1104-92-329 **Michele M Klingbeil*** (klingbeil@microbio.umass.edu), 639 North Pleasant Street, Amherst, MA 01003, and **Yuanan Diao** and **Javier Arsuaga**. *Multidisciplinary approaches to study the topological complexity in kinetoplast DNA.* Preliminary report.

Trypanosomes are unicellular parasitic protozoa that cause fatal diseases in humans and livestock. A distinctive feature of these organisms is their mitochondrial DNA known as kinetoplast DNA (kDNA), which is essential for parasite survival. kDNA is the most structurally complex DNA in nature composed of a few dozen maxicircles and thousands of minicircles that are topologically linked into a chainmail-like network. Network replication proceeds through a unique minicircle unlinking and relinking mechanism that requires a plethora of non-redundant activities such as primases, polymerases, and helicases. The network structure persists with changes in linking number. Formation of the network structure is still a puzzle in spite of numerous biochemical and molecular studies. Currently, there are no methods to study kDNA network formation in vivo. Mathematical modeling has defined minicircle volume confinement as the main contributing factor for network formation but cannot account for the in vivo linking number. To refine the model, we are using RNAi to silence essential kDNA associated proteins to produce network collapse. The topology of resulting networks (reduced stable structures before collapse) will help determine the critical and saturation densities for network formation. (Received September 03, 2014)