TiBE2020

ABSTRACT BOOK

METABARCODING and METAGENOMICS

9-10-11 DECEMBER 2020

Virtual event organized by

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ENVMETAGEN - *Capacity Building at InBIO for Research and Innovation using Environmental Metagenomics, is an* **ERA** *Chair project funded by the European Commission (Grant Agreement #668981).*
BIOPOLIS - *Teaming to Upgrade Excellence in Environmental Biology, Ecosystem Research and AgroBiodiversity, is a* **TEAMING** *project funded by the European Commission (Grant Agreement #857251).*

TiBE 2020 | METABARCODING AND METAGENOMICS

December 9 – 11, 2020 | Virtual Event

Welcome to TiBE - Trends in Biodiversity and Evolution Conference!

This is an annual meeting organized by CIBIO-InBIO, which aims to bring together senior researchers, post-graduate and graduate students working on the fields of biodiversity and evolutionary biology. In 2020, the aim of the meeting is to discuss cutting-edge findings in relevant topics related to metabarcoding and metagenomic techniques, and their application in ecological and environmental research, including biodiversity surveys, environmental assessment, ecosystem function and services, interaction networks and species autecology, among others.

The meeting will discuss exciting developments associated with the advent of ever more powerful DNA sequencing technology, which are opening possibilities to explore the living world in ways that were unimaginable just a decade ago. During three afternoons, participants will discuss new opportunities, challenges and pitfalls of metabarcoding and metagenomic approaches, with examples provided by a wealth of case studies where these new techniques contributed decisively to improve our understanding of biodiversity and ecosystem patterns and processes. Moreover, participants will discuss the application of metabarcoding and metagenomics to foster new and more cost-efficient environmental assessment and monitoring programs. The conference will be held in an informal but stimulating scientific atmosphere, on an online platform that will foster networking opportunities and allows poster presentations. The program includes both plenary and short presentations from selected abstracts.

TiBE2020 is organized by the CompBio and ApplEcol research groups of CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources – Research Network in Biodiversity and Evolutionary Biology (https://cibio.up.pt/). At the same time, TiBE2020 will be the closing meeting of the ERA Chair project ENVMETAGEN – Capacity Building at InBIO for Research and Innovation Using Environmental Metagenomics, funded by the European Commission (http://inbio-envmetagen.pt/).

The work presented in this conference is welcome to be submitted for publication as extended conference abstracts in the ARPHA Conference Abstracts (https://aca.pensoft.net/) and various research paper types in the Metabarcoding & Metagenomics Journal (https://mbmg.pensoft.net/) free of charge, thanks to the kind offer of the scholarly publisher Pensoft (https://pensoft.net/) and the DNAqua-NetCOST Action (https://dnaqua.net/).

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Identification of botanical origin of bee-collected mixed pollen samples: a comparison between palynological and DNA metabarcoding methods

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Identification of botanical origin of mixed pollen samples has several applications, including unraveling plant-pollinator interactions, determining botanical origin of honey, monitoring allergy-related airborne pollen sources, or even monitoring pesticide use in crops. These applications have typically been addressed using light microscopy, a costly approach that often provides low taxonomic resolution. However, with high-throughput sequencing (HTS) becoming increasingly affordable, DNA metabarcoding is emerging as a promising alternative to classical palynology. In addition to be time- and cost-effective for large sample sizes, metabarcoding has the potential to allow identification of pollen mixtures at the species level. However, before it can be widely employed in pollen analysis, the reliability of this molecular tool must be appraised. Herein, we compared the two approaches on 61 bee-collected pollen samples from eight European countries. The samples were homogenized and split into two sub-samples. One set of 61 sub-samples was analyzed by palynology experts from the "Institut für Bienenkunde", Germany, and the other one was subjected to HTS, using ITS2 as the barcode, in the labs of CIMO and CIBIO. Comparisons of the relative abundances at the family level show no significant differences ($P \geq 0.1057$, Wilcoxon signed-rank test) and high correlation values ($0.2736 \leq r \leq 1.000$, Pearson's correlation) between the two approaches. The highest correlation values were observed for Italian samples ($0.7245 \leq r \leq 0.9842$; global $r = 0.8958$) and the lowest for Greek samples ($0.0266 \leq r \leq 0.9703$; global $r = 0.5149$).

These results suggest that ITS2 metabarcoding offers a reliable alternative to classical palynology and this approach is now being employed in the European project INSIGNIA (https://www.insignia-bee.eu/), which is developing a standard protocol for using the honey bee as a tool for environmental monitoring. This study was funded by INSIGNIA "Environmental monitoring of pesticides use through honey bees" (SANTE/E4/SI2.788418-SI2.788452).

Changes in soil microbial diversity along gradients of land management intensity in São Miguel island grasslands (Azores)

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In the last decades, many natural areas were globally altered into rangeland or pastureland, which became one of the dominant land cover types. More than 50% of the land use in the Azores corresponds to pastureland, with agroindustry being a relevant socio-economic sector. With the world's climate changing at a rapid pace, a more sustainable management for food production is, more than never, required. The sustainability of production of agricultural land is, at a large scale, the result of soil microbial composition, abundance, and activity. São Miguel is an ideal study location, with habitats ranging from semi-natural to completely artificial found at relatively small distances. Three levels of management intensity were sampled for grasslands: semi-natural pasture, intermediate intensity pasture, high intensity pasture (corn rotation), in four sampling seasons (2 seasons/2 years) in a total of 54 soil samples. Data from above-ground flora diversity was also obtained. DNA extracted from the soil was sequenced by Illumina Miseq, followed by the assembly of operational taxonomic units (OTUs) from fungal and bacterial community marker genes. Numerical ecology, maximum likelihood and Bayesian methods are currently being applied to analyse the results. Preliminary results show clear differences in fungal diversity between both ends of the management gradient in the grasslands of São Miguel.

Assessing the diversity of coastal macroinvertebrate assemblages growing in artificial substrates based on morphology and DNA metabarcoding approaches

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