



Webinar Q&A

Holobionts and microbial flux within agri-food systems?

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Presenters:

- Emmanuelle Maguin (Holoflux Program Directorate, INRAE, FR)
- Manuel Blouin (Agroecology unit, INRAE, FR)
- Claire Rogel-Gaillard (Animal Genetics and Integrative Biology unit, INRAE, FR)

The webinar recording is available on the Phytobiomes Alliance YouTube channel at <https://youtu.be/CLdgp48vxEE>

Question answered by Manuel Blouin:

Concretely can you explain how you transfer the selected microbiota to the next generation ? What about the microbiota attached to roots ?

The full description will be published soon. A similar (but slightly different) protocol is described in Panke-Buisse et al. 2015 ISME Journal

I would like to know if similar studies have been performed to stabilize microbiota from the phyllosphere

Not to my knowledge.

I would like to read some papers related to your work. Is it possible if you could suggest some?

You can find: Blouin et al. 2015 Ecology Letters and Raynaud et al. 2019 Frontiers in Ecology and Evolution

Do you know if the microbes evolve in your experiment, or if the effect that you see is just driven by the ecological dynamics (changes in species abundances)?

No ways to know. It is clear that changes in species abundance occurred, but it could be either a cause or consequence of genetic changes at the individual level.

Question answered by Claire Rogel-Gaillard:

How we can differentiate between dynamic and mature stable microbiota in pigs?

Thanks for the question. I agree that it is not so easy to well define a "dynamic stability". We have to distinguish the stability linked to the microbial species and strains that are present (who is there) and the stability linked to the relative abundance of each microbial species. I would say that microbial diversification in early age contributes to shape the ecosystem by stabilizing quite early who is there and should remain present over life. The relative abundance of each species fluctuates according to environmental conditions, feed, etc. These fluctuations are dynamic and may lead to dysbiosis in cas of strong disequilibrium. During ageing and due to accumulations of

adaptive responses, microbial species may appear or disappear, thus adjusting and maturing the microbiome.

re: Enterotypes: the scatterplot makes it look like it's not so much 2 enterotypes as a continuum between two poles. How arbitrary is the cutoff between the two?

The method optimizes the number of clusters. Stratification of 60-day-old piglets in two main enterotypes has been published by Ramayo-Caldas et al. (2016, ISME Journal, 10(12):2973-2977). The method is based on the publication by Arumugan et al. (2011, Nature 473: 174–180). The relative abundances of OTU annotated to the genera Prevotalla, Mitsuokella, Ruminococcus and Treponema are statistically different between the two enterotype-based pig groups. However, I agree that some individuals seem to be inbetween the two groups.

Could you please specify how you calculated heritability in your experiment?

We use the relative abundance of genera as phenotypes. In the model, we included sex and animal batch as fixed effect.

