



METABAR-FOOD, a project for developing standardized metabarcoding and metagenomic analysis of fermented food

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Meeting on "High-Throughput Technologies Applied to Yeasts"

November 29th and 30th, 2018

Salle Louis Pasteur du Palais Universitaire
9 place de l'Université | 67000 Strasbourg | France

Program

Thursday November 29

9:15 Opening of the meeting by Cécile Fairhead, Université Paris Sud, France

9:30 - 9:55 [Bertrand Séraphin](#), IGBMC, Strasbourg, France [25 min]
Protein interaction in yeast: from high-throughput studies to detailed mechanisms

Session 1 - Genome sequencing, assembly and population analysis

Chair: [Jean-Luc Legras](#)

9:55 - 10:15 [Joseph Schacherer](#), University of Strasbourg / CNRS, France [20 min]
Yeast evolutionary history, natural variation and missing heritability

10:15 - 10:35 [Benjamin Istace](#), Genoscope / CEA, France [20 min]
Oxford Nanopore long reads sequencing and its applications at Genoscope

10:35 - 10:55 [Jonathan Grandaubert](#), Institut Pasteur, Paris, France [20 min]
Long-read sequencing and haplotype determination in *Candida albicans*

10:55 - 11:15 [Bart Theelen](#), Westerdijk Fungal Biodiversity Institute, Netherlands [20 min]
Malassezia genomics and hybridization

11:15 - 11:45 Coffee break

Session 2 - High-throughput screening and functional genomics

Chair: [Christophe d'Enfert](#)

11:45 - 12:10 [Josh Bloom](#), UCLA, US [25 min]
From genetic architectures and QTLs to causal variants: large designed crosses and parallel variant engineering in yeast

12:10 - 12:35 [Jolanda Vanleeuwen](#), Université de Lausanne, Switzerland [25 min]
Systematic analysis of genetic suppression interactions

12:35 - 13:00 [Gilles Charvin](#), IGBMC, Strasbourg, France [25 min]
Multiple inputs ensure yeast cell size homeostasis during cell cycle progression

13:00 - 14:30 Lunch

14:30 - 14:55 [Manuel Mendoza](#), IGBMC, Strasbourg, France [25 min]
Anaphase DNA synthesis ensures proper chromosome segregation

14:55 - 15:15 [Daniela Delneri](#), Manchester University, UK [20 min]
Functional analysis of ncRNAs and their genetic interactions in yeast

15:15 - 15:35 [Gianni Liti](#), IRCAN, Université de Nice / CNRS, France [20 min]
A comparative genotype-to-phenotype map from 10000 gametes

Session 3 - High-throughput screening and phenotypic diversity

Chair: [Agnès Michel](#)

15:35 - 16:00 [Yoshi Ohya](#), University of Tokyo, Japan [25 min]
From Genome to Morphology

16:00 - 16:25 [Dawn Thompson](#), Ginkgo Bioworks, Boston, US [25 min]
The synergy of rational design, natural genetic variation and evolutionary engineering in a high throughput biological foundry for industrial yeast strain improvement

16:25 - 16:55 Coffee break

16:55 - 17:20 [Scott McIsaac](#), Calico, San Francisco, US [25 min]
New technologies and strain collections for high-throughput profiling of single-cell aging

17:20 - 17:45 [Ed Louis](#), Leicester University, UK [25 min]
High throughput phenotyping and quantitative genetic analysis in *Saccharomyces* yeasts and hybrids

17:45 - 18:05 [Elodie Caudal](#), University of Strasbourg / CNRS, France [20 min]
Systematic characterization of background specific essential genomic regions in yeast

18:05 - 18:25 [Sergio Tusso](#), Uppsala University, Sweden [20 min]
TBD

Wine tasting party

Friday November 30

Session 4 - Large-scale genome editing in yeast

Chair: [Bertrand Llorente](#)

- 9:00 - 9:25 [Sibylle Vonesch](#), EMBL Heidelberg, Germany [25 min]
Multiplexed precision genome engineering in yeast
- 9:25 - 9:45 [Jing Hou](#), Donnelly Center, Toronto, Canada [20 min]
Conditional gene essentiality and beyond in the *Saccharomyces cerevisiae* species
- 9:45 - 10:05 [Alexandre Chamas](#), INRA, Montpellier, France [20 min]
Engineering of yeast genomes using CRISPR-Cas: principle and recent advances
- 10:05 - 10:25 [Gilles Fischer](#), Paris Sorbonne / CNRS, France [20 min]
Engineering reversible chromosomal translocations and shuffling the *Saccharomyces cerevisiae* genome with CRISPR-Cas9

10:25 - 11:00 Coffee break

Session 5 - High-throughput data analysis, bioinformatics pipelines

Chair: [Anne Friedrich](#)

- 11:00 - 11:20 [Hugo Devillers](#), INRA, Montpellier, France [20 min]
New functionalities in GRYC
- 11:20 - 11:40 [Olivier Lespinet](#), Université Paris-Sud, France [20 min]
FUNGlpath: a web service dedicated to the exploration of metabolism in fungi
- 11:40 - 12:00 [Toni Gabaldon](#), CRG, Barcelona, Spain [20 min]
PhyloDB and MetaPhORs: orthology, paralogy and gene phylogenies in the genome era

12:00 - 13:30 Lunch

Session 6 - Metagenomics and metabarcoding

Chair: [Cécile Neuvéglise](#)

- 13:30 - 13:55 [Eric Pelletier](#), Genoscope / CEA, France [25 min]
Ocean 'omics: A path to large scale analysis of marine organisms
- 13:55 - 14:15 [Pierre Renault](#), INRA, Jouy-en-Josas, France [20 min]
Metagenomics applied to food, more than easy!
- 14:15 - 14:35 [Delphine Sicard](#), INRA, Montpellier, France [20 min]
METABAR-FOOD, a project for developing standardized metabarcoding and metagenomic analysis of fermented food
- 14:35 - 14:55 [Marie-Elisabeth Bougnoux](#), Institut Pasteur, Paris, France [20 min]

A longitudinal study of the mycobiota in individuals undergoing third-generation cephalosporin therapy

Conclusion and perspectives

14:55 - 15:20 [Bernard Dujon](#), Institut Pasteur, France [25 min]
Conclusion and perspectives