

Metagenomic characterization of the MELiSSA waste degradation compartment (C1)

Key words: Microbial community, metabolic pathways, metagenome, mathematical modelling

Abstract: The MELiSSA loop, as a regenerative life support system, is designed to allow the recovery of human metabolic needs from the space mission wastes. Within the MELiSSA loop, the waste compartment, (i.e. C1), is responsible of the primary degradation of the waste material generated by the crew, to shorter molecules, ideally : CO₂, NH₄⁺,...

In order to respect robustness and safety requirements, the project follows a deterministic engineering approach. The associated approach is only possible through a deep knowledge of each sub-system (e.g. composition, behaviour, metabolism, kinetics, limitation, inhibition, etc..). Due to its complex microbial community, the development of the C1 model requires: - (i) the thorough characterization of the microbial community, - (ii) the elucidation of a validated metabolic network, - (iii) the identification of key microbial species and functions, - (iv) the definition of the driving metabolic reactions rates and associated parameters (performed by the key microbial species/functions) and -(v) the integration into a suitable mechanistic dynamic model that describes and predicts the conversion processes.

In a preliminary study, multiple “omic” approaches (genomic, transcriptomic, proteomic..) have been applied to characterize the C1 community in terms of taxonomy and functions resulting in the preliminary definition of microbial network. The proposed PhD project shall use meta-omics approaches to validate 1°) this preliminary microbial network, 2°) the corresponding metabolic pathways and 3°) the identified key species/functions/biomarkers of C1.

The C1 community metabolic model shall be further studied to allow to link any change in reactor performance and community/functional composition to changes in the C1 metabolome and hence in microbial metabolic pathways. A validated C1 community metabolic model, which indicates the metabolic interactions between species and/or functional groups, will be defined in a view of the future development of the C1 mechanistic model.

Impact on MELiSSA: definition of C1 community metabolic model and elaboration of C1 mathematical model equations

MELiSSA partners: U Mons (B), SCK.CEN (B), UClermont Auvergne (F), .

References:

Poughon, L.; Creuly, C.; Farges, B.; Dussap, C. G.; Schiettecatte, W.; Jovetic, S.; De Wever, H. (2013) Test of an anaerobic prototype reactor coupled with a filtration unit for production of VFAs, *Bioresource Technology*, 145, 240-247.

Desired knowledge: candidates preferably possess a degree in microbiology and molecular biology. They have to be familiar with anaerobic microbiology and metabolic pathways, bioinformatics and have notions of process engineering.