

Join the Tick Mitochondrial Genome Network!

Who

Us; that is all members of the tick research-community. You can participate by either sequencing a mitochondrial (mt) genome or two or three, or by contributing your favourite tick for sequencing by other members of the [Tick Mitochondrial Genome Network](#). Register at TTP10 to become an official member of the Tick Mitochondrial Genome Network; contribution of at least one vial of interesting ticks gets you into the network. Steve Barker and (University of Queensland, Qld, Australia), Ryo Nakao (Hokkaido University, Japan), Renfu Shao (University of the Sunshine Coast University, Qld, Australia) and Ben Mans (Onderstepoort Veterinary Institute) and will coordinate the network for the first three years.

What

The [Tick Mitochondrial Genome Network](#) is a network of tick enthusiasts who are keen to unravel the long evolutionary-history (phylogeny), and the complex population-genetics and phylogeography of ticks. All active members of the [Tick Mitochondrial Genome Network](#) will be invited to be authors on a scientific paper that will be prepared just before TTP11; this paper will report progress towards our aim of an entire mt genome for each species-group or similar level lineage of hard and soft ticks.

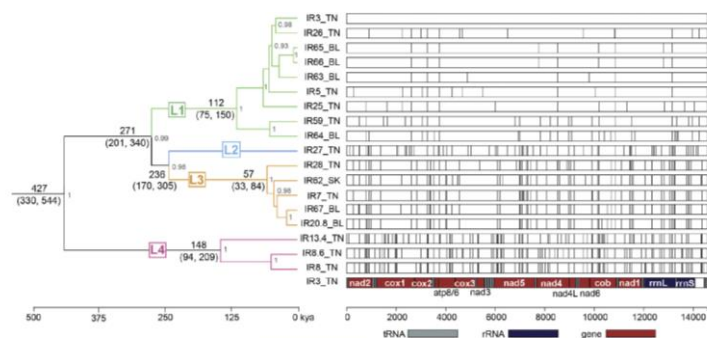
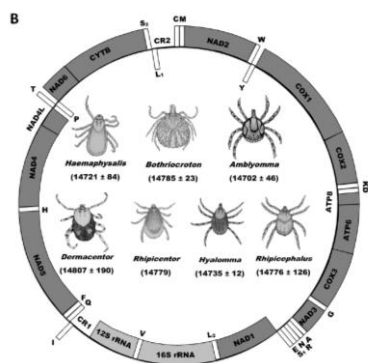
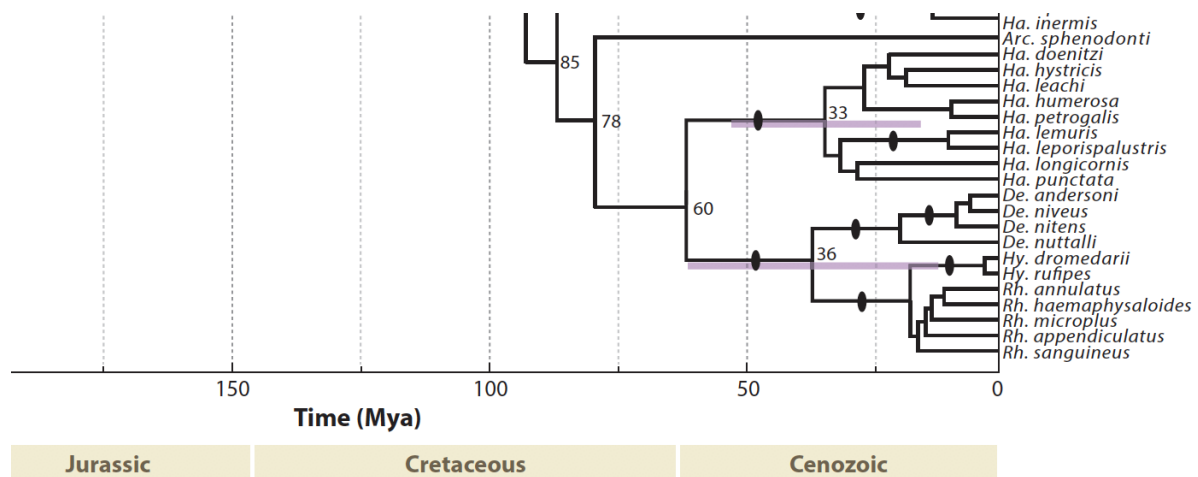


Fig. 2. Genetic diversity and phylogenetic relationships of 18 *I. ricinus* mt genomes. (A) Maximum Clade Credibility (MCC) phylogeny of the 18 independent *I. ricinus*



WHEN

The first meeting of the [Tick Mitochondrial Genome Network](http://www.zooparaz.net/ttp10) will be at TTP10, 24-28 August 2020, Murighiol, Danube Delta, Romania (www.zooparaz.net/ttp10), marked by a short plenary presentation. The second meeting will be at TTP11 in 2023. Bring your interesting ticks in ethanol (70% or 100%) to TTP10.

WHERE

All mt genomes will be deposited in GenBank in the usual way for easy access to all interested parties.

WHY

Mitochondrial genomes have been remarkably instructive about the evolutionary-history (phylogeny), population-genetics and phylogeography of ticks (brief reading list below). At present the tick-community has entire mt genomes for 125 of the 896+ species of ticks (160 mt genomes in total). We aim to have mt genomes for 300+ species of ticks by TTP11: 175 additional mt genomes.

HOW

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. Speakers in the short plenary presentation at TTP10 will tell you how.

