Weill Cornell Medicine

Pan-Cancer Mycobiome Analysis Platform to Predict Survival and Treatment Response

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Background & Unmet Need

- The tumor microenvironment (TME) is a complex ecosystem of immune cells, extracellular matrix, blood vessels, and other cell types
- While the microbiome (bacteria) has been shown to participate in the TME and influence response to cancer treatments, the role of the mycobiome (fungi) is poorly understood
- For instance, the gut microbiome plays a significant role in whether patients respond to anti-PDL1 treatment
- An improved understanding of the TME and the role of bacteria and fungi may lead to the development of improved diagnostics and treatments
- **Unmet Need:** Improved platform for analyzing the tumor microbiome and mycobiome

Technology Overview

- **The Technology:** A computational platform to extract fungal sequences from sequencing data of human tumor samples
- **The Discovery:** *Candida*-to-*S.Cerevisae* ratio were predictive of metastatic colon cancer
- Fungal species, specifically *C. albicans* and *S. Cerevisae* species, are prognostic markers of disease progression and worse clinical outcomes of GI cancers
- **PoC Data:** Fungal species associate with primary tumor samples and with different stages of disease, specifically in GI tumors
- The technology provides a novel method of screening and stratifying cancer patients who may be candidates for antifungal therapy

Inventors:
Iliyan Iliev
Anders Dohlman
Xiling Shen

Patents:
PCT Application Filed

Publications:
Dohlman et al. *Cell*. 2022.

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Technology Applications

- Computational platform to identify tumor-associated fungal species
- Development of a prognostic resource specifically for GI cancers where the technology has identified Candida ssp. as markers for disease progression and outcome
- Identification of potentially druggable fungal species to improve patient outcome

Technology Advantages

- The technology offers a unique framework to detect tumor associated fungal species
- The insights gained through the application of the technology could identify new prognostic markers and inform new treatment strategies such as anti-fungal therapies
- Future advances in detection of fungal DNA in blood samples could allow non-invasive diagnostics

Supporting Data / Figures

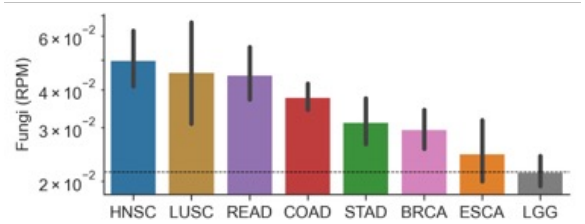

Figure 1: Fungi are present in human tumor samples. A rigorous multistep analysis is used to remove signal from spurious contamination. LGG, derived from brain tumors, serves as a negative control.

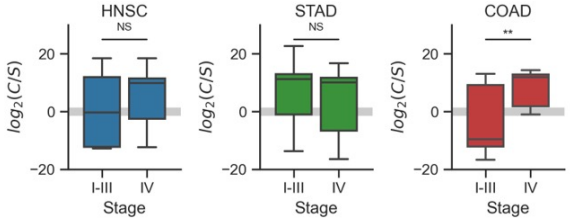

Figure 2: Candida levels associate with late-stage colon tumors (COAD) and metastasis, but not in head and neck (HNSC) and stomach cancer (STAD).

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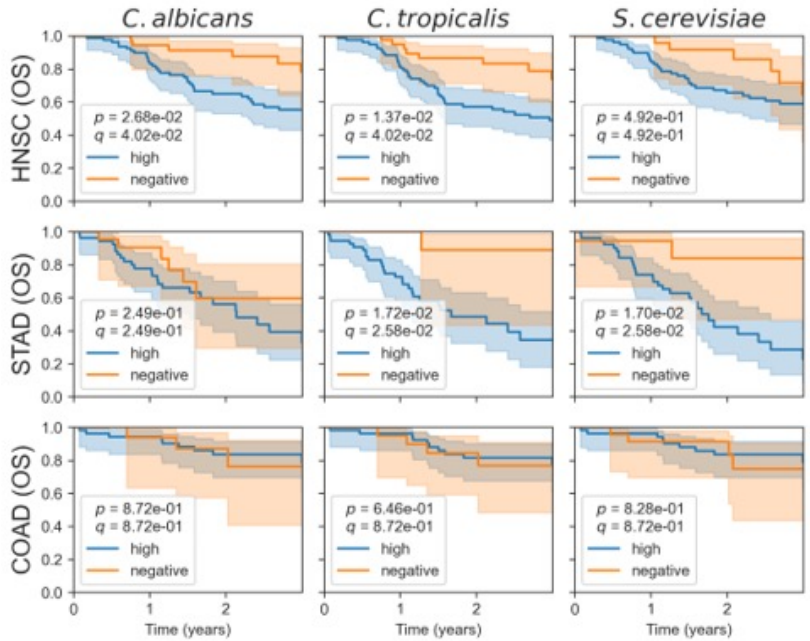

Figure 3: The presence of specific fungi are associated with overall survival. *C.albicans* levels are significantly associated with reduced survival in head and neck cancer. *C. tropicalis* levels are significantly associated with decreased survival in stomach and head and neck cancers. *Saccharomyces* spp. were associated with decreased survival in stomach cancer. No significant associations between fungi and survival were found for colon cancers.

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