

Department of Biochemistry and Molecular Biophysics Seminar

Wednesday, October 7 at 4:00 p.m. in Ackert 120

Coffee and cookies at 3:45 p.m. in Chalmers 168



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The invasive Asian longhorned tick from global
mitogenomes, the *Theileria* it carries, and a chromosome
that abolished sex

The Asian longhorned tick, *Haemaphysalis longicornis*, reached the United States in 2017 and now occupies more than twenty states. It exists in two forms: a diploid bisexual form and a triploid, obligately parthenogenetic form, and only the latter has spread across Oceania and North America. This seminar follows a decade of work on the species, from the first mitochondrial genomes of Japanese ticks, which revealed two maternal clades that map onto the two reproductive forms, through genotyping of Japanese populations and a global mitogenome survey that traced the North American population to multiple introductions from Asia. Along the way, the tick emerged as the vector of *Theileria orientalis* Ikeda, a cattle pathogen that we detected by screening public tick sequencing data, and as a target for RNA interference against tick proteins essential to feeding. By mapping every public genome and read set of the species to a single reference, we found that parthenogenetic clones arose many times from unrelated parents, yet a single chromosome may hold the answer.