

Next Generation Sequencing (NGS) for mycobiota analysis :

ECMM survey on goals and practices in european labs

& implementation of clinical studies

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While surveys on the mycobiota are more rare than bacterial microbiota investigation, NGS is an increasingly affordable and disposable technique in many european laboratories. It has been shown that diversities of mycobiome in various sites vary in different populations and conditions, for example according to the stages of diseases or the medications taken. Thus, it is probable that such investigation will become in the near future part of the diagnosis and management of many diseases. However, the wide domain of indication and diversity of the techniques used may alter comparisons and data interpretation.

The objectives of this study group are :

1/ to draw a picture of the use of NGS for mycobiota investigation in european labs in 2017

2/ to initiate a multicenter prospective analysis on the impact of this new tool on the management of the patients

3/ to organize a symposium during the TIMM 2019 in Nice

ECMM survey on goals and practices in european labs

Your country:

What is the City of your lab:

1. For you, the goals of using NGS to study the mycobiota are to:

- understand the pathophysiology of a dysbiosis
- contribute to a diagnosis
- implement a therapeutic strategy
- investigate an epidemy
- evaluate the exposome

2. Is NGS used in your routine practice: Yes or No

If yes, NGS is used in order to :

- contribute to a diagnosis
- implement a therapeutic strategy
- investigate an epidemy
- evaluate the exposome

3. Which Mycobiota site are you studying or plan to study:

- Lower respiratory tract
- Digestive tract
- Oral cavity
- Skin
- Environmental samples : please cite (air, water, other...)
- Other :

4. Regarding Lung, which diseases are concerned :

- Cystic fibrosis
- COPD
- Asthma
- Lung transplantation
- Pneumonia
- Other :

5. Regarding digestive tract which diseases are concerned:

- Crohn disease
- Chronic ulcerative colitis
- Pseudomembranous colitis (*Clostridium difficile colitis*)
- Other :

6. Other systemic diseases :

- Rheumatoid polyarthritis
- Diabetis mellitus
- AIDS
- Other :

7. Samples used for NGS processing

- Oral wash
- Sputum
- Broncho-alveolar lavage
- Stools
- Skin sample
- Environmental sample: please cite

8. Target used for the mycobiota :

- 18S rRNA
- ITS
- 18S rRNA + ITS

9. Do you consider that bacterial microbiota must be associated when studying the mycobiota:

- yes
- no

10. Do you use propidium monoazide pretreatment

- yes
- no

11. Data analysis

- reads shorter than 150 bases are not analysed
- Genbank database used for alignments
- CBS database used for alignments
- Both Genbank and CBS databases used for alignments
- Other databank

12. Are you interested in participating to an European study group : Yes - No

If yes :

- on the lung site
- on the digestive site?

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Projects of multicentre studies

With this working group, we aim at developing this emerging research field and setting-up large studies to decipher the relationship between microbial populations, organ inflammation and other covariates. Altogether, this working group will support mycobiota research development that will certainly call for a renewal of our understanding and management of numerous chronic diseases and will identify the research teams that may interact and be involved in multicenter prospective studies, for example:

- Comparison of the micro/mycobiota in the lung and the environment of asthmatic/cystic fibrosis patients
- Impact of antifungal treatment on the lung micro/mycobiota
- Impact of antibacterial treatment on the digestive micro/mycobiota
- Etc...

A symposium on NGS and the mycobiota will be organized during the TIMM 2019 in Nice.

References

- Riiser A. *The human microbiome, asthma, and allergy. Allergy Asthma Clin Immunol. 2015; 11:35.*
- Nguyen LD, Viscogliosi E, Delhaes L. *The lung mycobiome: an emerging field of the human respiratory microbiome. Front Microbiol. 2015;6:89.*
- Underhill DM, Iliev ID. *The mycobiota: interactions between commensal fungi and the host immune system. Nat Rev Immunol 2014 ; 14 : 405–16.*
- Marsland BJ, Gollwitzer ES. *Host–microorganism interactions in lung diseases. Nat Rev Immunol 2014 ; 14 : 827–35.*
- Dannemiller KC, Mendell MJ, Macher JM, et al. *Next-generation DNA sequencing reveals that low fungal diversity in house dust is associated with childhood asthma development. Indoor Air. 2014;24:236–47.*