S6.3c Adaptive dynamics in experimental populations of Aspergillus nidulans
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S6.3d Candida albicans commensalism in the oral mucosa is favored by limited virulence and metabolic adaptation
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S6.3 Fungal adaptation and evolution, September 22, 2022, 4:41 PM - 6:13 PM

A total of 12 replicate populations initiated with a laboratory strain of the anamorphic fungus Aspergillus nidulans evolved on synthetic minimal glucose agar medium for 1 year, using weekly transfers of 3% of the produced aerial spores to fresh medium. This Aspergillus short-term evolution experiment (ASEX) was designed to understand how filamentous fungi adapt to growth on limited carbon in a spatially structured environment. We observed no systematic improvement in the fitness component normal and neither in the competitive fitness relative to the ancestor line; instead, we observed the sequential evolution of at least two morphotypes, with a fully-like (FL) or an anamorphic (AN) colony morphology, leading to interspecific fitness interactions among isolates in two selected populations. The genotypic analysis of clones from all 12 populations at an early (week 10) and the final time point (week 52), show a clear role of natural selection during ASEX. We also observed a shared genetic basis and different timing of adaptations of AS and FL types. In addition, in most populations, both morphotypes do not form monomorphic groups, but they frequently disappear and re-evolve from ancestral forms of both types. Reduction in aerial spore yield, the most evident parallel phenotypic change found in all our evolved populations, is not due to the direct selection of genes involved in aerial reproduction. Instead, we argue that reduced spore yield is a pleiotropic effect of adaptive changes in metabolism.

S6.4 One health approach for endemic mycoses in the Americas, September 22, 2022, 4:41 PM - 6:13 PM

Objective: To present a series of cases of primary cutaneous coccidioidomycosis, to highlight this mycosis that can start as cutaneous implantation, after trauma, and to emphasise the classification criteria.

Methods: A series of cases of primary cutaneous coccidioidomycosis will be presented, all of them confirmed mycologically, with examination, stains, and cultures, as well as their molecular identification, also confirmed by histopathology.

Results: A series of 22 cases of primary cutaneous coccidioidomycosis is presented, 16 (72.8%) in men, 6 (27.2%) in women. With an average age of 35.2 years, the lowest case in a 14-year-old child and the highest in 74 years. All from rural and endemic areas. A total of 11 (49%) with childhood and the rest due to various injuries. The otopathological agent was isolated in all of them: Coccidioides posadae in 14 (72.8%), C. immitis in 3 and one as Coccidioides sp. 20 cases were treated with itraconazole, with an average of 8 months and two more with a cycle of amphotericin B and subsequent itraconazole.

Clinical and mycological cure was obtained in all.

Discussion: Primary cutaneous coccidioidomycosis is considered an important mycosis, similar to other endemic ones, it occurs between 2%-10% of cases. It begins with trauma that inoculates the fungus, such as a primary lesion. To confirm that it is a primary form, Wilson’s criteria must be met: the presence of skin trauma, regional lymphadenopathy, no evidence of pulmonary involvement, positive intradermal reaction, and low antibody titer. It may present auto-inoculation and in immune-suppresse patients, it can spread.

Conclusion: The initial cutaneous form of coccidioidomycosis is rare, usually seen in patients living in endemic areas, and usually prone in patients with rural occupations. It has a variety of clinical forms, being confused with other diseases. Its diagnosis is simple, being the biopsy the most useful, and it must be confirmed by mycological tests. It has a good prognosis and its main management is with itraconazole.

S6.5 Candida albicans commensalism in the oral cavity is favored by limited virulence and metabolic adaptation
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S6.5 Fungal adaptation and evolution, September 22, 2022, 4:41 PM - 6:13 PM

Objective: As part of the human microbiota, the fungus Candida albicans colonizes the oral cavity and other mucosal surfaces. Commensalism is tightly controlled by complex fungus-host interactions that provide fungal elimination but also fungal overgrowth and invasion that would result in disease. As such, defects in antifungal T cell immunity render individuals susceptible to oral thrush due to unregulated immunocompetence. The factors that promote commensalism and immune persistence of C. albicans in a fully immunocompetent host remain less clear. In this study, we aimed at identifying determinants of C. albicans commensalism in the oral cavity.

Methods: We used an experimental model of C. albicans oral colonization in mice, profiling the transcriptome of the fungus in the mucosal tissue, and conducted functional studies with the prototypical commensal isolate 101 in host-free and host-involved conditions.

Results: C. albicans commensalism is associated with a characteristic metabolic profile tailored to the nutrient-poor conditions in the estrumen of the epithelium where the fungus resides. Metabolic adaptation of the commensal isolate 101 was also reflected in enhanced nutrient acquisition when grown on oral mucosa substrates. Potent colonization of the oral mucosa by C. albicans also correlated strongly with the capacity of the fungus to induce epithelial cell damage and to elicit an inflammatory response. These immune evasion properties of isolate 101 are explained by a strong attenuation of numerous virulence genes, including those linked to fermentation. Disruption of the hyphal program by deletion or conditional repression of the transcriptional repressor NRG1 abolished the commensal behavior of isolate 101.

Conclusions: This study establishes a central role of NRG1 in the commensal lifestyle of C. albicans in the oral niche of the host.
Mycetoma is a debilitating disease recognized as a neglected tropical disease by the World Health Organization. The etiology of mycetoma is poorly understood; ~60% of cases are caused by fungi and the rest are bacterial, although this varies by region. The pathogenic fungus, Madurella mycetomatis, is most frequently identified in mycetoma cases. Here, we present a high-quality genome assembly of M. mycetomatis and the results of the whole genome sequence analysis of 25 isolates from Sudan. We demonstrate evidence of at least seven genetically diverse lineages and extreme clonality among isolates within these lineages. Shotgun metagenomic analysis of DNA from mycetoma grains confirmed that M. mycetomatis was the predominant causative agent of mycetoma Sudan; however, 10% of grains also contained bacterial reads suggestive of secondary infections. A thorough understanding of the genetic structure and diversity of fungi causing mycetoma is essential for the development of new diagnostic methods and for identifying potential drug targets.