Abbreviated reading-list (please notify the coordinators if we failed to list your papers that contain an entire mt genome)

- Burger, T. D., R. Shao, and S. C. Barker. 2013. Phylogenetic analysis of the mitochondrial genomes and nuclear rRNA genes of ticks reveals a deep phylogenetic structure within the genus *Haemaphysalis* and further elucidates the polyphyly of the genus *Amblyomma* with respect to *Amblyomma sphendonti* and *Amblyomma elaphense*. *Ticks & Tick-borne Diseases* 4: 265-274.
- Burger, T. D., R. Shao, and S. C. Barker. 2014. Phylogenetic analysis of mitochondrial genome sequences indicates that the cattle tick, *Rhipicephalus (Boophilus) microplus*, contains a cryptic species. *Molecular Phylogenetics & Evolution* 76: 241-253.
- Burger, T. D., R. Shao, M. B. Labruna, and S. C. Barker. 2014a. Molecular phylogeny of soft ticks (Ixodida: Argasidae) inferred from mitochondrial genome and nuclear rRNA sequences. *Ticks & Tick-borne Diseases* 5: 195-207.
- Burnard, D., and R. F. Shao. 2019. Mitochondrial genome analysis reveals intraspecific variation within Australian hard tick species. *Ticks & Tick-borne Diseases* 10: 677-681.
- Charrier, N. P., A. Hermouet, C. Hervet, O. Lambert, A. Agoulon, S. C. Barker, D. Heylen, C. Toty, K. D. McCoy, O. Plantard, and C. Rispe. 2019. Transcriptome-based phylogenetic study of the hard ticks. *Scientific Reports*. in press.
- de Lima, P. H. C., R. M. Barcelos, R. C. Klein, P. M. P. Vidigal, C. E. Montandon, M. H. Fabres-Klein, J. A. Dergam, and C. Mafra. 2017. Sequencing and comparative analysis of the *Amblyomma sculptum* mitogenome. *Veterinary Parasitology* 247: 121-128.
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- Lima, P., R. K. Rafael Barcelos¹, Pedro Vidigal², Mary Fabres-Klein¹, Jorge Dergam³, Carlos Montandon¹, José Venzal⁵, and C. Mafra. 2017a. The *Nothoaspis amazoniensis* complete mitogenome: organizational characteristics
- Lima, P., R. K. Rafael Barcelos¹, Pedro Vidigal², Mary Fabres-Klein¹, Jorge Dergam³, M. S. Marlene Olegário⁴, Carlos Montandon¹, ⁵, and C. Mafra. 2017b. Organizational characterization and comparative analysis of *Amblyomma sculptum* mitogenome. ...
- Liu, G. H., F. Chen, Y. Z. Chen, H. Q. Song, R. Q. Lin, D. H. Zhou, and X. Q. Zhu. 2013. Complete mitochondrial genome sequence data provides genetic evidence that the brown dog tick *Rhipicephalus sanguineus* (Acari: Ixodidae) represents a species complex. *International Journal of Biological Sciences* 9: 361-369.
- Liu, Z. Q., Y. F. Liu, N. Kuermanali, D. F. Wang, S. J. Chen, H. L. Guo, L. Zhao, J. W. Wang, T. Han, Y. Z. Wang, J. Wang, C. F. Shen, Z. Z. Zhang, and C. F. Chen. 2018. Sequencing of complete mitochondrial genomes confirms synonymization of *Hyalomma asiaticum asiaticum* and *kozlovi*, and advances phylogenetic hypotheses for the Ixodidae. *Plos One* 13.
- Mans, B., J. Featherston, M. Kvas, K. A. Pillay, D. G. de Klerk, R. Pienaar, M. H. de Castro, T. G. Schwan, J. E. Lopez, P. Teel, A. A. P. de Leon, D. E. Sonenshine, N. I. Egekwu, D. K. Bakkes, H. Heyne, E. G. Kanduma, N. Nyangiwe, A. Bouattour, and A. A. Latif. 2019. Argasid and ixodid systematics: Implications for soft tick evolution and systematics, with a new argasid species list. *Ticks & Tick-borne Diseases* 10: 219-240.
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- Mans, B. J., D. de Klerk, R. Pienaar, M. H. de Castro, and A. A. Latif. 2015. Next-generation sequencing as means to retrieve tick systematic markers, with the focus on *Nuttalliella namaqua* (Ixodoidea: Nuttalliellidae). *Ticks & Tick-Borne Diseases* 6: 450-462.
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- Shao, R., F. Masahito, and S. C. Barker. Year. Published. The mitochondrial genomes of ticks and their kin: a review, plus the description of the mitochondrial genomes of *Amblyomma triguttatum* and *Ornithodoros porcinus*. In, Proceedings of the 5th International Conference on Ticks and Tick-Borne Pathogens, (2005b) 2005a, Neuchatel, Switzerland. Universite de Neuchatel.
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- Tian, J. H., M. H. Ge, H. B. Xu, T. P. Wu, B. Yu, and C. L. Lei. 2019. The complete mitochondrial genome and phylogenetic analysis of *Haemaphysalis hystrix* (Parasitiformes: Ixodidae). *Mitochondrial DNA B* 4: 1049-1050.
- Williams-Newkirk, A. J., M. Burroughs, S. S. Changayil, and G. A. Dasch. 2015. The mitochondrial genome of the lone star tick (*Amblyomma americanum*). *Ticks & Tick-borne Diseases* 6: 793-801.
- Xu, P., Q. Zhao, X. Li, J. Wang, L. Guo, and X. G. Liu. 2016. Complete mitochondrial genome of cattle tick (*Rhipicephalus microplus*). *Mitochondrial DNA A DNA Mapp Seq Anal* 27: 529-530.
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