Hansen's disease in Northeast Brazil

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Background: Hansen's disease is an infectious malady with an insidious evolution caused by *Mycobacterium leprae.* This bacteria is transmitted through contact with damaged skin/mucosa or oropharyngeal/nasal secretions of infected patients. Peripheral nerves can be affected by this disease too, which can be incapacitating if left untreated. In spite of the Brazilian government efforts to contain the dissemination of Hanseniasis, it is still an important public health problem, mainly in the poorer areas of the country, including the Northeast region. Knowing the disease epidemiology, making early diagnosis and initiating adequate treatment and follow up are indispensable tools to achieve its control. In order to understand the epidemiology of Hansen's disease in our city, we conducted the present study.

Methods: This is a retrospective cohort study of all the patients with Hansen's disease diagnosed and treated in the Dona Libânia Dermatology Reference Center, in Fortaleza, Ceará, Northeast Brazil, in 2008. Patients' medical records were reviewed and the data collected was analyzed utilizing the Epi Info 3.5 program.

Results: A total of 273 patients were included in the study and 52% were female. Most prevalent age intervals were 41-60yrs (39,19%) and 20-40yrs (35,16%). Hypochromic or eritematous patches, presence of skin nodules or plaques, neuropathic pain and functional sequelae were the most frequent signs/symptoms found on admission, with prevalence of 81,7%, 59,6%, 23,1% and 13,3% respectively. In 27,8% patients the disease could not be classified. The remaining was classified as follow: 37% borderline, 20,5% tuberculoid, 11,4% lepromatous and 3,3% indeterminate. Only in 16,5% of the patients a household contact was identified as a reservoir of the bacteria.

Conclusion: Hansen's disease is still a prevalent disease in our city. Most of the patients were adults, in productive working ages. Some of them presented with functional incapacity or advanced neural damage on admission suggesting an unacceptable delay in the diagnosis. Our findings point to the necessity of a better identification of risk factors, investigation of reservoirs and the use of more sensitive methods for early detection of leprosy in order to achieve adequate control of the disease.

31.004

Identification of immunogenic proteins of *Mycobacterium avium* with diagnostic potential

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Background: Non-tuberculous mycobacteria (NTM) is the term used to define all the remaining species from *Mycobacterium tuberculosis* complex species (MTC). The major ness. Members of the *Mycobacterium avium* complex (MAC) may be found in drinking water systems and is now more frequently isolated than MTC and represents the 26% of the total mycobacterial isolates from chronic pulmonary disease of NTM. Since the ubiquitous occurrence of MAC organisms in the environment, and the clinical presentation may be indistinguishable from tuberculosis, the diagnosis of pathogenic agent is important to apply the correct antibacterial treatment. In order to find a diagnostic tool to distinguish between MAC from MTC, we have use an immunoproteomic approach to find immunogenic proteins from *M. avium* and *Mycobacterium bovis* BCG strain México to represent MAC and MTC respectively.

Methods: With a panel of 52 serum samples classified into four groups: patients with active pulmonary tuberculosis, patients with chronic pulmonary by NTM, subjects with positive reaction to protein derivative (PPD) who were healthy household contacts and those with negative reaction who were the healthy uninfected controls, ELISA test was performed for titration of IgG2 against 16 mycobacterial strains from three groups: *M. tuberculosis*, *M. bovis* BCG and NTM. The sera with higher titers were used to obtain the immunoproteomes. A standard proteomic analysis of BCG Mexico and *M avium* M7 began with the separation and visualization of the protein mixture using two-dimensional polyacrylamide gel electrophoresis (2-DE) followed by Western blotting for the screening of immunogenic proteins using selected sera.

Results: The comparison between the immunodetection of different sera: TB, MNT and PPD+/− against BCG Mexico gave about 80% of unique proteins and 20% of proteins shared among different sera. The immunodetection in *M. avium* gave 90% of unique proteins and 10% of proteins shared among the same sera.

Conclusion: The comparative analysis between immunoproteomes of BCG Mexico and *M. avium* allowed the identification of candidate proteins for the differentiation between pulmonary disease caused by NTM and BCG Mexico as a member of MTC.

31.005

Characterization of nontuberculous mycobacteria isolated of potable water distribution system and wastewater of Mexico City Metropolitan Area

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Background: Background: Nontuberculous mycobacteria (NTM) are normal inhabitants of the environment and they are found in soil, dust and water including natural and potable water and since there is no evidence of person-to-person transmission, the water is considered the main vehicle for transmission of nontuberculous mycobacteria. Some studies have shown that the rate of infection by nontuberculous mycobacteria is increasing in predisposing hosts as well as healthy persons. On the other hand NTM may alter replication of vaccine *Mycobacterium bovis* Bacillus