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Comparative study of clinical and biochemical parameters in leptospirosis and dengue

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Background: Leptospira and dengue can affect many different human tissues, producing a wide array of clinical manifestations, ranging from a mild undifferentiated febrile illness to severe multi-organ failure and death especially in tropical countries. Early differentiation between both the diseases is necessary since management of either condition varies considerably. Study was undertaken to compare clinical and laboratory parameters of dengue and leptospirosis and to identify parameters for early differentiation.

Methods: The study was undertaken at patients admitted at the Kasturba Hospital, Manipal, Indiafor 3 yrs. This was a prospective study and included 200 patients with 100 each of dengue and leptospirosis. A detailed history and examination were performed. Laboratory investigations included hematological, biochemical, radiological and microbiological studies.

Results: Of the 100 cases of each, 73 leptospirosis patients and 68 dengue patients were male and the rest female. The mean age was 46.19 years for leptospirosis and 34.8 years for dengue cases. Oliguria, icterus and muscle tenderness were more commonly seen in leptospirosis. Low hemoglobin, low total leukocyte count, thrombocytopenia, elevated ESR were more common in leptospirosis as compared to dengue. Renal and liver functions alteration and ARDS were altered more in leptospirosis. Mortality was 18% in leptospirosis as compared to 1% in dengue.

Conclusion: Leptospirosis had a greater incidence of muscle tenderness, icterus, oliguria and pancreatitis as compared dengue. Mortality is significantly high in leptospirosis than dengue.

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Etiological and molecular diagnostic of Carrion's disease in patients from Cajamarca - Perú

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Background: Bartonellagenus is a group of facultative intracellular pathogens that posses able to survive and proliferate inside of erythrocytes. Classified within this genus,Bartonella bacilliformisis of special relevance. This microorganism is the etiological agent of the so called Carrion's Disease (Human bartonellosis). Additionally the presence of sub-clinical cases (asymptomatyc carriers) is of special interest, because acts as a reservoir of this illness.

Carrión's Disease is an endemic illnes in Perú, affecting in a special manner the north interandean valleys. However, the current in use diagnostic techniques (Giemsa Stain) possess low sensitivity and specificity, and due to the fact thatB. bacilliformispossess a low growth (weeks), bacterial cultures lacks of clinical utility. Thus suspictious cases frequently are not confirmed, and the real relevance of this illness remains underestimated.

This work is addressed to the direct identification from blood samples ofBartonella baciliformisusing a conventional PCR. All patients were from the Cajamarca area being enrolled by the Epidemiological Surveillance program of DIRESA.

Methods: The samples were processed at arriving to the laboratory, by molecular and microbiological techniques. Thus samples were cultured in Blood Columbia Agar (10%), in anaerobic conditions at 28 °C for a period of 2 months. Positive cultures were both Giemsa stained and identified by the amplification of a fragment the 16S rRNA gene.

Genetic material was directly extracted from blood samples using the Kit High Pure (Roche diagnostic), and a fragment of 438 bp of the 16S rRNA gene was amplified withBartonellagenus specific primers. All positive PCR were sequenced (Macrogen-Korea).

Results: A total of 134 blood samples were processed, from this 12 (8.9%) grown in blood agar, while in 18 (13.4%), including the aforementioned 12, the 16 s rRNA gene was amplified. In all cases the sequence analysis showed the presence ofB. bacilliformis

Conclusion: Although microbiological culture is the gold standard in the identification ofBartonellaspp., this technique possess strong limitations due to the low growth of these microorganisms. However, the PCR is a rapid technique, possessing a high sensibility and specificity that may be used as routine diagnostic tool for the identification of Carrion's Disease.

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Eco-bio-social determinants of Aedes infestation in Dhaka, Bangladesh

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Background: Globally, vector borne diseases are becoming a significant public health problem, with a number of 'old' diseases resurging in recent years alongside newly emerging infectious diseases. Among them, Dengue has become most prominent example. While dengue is regarded as one of the most alarming infectious diseases, its resurgence reflects the failure of traditional reductionistic disciplinary approach in understanding dengue disease transmission process as well as in eliminating and controlling dengue vectors (i.e., *Aedesaegypti* and *Aedesalbopictus*). My research is based on the notion that the understanding of the dengue transmission requires the development of a holistic epistemology that can assess the eco-bio-social determinants and their interactions with human action and vice versa. The proposed study has four components: i) determination of dengue virus prevalence, ii)determination of vector density and its correlation with dengue prevalence; iii) effects of local-level social-ecological and human behavioural factors on vector density; and iv) enhancement oflocal community capacity for public participation in health intervention and development policyforums.

Methods: The proposed research has adopted a transdisciplinary approach as the basis forunderstanding dengue transmission in Bangladesh and for identifying community-centered interventions.In order to attain the objectives of the research, a total of 842 households from 12 urban wards were surveyed with a specific survey instrument. Vector distribution was monitored and vector density has been calculated by the commonly used larvalindices and the human-hour catch and per room collection of adult vector population. For in-depth understanding and identification of potential interventions, Focus Group Discussions were held in three selected wards of the City of Dhaka. These were supplemented by semi-structured interview of 30 stakeholders representatives; responses from 300 ward/community members; 12 policy- and/or decision makers (national and local institutions), and Mental Map construction of 24 ward representatives (supplemented by 300 ward members).

Results: Overall, the findings have revealed that vast majority of the community members are well aware of Aedes infestation, however, very few have taken specific measures to control them in their household and in the neighbourhood.

Conclusion: It is suggested that more community ownership will be required to make Aedes control a success.

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Developing an economic-epidemiological model system to allow economic evaluation of pandemic influenza preparedness policies

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Background: Recent estimates suggest that emergence of an influenza strain similar to the 1918 pandemic may cause up to 62 million deaths globally, but importantly 96% of these are predicted to occur in low income countries. Zoonotic H5N1 avian influenza continues to infect and kill humans, including recent deaths in Cambodia and Indonesia. Although the risk from pandemic influenza is real, poor countries present a range of opportunities for inexpensive public health gains, which pandemic preparedness policies must be compared against when considering investment.

While there have been economic evaluations of pandemic influenza preparedness policies in high income countries there are none which look specifically at low income countries. These studies tend to focus of influenza specific interventions, ignoring investment in general hospital resources to strengthen surge capacity, do not explore intra-country geographic variation and neglect aspects of uncertainty in the timing and virulence of disease.

Methods: Through reviewing state-of-the-art methods in health economic and infectious disease transmission modelling we identify approaches to facilitate economic evaluation of pandemic influenza policy. Models were developed using the statistical package R and apply sets of differential equations to describe populations and processes within the model structure.

Results: The developed model system contains four components:

i) An influenza transmission model
ii) A health system resources model
iii) A pandemic cost of illness and economic impact model
iv) A cost of pandemic preparedness policy option model

The transmission model describes Susceptible (S), Exposed (E), Infectious (I) and Recovered/Dead (R) populations separately per province of Cambodia. The populations are heterogeneous, with separate mixing patterns for different age groups. Health impact is estimated through the interaction with the transmission (i) and resource (ii) models. For each pandemic scenario the net cost is calculated from the pandemic (iii) and policy (iv) cost models.

Using 'Monte Carlo' simulation we vary the virulence of the pandemic strain and the timing of the pandemic event allowing probabilistic analysis of policies across a high number of possible future scenarios.

Conclusion: We have developed a sophisticated model system which incorporates variability in population, health system and pandemic characteristics.

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