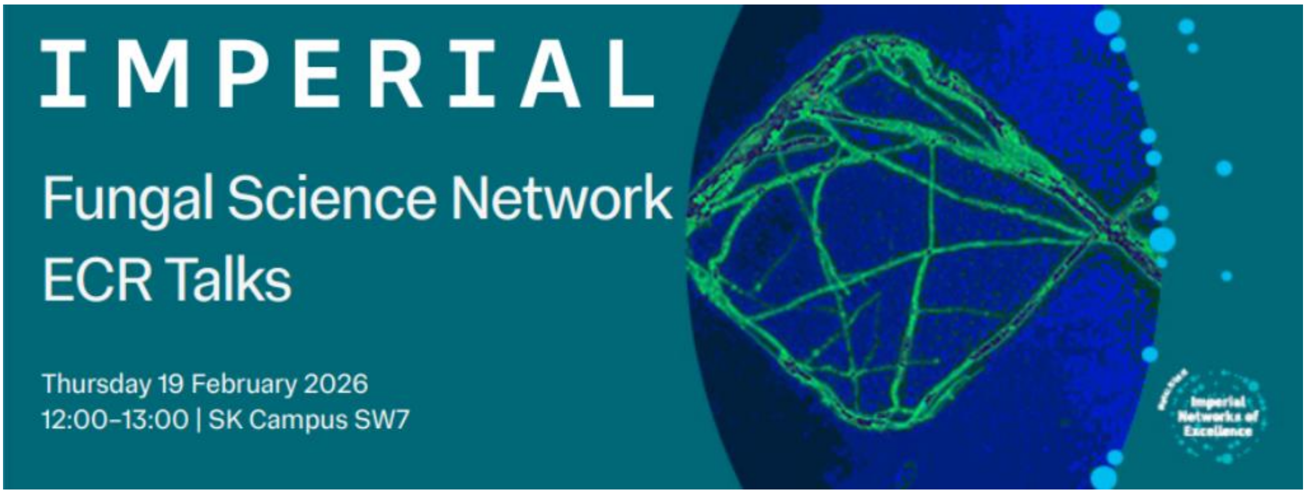


IMPERIAL

Fungal Science Network ECR Talks

Thursday 19 February 2026
12:00–13:00 | SK Campus SW7

We warmly invite you to attend the Imperial Fungal Science Network Seminar on

📅 Thursday 19th February, 12:00 - 13:00

📍 G47 Flowers Building, South Kensington Campus, Armstrong Road, London SW7 2AZ 3A on map

in-person (walk in; refreshments from 11:30am)
or online (via Teams)

no registration required

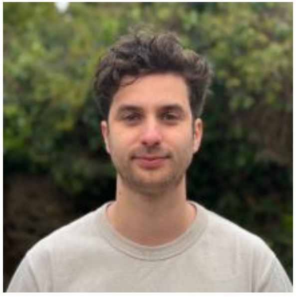
Microsoft Teams Need help?

Join the meeting now

Meeting ID: 337 087 815 982 04
Passcode: eg6Rc99x

>click here - live event info IFSN Seminar | 12noon Thurs 19 Feb | ECR Talks

Biotechnology and engineering

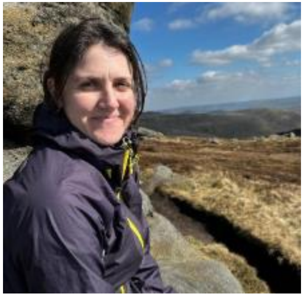


Louis Cohen (Stanley Lab, Department of Bioengineering, Imperial College London)

"Mycorrhiza-on-a-chip" – developing microfluidic systems for studying root-fungal symbioses

The relationship between plant roots and mycorrhizal fungi is ancient and laid the foundation for terrestrial life on earth. Today, this relationship underpins agricultural yields and ecosystem stability. How individual mycorrhizal fungal hyphae initiate a symbiosis-specific response from plant hosts is still largely unknown. Microfluidic technology is a useful tool to engineer custom simplified microenvironments to monitor these pre-symbiotic interactions in real time, and gain insights into the mechanisms that drive symbiotic crosstalk.

Pathogenesis of fungal diseases



Dr Lauren Dineen (Armstrong-James Lab, Department of Infectious Disease, Imperial College London)

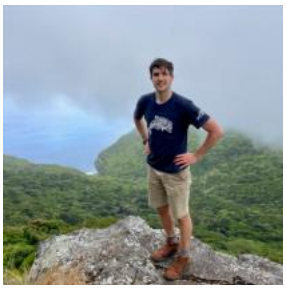
Exploring tRNA diversity in yeast using machine learning and direct RNA sequencing approaches

Up until recent decades, tRNA were thought to be passive molecules in translation. We now know that tRNA are important regulatory molecules that influence translation dynamics and other cellular processes. Despite leaps in the field, significant gaps in knowledge of fundamental tRNA biology remain. I will talk about my recent work focused on tRNA diversity within the Saccharomycotina yeast subphylum using both computational and direct RNA sequencing approaches.

Ecology, evolution and the environment

Dr Marco Balducci (Savolainen Lab, Department of Life Sciences, Silwood Park, Imperial College London)

Can symbiosis underpin local adaptation?



Using metabarcoding and meta-transcriptomics, we examine how *Howea* palms and their arbuscular mycorrhizal fungal (AMF) communities vary with host identity and soil environment. Metabarcoding reveals that AMF community composition is structured by both host species and habitat, while meta-transcriptomic analyses show coordinated shifts in fungal function, stress tolerance, and cross-kingdom gene co-expression across soils. Together, these patterns suggest that environmentally structured plant–microbiome interactions contribute to local adaptation in a natural system.

Imperial Fungal Science Network leadership team
Fungal Science Network | Research groups | Imperial College London
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