



## EMERGENCE OF VECTOR BORNE ZOOONOTIC DISEASES

### Background

Over 60% of emerging human diseases are zoonotic or caused by microorganisms that are transmitted from wildlife to humans. Vector borne zoonotic diseases (VBZDs) are transmitted by blood-feeding, or hematophagous arthropods, and are at an increasing rate relative to directly transmitted infectious diseases that lack an arthropod intermediary. VBZDs comprise 22% of all emerging infectious diseases in humans. The most recent compilation of data about emerging vector borne diseases is from Jones et al., *Nature* 451: 990-994 (2008). Swei et al. have now conducted a literature review to assess VBZDs emergence and discuss key ecological and evolutionary characteristics of vector borne diseases in contrast to non-vector borne diseases.

### Results

Standardized database searches were conducted on BIOSIS Citation Index and Web of Science on July 2018 and included the search terms „emerging AND infectious AND disease AND vector in the topic field” and the year range was 1940-2018, which generated a list of 348 articles. A total of 131 emerging vector borne diseases in the peer-reviewed literature from the years 1940 to 2018 were identified. The authors identified 53 emerging vector borne diseases since 2005, in addition to the 78 originally described by Jones et al. (2008). In nearly 90% of all emerging VBZDs acari (ticks and mites) and diptera (flies) are involved. Within these two groups, the vectors are dominated by hard ticks (family Ixodidae) and mosquitoes (family Culicidae), respectively, and are responsible for vectoring approximately three-quarters of all documented emerging VBZDs: Ixodidae ticks (e.g. *Ixodes*, *Dermacentor* and *Amblyomma* spp.) transmit 40% of documented emerging VBZDs and mosquito vectors (e.g.

*Aedes*, *Anopheles* and *Culex* spp.) 36%, respectively. The pathogens transmitted by these two most prominent vector groups are dominated by bacteria of the family Rickettsiaceae and a variety of viruses, including Flaviviridae, Bunyaviridae, Togoviridae (and rarely Reoviridae). Of the emerging pathogens transmitted by arthropod vectors, bacteria are responsible for 59% of all VBZDs, followed by viruses (27%) and then by protozoa (15%). Rickettsiaceae account for over a quarter of all emerging pathogens at the family level. The highest number of vector-borne pathogen emergence events were in North America (27%), followed by Europe (21%) and Asia (20%). There is, however, an unequal surveillance effort across continents which may influence the detection of emergence events and using a correction, Africa may have the most emerging vector borne pathogens. One of the most noted reasons for the emergence of VBZDs was changes of land use (26%), followed by unspecified or unknown drivers (14%) and international trade and commerce (11%), reflecting increasing globalization and then followed by weather-related factors (10%) as drivers.

### Discussion

This literature review revealed the importance of Rickettsiaceae among emerging VBZDs, bacteria, which are always transmitted by ticks, while the viruses Bunyaviridae and Flaviviridae are predominantly transmitted by *Aedes* or *Culex* mosquitoes. A common feature among arthropod vectors of pathogens is blood feeding or hematophagy. Although blood is a rich source of protein as well as fluid, it lacks some key nutrients, particularly B-vitamins such as biotin and folic acid. Many hematophagous arthropods rely on obligate bacterial endosymbionts to synthesize these important nutrients, e.g.



*Francisella*, *Rickettsia* or *Coxiella* in ticks (see also Snapshot week [36/2018](#)) and notably many of these endosymbionts are closely related to pathogens. Many *Rickettsia* species once thought non-pathogenic are now known to be pathogenic (e.g. *R. helvetica*, *R. slovacca*, *R. parkeri*). Likewise, *Coxiella burnetii*, the etiological agent that causes Q fever, has evolutionary origins in an endosymbiotic *Coxiella* group. The close phylogenetic relationships between tick symbionts and pathogens suggest that the importance of ticks as vectors of emerging infectious diseases may stem partially from the dependence on symbiotic microorganisms. Furthermore, vector-borne viral pathogens in the families *Flaviviridae* and *Bunyaviridae* share ancestry with mosquito restricted viruses that were presumably non-pathogenic. Close symbiotic relationships between vectors and microorganisms may thus comprise an important source for emerging pathogens.

## Literature

Swei et al.

Patterns, drivers, and challenges of vector borne disease emergence

*Vector Borne Zoonotic Dis.* 2019, in press, doi: 10.1089/vbz.2018.2432

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