

Molecular characterization of *Aspergillus terreus* species complex clinical isolates: a multicentre study in eight university hospitals

27th **ECCMID** Vienna, Austria
22 – 25 April 2017
EP390 The congress of ESCMID

S. Imbert^{1,2,3}, A-C Normand⁴, S. Ranque⁴, JM. Costa⁵, C. Hennequin⁶, I. Accoceberry⁷, C. Bonnal^{1,8}, S. Houzé⁸, A. Fekkar³, N. Bourgeois⁹, R. Piarroux⁴, E. Dannaoui^{2,10,11}, F. Botterel^{1,2}

¹ Unité de Parasitologie - Mycologie, Département de Microbiologie, DHU VIC, CHU Henri Mondor, AP-HP, Créteil, France; ² EA Dynamyc 7380 UPEC, ENVA, Faculté de Médecine de Créteil, Créteil, France; ³ Service de Parasitologie-Mycologie, CHU La Pitié-Salpêtrière, AP-HP, Paris, France; ⁴ Service de Parasitologie-Mycologie, Hôpital de la Timone, Marseille, France; ⁵ Laboratoire CERBA, Saint Ouen L'Aumône, France; ⁶ Service de Parasitologie-Mycologie, AP-HP, Hôpital Saint Antoine, Paris, France; ⁷ Service de Parasitologie-Mycologie, CHU Bordeaux, France; ⁸ Service de Parasitologie-Mycologie, AP-HP, Hôpital Bichat, Paris, France; ⁹ Service de Parasitologie-Mycologie, CHU Montpellier, France; ¹⁰ Hôpital Européen Georges Pompidou APHP, Paris France; ¹¹ Université Paris Descartes, Paris France.

Introduction

- *Aspergillus terreus* is one of the 5 most frequent pathogenic *Aspergillus* species after *A. fumigatus*.
- Infections due to *A. terreus* can be problematic to manage because of its intrinsic resistance to amphotericin B.
- *A. terreus* has been shown to be part of the *A. terreus* species complex, currently comprising 14 recognized cryptic species. All these species share morphological characteristics and their prevalence in clinical samples is largely unknown.

Aim of the study

- In this study we present the molecular characterization of a panel of clinical isolates belonging to the *A. terreus* species complex and collected from 8 French university hospitals.

Methods

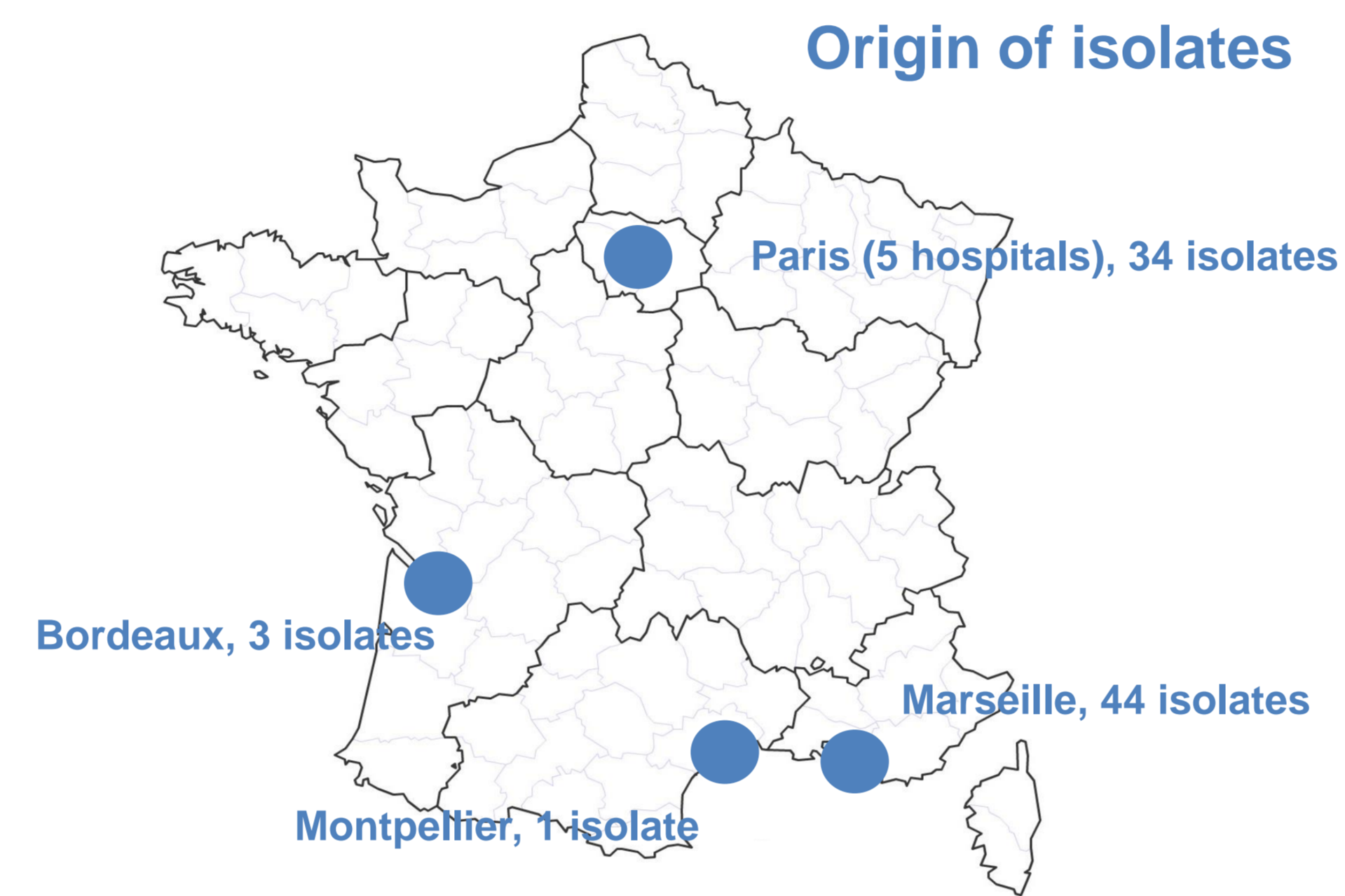
- Eighty-two clinical isolates were recovered from a variety of specimens over a 13-year period (2003-2015).
- For each isolate, age, sex, underlying disease of the patient, site of isolation and clinical form of aspergillosis were retrieved.
- Isolates were initially identified as members of *A. terreus* species complex by morphological characteristics.
- Each isolate was identified to the species level by sequencing a part of the β -tubulin and calmodulin genes.
- Neighbor-joining trees were built to perform phylogenetic analyses (MEGA 6.0 software).

