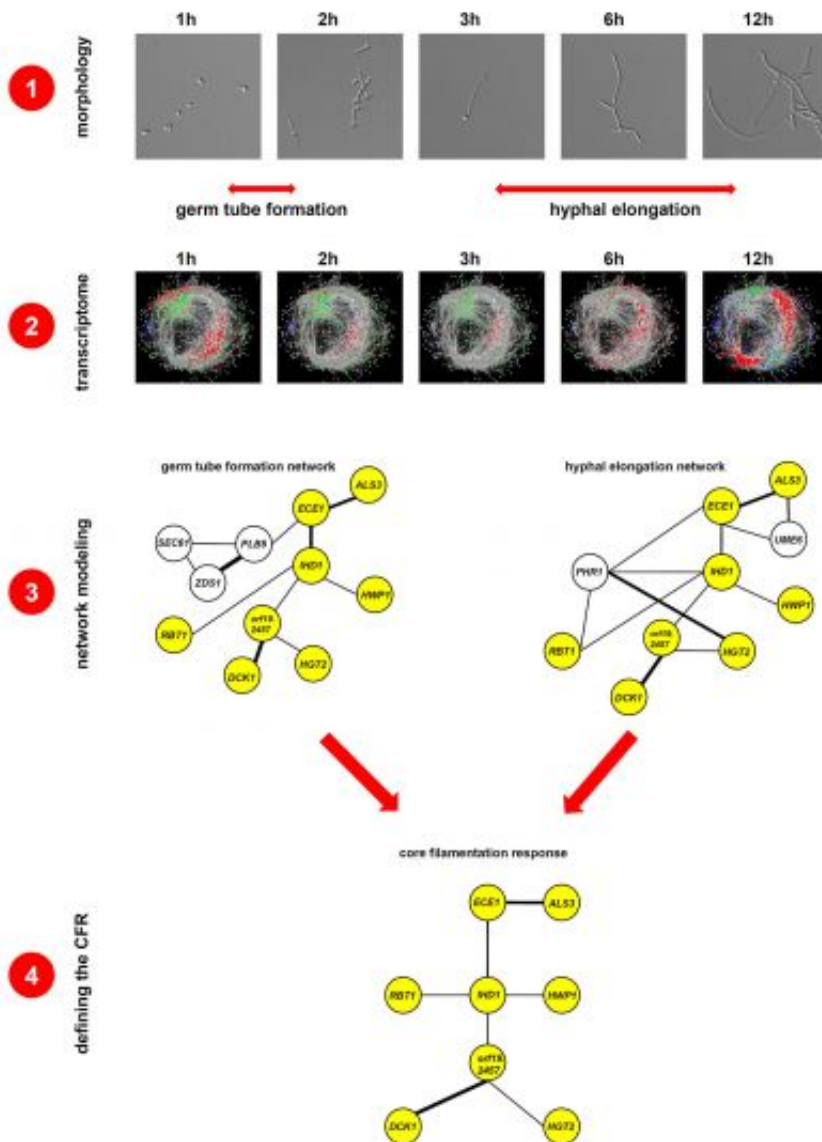


Pathogenic biology of *Candida* species

defining a core filamentation response (CFR) in *Candida albicans*



— Analyse der Core Filamentation

Response von *C. albicans*

The virulence of yeast fungi of the *Candida* species is closely linked with the ability to react to changing environmental conditions. *Candida albicans* is able to react on changes of environmental conditions with morphologic changes between the yeast form and filamentous forms. This morphologic plasticity is a core virulence factor. We analyse mechanisms of such morphotype-changes and investigate both the genes whose expression is bound to the change in growth form and regulators of morphologic plasticity. Based on the experimentally derived transcriptome data of differently stimulated fungi, we have been able to generate a *Core Filamentation Response* network by means of biomathematical methods. This network consists of genes that are expressed independent of the morphotype-induced stimulus within the frame of filamentation (Matrin *et al.*,

2013). In contrast to *C. albicans*, *C. glabrata* is monomorphic. Therefore, the second most common pathogen of invasive *Candida*-infections possesses different adaptation mechanisms. In cooperation with F. Mühlschlegel (Canterbury, UK), a molecular mechanism of CO₂ adaptation that is conserved in yeasts was described that is independent of already known adenylatcyclase-mediated signal transduction. Rca1 was identified as the central transcription factor in *C. albicans* (Cottier *et al.*, 2012). The work approaching the further characterisation of the Rca1-cascade in *C. glabrata* has been funded by the DFG since 2013.