THEME 3

- **Create strain collections of all identifiable species (freely available)**
- **Agreed reference methods, systems and standards**

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Strain collections, some examples

Common Access to Biological Resources and Information (CABRI)

- Total : 140,000 strains
- BCCM (Belgium).
- CABI (UK).
- CBS (Netherlands).
- CRBIP (France).
- DSMZ (Germany).

European Culture Collections' Organisation (ECCO)

- Total : 350.000 strains (including Cabri)
- 61 members from 22 European countries.

Other national / international / private collections

USA 18,000 strains

Japan 12,000 strains

France & USA 100,000 strains

- Every collection is specific
- Building and maintaining a collection is a multi-year and costly effort
- Totally free access to those collections is unlikely
- A low fraction of bacteria is cultivable : combined culturomics / metagenomics

Data bases, some examples

silva
high quality ribosomal RNA databases

Germany, 5.7 Mseq.
Free for academic users

GREENGENES
The 16S rRNA Gene Database and Tools

USA, *x* Mseq
Attribution-ShareAlike 3.0 Unported

NCBI RefSeq

USA, 45 non-redundant kseq.
Open

EZ BioCloud

Korea, 82 kSeq
Open for academics

rdp

USA, 3.4 Mseq
Attribution-ShareAlike 3.0 Unported

EMBL-EBI

BBSRC
bioscience for the future

RNAcentral

42 Expert Databases

enterome

BIOMÉRIEUX
PIONEERING DIAGNOSTICS

Proprietary and internal databases

- Very diverse in contents, level of curation, metadata, etc.
- Mainly isolated microorganisms, much less real microbiome samples
- Often poorly populated below the level of species
- Poor coverage of the “microbial dark matter”
- More and more coupled with (on-line) analysis tools
- Frequent upgrades impact reproducibility
- Multiple taxonomies
- Different licensing regimes

Ongoing efforts to standardize

Efforts to standardize protocols for metagenomics, including sample collection, nucleic acid extraction, library preparation, sequencing, and computational analysis are underway. Examples:

- Microbiome Quality Control (MBQC)
- Genome Reference Consortium (GRC)
- International Metagenomics Microbiome Standards Alliance (IMMSA)
- Critical Assessment of Metagenomics Interpretation (CAMI)
- International Human Microbiome Standards (IHMS) (→2015)
- and others.

Needs and Rationale

Access to relevant **collections / databases / tools** is key for the development of any application. The medical nature of a future IMI microbiome program should impose higher quality standards.

Beyond meta-genomics, other fields and corresponding databases should be considered :

- meta-proteomics, meta-metabolomics
- application driven databases (*e.g.* dietary data, resistome, virulome)

Like in theme 2:

Robustness, reproducibility, automated quality indicators for **end-to-end workflows** are key features to pave the way for **standardization** and market access.

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Need for public-private collaborative research

Identical to theme 2

Depending on the application, numerous features can be optimized :

- **fundamental performances** (*e.g.* sampling, sensitivity, specificity, speed).
- **global functionalities** (*e.g.* traceability, reproducibility, controls, ergonomics).

Double advantage of working in a public-private collaborative setting :

1. it offers the possibility to **assemble the best bricks** coming from the two communities in order to build the best tools.
2. it allows **extensive testing** in various and demanding conditions of any new piece of software of interest.

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Objectives, deliverables

Overall objectives

This theme is designed as a **generic and enabling set of tools** for any study related to microbiome, allowing scientists to focus on their specific applicative objectives.

Medical (or nutrition) applications are the final objective, implying more stringent quality requirements than usual.

Suggested key deliverables

- Construction and/or access to **specialized and curated biological and digital collections**, under clear IP terms.

Common to themes 2 and 3 :

- Guidelines, validated protocols and pipelines, possibly **standards** for microbiome-based and omics studies.
- **Benchmark exercises.**

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Open questions

- Collections : do we really want to *create* new strain collection(s) ?
- What about *sample* collections ? Useful ? Technically and legally feasible ?

Like in theme 2 :

- Meta-genomics only ? Meta-proteomics / meta-metabolomics ? Others ?

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Thank you

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