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Adverse reactions to field vaccination against lumpy skin disease in cattle

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Background: Lumpy skin disease (LSD) is an emerging pox disease that can cause serious losses in cattle industry due to decreased productivity, cost of veterinary treatments, death, and impact on the international trade of live animals and animal products. The disease originated from Africa, but it has spread to countries of the Middle East and poses a serious threat to Europe and Asia. Recently, field veterinarians in Jordan reported a range of clinical signs seen after the LSD vaccination in cattle.

Methods & Materials: During the outbreak of LSD in Jordan, farmers outside the outbreak governorate (Irbid) were recommended to vaccinate their cattle of all ages, types and sexes using a sheep pox virus (SPPV) RM65 vaccine, Jovivac. After the vaccination campaign was initiated, post vaccinal reactions were suspected. Affected farms were investigated and data collected about animals on each farm that practiced vaccination against LSD.

Results: Sixty-three dairy cattle farms, with a total of 19,539 animals, were included in the study. Of those, 56 farms reported adverse clinical signs after vaccine administration. The duration between vaccine administration and appearance of adverse clinical signs ranged from 1 to 20 days (Mean = 10.3, SD 3.9). Clinical signs were similar to those observed with natural cases of lumpy skin disease.

These included fever and variable sized cutaneous nodules that could be seen anywhere on the body. Some cattle had swollen lymph nodes, while a few pregnant animals aborted. The percentage of affected cattle ranged from 0.3 to 25% (Mean = 8, SD 5.1). Fever, decreased feed intake, and decreased milk production were seen in 83.9, 85.7, and 94.6% in cattle on the affected farms, respectively. All affected cattle displayed skin nodules over their entire bodies. No mortalities were reported due to vaccine adverse reactions. Duration (course) of clinical signs ranged from 3 to 20 days (Mean = 13.7, SD 4.1).

Conclusion: LSD vaccines can be associated with severe reaction that can be confused with natural infection. Further studies are warranted to identify safe vaccines for this disease.

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Maximizing detection of dengue virus serotypes by a modified reverse transcription-polymerase chain reaction assay in India: presence of co-infection with multiple serotypes

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Background: Dengue surveillance uses reverse transcription-polymerase chain reaction (RT-PCR), although no standardized method for Indian serotypes exists. We compared efficacies of known and modified primer sets targeting envelope (*Env*) and capsid pre-membrane (*C-prM*) genes for detection of circulating dengue virus (DENV) serotypes in southern India.

Methods & Materials: Acute samples from children with clinically-diagnosed dengue were tested for NS1/anti-dengue-IgM. Viral RNA was extracted and two-step nested RT-PCR was done using 3 methods; in the first, consensus primers targeted 654bp of *C-prM* (*CprM654*) with a modified reverse primer; the second targeted 511bp of *C-prM* (*CprM511*), and the third targeted 641bp of *Env* (*Env641*). To ensure accuracy, sequencing (ABI, Applied Biosystems) was done on all RT-PCR-positive samples; DENV sequences were aligned using ClustalW, and compared with NCBI's GenBank database.

Results: Among 162 children (mean age 6.9yrs ± 4.3; males 61.0%) hospitalized between Nov 2014-Mar 2015, 113 were 'dengue-positive' (111 NS1-positive and 2 dengue-IgM-positive), and 49 were 'negative' (undetectable NS1/dengue IgM/IgG). Among 113 positives, PCR detected 84 (74.3%) by *CprM654*, 66 (58.4%) by *CprM511*, and 72 (63.7%) by *Env641*, suggesting high suitability of *CprM654* for regional DENV serotyping. Among 49 'negative' samples, 10 (20.4%) were detected by *CprM654*, 11 (22.5%) by *CprM511*, and 11 (22.5%) by *Env641*. Overall detection rate using all three methods sequentially was 81.4% (92/113) among positive and 38.7% (19/49) among negative samples. Consensus serotype distribution (including multiple-serotype co-infection) was DENV-1 (66, 59.4%), DENV-2 (28, 25.2%), DENV-3 (19, 17.1%) and DENV-4 (1, 0.9%). Co-infections with multiple serotypes were seen in 8 children (4.9%); among these, increased severity and death was seen in one child, and moderate severity in 4 children. Discordant results were seen in 6 (3.7%) samples, signifying either varying sensitivities among RT-PCR methods, or presence of recombinant virus.

Conclusion: This is the first sequencing-confirmed optimization study showing improved detection of circulating DENV serotypes from symptomatic Indian children, using a modified RT-PCR method and a testing algorithm. Our results showed a significant rate of co-infection with multiple serotypes. This method may be used with immediate effect for national dengue surveillance, which

is critical in hyper-endemic countries like India, and for future vaccine studies.

