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

Delphine Sicard

To cite this version:

Delphine Sicard. METABAR-FOOD, a project for developing standardized metabarcoding and metagenomic analysis of fermented food. i-Genolevure, "High-Throughput Technologies Applied to Yeasts", Nov 2018, Strasbourg, France. hal-02006837

HAL Id: hal-02006837
https://hal.science/hal-02006837
Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Meeting on "High-Throughput Technologies Applied to Yeasts"

November 29th and 30th, 2018

Salle Louis Pasteur du Palais Universitaire
9 place de l'Université I 67000 Strasbourg I 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, Gingko 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

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 CRIPSR-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 CRIPSR-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]
FUNGIpath: a web service dedicated to the exploration of metabolism in fungi

11:40 - 12:00 Toni Gabaldon, CRG, Barcelona, Spain [20 min]
PhylomeDB 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