

P30 & FP – Airway mycobiota in severe asthma: isolation from the exhaled breath condensate

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Background: There is current evidence to demonstrate a close association between fungal sensitisation and asthma severity. This can be due simply to exposure to high levels of fungal spores where they have been implicated as a cause of severe exacerbations. Exhaled breath condensate (EBC) collection potentially offers a less invasive alternative for lung mycobiota sampling.

Objective: This study was carried out to investigate the clinical and immunological features of severe asthmatics with a fungal colonization detected in EBC.

Methodology: We enrolled 27 subjects with a diagnosis of severe asthma. They underwent to spirometry, fractional exhaled nitric oxide (FeNO) analysis, skin prick tests, total IgE and blood and sputum count cell collection. Selected EBC were plated directly onto fungal specific culture and fungi were identified by morphology and species identity was confirmed by DNA sequencing.

Results: A fungal sensitisation to at least 1 fungal allergen in the EBC of 66.7% of enrolled subjects with severe asthma was detected. The most common species were *Cladosporium spp* (72.2%) followed by *Aspergillus* (50%), *Penicillium* (44%) and *Alternaria* (22%) species. Fungal colonization was higher in female, non-atopic and obese severe asthmatics with an eosinophilic inflammation and a fixed airflow obstruction.

Conclusions / Implications for practice: The association of a positive EBC culture in severe asthmatics with an eosinophilic inflammation, without atopy and with fixed airway limitation support the hypothesis that a chronic fungal airway colonization might have an important role in the pathogenesis of this severe asthma phenotype and encourages the use of the analysis of exhaled mycobiota in these subjects.

References

1. Agbetile J, Fairs A, Desai D, Hargadon B, Bourne M, Mutalithas K, Edwards R, Morley JP, Monteiro WR, Kulkarni NS, Green RH, Pavord ID, Bradding P, Brightling CE, Wardlaw AJ, Pashley CH. *Isolation of filamentous fungi from sputum in asthma is associated with reduced post-bronchodilator FEV1*. Clin Exp Allergy. 2012 May;42(5):782-91.
2. Carpagnano GE, Malerba M, Lacedonia D, Susca A, Logrieco A, Carone M, Cotugno G, Palmiotti GA, Foschino-Barbaro MP. *Analysis of the fungal microbiome in exhaled breath condensate of patients with asthma*. Allergy Asthma Proc. 2016 May;37(3):41-6.