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RESEARCH AREA

Besides the bacterial flora, several fungal species are also long-term occupants of the oral microbiota. Among these, *Candida* are the most abundant species. Although the role of the human bacteriota and virome is well characterized, less is known about the composition of the mycobiota, let alone its role in the host. Therefore, one purpose of our project is to examine how do normal oral epithelial cells respond to the presence of commensal *Candida* species. We aim to explore their recognition, the corresponding signal transduction mechanisms and potential effector functions in the presence of various fungal stimuli. Since the last decade, numerous studies report alterations in the diversity of the oral microflora of immunocompromised and cancer patients (e.g. with oral squamous cell carcinoma), allowing the overgrowth of opportunistic pathogenic species (such as *C. albicans* and *C. parapsilosis*). Besides the increased probability of oral candidiasis in these patients, the abnormally altered microbiota might also influence the underlying diseases' progression. In addition to investigating the immune response regulatory effect of normal oral epithelial cells, we further aim to examine the potentially altered immunomodulatory effects of oral squamous cell carcinoma cells and to explore signaling routes that might be associated with tumor progression following fungal stimuli.

TECHNIQUES AVAILABLE IN THE LAB

Establishment/ optimization/ handling of *in vitro* co-infection models to examine fungal infections, using human monocytic, epithelial and murine cell lines and primary cells; phagocytosis and killing experiments; RNA preparation; real-time PCR; ELISA; flow cytometry; metabolic activity; cell adhesion and host cell killing (LDH) assays, live cell imaging. Next-generation sequencing, RNA-seq, micro RNA investigations.

SELECTED PUBLICATIONS

Toth, R., Nosek, J., Mora-Montes, H., Gabaldon, T., Bliss, J.M., Nosanchuk J.D., Turner, S.A., Butler, G., Vagvolgyi, Cs., Gacser, A. (2019) The emergence of Candida parapsilosis: from genes to the bedside. **Clin Microbiol Rev 32:** e00111-18.

Toth, R., Cabral, V., Thuer, E., Bohner, F., Nemeth, T., Papp, Cs., Nimrichter, L., Molnar, G., Vagvolgyi, Cs., Gabaldon, T., Nosanchuk, J.D., Gacser, A. (2018) Investigation of Candida parapsilosis virulence regulatory factors during hostpathogen interaction. **Sci Rep 8:** 1346.

Toth, R., Toth, A., Vagvolgyi, Cs., Gacser, A. (2017) Candida parapsilosis secreted lipase as an important virulence factor. **Curr Protein Pept Sci 18:** 1043-1049.

Nagy, L.G., **Toth, R.**, Kiss, E., Slot, J., Gacser, A., Kovacs, G.M. (2017) Six Key Traits of Fungi: Their evolutionary origins and genetic bases. **Microbiol Spectr 5.**

Toth, R., Toth, A., Papp, Cs., Jankovics, F., Vagvolgyi, Cs., Alonso, M.F., Bain, J.M., Erwig, L.P., Gacser, A. (2014) Kinetic studies of Candida parapsilosis phagocytosis by macrophages and detection of intracellular survival mechanisms. **Front Microbiol 5: 633.**