Towards standardization for mycological examination of sputum samples from Cystic Fibrosis patients: From the French multicenter experience to an international study

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Résumé en anglais	**Introduction:** Prognosis of cystic fibrosis (CF) essentially depends on impairment of the lung function. While considerable attention therefore has been paid over recent decades to the prevention and treatment of bacterial respiratory infections, leading to a marked increase in life expectancy of the patients, prevalence of colonization of the airways by filamentous fungi or yeasts, sometimes leading to true respiratory infections, has been regularly increasing. However, recently, Borman et al. (2010) reported wide variations in the range of the causative fungal pathogens and in their prevalence, related at least to a lack of standardization in the methods used to detect these microorganisms. **Here, our aims are:** • to analyze the impact of the culture conditions used on the detection of specific fungal pathogens throughout the French multicenter experience, and • to discuss the methods used in various European or Australian laboratories, in order to carry out an international prospective study that will make possible a standardized protocol for efficient detection of the whole fungal biota that can be encountered in respiratory secretions of CF patients. **Results:** First, from January 2007 to the end of 2009, a multicenter study was conducted in France encompassing 7 university or general hospitals which agreed to use the same procedure for mycological analysis of sputum saples from CF patients, including prior digestion of the sample with dithiolbutane and inoculation of the digested sample on 6 semi- selective agar-based media ("MucoFong" study – PHRC1902). Data obtained during one year were analyzed using the CHAID (Chi-squared Automatic Interaction Detector) method, which is a statistical approach able to give best association of media to detect a specific pathogen. CHAID is a type of decision tree technique, based upon adjusted significance testing that we apply to our data in order to define the best set of semi-selective media able to isolate 99.99% of the fungal pathogens that were detected in our CF population. Second, the major data of the international survey will be presented, and discussed with the purpose of developing a standardized approach for mycological examination of respiratory secretions from CF patients. **Conclusion:** Defining the optimal method for mycological analysis of the fungal components of CF lungs microbiome through a large international study is becoming a major requirement. This will make possible not only to analyze the role of some "rare" filamentous species in CF exacerbation or the existence of geographic variations in the fungal species that colonize the airways, but also to study the complexity of the CF lung microbiome as well as its dynamics.
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