Environmental and Agronomical Genomics Symposium

February 14-16, 2024
Marthe Condat Auditorium, administrative building, Paul Sabatier University, Toulouse, France
Wednesday February 14th

12:30 - 14:00 Welcoming participants, main hall (Lunch not included, welcoming tea/coffee only)

14:00 - 14:15 Introductory speech, Scientific committee, Marthe Condat Auditorium

Monitoring of ecosystems functioning and health / Eco exposome (chair: J.C. Simon)

14:15 - 14:45 [01] Applications of environmental DNA & RNA in freshwaters ecosystems: recent advances, expectations for operational biomonitoring, challenges and prospects, Isabelle Domaizon, INRAE Thonon les Bains, France

14:45 - 15:05 [02] Meet the bushmeat pathogens: A metabarcoding snapshot of the bacterial diversity in the bushmeat sold in West Africa, Marine Montblanc, CRBE Toulouse, France

15:05 - 15:25 [03] What is the importance of genetic load in successful biological invasions of pests? Barbara Porro, Genoscope Evry, France

Exploring ecosystems using metagenomics 1/2 (chair: P. Wincker)

15:25 - 15:45 [04] Revealing the potential for lignin degradation by the termite gut microbiome. Guillermia Hernandez-Raquet, TBI Toulouse, France

15:45 - 16:05 [05] Exploring microbial disease dynamics in natural phyllospheres. Paloma Duran, LIPME Toulouse, France

16:05 - 16:35 Coffee Break, main Hall

Exploring diversity and evolution of Life 1/2 (chair: L. Bittner)

16:35 - 16:55 [06] The ecology of bacterial immune systems. Pedro Oliveira, Genoscope Evry, France

16:55 - 17:15 [07] Unravelling the molecular mechanisms underlying nutritional polyphenism in the bird cherry-oat aphid Rhopalosiphum padi. Aurélie Etier, IGEPp Rennes, France

17:15 - 17:35 [08] Phylogeny-guided environmental genomics of giant viruses. Tom Delmont, Genoscope Evry, France

17:35 - 17:55 [09] Disparate genetic divergence patterns in three corals across a pan-Pacific environmental gradient highlight species-specific adaptation trajectories. Didier Forcioli, Côte D’Azur Univ, France

Thursday February 15th

08:00 - 08:30 Welcoming participants

*Ancient DNA and paleo-environments (chair: P. Wincker)*

08:30 - 09:00 [11] Microbial time travellers: preserving the past, shaping the future. *Antonio Fernandez Guerra, Copenhagen Univ., Denmark*

09:00 - 09:20 [12] Diversity of ancient rhizosphere microbial communities preserved in herbaria, a paleomicrobiological approach. *Gianluca Grasso, Torino Univ., Italy*


*Environmental genomics and participatory science, openness to society 1/2 (chair: D. Faure)*

09:40 - 10:10 [14] Climate change microbiology: novel insights into methane cycling archaea. *Cornelia Welte, Radboud Univ, Nijmegen, The Netherlands*

10:10 - 11:10 Coffee Break/Poster session (ODD NUMBERS), main Hall


*Pangenome and structural variants 1/2 (chair: D. Milan)*

11:40 - 12:10 [16] Reference-free pangenomics and other large indexes. *Camille Marchet, CRISTAL, Lille Univ., France*


12:30 - 12:50 [18] Overdominance likely maintained large structural variants polymorphism in pearl millet. *Marine Salson, DIADE, Montpellier, France*

12:50 - 14:00 Lunch (main hall)

*Pangenome and structural variants 2/2 (chair: D. Milan)*

14:00 - 14:30 [19] Ten years of pangenomics in rices, lessons and knowledge. *François Sabot, IRD Montpellier, France*

14:30 - 14:50 [20] The pangeneome of the cosmopolitan picophytoplankton *Bathycoccus prasinos*: Understanding latitudinal and seasonal adaptation. *Louis Dennu, INSU Banyuls, France*


*Technological advances: producing and analyzing genomic data (chair: E Pelletier)*


15:40 - 16:00 [23] RdRp-scan: A bioinformatic resource to identify and annotate divergent RNA viruses in metagenomic sequence data. *Justine Charon, INRAE, Bordeaux Univ., France*

16:00 - 16:20 [24] EPIK: Evolutionary Placement with Informative K-mers for scalable taxonomic identification. *Benjamin Linard, MIAT INRAE Toulouse*

16:20 - 16:50 Coffee Break, main Hall

*Genomics of plants and animals and their microbiota (chair: E Pelletier)*

16:50 - 17:30 [25] The Ocean and Coral Reefs as Microbial Treasure Troves. *Shinichi Sunagawa, ETH, Switzerland*

17:30 - 18:00 [26] From the diversity of the diploid progenitors to a new diversity in a polyploid crop, oilseed rape. *Anne-Marie Chèvre, INRAE, Rennes Univ., France*
Friday February 16th

08:00 - 08:30 Welcoming participants, main hall

Exploring diversity and evolution of Life 2/2 (chair: L. Bittner)

08:30 - 08:50 [27] Introducing an integrative and generalizable approach to elucidate cryptic diversifications using mouse lemurs as a model system. Anne Yoder, Duke Univ., Durham, USA

08:50 - 09:10 [28] Exploring horizontal gene transfers in phytoparasitic nematodes through soil metagenomes. Carole Belliardo, Sophia Agrobiotech, France

Genomics of biological interactions : holobionts, pathogens, symbionts 1/2 (chair: JC Simon)


09:50 - 10:10 [30] A genomic map of local adaptation in Arabidopsis thaliana to native non-pathogenic bacteria: from mono-infections to complex communities. Fabrice Roux, LIPME Toulouse, France

10:10 - 10:30 Coffee Break/Poster session (EVEN NUMBERS), main Hall

Genomics of biological interactions : holobionts, pathogens, symbionts 2/2 (chair: JC Simon)

10:30 - 11:30 [31] Comparative genomics of Xylella fastidiosa subsp. multiplex strains from France reveals pathogen dynamics after its introduction. Jessica Dittmer, INRAE Angers Univ., France

Exploring ecosystems using metagenomics 2/2 (chair: P. Wincker)

11:30 - 12:00 [32] Hologenome 2.0: taking the genomes of social partners into account. Amélie Baud, CRG Barcelona, Spain

12:00 - 12:20 [33] Genomics of palm tree-palm weevil interactions. Emmanuelle Jacquin-Joly, IESE Paris, France

12:20 - 12:40 [34] Signals of generalist plant species adaptation to local pollinator communities and abiotic factors. Léa Frachon, INRAE Agroecologie Dijon, France

12:40 - 14:00 Lunch (main hall)

14:00 - 14:20 [35] Metagenomics reveal contrasted and dynamic responses of microbial soil communities to in situ wheat straw amendment in croplands or grasslands. Domitille Jarrige, Bourgogne Univ., France


14:40 - 15:00 [37] Combined metabarcoding and metatranscriptomic approaches unravel functional and taxonomic diversities of a coastal sediment microbiome and its reaction to hypoxia. Pascal Mirleau,IRD Marseille, France

15:00 - 15:20 [38] Genomic basis of temporally persistent and narrow prokaryotes in a coastal marine ecosystem. Clarisse Lemonnier, INRAE Thonon les Bains, France

Environmental genomics and participatory science, openness to society 2/2 (chair: D. Faure)


15:50 - 16:00 Conclusions