



Webinar Q&A

Circles H2020: Can natural microbiomes be exploited for more sustainable, safe, productive and nutritious food production?

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The webinar recording is available on the Phytobiomes Alliance YouTube channel at <https://youtu.be/yLJgmQwj-1w>

Question regarding labels: do you mean listing microbiome inside of the fruit/vegetable? Because I do not know how practically you can ensure stability of microbiome on the surface of fruit/vegetables (during harvesting, handling during transport, washing before consuming, etc).

MTLs/ Microbiome transparent labels will provide the consumer with information on the microbiome regarding if a plant has been grown with a microbiome that has enhanced the quality of the plant (higher nutrient content for example) or contains microorganisms within the tissue that may benefit human health. Although with some inevitable degree of uncertainty, microbiome will be monitored also at the processing stations providing some insights into its dynamic on the food products.

What happens if you detect human or plant pathogens in the core microbiome?

CIRCLES includes partners which are established food producers. These companies already have stringent protocols and quality guidelines with the food they produce to detect pathogens and, as is already the case, food that does not meet these rigorous standards will not be available for human consumption.

How big sample size (how many plant per hectare) should be tested to be representative for the whole field? (in regard to field uniformity/variability)?

These are actual farm and the size of the field varies. However, we have a minimum of 50 samples/field (i.e., individual spinach plantlets with root and rhizosphere) collected across the "diagonal" of the field.

How did you choose your food systems?

The food systems were selected based on their relevance to the European economy and how much are sold. Spinach and tomato were chosen because they are often eaten raw in addition tomato is a core food product in Europe and spinach is often frozen, so this gives an opportunity to track microbiomes through different manufacturing processes.

Are you analyzing microbiota with OTU or sequence Variants?

Historically, in line with others in the field at the time we used OTUs. However, we have shifted to the use of ASVs using SILVA 138 in line with the movement of the research field.

Are you planning co-occurrence network analyses to identify hub taxa linked to particular traits (yield, agronomic practice...)?

A combination of 16S, ITS and functional metagenomics will be used to identify taxa and function that is common and differentiated between several factors including yield, resistance to disease, nutritional content etc.

If I understood right, you characterized the core microbiota of tomato plants. Does it mean you have identified a core tomato microbiota that promotes health in tomato plants? If we want to test the effect of the core microbiota you have characterized, can you for example provide a synthetic mix (SynComs) of them?

We haven't yet identified a core tomato microbiota, but we have identified a preliminary core spinach microbiota. However, it will require additional sampling seasons to verify this and it will be important to explore conserved functionality within this data too to elucidate the relevance of this observation.

Given plant microbiomes may be compromised by environmental stresses, would microbes introduced to plants in these environments actually survive in natural conditions?

That's the big question. It's quite common for inoculants to fail to thrive in the natural environment vs laboratory conditions. However, due to the work with several agrotech companies, combined with scientific observation and knowledge this puts us in a strong position to create treatments that can persist or complement the existing microbiota. In addition, the treatments being explored are also bioboosters that may naturally enhance the existing soil microbiota without the requirement for inoculants.

Which interventions can be done to improve the quality of soils? Add biofertilizers? Add other type of compounds to modify the composition of the soil microbiota? others?

Planning crop rotations with long gaps between crops combined with intercropping - particularly with legumes is a good way to improve soil health. Emphasis on crops that increase the organic matter of soil also helps to enrich the natural microbiota.

Which considerations you may take into account about the impact on the soil ecology when developing a new product based on biofertilizers?

Our hypothesis is that differences in crop productivity and soil fertility are dictated by a "disbiosis" of the microbiota (due to e.g., the history of the field and/or a plant genotype not capable of recruiting probiotic members of the microbiota): put it simply we will select inoculants that, from taxonomy and functional point of view, complement what is "missing" in problematic fields compared to "healthy" ones. We believe this type of intervention will be less impacting (than just an inoculation per se) on the endogenous soil biota.

What characterizes the core microbiome? What specific taxonomic bacteria and fungi are found in the core microbiome?

At the moment the core spinach microbiome data is very provisional as further sampling seasons, ITS and metagenomics must also be incorporated in to the data set. However, what we can see emerging is that at phylum level almost 50% of the core microbiota is represented by Gammaproteobacteria, followed by Bacteroidia, Alphaproteobacteria, Actinobacteria and Verrucomicrobiae. This encompasses at genus level Flavobacterium, Massilia, Rhizobium, Variovorax, Devosia, Pedobacter, Pseudomonas, Acidovorax, Sphingomonas, Streptomyces and around 20% unknown genera.

