USE OF ARTHROPOD CELLS AND CELL LINES TO ISOLATE PATHOGENS FROM TICKS

Background

By means of modern sequencing techniques, medically important microorganisms and endosymbionts have been detected in ticks. However, it is challenging to evaluate the roles of these microorganisms in ticks and their pathogenic potential solely based on their genome sequence. Therefore, it is warranted to isolate the microorganisms from ticks and study them by cultivation in arthropod cells.

Results

Thu et al. have prepared extracts from 15 different tick species collected in Japan and inoculated two permanent arthropod cell lines, the ISE6 cell line (derived from *Ixodes scapularis*) and the C6/36 cell line (derived from the mosquito *Aedes albopictus*) and cultured these infected cells for a period of up to eight weeks. When the cells showed bacterial infections, DNA was extracted and analyzed. Among 170 tick homogenates, the authors revealed 114 positives for Rickettsia and other bacteria like *Rickettsiella, Spiroplasma, Bacillus, Pseudomonas* and *Mycobacterium*. Based on phylogenetic analysis, several rickettsial species could be identified including Rickettsia. sp. LON (an unnamed rickettsial agent previously isolated from *Haemophysalis longicornus*). For the first time, *R. monacensis* could be isolated from Japan, which has not been reported so far in Japan and for the first time, the isolation of *Rickettsiella* from ticks and propagation in arthropod cells could be demonstrated. The role of this bacterium in ticks is yet not known. Various *Spiroplasma* could be isolated. This symbiont may have various functions in arthropodes (may be beneficial or e.g. male killing). The isolates described in this study are useful materials to further analyze the pathogenic potential in vertebrates and their roles as symbionts in ticks.

Palomar et al. have used another approach. They primary raised cells derived from eggs laid by *Ixodes ricinus* and *Dermacentor reticulatus* female ticks collected in the field from various regions of Eurasia and cell lines were inoculated with organs of various unfed and partially-fed ticks of different genera. Primary cell cultures and cell lines inoculated with adult tick organs were raised for several weeks to months. By this approach, various bacteria could be isolated, e.g. four new *Spiroplasma* (for the first time originating from The Netherlands, Poland and Spain and for the first time isolated from *D. reticulatus*). The authors could detect *Mycobacterium* sp. from dissected internal organs of a tick, which could be successfully cultured for a long time in tick cells and support the view that mycobacteria may have originated from inside the tick rather than from external surface.

Discussion

For the isolation of tick-borne microorganisms, it is necessary to have culture conditions suitable for supporting survival and growth of these microorganisms, whether they are intracellular or extracellular. Using either permanent arthropod cell lines or primary tick cell lines, it was shown that this is a useful tool to detect tick-borne microorganisms, even if they are present at a very low level in ticks or if they are slow-growing. Tick and arthropod cell lines from various origins may differ in susceptibility to infection of different microorganisms and differences in susceptibility to, and intensity of infection and propagation could be used to study the host range of bacterial species. The isolation and propagation of bacteria

in primary and permanent cell lines can increase the confidence that a bacterium which has previously been detected solely by molecular methods is really tick-borne and not just a surface contaminant.

Literature

Thu et al.

Isolation of Rickettsia, Rickettsiella, and Spiroplasma from questing ticks in Japan using arthropode cells

Vector Borne Zoonotic Dis. 2019, in press, DOI: 10.1089/vbz.2018.2373

Palomar et al.

Isolation of known and potentially pathogenic tick -borne microorganisms from European ixodid ticks using cell lines

Ticks Tick Borne Dis., 2019, in press, DOI: 10.1016/j.ttbdis.2019.02.008

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