

# STUDY OF THE EVOLUTION OF MICROORGANISMS COMMUNITIES IN AN AQUAPONIC SYSTEM OVER THE COURSE OF A FULL LETTUCE GROWTH CYCLE

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## Introduction

Aquaponics is a combination of recirculating aquaculture and hydroponics techniques that enables the recycling of the nutrient-enriched aquaculture effluents whilst at the same time avoiding the use of mineral fertilisers for the growth of plants. Aquaponics is also a system based on a fragile equilibrium between 3 groups of living organisms i.e. fish, plants and microorganisms. Except for the nitrification process, little is currently known on the roles and properties of these microorganisms and even less when it comes to the bacteria and fungi which may be involved in plant beneficial interactions. The nitrification process is crucial in aquaculture and has therefore been studied in depth. The principal bacteria involved in the transformation of ammonia to nitrite are *Nitrosococcus*, *Nitrosospira* and *Nitrosomonas* while the bacteria responsible for the conversion of nitrite to nitrate are *Nitrobacter*, *Nitrospira* (Rurangwa and Verdegem, 2015), *Nitrococcus* and *Nitrospina* (Itoi et al., 2007). The aim of this work is thus to thoroughly study the microorganisms communities harboured by the closed-loop aquaponic system of Gembloux Agro-Bio Tech throughout a full lettuce cycle, in real conditions. To this end, high throughput sequencing is used to sequence microorganisms' DNA and bioinformatics tools are then used to assign taxonomic identification. Gaining a better understanding of the role of microorganisms in aquaponics could help foster the development of more viable and productive systems.

## Material and methods

A first experiment was conducted between the 5<sup>th</sup> and 19<sup>th</sup> of May 2017 in the PAFF Box aquaponic system (Delaide et al., 2017) in Gembloux Agro-Bio Tech, which was at the moment hosting a variety of plants in the greenhouse compartment and Nile tilapias (*Oreochromis niloticus*) in the tank compartment. One sump sample and one biofilter sample per week were collected in the system. Bacterial DNA was then extracted from the samples and the 16S rRNA gene was sent for Illumina sequencing. The aim of this first trial was to gain a first insight of the evolution of the bacterial communities in our aquaponic system. To obtain a more in depth view, a second experiment was launched in 2019. 90 lettuces (*Lactuca sativa* var. Lucrecia) were sown on the 27.02.19 in rockwool plugs and were then transferred in the floating raft compartment of the PAFF Box (Delaide et al., 2017) aquaponic system on the 11.03.19. The system was at the moment hosting 34 Nile Tilapias (*Oreochromis niloticus*). Microbiota samples were collected twice per week during the first three weeks and then once per week during the last three weeks. Samples were harvested from the sump, the biofilter, the roots' rhizoplane and the roots' endosphere. DNA was then extracted with the FAST DNA

Spin Kit (Mp, Biomedicals) and is currently being sequenced on an Illumina MiSeq machine. Data will be analyzed with the QIIME 1.9.1 program (Caporaso et al., 2010).

## Results and discussion

The results of the first experiment showed that there seemed to be different communities harboured in the sump and in the biofilter with the biofilter community being significantly more diverse. No significant difference was observed in any community over the course of the three weeks.

Results from the second experiment are now awaited to answer our new hypotheses:

- Can we observe changes in the composition of the microbial communities when the aquaponic system is relaunched after the winter break?
- Do the bacterial AND fungal communities evolve over the course of a complete lettuce cycle of 6 weeks?
- What is the composition and the evolution of the microbial community present on the lettuces' roots?

## References

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