27th ECCMID Vienna, Austria 22 – 25 April 2017

The congress of ESCMID

Session: P071 Epidemiology of fungal infections II

Category: 6a. Fungal disease epidemiology & clinical trials

24 April 2017, 13:30 - 14:30
P1440

Exploring the epidemiology and diversity of fungal isolates in a large tertiary haematology unit in London, UK

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Background: Fungal infection is a major cause of morbidity and mortality in patients with haematological disease. With growing concerns of antifungal resistance and a limited pool of antifungal classes for the management of such infections, there is a paucity of data describing the epidemiology and diversity of fungal isolates and resistance patterns within haematology cohorts in the UK. We describe the fungal isolates identified within a large tertiary haematology unit in London, UK that manages adult patients, including performing stem cell transplantation.

Material/methods: Electronic microbiology records were reviewed to identify all positive fungal cultures identified between June 2011 and January 2015. Demographics, clinical case histories, antifungal therapy (including prophylaxis), and outcome data for individuals with positive isolates was extracted from electronic medical records. Data was analysed using SPSS (22.0, IBM).

Results: Between June 2011 and January 2015 56 individuals had 78 positive fungal cultures. Median (IQR) age of the cohort was 57(40-69) years and the majority were male (39/56;70%) and white ethnicity (33/56;59%). 51/57(89%) had a haematological malignancy with 31/57(54%) pre- stem cell transplantation receiving chemotherapy and 20/57(35%) in the post-transplant period. At the time of fungal culture patients were neutropaenic (<0.5 $x10^9$/L) in 14/70 (20%) of cases and median (IQR) C-reactive protein was 74(22-127) mg/L.

Of the 78 identified organisms, yeasts predominated with commonly cultured species including *Candida albicans* (18/78;23%), *Candida glabrata* (11/78;14%), *Saccharomyces cervisiae* (9/78;12%), and *Candida krusei* (7/78;9%). *Aspergillus fumigatus* was the commonest filamentous species (6/78;8%). The commonest site for fungal isolation was in the lower respiratory tract with 45/78(58%) isolates in sputum and a further 5/78(6%) samples cultured from bronco-alveolar lavage (BAL). Blood stream infection was identified in 9/78(12%) of cultures with a further 1/78(1%) culture from a central venous line. A further 18/78(23%) samples were identified in other sites.

Of the 56 individuals with positive fungal cultures 36/56(64%) have died with median (IQR) time between first positive fungal culture and death 151 (53-469) days. 8/10(80%) of the blood stream / line cultures were associated with mortality. *Candida albicans* was the commonest species associated with mortality (8/36;22%), with *Saccharomyces cervisiae* (5/36;14%) and *Aspergillus fumigatus* (4/36; 11%) second and third, respectively.

Conclusions: We have described the epidemiology of fungal infections from a large haematology transplantation centre in the UK. Yeasts were the most commonly isolated fungi with respiratory samples being the most common source for positive culture. Blood stream and BAL positive cultures were associated with high mortality. Further work must be undertaken to explore the distribution of antifungal resistance within this cohort and investigate the potential unintended consequences of long term antifungal prophylaxis used within this population.