Relative abundance and geospatial stratification of airborne Mucoromycota are poor predictors of Mucormycosis

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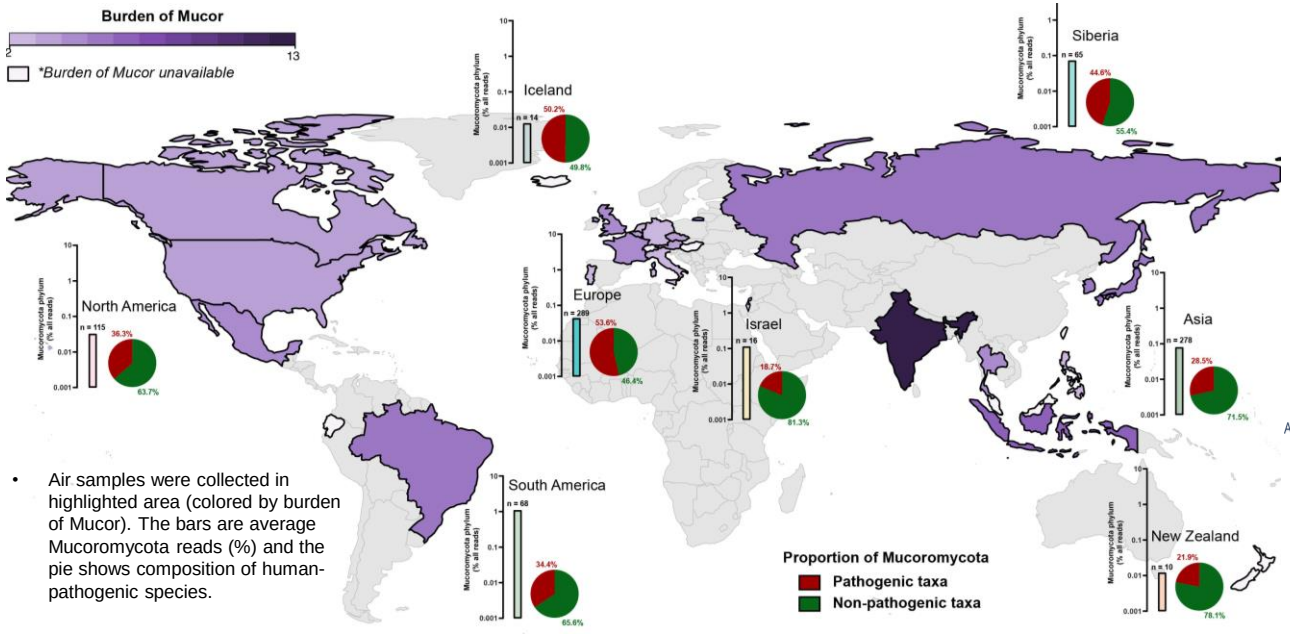
Introduction and Methods

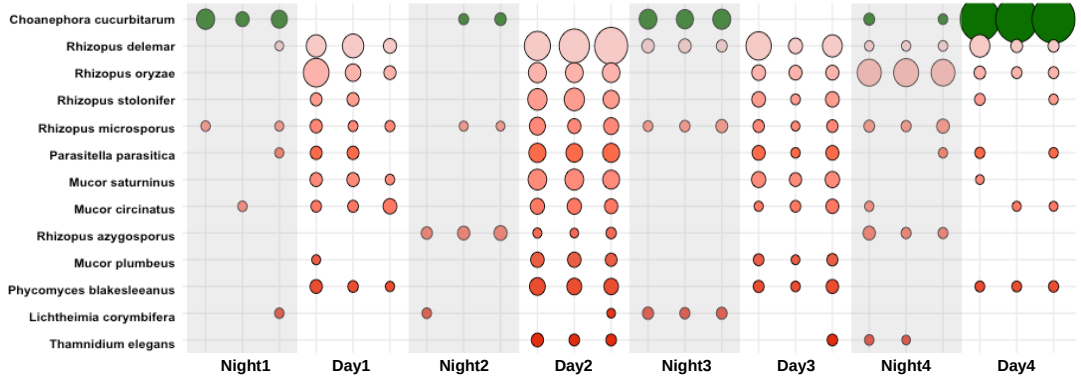
- Despite mucormycosis being increasingly recognized as an important, invasive, and severe complication related to COVID-19 (CAM), no globally standardized datasets are available for evaluating the human exposure to this species-rich group of fungi.
- Employing our synoptic analysis of 8,937 metagenomic samples (7,475 air and 1,462 dust) from 30 countries we demonstrate the relative abundance and geospatial stratification of Mucorales.

