. Reference to external standard used for this field.
 - 3.7. Samples of correct coding for this field.

Description of each subfield is assumed to follow the same schema.

An obvious barrier for the future development seem to be the inconsistency of the previous microbiological standards with the new ones focused on genetic information, such as MIMS / MIGS of the GSC consortium. One of the approaches toward harmonizing them might be the inclusion of subfields dealing with functional genes in some phenotype-related sections, for example, "enzymes".