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Modifying the clinical case definition of pertussis increases the sensitivity of diagnosis in children suspected of Bordetella pertussis infection



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Background: The WHO defines a surveillance clinical case of pertussis as one with a cough of at least 14 days duration and one of paroxysms, post-tussive vomiting or an inspiratory whoop. Laboratory confirmation is not essential for notification and remains unavailable in most of the developing world where current notification trends suggest that cases are being missed.

We aimed to determine the sensitivity and specificity of changing the WHO's clinical case definition in a cohort of children suspected of Bordetella pertussis infection.

Methods & Materials: A retrospective folder review was undertaken between December 2012 and April 2013. Patients from the Red Cross War Memorial Children's Hospital, Cape Town, who had a PCR (ptx A) for suspected pertussis between May 2009 and December 2012 were included.

Data including history on admission, examination and results of investigations were extracted. Receiver operating characteristic (ROC) analysis, using different cut-offs was used to define a clinical

Results: There were 305 folders with sufficient data included in the review. The median age of the childen was 2.3 (IQR 1.4 - 4.0) months. Of the 279 children with known immunization status, 233 (84%) were up to date with vaccines for age. Only 74/279(27%) had completed a primary pertussis vaccination schedule.

Infection was confirmed in 75/305 (26%) of the children. The WHO clinical case definition for pertussis was fulfilled in 50/305 (16%). This proportion was higher in the PCR positive compared to the negative group (RR 2.3; 95% CI 1.5 – 3.3). Only 23/75 confirmed cases (31%) fulfilled the clinical case definition.

The proportion of confirmed infections fulfilling case definition increased to 55% (41/75) when apnoea was added to the WHO definition. The sensitivity increased to 84% (58/75) when duration of cough was omitted from the definition. The specificity however declined from 88% to 56% with this modification.

Conclusion: Modifying the WHO case definition of pertussis increases the sensitivity of pertussis clinical case detection. There is an urgent need to adopt a revised clinical case definition that takes into account the "atypical" clinical presentation in young and partially immunized children as well as limited access to laboratory diagnosis.

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Geospatial distribution of the primary vectors of Rift Valley Fever (RVF) (Ae. Mcintoshi and Ae. ochraceous) along the Livestock Migration Routes (LMR) in Garissa and Lamu Counties Kenva



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Background: The ecology distribution and abundance of various mosquito vectors is important in the determination of disease prevalence in disease endemic areas. The geospatial distribution of primary vectors of Rift Valley Fever (RVF) in natural ecosystem and the species relative abundance was studied between November 2012 and October 2013 along the major livestock movement routes (LMR) in Garissa and Lamu Counties in Kenya. This ecological study focused on the taxonomy, frequency, and distributions of Ae. mcintoshi and Ae. ochraceous which among other vectors play important role in RVF transmission in the region.

Methods & Materials: Carbon dioxide baited CDC light traps were used to collect mosquitoes in five foci (Bothai, Fafi, Boni, Mlimani and Mangai) along the LMR which traverse diverse natural ecosystem. Ten traps were set 3 times in each study site at 1800 hrs and retrieved at 0600 hrs. The collected samples were sorted and morphologically identified to species level in the laboratory with the aid of a dissecting microscope.

Results: Over 50,000 mosquitoes comprising the primary vectors of RVF, Ae. (Neomelaniconion) mcintoshi and Ae. (Aedimorphus) ochraceus were identified. Other species collected from the five sites during this study includedAe. sudanensis, Mn. africana, Cx. pipiens, An. squamosous and An. gambiae. This study revealed high species diversity and richness associated with different study sites. The data revealed high species richness in the savannah forest areas than open grassland. Distribution of the primary vectors of RVF along the LMR was evident with most study sites representing proportions of this vector population. This shows the high risk level associated with the livestock movement in amplification and circulation of the virus during the outbreaks.

Conclusion: During this study a map showing the spatial distribution of the major RVF vector species was generated. The association of vector species with different study sites was documented. The nomadic communities annually migrate with livestock and there is high level of interaction between humans, wildlife, livestock and mosquito vectors in the migration routes. The findings of this study therefore demonstrate the potential vulnerability of nomadic communities to infection by arboviral diseases transmitted by RVF vectors. This calls for comprehensive mechanisms of vector control and management.