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Prevalence of different *Aspergillus* species in the United States: one-year surveillance study of clinical isolates from a reference laboratory

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Background: Invasive aspergillosis is the most common invasive mould infection in highly immunocompromised individuals, including solid organ and hematopoietic stem cell transplant recipients, and patients with hematologic malignancies. Although species such as *A. fumigatus*, *A. flavus*, *A. niger*, and *A. terreus* remain the primary causes of invasive infections, other rare species have been associated with disease in profoundly immunocompromised hosts. Our objective was to evaluate the prevalence of different *Aspergillus* species received by our reference laboratory during a 1 year period.

Material/methods: Clinical isolates of *Aspergillus* species, received by the Fungus Testing Laboratory at the UT Health Science Center San Antonio as part of a surveillance study between October 2015 and September 2016, were included. These included isolates from various institutions across the United States. All species identifications were made by combined morphologic/phenotypic characterization, including microscopic analysis and temperature studies, and by DNA sequence analysis of the partial β -tubulin and calmodulin genes.

Results: 854 clinical *Aspergillus* isolates were included. Species within section *Fumigati* were the most prevalent, consisting of 57.6% of all isolates, followed by those in sections *Nigri* (17.7%), *Flavi* (8.8%), *Terrei* (6.8%), *Nidulantes* (2.7%), *Usti* (2.6%), *Versicolores* (2.3%), *Circumdati* (0.9%), and *Aspergillus* (0.6%). Within section *Fumigati*, *A. fumigatus* was the most prevalent (95.5% within section, 55% overall). Several cryptic species within section *Fumigati* were identified, including *A. hiratsukae* (n = 6), *A. lentulus* (n = 7), *A. thermomutatus* (4), *A. udagawae* (4), and *A. viridinutans* (1). Cryptic species were also identified within other sections (e.g., *A. nomius*, *A. tamarii*, *A. alabamensis*, *A. citrinoterreus*, *A. delacroixii*, *A. tubingensis*, *A. welwitschiae*). Just over half of the isolates (50.1%) were collected from a respiratory-tract source (bronchial-alveolar lavage fluid, bronchial wash, lung tissue, sputum).

Conclusions: Aspergillosis is caused by a variety of different species within the U.S. Species within *Aspergillus* section *Fumigati* were the most prevalent, with *A. fumigatus* being the most common of all species identified. Several cryptic species were also identified during this one year period, many of which are known to have reduced susceptibility to different antifungal classes. Most isolates were from a pulmonary source, but many were collected from sites outside of the respiratory tract.