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What have we learned from the first 600 mitochondrial genomes of Acari?*

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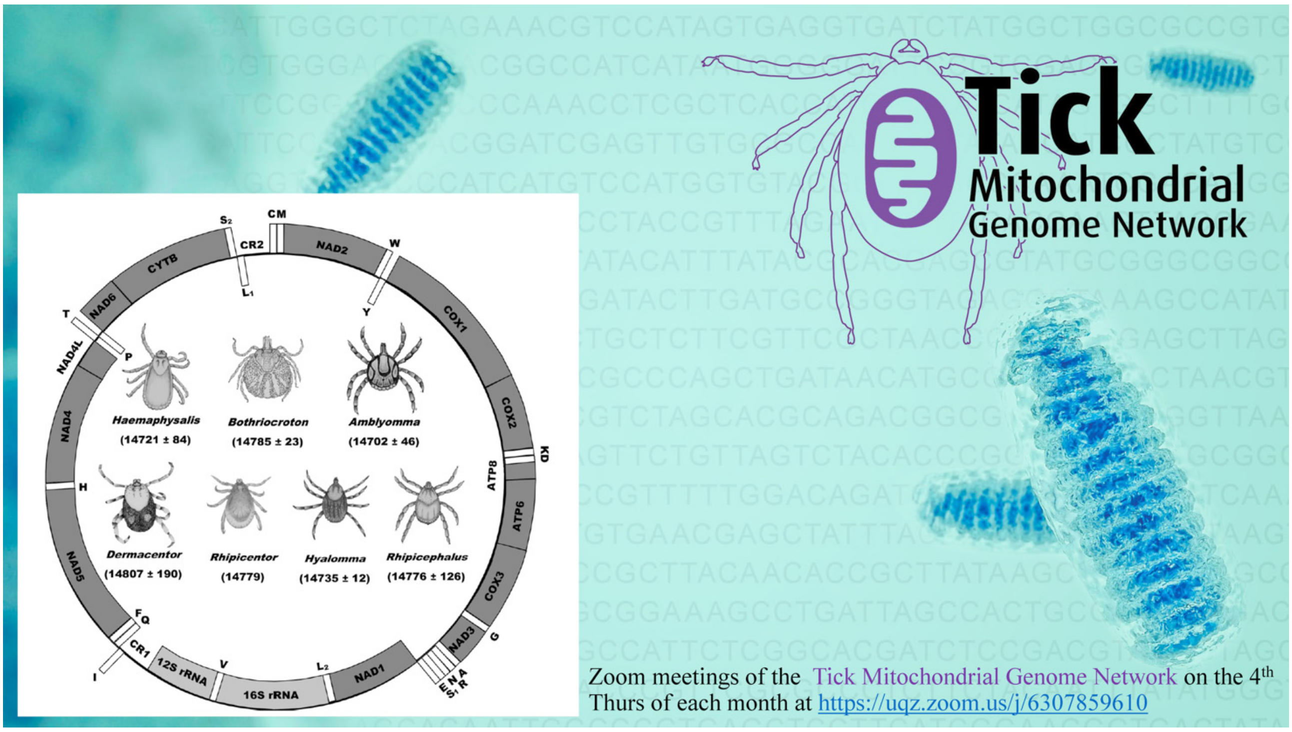
Mitochondrial genomes have been remarkably instructive about the evolutionary-history (phylogeny), population-genetics and phylogeography of Acari, particularly the ticks. At present we have entire mt genomes for 125 of the 896+ species of ticks (316 mt genomes in total), and for 146 of the thousands of other species of Acari (296 mt genomes in total). Total number of mt genomes available for the Acari is 612 [we aim to have mt genomes for 400+ species of ticks and other Acari in time for the XVII International Congress of Acarology]. It has never been easier to sequence entire mt genomes. Any lab with basic wet-lab capability can do this by using commercial sequencing companies. In 2021, Barker & Kelava precipitated the Tick Mitochondrial Genome Network with a YouTube Channel of the monthly meetings [https://www.youtube.com/channel/UCnBhfhYxjC4rsJmVpBwHT0g/featured]. This is a worthwhile resource for people wanting to join our enterprise. We study mitochondrial genomes and nuclear genes, like the internal transcribed spacer 2 (ITS2), to address phylogenetic questions and questions about species-level taxonomy of ticks and other mites.



Zoom meetings of the Tick Mitochondrial Genome Network on the 4th Thurs of each month at https://uqz.zoom.us/j/6307859610

Selected insights and outcomes will be discussed in our talk, including: (i) phylogenetic trees that led Ben Mans and us to propose that the genus *Carios* s.l. be dissolved and the subgenera *Alectorobius*, *Antricola*, *Nothoaspis*, *Reticulinasus* and *Subparamatus* be raised to genus level; (ii) an extraordinarily re-arranged mt genome arrangement in *Amblyomma* (*Africaniella*) *transversale* that prompted the elevation of the subgenus *Africaniella* back to a genus; (iii) recent insights into the phylogeny of the genera *Robertsicus*, *Amblyomma* and *Haemaphysalis*; (iv) the tick-box

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motif may be involved in the insertions of 132 to 312-bp in two *Haemaphysalis* species (*H.* (*Al.*) *inermis* and *H.* (*Al.*) *kitaokai*) and *R.* (*B.*) *geigyi*; (v) assignment of several ticks to subgenera including: *Ixodes woylie* and *I. barkeri* to *Endopalpiger*; (vi) realization that *Ixodes anatis*, the kiwi tick, may be closely related to the ticks of marsupials of Australia and Papua New Guinea.

We will also touch on the question "is the Acari monophyletic?" Mitochondrial genomes have been used to address this topic. Take for example Lozano-Fernandez *et al.* (2019), who argued that the Acari is monophyletic, whereas on the other hand Arribas *et al.* (2020) argued that the Acari was not monophyletic.

Keywords: Ixodida, phylogeny, evolution, phylogeography

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