

CARIBBEAN SCIENCE & INNOVATION MEETING

Coopérer sur les problématiques communes aux territoires caribéens



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ABSTRACTS BOOK

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TICK-BORNE PATHOGEN DETECTION IN CARIBBEAN TICKS USING NGS AND HIGH-THROUGHPUT MICROFLUIDIC REAL-TIME PCR (DOMOTICK PROJECT).

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Abstract : Ticks transmit the greater variety of pathogens of public and veterinary health importance. The diversity of tick-borne pathogens in the Caribbean is little known. We report here on the detection of tick-borne pathogens in individual Caribbean ticks by using a combination of NGS and high-throughput microfluidic real-time PCRs.

Of 27,544 NGS contigs generated from 588 ticks collected in Guadeloupe and Martinique (*Amblyomma variegatum*, *Rhipicephalus microplus*), 1, 2 and 30% matched viral, bacterial and parasitic sequences, respectively. No known pathogenic viruses were detected. However, four new viruses were discovered, of which, one is a suspected human pathogen. Five bacterial genus were identified: *Rickettsia*, *Coxiella*, *Anaplasma*, *Borrelia* and *Ehrlichia*. At the species level, only *Rickettsia africae* (human) and *Anaplasma marginale* (bovine) were consistently detected. Two parasite genus were found, *Babesia* and *Theileria*, but only *Babesia bigemina*, a bovine pathogen was further identified.

The prevalence of tick-borne pathogens was determined using the BioMark™ dynamic arrays allowing the simultaneous detection of 30 bacterial, 17 parasitic and 22 viral species in 94 individual ticks. Of the four interesting viruses found by NGS, one was preferentially found in *Amblyomma* (23%) while the others were preferentially in *Rhipicephalus* (30-90%, no differences between Guadeloupe and Martinique).

Rickettsia africae (96% *Amblyomma*), *Ehrlichia ruminantium* (5.1% *Amblyomma*) and *Anaplasma marginale* (4 to 40% *Rhipicephalus*) were the most detected bacteria.

Babesia bigemina (1 to 12% *Rhipicephalus*) and *Babesia bovis* (0.7% *Rhipicephalus*), *Theileria velifera* (25% *Rhipicephalus* and 42% *Amblyomma*) and *Theileria mutans* (1.5-2% in both ticks), all pathogens of bovine, were also identified.

Co-infections were frequent, with more than 10% and 2% of the ticks hosting 2 and 3 pathogens, respectively. Eleven and one ticks were infected with 4 and 5 different pathogens, respectively.

These results support the importance of these arthropods in terms of public and veterinary health.