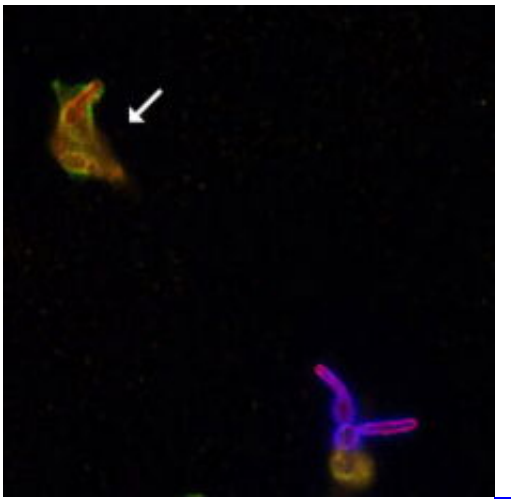
Infection models with human immune cells

For the analysis of the pathogen-host-interaction within the scope of systemic infections and sepsis, we use – also in cooperation with numerous groups at the HKI – infection models for primary human immune cells including neutrophile granulocytes [PMN], monocytes [MoC], dendritic cells [DC] and natural killer cells [NKC] (Heddergott et al., 2012; das Gupta et al., 2014, Miramon et al., 2014). Live-cell-imaging plays a key role with regard to those analyses. We were able to show evidence of both a pro-inflammatory and an antifungal activity of NK cells over *C. albicans* and show that the fungus is phagocyted by NKC. Moreover, NKC modulate the antifungal activity of PMN (Voigt et al., 2013). In cooperation with the FG MI, the pro-inflammatory role of the NKC in the case of a *C. albicans*-sepsis was further investigated using a mouse model. NKC-depleted mice have proven a longer life expectancy as a consequence of a decreased inflammatory reaction (Quintin et al., 2014). To be able to analyse the interactions of different human immune cells in response to pathogenic fungi, a whole-blood infection model was established. This allows the analysis of the pathogen distribution to different compartments. At the same time, the activation of immune cells and the pathogenic adaptation can be quantified. In cooperation with the FG ASB, a virtual infection model has been developed that allows the measurability of the dynamics of this interaction. (Hünniger et al., 2014).

-  Auskeimende Zellen der humanpathogenen Hefe *C. albicans* werden von einer NK Zelle phagozytiert.
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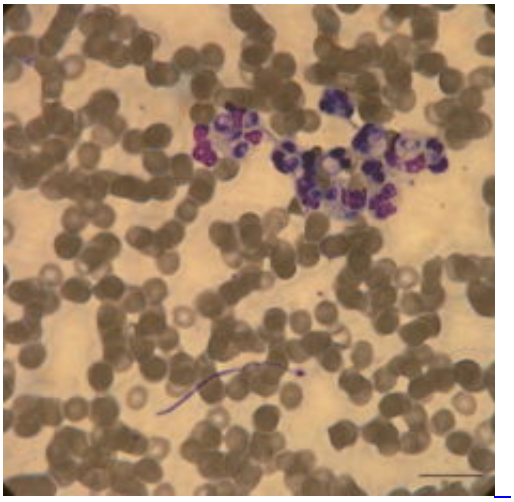 *C. albicans* assoziiert im Blut vorwiegend mit neutrophilen Granulozyten.