References

1. Guinea J, 2015. J Clin Microbiol 53(2): 611-7
2. Hachem R, 2014. J Antimicrob Chemother 69: 3148-55

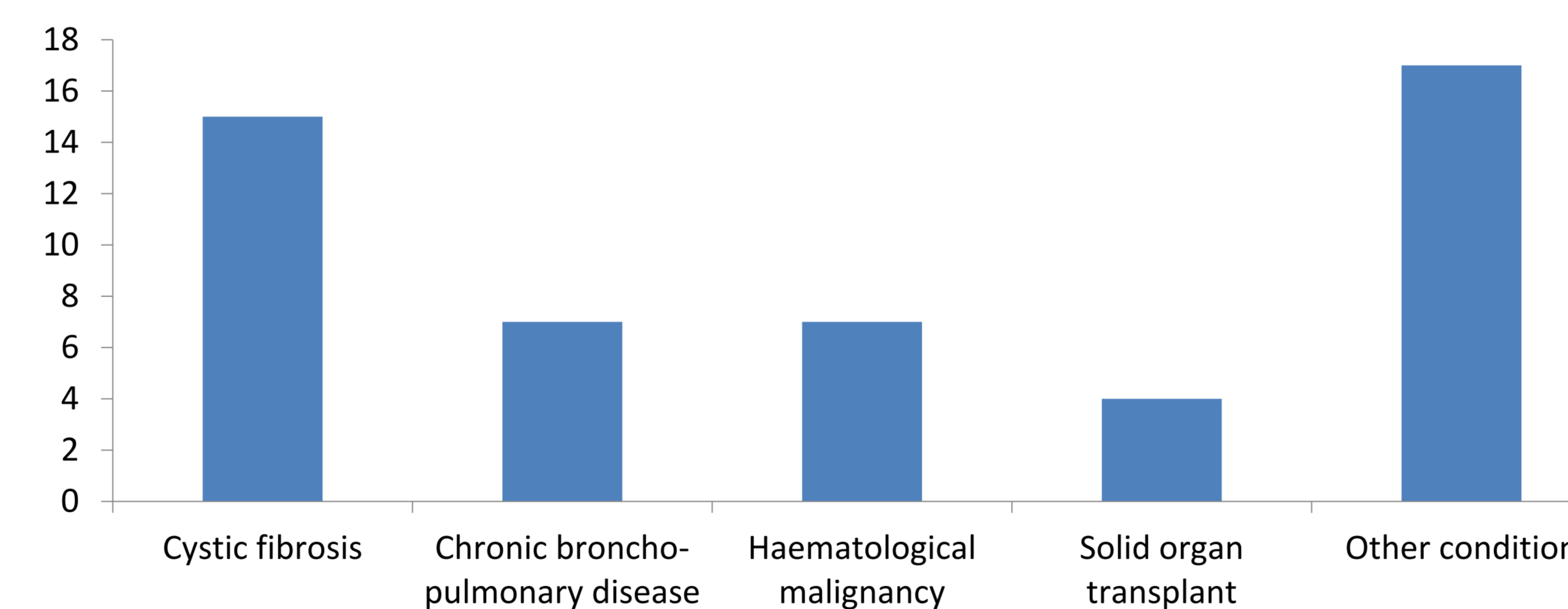
Contact : francoise.botterel@aphp.fr, eric.dannaoui@aphp.fr

