

Molecular epidemiology and virulence assessment of *Aspergillus fumigatus* isolates from white stork chicks and their environment.

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Abstract

Aspergillus fumigatus is a common pathogen in poultry and captive wild birds and an emerging opportunistic fungal pathogen in immunocompromised humans. Although invasive aspergillosis is frequently reported in free-ranging wild birds, the incidence and epidemiology of the disease in a natural setting is unknown. We recently reported endemic outbreaks of invasive aspergillosis at white stork nesting sites close to human habitation in Germany with significant subsequent breeding losses. Therefore, we hypothesized that *A. fumigatus* strains with higher virulence in birds may have evolved in this environment and performed the first epidemiological analysis of invasive aspergillosis in free-ranging wild birds. Sixty-one clinical and environmental *A. fumigatus* isolates from six affected nesting sites were genotyped by microsatellite analysis using the STRAf-assay. The isolates showed a remarkable high genomic diversity and, contrary to the initial hypothesis, clinical and environmental isolates did not cluster significantly. Interestingly, storks were infected with two to four different genotypes and in most cases both mating types MAT-1.1

and MAT-1.2 were present within the same specimen. The majority of selected clinical and environmental strains exhibited similar virulence in an in vivo infection model using embryonated chicken eggs. Noteworthy, virulence was not associated with one distinct fungal mating type. These results further support the assumption that the majority of *A. fumigatus* strains have the potential to cause disease in susceptible hosts. In white storks, immaturity of the immune system during the first three weeks of age may enhance susceptibility to invasive aspergillosis.

Involved units

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