Automated quantification of the phagocytosis of *Aspergillus fumigatus* conidia by a novel image analysis algorithm.

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Details

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Abstract

Studying the pathobiology of the fungus *Aspergillus fumigatus* has gained a lot of attention in recent
years. This is due to the fact that this fungus is a human pathogen that can cause severe diseases, like
invasive pulmonary aspergillosis in immunocompromised patients. Because alveolar macrophages belong to the first line of defense against the fungus, here, we conducted an image-based study on the

host-pathogen interaction between murine alveolar macrophages and *A. fumigatus*. This is achieved
by an automated image analysis approach that uses a combination of thresholding, watershed segmentation and feature-based object classification. In contrast to previous approaches, our algorithm allows for the segmentation of individual macrophages in the images and this enables us to
compute the distribution of phagocytosed and macrophage-adherent conidia over all macrophages.
The automated imaged-based analysis provides access to all cell-cell interactions in the assay and thereby represents a framework that enables comprehensive computation of diverse characteristic parameters and comparative investigation for different strains. We here applied automated image analysis to confocal laser scanning microscopy images of the two wild-type strains ATCC 46645 and
CEA10 of *A. fumigatus* and investigated the ability of macrophages to phagocytose the respective conidia. It is found that the CEA10 strain triggers a stronger response of the macrophages as revealed
by a higher phagocytosis ratio and a larger portion of the macrophages being active in the phagocytosis process.

Study data: http://www.leibniz-hki.de/en/pictures.html

Involved units

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