Prognostic markers and out comes in severe leptospirosis in a tertiary care hospital from south India

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Background: Leptospirosis is a common zoonotic disease causing epidemics all over the world. Severe leptospirosis with multiple organ involvement causing high mortality is common along costal India. APACHE III is the most recent version of the scoring system developed by Knaus and colleagues. So far no studies are available using APACHE III in severe leptospirosis in Indian setting. Develop simple scoring in leprospirosis to predict outcome. Prospective clinical study of APACHE III score and other independent variables as a predictor of mortality in patients with severe Leptospirosis. To develop simple scoring system to predict outcome measure.

Methods: 61 patients with diagnosis of severe Leptospirosis admitted in Kasturba Hospital Manipal, tertiary care hospital in south India during the period of May 2006 to June 2008.

Results: During 2 year study period (May 2006- June 2008) 61 patients with Severe Leptospirosis were admitted in different ICUs of Kasturba Hospital, of whom13 were females and 48 were males.21 patients succumbed to their illness and 40 survived. Mean age was 48.38 ± 18.31 years among those who succumbed to Leptospirosis. All patients in dead group had hypotension in comparison to 25(65%) patients out of 40 patients in alive group. 20 out of 21 patients who succumbed had acute lung injury or acute respiratory distress syndrome. Artificial ventilation was associated with increased mortality ($P < 0.001$)Alterations in renal functions such as raised creatinine or raised blood urea nitrogen had no correlation with mortality, however low urine output had a significant correlation ($p < 0.001$). Alterations in liver function tests such as low albumin, high total bilirubin, AST, ALT, ALP or a prothrombin time had no correlation with outcome Hematological alterations such as low hematocrit, high counts or low platelets were not associated with increased mortality Mean APACHE III scoring among alive patients was 56.32 ± 31.0 and among dead patients was 100.33 ± 26.37.The scores were compared by using Independent T test and the scores were highly statistically significant ($p < 0.005$).

Conclusion: 1. APACHE III is very good prognostic marker in predicting mortality in severe leptospirosis 2. Older age, hypotension, oliguria and ARDS predict independently high mortality and need for ICU monitoring and aggressive treatment.

Multilocus sequence typing of *Enterococcus faecalis* clinical isolates in Cuba

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Background: Enterococcus faecalis has recently emerged as an important multidrugresistant nosocomial pathogen. However, studies on population structure and global epidemiology of this species are limited. We carried out the first study in Cuba by multilocus sequence typing (MLST) of *E. faecalis* clinical isolates and to link the molecular typing data with the presence of virulence determinants and the antibiotic resistance genes.

Methods: A total of 23 *E. faecalis* isolates recovered from several clinic sources and geographic areas of Cuba during a period between 2000 and 2005 were typed by MLST. Different antibiotic resistance genes [*aac(6′)-aph(2″), aph(3′), ant(6), ant(3″)(9), aph(2″)-Id, aph(2″)-Ic, erm(B), erm(A), erm(C), mef(A), tet(M), tet(L)*] and virulence genes (*agg, gelE, cylA, esp, ccf* and *efaAfs*) were searched by PCR in the selected isolates.

Results: The MLST data revealed 13 sequence types (STs) of which the five STs were novel type. The most frequently types were ST 64 (CC8), ST 6 (CC2), ST 21(CC21), and ST 16. The ST16 showed a great dissemination and persistence among Cuban hospitals and community. Sixty seven percent of STs corresponded to STs reported previously in Spain, Poland and Netherland, and other STs (ST115, ST64, ST6 and ST40) were close to those detected in USA. Aminoglycoside resistance gene *aac(6″)-Ie-aph(2″)-Ia, aph(3″), ant(6), ant(3″)(9)* were more frequently detected in ST6, ST16, ST23, ST64 and ST115. The multidrug resistance was distributed to all the clonal lineages detected, except ST117 and singleton ST225. The *ccf* and the *efa* genes were carried by all *E. faecalis* isolates, while 61.5%, 46%, 38.5% and 23% of isolates carried the *esp, gel, agg and cyl* genes, respectively. The presence of *cyl* gene was specifically linked to the CC64 and ST16. Presence of the *esp, gel* and *agg* genes was not specific to any particular ST.

Conclusion: This research provided the first insight into the population structure of *E. faecalis in* Cuba. Most Cuban strains are related to European strains, and others strains are related to US strains. The CC2, CC21 and CC8, three of the biggest CCs in the world are evident in Cuba circulating with multidrug resistance and virulence traits.