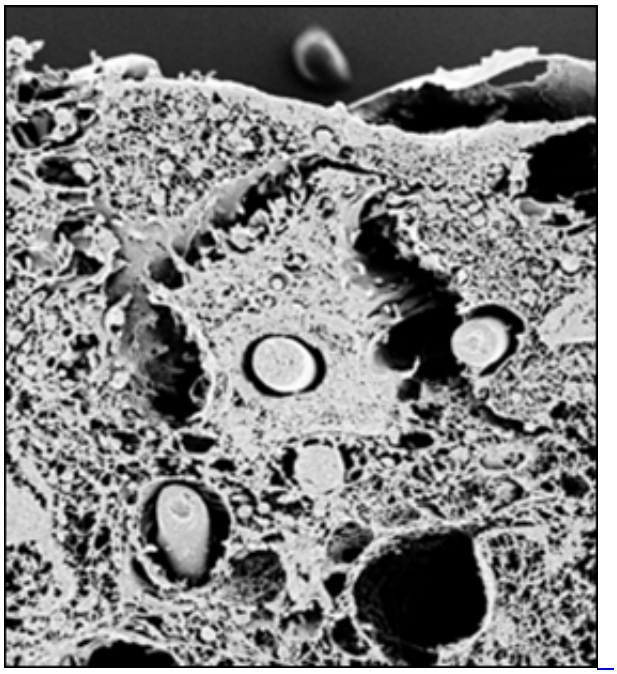
Molecular mechanisms of *Candida* sepsis



Scanning electron micrograph showing *C. albicans* interacting with epithelial cells. Hyphae penetrate through and between the epithelial cells leading to tissue destruction.

The most common fungal pathogen of the genus *Candida* is *Candida albicans* (*C. albicans*). During systemic infections, *Candida albicans* can infect almost all organs, which can cause disregulation of the immune system and organ failure. In the murine model of haematogenously disseminated candidiasis, mice die of progressive sepsis, kidney inflammation and failure, while fungal load declines in all other infected organs without causing pathological alterations. This data suggests that fungal pathogenicity is not only due to damage caused by the fungus, but also due to an inappropriate host response leading to damage caused by immune cells.

In this project, we aim at understanding the molecular mechanisms of sepsis induction triggered by *C. albicans* by identifying fungal genes, factors or activities which are responsible for or contribute to the organ-specific host responses. We propose that fungal genes exist, which are required for an organ-specific host response which is either protective or non-protective. We will use in vivo transcriptional profiling and large scale *C. albicans* mutant collection screening to identify such genes. The knowledge of these genes and their role during systemic *C. albicans* infection provide new options for antifungal therapies, which are urgently required due to the high mortality rates caused by *C. albicans*.