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In silico MLST for *Aspergillus* species identification and CYP51 gene characterization.

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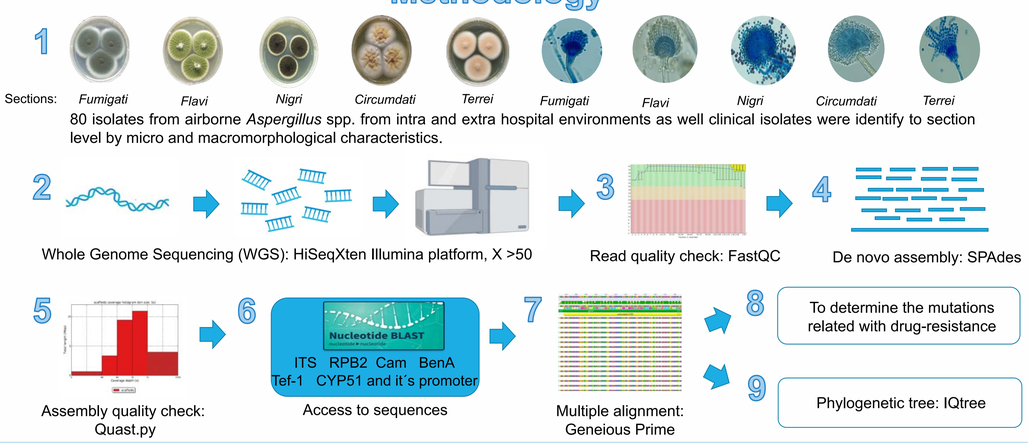
Introduction

Aspergillus spp. is an environmental fungi that can causes from localized infectious and allergic forms, to severe invasive disseases[1]; these clinical entities are a major health problem, with a rapidly evolving epidemiology and new groups of patients at risk[2].

A. fumigatus is the major etiologic agent of aspergillosis, but a few other *Aspergillus* species such as *A. niger*, *A. flavus* and *A. terreus* can also cause infections[3]. While most of these pathogens are phenotypically distinguished to section level, there is not enough resolution power to identify the species between the same section as they share near identical morphological characteristics[4]. For that reason, genomic identification of *Aspergillus* species is an alternative with better resolution power; and it provides additional information about biological, virulence and drugs resistance characteristics.

The objective was to identify *Aspergillus* species through MLST and characterize the *CYP51* gene.

Methodology



Results

Section	Percentage (%)
Fumigati	32.9
Nigri	28,6
Flavi	25,2
Terrei	6,1
Circumdati	3,6
Nidulantes	3,6

Table 1. *Aspergillus* sections distribution identified by morphological characteristics.

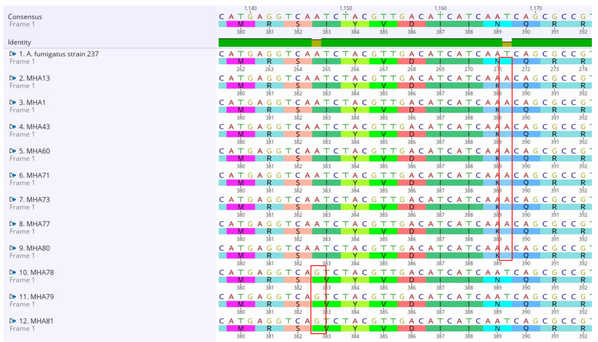


Figure 1. CYP51A mutations I242V and N248K related to azole drug-resistance in strains isolated.