Global Distribution of Mucoromycota (Spatial variation)



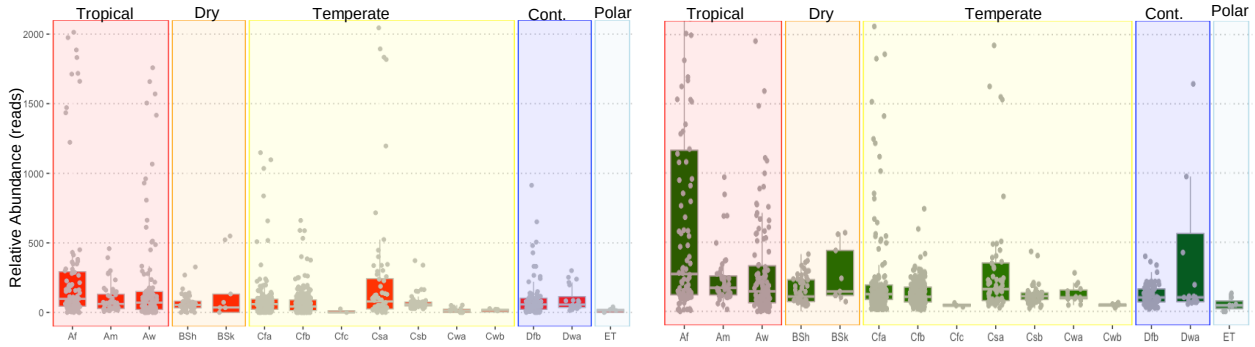
- Air samples were collected in highlighted area (colored by burden of Mucor). The bars are average Mucoromycota reads (%) and the pie shows composition of human-pathogenic species.

Diel dynamics of Mucoromycota (Temporal variation)



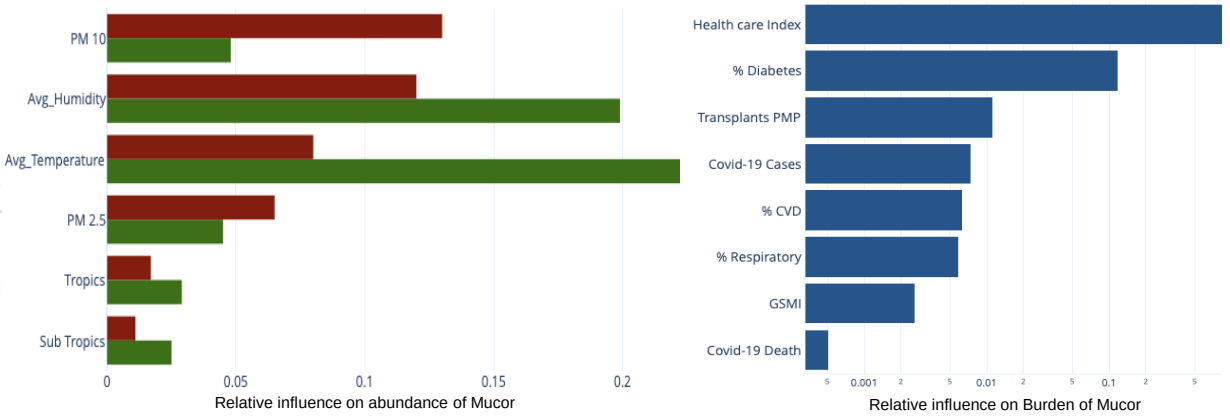
- Mucoromycota abundance follows a daily cycle like most other taxa
- The cycles of plant and human related species are unsynced

Eco-region distribution of Mucoromycota (Ecosystem Variation)



- Both Plant and Human associated Mucoromycota are more abundant in Tropical region (Af, Am)

Impact of Environmental, Clinical and Social Predictors



A perfect storm in India:
The increased covid burden on the health care system combined with a substantially high number of susceptible hosts with comorbidities caused for a perfect breeding ground for Mucor in India.

Conclusion and Acknowledgement

- The environmental burden of Mucorales can be excluded as a key contributor to emergence cases of CAM, suggesting host genetics, co-morbidities (diabetes), high steroid use and yet undescribed factors to be of greater explanatory power.
- This study concludes that the identification of global hotspots and avoidance of airborne Mucoromycota is not a viable public health intervention aimed at controlling the ongoing Mucormycosis 'epidemic within the pandemic'.
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