S6.3c
Adaptive dynamics in experimental populations of Aspergillus nidulans
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6.5 Pinal fungal adaption and evolution, September 22, 2022, 4:47 PM - 6:13 PM

A total of 12 replicate populations initiated with a laboratory strain of the ascomycete 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 components total and neither in the competitive fitness relative to the ancestor. Instead, we observed the repeated evolution of at least two morphotypes, with a fully-like (FL) or an aerial-like (AL) colony morphology, leading to inter-specific fitness interactions among isolates in two selected populations. The genome 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 adaptive changes of AL and FL types. In addition, in most populations, both morphotypes do not form monomorphic groups, but they frequently disappear and re-appear 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 plastic effect of adaptive changes in metabolism.

S6.3d
Candida albicans communisation in the oral mucosa is favored by limited virulence and metabolic adaptation
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6.5 Pinal fungal adaption and evolution, September 22, 2022, 4:41 PM - 6:13 PM

Objectives: As part of the human microbiota, the fungus Candida albicans colonises the oral cavity and other mucosal surfaces. Communisation is tightly controlled by complex fungus-host interactions that promote 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 uncontrolled intramycocellulare. The factors that promote communisation 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 communisation in the oral cavity.

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

Results: C. albicans communisation is associated with a characteristic metabolic profile tailored to the nutrient-poor conditions in the stratum corneum of the epithelium where the fungus resides. Metabolic adaptations of the communal isolate 101 was also reflected in enhanced antifungal acquisition when grown on oral mucosa substrates. Permanent colonization of the oral mucosa by C. albicans also correlated inversely 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 activation of numerous virulence genes, including those linked to filamentation. De-repression of the hyphal program by deletion or conditional repression of the transcriptional repressor NRG1 abolished the communal behavior of isolate 101.

Conclusions: This study establishes a central role of NRG1 in the communal lifestyle of C. albicans in the oral niches of the host.

S6.4c
Primary cutaneous implantation coccidioidomycosis
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6.4 One health approach for endemic mycoses in the Americas, September 22, 2022, 4:41 PM - 6:15 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 by mycological studies, both immunostains, 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 (72.7%) in men, 6 (27.2%) in women. With an average age of 35.2 years, with the lowest case in a 14-year-old child and the highest at 72 years. All from rural and endemic areas. A total of 11 (50%) with childhood and the rest due to various injuries. The etiological agent was isolated in all of them: Coccidioides posadasii in 14 (72.7%), C. immites in 3 and one by Coccidioides sp. 20 cases were managed with itraconazole, with an average of 8 months and two with a cycle of amphotericin B and subsequent itraconazole. Clinical and mycological cure was obtained in all.

Conclusions: Primary cutaneous coccidioidomycosis is considered an implantation mycosis, similar to other endemic ones, it occurs between 2%-10% of cases. It begins after trauma that inoculates the fungus, such as a primary chance. 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 rate. It may present auto-inoculation and in immunosuppressed patients, it can spread.

Conclusion: The cutaneous form of coccidioidomycosis is rare, usually seen in patients living in endemic areas, and rarely present 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 used, and it must be confirmed by mycological tests. It has a good prognosis and its main management is with itraconazole.