Draft Genome Sequence of 11 clinical and environmental Colombian isolates of genus Aspergillus.

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Background: The genus Aspergillus is a group of opportunistic fungi that cause infections, with high morbi-mortality in immunosuppressed patients. Approximately 350 species have been described in this genus, classified in 4 subgenus and 20 sections. In Colombia, *Aspergillus fumigatus* is the most frequent species in these infections. However, in the last years an increase in the incidence of other species has been observed. This added to an increase in the quantity and diversity of Aspergillus isolates in hospital environments.

Aims: Characterize the phenotype and genotype of clinical and environmental Colombian isolates of *Aspergillus spp.*

Methods: We collected 11 Colombian isolates of Aspergillus: 4 from diferents clinical samples, 6 from hospital environments and 1 from extra-hospital environments. The isolates were identified according to their macro and microscopic characteristics. Genomic DNA for sequencing was prepared from mycelium culture using phenol/chloroform extraction. Library preparation and 150-bp paired-end sequencing was performed using the Illumina HiSeq 2500 platform. The reads was *de novo* assembled using SPAdes 3.10 pipeline. The draft genome assembly quality was analyzed by QUAST. Augustus v3.0.1 and GlimmerHMM were used for gene prediction. Inference by sequence homology was performed with OrthoFinder v2.0.9. IQtree v1.4.4software was used for phylogenetic reconstruction by ML.

Results: In this study, four of the eleven isolates classified phenotypically were re-classified correctly after genome analysis. We obtained whole genome sequence of 4 clinical and 7 environmental isolates, including 3 novel genome sequences of the genus *Aspergillus* not reported in the databases: *A. tritici* (Clinical)*, A. tamarii* (hospital environment) and *A. amoenus* (extra-hospital environment).

Conclusion: The results of this study provide useful data for the genomic comparison between clinical and environmental isolates of Aspergillus. Valuable information that can be used to understand the evolutionary relationships, determine the diversity and level of production of enzymes and secondary metabolites, predict the pathogenicity and response of this opportunistic fungus to antifungal agents.