

## The *Ixodes scapularis* Genome Project

Catherine A. Hill<sup>1</sup> & S. K. Wikel<sup>2</sup>

<sup>1</sup>Purdue University, Department of Entomology, West Lafayette, IN, 47907;

<sup>2</sup>Center for Microbial Pathogenesis School of Medicine

University of Connecticut Health Center, Farmington, CT 06030

Ticks (subphylum Chelicerata, class Arachnida) transmit a diverse array of infectious agents and are second only to mosquitoes as vectors of human pathogens. Current knowledge of ixodid tick biology is limited and methods to control ticks and the diseases they transmit are needed. In 2004, the National Institutes of Health and the international tick research community initiated an effort to sequence the genome of the Lyme disease tick, *Ixodes scapularis*. In the USA, *I. scapularis* transmits the causative agents of Lyme disease, babesiosis and human granulocytic anaplasmosis. The *Ixodes* Genome Project (IGP), the first to sequence a tick genome, is a major advance for vector biology research. The IGP represents an unparalleled resource for studying tick biology and tick–host–pathogen relationships, and identifying novel targets for tick and tick-borne disease control. The IGP will be the first genomic analysis of a member of the subphylum Chelicerata and will significantly expand comparative and evolutionary analyses in eukaryotes. An overview of the IGP including current status of the project and data availability will be provided. Ongoing activities include the production of cDNA, BAC and genomic libraries for sequencing. We are currently undertaking cytogenetic studies in the Ixodidae to understand tick chromosome biology and genome organization and to facilitate genome assembly. Further information regarding the IGP can be found at: <http://www.entm.purdue.edu/igp/default.html>