

Regulatory control of epithelial damage during *Aspergillus fumigatus* infection

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1. Introduction

- A unifying feature of *Aspergillus fumigatus* lung disease is epithelial damage, the regulatory control and the mechanistic basis of which is poorly characterised.
- Previous studies¹ have identified a number of fungal attributes such as epithelial adhesion, spore uptake, germination, hyphal penetration and release of secreted factors as critical contributors to epithelial damage during *A. fumigatus* invasive infection.
- This study aims to identify, characterise and mechanistically understand the *A. fumigatus* transcription factors driving those activities during epithelial infection.

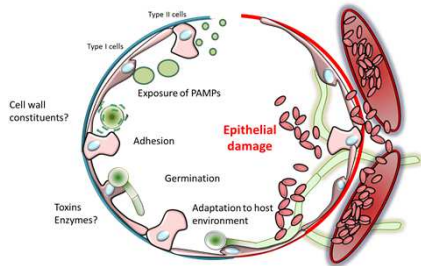


Figure 1: Schematic of interaction of *A. fumigatus* inside the alveoli of a lung. *A. fumigatus* conidia initiate pathogenesis by a series of events leading to epithelial disintegration causing invasive disease.

2. High-throughput screening for epithelial damage

In order to identify the regulators of epithelial cell damage, an A549 epithelial cell model was challenged with 479 *A. fumigatus* transcription factor mutant strains and epithelial damage was assessed by screening for cell detachment and cell lysis.

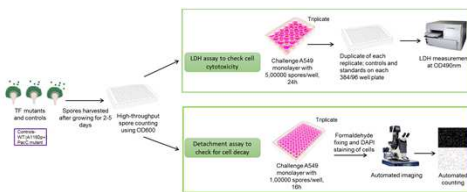


Figure 2: High-throughput methodologies used for screening epithelial damage. The TF mutant library was grown for 2-5 days to harvest sufficient spores; the spores were counted using OD⁶⁰⁰ measurement and were challenged against A549 cells. LDH in cell supernatant was measured by OD⁴⁹⁰ after 24 hours in a 96 or 384 well plate for quantitation of cell lysis. Detachment of epithelial cell monolayer after 16 hours was imaged and quantitated automatically in a 96 well plate to determine cell decay.

3. Regulators of epithelial damage

3.1 Epithelial cell detachment

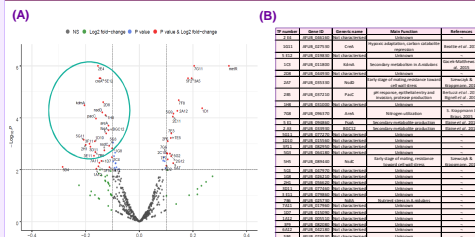


Figure 4: Screening for regulators of epithelial cell detachment. (A) Volcano plot showing the output from the detachment screen transformed as fold change number of adherent cells for the 479 *A. fumigatus* TF mutants, with biological difference in the x axis and statistical difference in the y axis. (B) Table showing the identified TFs driving epithelial cell detachment.

3.2 Epithelial cell lysis

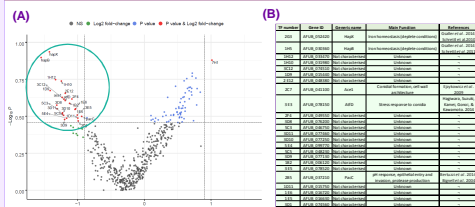


Figure 5: Screening for regulators of epithelial cell lysis. (A) Volcano plot showing the output from the LDH screen for the 479 *A. fumigatus* TF mutants, with confidence interval from bio-informatic analyses on the y axis versus fold change LDH to the WT on the x axis (B) Table showing the identified TFs driving epithelial cell lysis.

4. Epithelial damage and growth

Screening of the 479 *A. fumigatus* TF mutants for growth using OD measurement at 24 hours identified the slow growing TF mutants.

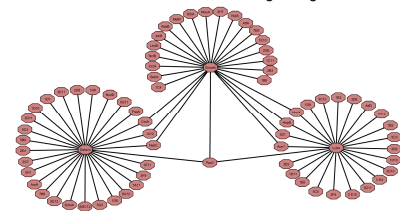


Figure 6: Correlation of *A. fumigatus* regulators of epithelial damage with growth. *A. fumigatus* TFs driving epithelial cell detachment (in left) and epithelial cell lysis (in right) and their relation with slow growing mutants (in centre).

5. Attributes driving epithelial damage

In order to identify factors driving epithelial damage by the identified regulators of epithelial damage, the TF mutants were tested for attributes previously reported to contribute to epithelial damage¹.

5.1 Adhesion capacity to epithelial cells

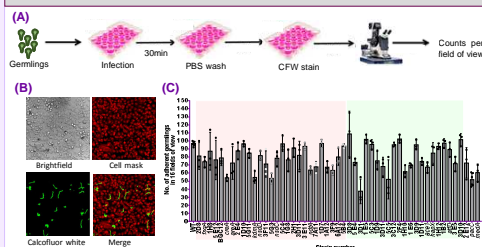


Figure 7: Adhesion capacity of *A. fumigatus* mutants to A549 cells. (A) Germlings incubated with A549 cells for 30 min to enable adhesion were washed to stain and visualise only the adherent germlings (B) Representative images of brightfield, cell mask stained A549 cells and calcofluor white stained germlings captured with TCS-SP8 confocal microscope at 40x magnification (C) Total number of adherent germlings for the identified *A. fumigatus* TF mutants. WT=parental strain

5.2 Germination efficiency and hyphal extension

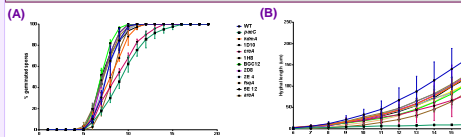


Figure 8: Germination efficiency and hyphal lengths of *A. fumigatus* mutants. (A) Percentage germinated spores and (B) hyphal lengths of the identified TF mutants calculated by assessing growth using time-lapse imaging with the TCS-SP8 confocal microscope. WT=parental strain

5.3 Spore internalisation by epithelial cells

