## Mathematical modelling of DNA repair of MELiSSA strains when exposed to cosmic radiations Beyond Earth Orbit.

Key words: Cosmic radiation, DNA repair, mathematical modelling

Abstract: The MELiSSA loop as a regenerative life support system has to maximize the recovery of the main elements from the mission wastes. Although the MELiSSA gather a large number of processes and technologies, part of these processes are biologically based and consequently more sensitive to radiations. The genetic/transcriptomic/proteomic stability of MELiSSA strains (Arthrospira platensis, nitrifying bacteria, plant-growth promoting bacteria) is of paramount importance to detect any metabolism drift linked to potential surges of cosmic radiations in spaceflights and planetary stations and to check the linked process robustness. Up to now, the understanding of DNA repair and its associated mathematical modelling has been poorly investigated.

This PhD work mainly concerns prokaryotes, and will first focus on the study, evaluation and trade-off mathematical methodology to understand and predict DNA repair.

- Badri H, Monsieurs P, Coninx I, Wattiez R, Leys N (2015) Molecular investigation of the radiation resistance of edible cyanobacterium Arthrospira sp. PCC 8005. MicrobiologyOpen. doi:10.1002/mbo3.229
- Chain P, Lamerdin J, Larimer F, Regala W, Lao V, Land M, Hauser L, Hooper A, Klotz M, Norton J, Sayavedra-Soto L, Arciero D, Hommes N, Whittaker M, Arp D (2003) Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea. J Bacteriol 185 (9):2759-2773
- Janssen PJ, Morin N, Mergeay M, Leroy B, Wattiez R, Vallaeys T, Waleron K, Waleron M, Wilmotte A, Quillardet P, de Marsac NT, Talla E, Zhang CC, Leys N (2010) Genome sequence of the edible cyanobacterium Arthrospira sp. PCC 8005. J Bacteriol 192 (9):2465-2466. doi:10.1128/jb.00116-10

MELISSA Partners: UClermont Auvergne (F), SCK.CEN (B), U Mons (B)

## Impact on MELiSSA:

This study is the first step of safety studies related to genetic elements. It will allow a preliminary risk evaluation

**Desired knowledge**: Candidates preferably possess a degree in mathematics, biology, chemistry or bioengineering with experience in genetics and molecular biology. They have to be familiar with genomic (trancriptomic, proteomic) databases and annotation platforms.