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# Fungal genetics, host pathogen interaction and evolutionary ecology

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## PROGRAM & ABSTRACTS



The genomes of organisms living in diverse environments can reflect adaptations to diverse environmental conditions. Anthropogenic disturbances such as soil pollution can quickly create steep environmental gradients that likely induce adaptation and imprint genomic signatures of selection. Fungi are ubiquitous in soil environments and are key players in soil systems processes, however little is known about how they evolve in face of anthropogenic soil pollution. We used population genomics to investigate incipient local adaptation to heavy metals in *Suillus luteus*, a widespread symbiotic ectomycorrhizal fungus associated with pine trees. Available phenotypic data show that *S. luteus* isolates from the same population have variable heavy metal tolerance with some isolates tolerating high metal concentrations, while others show reduced growth and death when exposed to heavy metals. Whole genome scans across isolates from both habitats revealed genomic signatures associated with colonizing polluted sites, with a strong enrichment for transmembrane transporters. Candidate genes underlying heavy metal adaptation in *S. luteus* were involved in metal exclusion, immobilization, and detoxification, and displayed both allelic and copy number variation. Results from our study revealed incipient local adaptation to heavy metals in *S. luteus* and elucidate on the evolutionary processes involved in environmental adaptation in fungi.

### **Novel insights into population dynamics and lineage differentiation of the coffee leaf rust pathogen *Hemileia vastatrix***

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Coffee Leaf Rust, caused by *Hemileia vastatrix* (Hv), has been the major constraint to global coffee production for more than a century. Only recently the population evolutionary history of this pathogen began to be unveiled. Silva *et al.* (2018) found for the first time the species to be structured into three divergent genetic lineages with marked host tropism (C1 and C2 infecting diploid coffee species; and C3 infecting tetraploid coffee species), and signals of introgression. Nevertheless, no significant structuring was found within the C3 lineage, which represent the most widespread and epidemiological relevant Hv group. Here, we extended the investigation to a worldwide scale sampling for obtaining a deeper insight on the dynamics and adaptive evolution of Hv populations. We used restriction site-associated DNA sequencing (RADseq) to generate around 21,520 SNPs

across 108 Hv isolates. Phylogenetic analyses corroborated the existence of the three well-diverged Hv groups, but furthermore showed a well-supported structuring within C3, with three main sub-groups: African, Asian and Timor. This pattern seems to reflect Hv geographical origin associated to the historical distribution and exchange of coffee materials. The Asian origin clade comprises the higher number of isolates and exhibits a ladder-like diversification pattern, with relatively low genetic diversity, suggesting rapid evolution and population expansion. On the contrary, the African and Timor populations appear to more restricted, revealing some degree of differentiation. In addition, our results reinforce the potential role of introgression in Hv lineage and virulence evolution. From the 7909 loci (comprising 9628 “diagnostic” SNPs) differentiating C2 and C3 groups, 2,63% mapped against NCBI nt database, with the majority of the hits corresponding to retrotransposons (82,76%) and putative secreted protein genes (9.58%)

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## Emergence and diversification of a highly invasive tree pathogen lineage

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Invasive microbial species constitute a major threat to biodiversity, agricultural production and human health. Microbial invasions are often dominated by one or a small number of genotypes, yet the underlying factors driving invasions are poorly understood. A prime example for a successful invasion is the recent outbreak of the chestnut blight fungus *Cryphonectria parasitica* in Southeastern Europe. *C. parasitica* is native to East Asia and has colonized North America and Europe during the first half of the 20<sup>th</sup> century. We investigated the genetic structure of 188 European strains of the pathogen using 17'873 genome-wide single-nucleotide polymorphisms (SNPs). Genotypes showed high levels of diversity with evidence for frequent and ongoing recombination. European populations also exhibit a longitudinal gradient in genetic diversity. We found that the invasive S12 lineage dominating Southeastern Europe is genetically homogeneous. Our data strongly suggests that S12 emerged from the highly diverse pool of European genotypes rather than a secondary introduction from Asia. The S12 lineage is predominantly composed of a single mating type and the observed genetic diversity is consistent with mutation accumulation. Despite little or no evidence for recombination, we show experimentally that the lineage retained the ability to reproduce sexually. Overall, our findings show that an invasive pathogen lineage can arise through an intermediary, highly diverse bridgehead population. The combination of genetic and epidemiological evidence suggests that the invasive lineage switched the dominant reproductive mode and gained crucial adaptive