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The role of diabetes in the severity of 2009 influenza A (H1N1) and the Middle East respiratory syndrome coronavirus (MERS-CoV): A systematic review and meta-analysis

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Background: A number of acute respiratory infections outbreaks such as the 2009 influenza A (H1N1) and the Middle East respiratory syndrome coronavirus (MERS-CoV) have emerged and presented a considerable global public health threat. Epidemiologic evidence suggest that diabetic subjects are more susceptible to these conditions. However, the global influence of diabetes to the severity of H1N1 and MERS-CoV is yet to be evaluated.

Objective: The aim of this study was to carry out a systematic review and meta-analysis documenting the prevalence of diabetes in sever H1N1 and MERS-CoV to enable estimating its contribution to the severity of these conditions.

Methods & Materials: A search strategy was developed for online databases (PubMed, Ovid MEDLINE, Embase and Embase Classic) using H1N1, MERS-CoV and DIABETES as search terms. Reports documenting the prevalence of diabetes in these conditions were identified. Meta-analysis for the proportions of diabetes in sever conditions (95% confidence intervals, CI) was carried out (29 H1N1 studies, *n*=92,948 subjects and 9 MERS-CoV studies, *n*=308). Weighted averages of the extracted information and subgroup analysis (by region) were carried out.

Results: Average age of H1N1 patients (38.0 ± 9.2 yrs) was lower than that MERS-CoV patients (54.9 ± 10.1 yrs, $p<0.05$). The prevalence rates of clinical symptoms such as pyrexia, dyspnea, pharyngitis and pertussis were comparable between the two conditions. Compared to MERS-CoV patients, H1N1 subjects exhibited 3-fold lower prevalence of cardiovascular diseases and 2- and 4-fold higher obesity and immunosuppression rates, respectively. The prevalence of diabetes in sever H1N1 was 14.6% (95%CI: 12.3-17.0%; $p<0.001$), a 3.7-fold lower than in MERS-CoV (54.4%; 95%CI: 29.4-79.5; $p<0.001$). The contribution of diabetes to the severity of H1N1 from Asia (18%) and North America (20%) was 2-fold higher than that from South America (9.8%) and Europe (10%).

Conclusion: The effect of diabetes is 4-fold higher in MERS-CoV than in H1N1 and may play a significant role in the susceptibly to these conditions and vulnerability to their ensuing sever complications. The high prevalence of diabetes in H1N1 in North America and Asia may reflect its elevated prevalence in these regions.

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Concurrent dengue and malaria coinfection: Observations from a central Mumbai hospital

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Background: Coinfection by Dengue and Malaria is not uncommon,though studies are scarce. Both remain among the major causes of acute febrile illnesses in India. The objective of this study is to understand and observe the interplay of Dengue and Malaria,compare their clinical and laboratory features and analyze the outcomes.

Methods & Materials: A comparative, retrospective study of Dengue, Malaria and their coinfections was carried out, during 2 consecutive monsoons (June-November;2014 and 2015), in a Mumbai hospital. Febrile patients,during this period,were investigated for both Dengue and Malaria simultaneously. Elisa(NS-1/IgM) and peripheral smear examination was done to confirm Dengue and Malaria respectively. Clinical comparison of signs and symptoms,severity and outcomes, as per predefined criteria was systematically carried out.. Relevant laboratory parameters were compared.

Results: During 2014,of 156 included febrile cases,85(54.48%) were Dengue monoinfection,55(35.25%) isolated Malaria and 16(10.25%) coinfection cases,whereas in 2015, of 417 febrile cases,272(65.2%)were Dengue,117(28.05%) isolated Malaria and 28(6.7%) were coinfection cases. The coinfection and Dengue groups presented with a similar clinical picture. Among compared laboratory parameters,transaminitis was statistically significant in the coinfection group($p<0.001$). Anaemia was significant in the Malaria group,whereas,the Dengue group presented with raised haematocrit and thrombocytopenia. The coinfection group, with low haemoglobin and haematocrit, was consistent with concurrent Malaria coinfection. Among compared severity parameters,bleeding manifestations,renal dysfunction and jaundice, was notable in the coinfection group,compared to the Malaria group(12% & 3.6% and 6.3% & 3.6% each respectively) with 3 mortalities in the Malaria and 1 in the coinfection group during 2014. During 2015,despite increased Dengue and coinfection cases,numerically, with increased jaundice and bleeding manifestations(16% &8% and 8% & 6% respectively),recovery was total.

Conclusion: Dual infection by Dengue and Malaria was observed by us, for the first time, in 2014. This phenomenon,was noticed to recur, subsequently,during 2015. as well; and therefore merits further studies. Awareness and thus routine testing for both,helps in effective management and reducing mortality as observed.

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