- Eighty-two isolates were collected from 50 patients



- Mainly from respiratory samples (89%)

Underlying diseases



- Clinical forms

Mainly bronchial colonization: n = 44

Invasive aspergillosis: n = 5 (*A. terreus sensu stricto*)

Onychomycosis: n = 1 (*A. hortai*)

Results

- Species identification

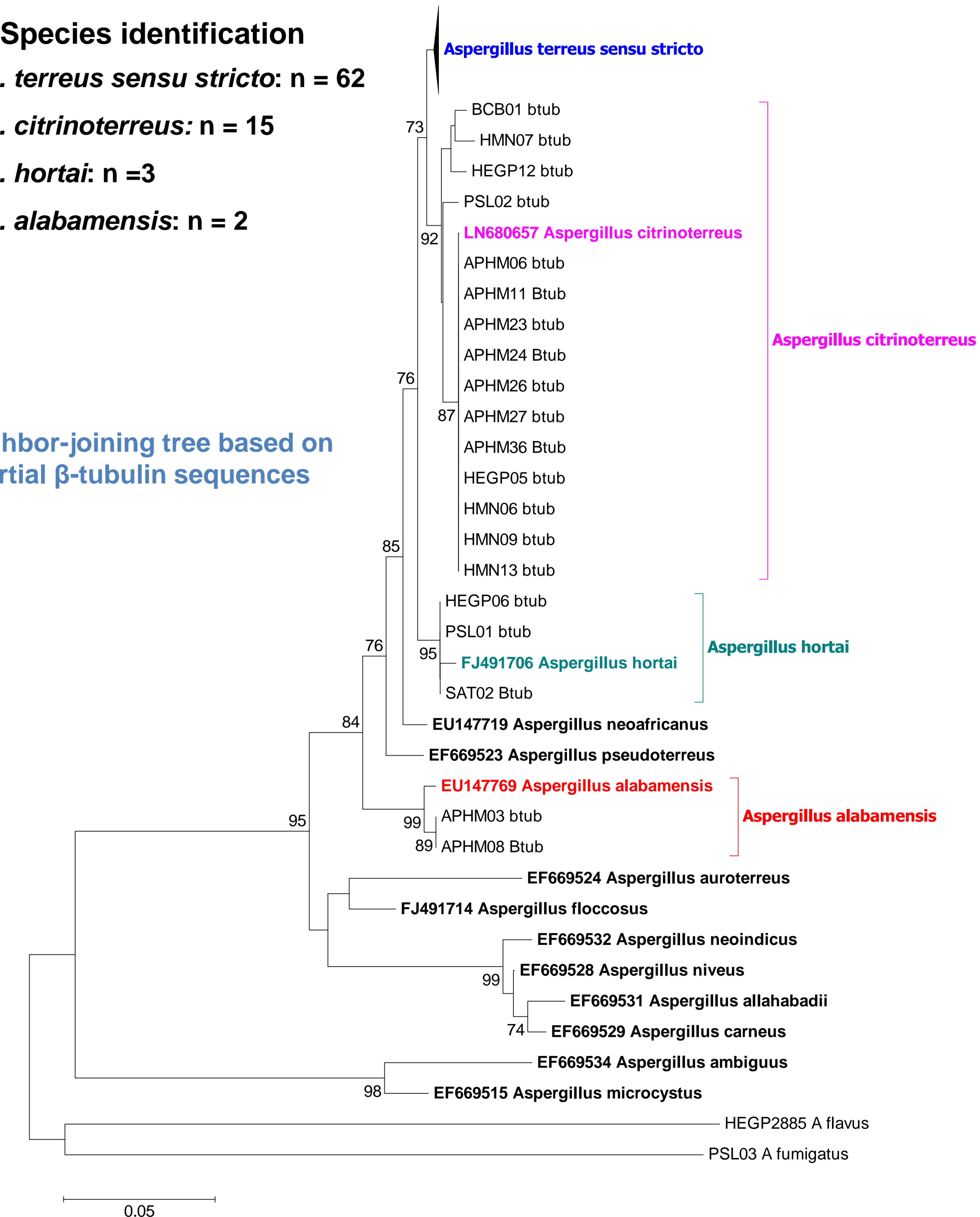
A. terreus sensu stricto: n = 62

A. citrinoterreus: n = 15

A. hortai: n = 3

A. alabamensis: n = 2

Neighbor-joining tree based on partial β -tubulin sequences



Conclusion

For the first time in France, we molecularly characterized a large collection of clinical isolates belonging to *A. terreus* species complex. *A. terreus sensu stricto* was the most common species and was responsible for the 5 cases of invasive aspergillosis. However, 25% of these clinical isolates were cryptic species other than *A. terreus sensu stricto*. Further studies are warranted to investigate the clinical impact of these cryptic species, as well as their antifungal susceptibility.