

## **Current trends in environmental microbiome amplicon sequencing in the framework of risk assessment - harmonisation strategies**

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### **INTRODUCTION**

The analysis of environmental microbiome structure is now being explored for its possible utility in the framework of risk assessment. Aiming to analyse microbial communities with appropriate tools may also allow for the detection of pathogens. Besides this direct identification, investigating the microbiome structure can also highlight unbalanced community structures or an increase in some defined taxa, possibly indicating the detrimental influence of an external factor like a pollutant or a pathogen. The advent of high-throughput sequencing technologies enabled the development of amplicon sequencing strategies where taxonomically informative sequences are massively sequenced in order to assess the microbial composition of studied samples. This approach involves multiple steps. Different procedures are available for each of them. Recently, a joint project between the Walloon Agricultural Research Center (CRA-W), the Catholic University of Louvain (UCLouvain) and EFSA (GP/EFSA/ENCO/2020/02) has started to inform a possible way forward and includes a work package covered with this poster.

### **METHODOLOGY**

In order to use amplicon sequencing of environmental microbiomes as a tool for risk assessment (e.g. under EFSA's remit), a review of the scientific literature has been carried out to highlight current trends in the field. In addition, particular attention has been paid to possibilities to harmonise methodologies. Relevant initiatives already underway are reported.

### **RESULTS**

Studies identified following the literature review showed that the ways chosen for studying environmental microbiome structure through amplicon sequencing are very diverse. Despite some similarities like the barcode sequences targeted to study the different microbiome populations, other steps in the workflow revealed a very high heterogeneity among studies, like for the bioinformatics processing of sequencing data. Two major initiatives (i.e. the

Australian Microbiome Initiative and the Earth Microbiome Project) attempting to characterise microbial diversity from different ecosystems were highlighted. Interestingly, one of their major concerns is the development of standardised protocols so that every study carried out in their framework uses these harmonised procedures to provide results that can be easily compared.

## DISCUSSION

When aiming for the use of amplicon sequencing as a tool to analyse environmental microbiomes in the framework of risk assessment, comparing results from different situations and different studies is unavoidable. To do so, as a great heterogeneity has been highlighted in the way to produce results, it is crucial that analysis workflows use harmonised procedures to be able to perform relevant comparisons. In this regard, some initiatives are already underway in the field and it would be interesting to take advantage of their harmonisation efforts to evaluate how they can be integrated in a risk assessment approach.