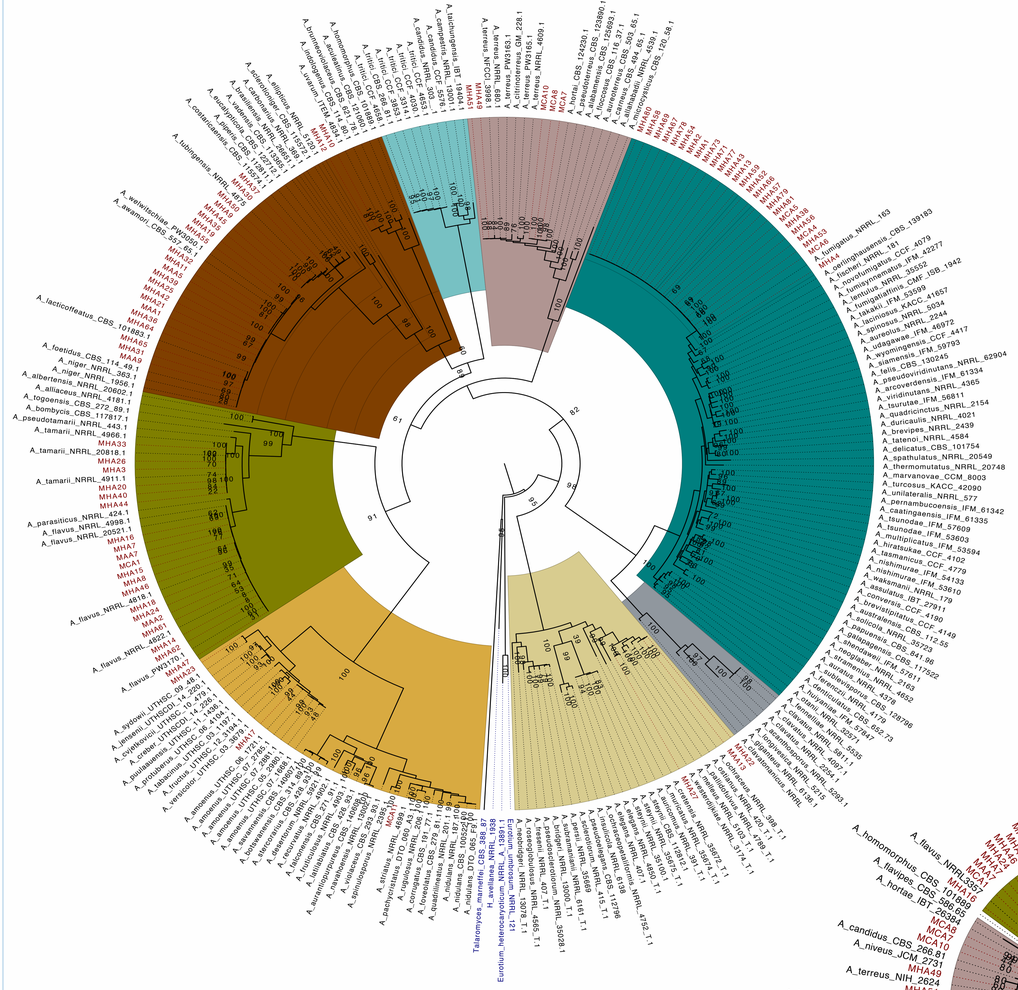


Figure 3. Phylogenetic tree based on single data set of **exon 4 Tef-1a** sequences showing the relationship between *Aspergillus* species. The probability values and bootstrap percentages of the maximum likelihood analysis are presented at the nodes. *Talaromyces marneffei* was used as outgroup. Colors represent different *Aspergillus* sections. Reference sequences where obtained from NCBI and Mycocoms database and they are colored in black. Isolates from this study are colored in red.

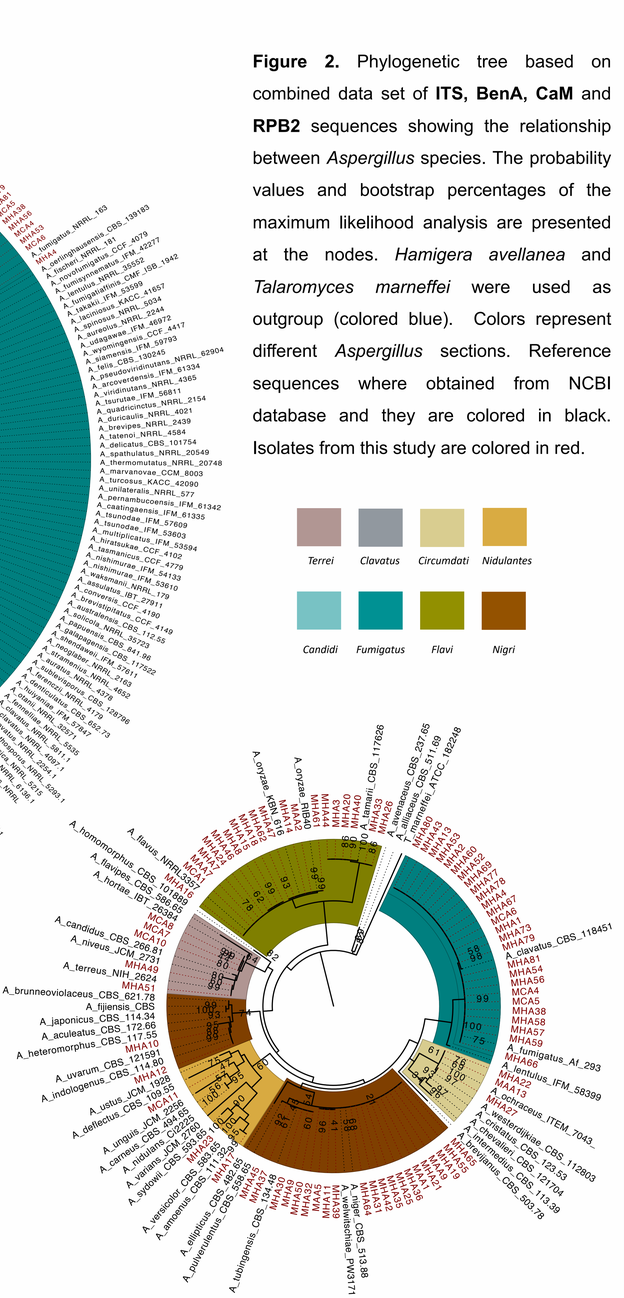


Figure 2. Phylogenetic tree based on combined data set of **ITS, BenA, CaM** and **RPB2** sequences showing the relationship between *Aspergillus* species. The probability values and bootstrap percentages of the maximum likelihood analysis are presented at the nodes. *Hamigera avellanea* and *Talaromyces marneffei* were used as outgroup (colored blue). Colors represent different *Aspergillus* sections. Reference sequences where obtained from NCBI database and they are colored in black. Isolates from this study are colored in red.

Conclusions

- The morphological classification to section level had good correlation with the subsequent molecular classification. Species identification was achived using MLST analyzes of BenA, CaM and RPB2 genes, however some of the isolates will need extra analysis using whole genome sequences from this study and the ones reported on database (e.g Section *Nigri* and *Flavi*).
- The exon 4 of Tef-1a has great discriminatory power, however, more reference sequences will be includ for further analysis. Phylogenetic analysis showed similar classification as in figure 2.

References:

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Acknowledgments:

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