INTRODUCTION

- Aspergillus bronchitis is a chronic non-invasive infection of the lower respiratory airways that affects immunocompetent patients, although the global burden of disease is unknown (1).
- Patients with symptoms of chronic pulmonary disease, microbiological evidence of Aspergillus in the airways (culture or PCR) and Aspergillus-specific IgG antibodies that do not fulfill the diagnostic criteria for chronic pulmonary aspergillosis, allergic bronchopulmonary aspergillosis or invasive aspergillosis may have Aspergillus bronchitis (2).
- Although A. fumigatus is the most common species isolated from lungs of individuals with Aspergillus bronchitis, other Aspergillus species have been described as causative agents. Bacterial pathogens are also commonly observed in Aspergillus bronchitis (2).
- Our objective was to define host and pathogen factors contributing to Aspergillus bronchitis.

HOST FACTORS

- We have previously described a mutation (rs35699176) in the human transcription factor ZNF77 associated with lung colonisation of the respiratory airways of patients with allergic bronchopulmonary aspergillosis (3).
- The presence of the genetic variant in rs35699176 was analysed on 46 DNA samples from patients with Aspergillus bronchitis. A 663 bp amplicon of the genomic region containing the genetic variant rs35699176 was amplified by PCR and sequences were resolved by Sanger sequencing (3).
- Prevalence of the genetic variant was compared to that found in patients with allergic bronchopulmonary aspergillosis in our previous study or in the healthy population.

RESULTS

- ZNF77(rs35699176) (GA) was present in 19% of patients with Aspergillus bronchitis. Allele frequency for the variant associated with fungal colonisation was higher in patients with Aspergillus bronchitis than in those with allergic bronchopulmonary aspergillosis (ABPA, 9%) or healthy controls (0%) (Figure 1).
- ABPA vs Aspergillus bronchitis: P = 0.09; OR: 0.37 [95% IC = 0.1307 to 1.011]; Aspergillus bronchitis vs healthy: P < 0.0001: OR: 0.02 [95% IC = 0.004 to 0.084].

CONCLUSIONS

- The prevalence of the fungal-colonisation at risk allele rs35699176 in patients with Aspergillus bronchitis was higher than the reported for patients with fungal allergy.
- The mycobiome of patients diagnosed with Aspergillus bronchitis indicates high levels of Cladosporium and Alternaria, raising the possibility that this clinical entity is actually ‘fungal bronchitis’, ‘airway mycosis’ or ‘fungal-associated airways disease’ rather than aspergillosis.
- Further research is needed to investigate the link between the presence of rs35699176 and the colonisation of the airways by non-Aspergillus species.

REFERENCES