



NEW VIRUSES DISCOVERED IN TICKS

Background

Ticks are well recognized as vectors of several highly pathogenic viruses. However, until a decade ago, only a few tick viruses were known and, among these, flaviviruses were the most well characterized viruses (e.g. TBE virus, Powassan virus, Omsk hemorrhagic fever virus, louping ill virus).

Other well-known viruses include the Crimean Congo hemorrhagic fever virus and the Colorado tick fever virus. The metaviromics approach has led to the identification of a plethora of new tick viruses, which are genetically highly diverse. Although metaviromics is highly efficient in identification all viruses in a sample, the confirmation of an infection requires the isolation of an infectious virus. In this review, the origin, ecology and biological properties of new viruses and their relevance for public health has been described.

Results

Comparing the metagenomic-based virome of ticks collected from the United States, Norway, France, Australia and China revealed the near absence of DNA viruses in the global tick virome. The global virome of ticks is dominated by RNA viruses that include viruses with single-strand or double-strand, negative- or positive-sense, monopartite or segmented genomes. Among the single-stranded RNA viruses of positive-sense genome, Flaviviruses were the most common. The most common constituents of tick viromes were single-strand negative-sense RNA viruses belonging to the orders *Bunyavirales* and *Monogenavirales*. The only double-strand RNA viruses found in ticks belonged to the *Reoviridae*.

Tick phleboviruses in the order of *Bunyavirales* include Severe Fever with Thrombocytopenia Syndrome virus (SFTS virus) and Heartland virus as well as recently identified viruses such as

Phlebovirus type 1, 2 and 3 (USA), Norway Phlebovirus 1, and Beiji Phlebovirus (China). Comparative phylogenetic analyses indicate that the new tick phleboviruses are highly divergent.

Among the flaviviruses, the most interesting new tick virus is the Jingmen tick virus (JMT virus), which is the first segmented flavivirus. The JMT virus genome contains four single-strand positive-sense RNA segments that encode a flavivirus-like helicase, a polymerase and structural proteins. The virus was first identified in China from *Rhipicephalus microplus* ticks. Evidence of JMT virus infections have been reported from rodents and cattle, and a JMT virus-related virus, the Alongshan virus, was reported from humans with febrile illness. Recently, the Alongshan virus has been detected in *Ixodes ricinus* ticks in Finland (see [Snapshot week 30/2019](#)). Similar viruses have been found in mosquitoes and were shown to be capable of infecting mammalian hosts. Comparative analyses of JMT virus-related viruses from ticks and mosquitoes indicate that they form two distinct genetic clusters. Cross-species transmission from ticks to mammals including primates and humans warrant further investigation into the origin, ecology and host tropism of these new viruses.

Discussion

The knowledge of viruses present in ticks has substantially increased in the last few years. Two ways to improve the analysis of the tick virome include metagenomics of large numbers of individual ticks and/or the enrichment of samples for viruses that are most likely to infect mammalian cells. Tick homogenates can be inoculated in cell lines (which has unfortunately not been effective e.g. in the study discussed in Snapshot week 30/2019) or animal models to enrich viruses with the potential to infect vertebrate hosts, followed by metaviromic-based



identification. We yet know only little about the origin and ecology of these newly discovered viruses and the complete host range of these viruses is still not fully understood since most of these viruses cause a transient viremia in the vertebrate host that may be or may not be detected using PCR-based assays. Serological assays can reveal the real infection prevalence of these new viruses, since the presence of antibodies can indicate both prior and ongoing viral infection.

Literature

Vandegrift, KJ and Kapoor, A

The ecology of new constituents of the tick virome and their relevance to public health

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