

brugian parasite has been detected over the recent past, raising a concern from a one health perspective.

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Molecular identification of sibling species of the members of the *Anopheles punctulatus* group in the Jayapura regency, Papua province, Indonesia

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Purpose: Precise mosquito species identification is an essential step for proper management and control of malaria vectors. Misidentification of members in the *Anopheles punctulatus* group, some which are primary malaria vectors in Papua (Indonesia), Papua New Guinea (PNG), Solomon Islands, Vanuatu and northern Australia, remains problematic because of indistinguishable or overlapping morphological characters between sibling species. Distinguishing these species from each other requires molecular diagnostic methods.

Methods & Materials: Mosquitoes obtained from seven districts of Jayapura regency, Papua province, Indonesia representing a variety of habitats were analyzed by using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) of the ribosomal DNA (rDNA) internal transcribed spacer 2 (ITS2).

Results: Results of the identification based on morphological characteristics of the members of the *An. punctulatus* group found in Jayapura Regency are: *An. farauti*, *An. koliensis* and *An. punctulatus*. Further species identification using PCR-RFLP for sibling species of the *An. punctulatus* group was found four species in Jayapura Regency: *An. farauti* s.s., *An. farauti* 2, *An. farauti* 4 and *An. koliensis*. Morphological species *An. farauti* identified using PCR-RFLP were shown to be three sibling species: *An. farauti* s.s., *An. farauti* 4 and *An. koliensis*, the morphological species of *An. koliensis* were shown to be two sibling species: *An. farauti* 2 and *An. koliensis* while the morphological species of *An. punctulatus* to be one sibling species: *An. koliensis*

Conclusion: This PCR assay is simpler, quicker, cheaper and readily interpreted. This study is the first effort to make malaria vector mapping in Indonesia base on molecular approach.

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West Nile Virus in Africa: Current Epidemiological Situation and Knowledge Gaps

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Purpose: West Nile virus (WNV) is an arthropod-borne zoonotic pathogen which represents a continuous source of concern for public health worldwide due to its expansion and invasion into new regions. Its distribution and circulation intensity in African countries is only partially known. The aim of the present study is to provide an updated overview on the current knowledge of WNV epidemiology in Africa, providing available data on incidence

in humans and animals, the circulating lineages and clades, other than an updated list of the principal arthropod vectors identified and the availability of vector competence studies.

Methods & Materials: We searched pertinent articles to be included in the Scoping Review according to PRISMA and QUORUM criteria. We searched PubMed and Google Scholar electronic databases on January 21, 2020, using selected keywords. From the references of each article, we explored further references as appropriate. Additional references have been later identified and added accordingly to expert opinion.

Results: This review, based on the analysis of 150 scientific papers published between 1940 and 2020, highlights: (i) the co-circulation of WNV-lineages 1, 2, and 8 in the African continent; (ii) the circulation of Koutango virus in Senegal, Gabon, Somalia, and Niger (iii) the presence of diverse WNV competent vectors in Africa, mainly belonging to the *Culex* genus; (iv) the lack of vector competence studies for several other mosquito species found naturally infected with WNV in Africa; (v) evidence of circulation of WNV among humans, animals and vectors in at least 28 Countries; and (vi) the lack of knowledge on the epidemiological situation of WNV for 19 Countries.

Conclusion: This study provides the state of art on WNV investigation carried out in Africa, highlighting several knowledge gaps regarding i) the partial knowledge on the current WNV distribution and genetic diversity, ii) its ecology and transmission chains including the role of different arthropods and vertebrate species as competent reservoirs, and iii) the real disease burden for humans and animals, therefore highlighting the needs for further research and surveillance studies to be addressed with high priority in this Continent.

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A Qualitative Risk Assessment for the Introduction of Crimean-Congo Haemorrhagic Fever (CCHF) in Bhutan

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Purpose: Crimean-Congo Haemorrhagic Fever (CCHF) has been widely reported in India but no cases have been reported in humans in Bhutan. However, a serological study conducted in 2015, detected CCHF virus specific IgG antibodies in imported goats from the southern parts of Bhutan. The disease is often non-clinical in animals but can cause severe haemorrhagic fever in humans. CCHF is transmitted through the bites of an infected tick, crushing infected ticks, and direct contact with infected blood and tissues of viraemic livestock and humans. The porous border with the neighboring states of India facilitates free and unregulated movement of animals, posing continuous risk of disease incursion into the country. Furthermore, due to anthropogenic factors, such as increasing human travel, increased import of animal and meat from India, there is a risk of CCHF introduction into Bhutan.

Methods & Materials: In this study we estimated the risk of CCHF introduction into Bhutan by performing a qualitative risk assessment based on an import risk assessment method developed by World Organization for Animal Health (OIE). Our assessment