RAD Sequencing of SNPs in the *Ixodes scapularis* (Lyme Disease Tick) Genome: Toward an Integrated Genetic and Physical Map

EXECUTIVE SUMMARY:

Project PI: Catherine A. Hill, Associate Professor, Department of Entomology, Purdue University, West Lafayette, IN., 47907; email: hillca@purdue.edu; tel: 765-496-6157

Disease Vectors: This project will generate novel genomic and biological resources made publically available through VectorBase (VB) (Lawson et al., 2009) and Purdue University to accelerate research on the Lyme disease tick, *Ixodes scapularis*. More broadly, it will support genome-driven research in multiple tick and mite vectors of disease.

Project Description: This Driving Biological Project (DBP) addresses the current lack of a high-quality genomic sequence for a tick vector of disease that is fully integrated with genetic and physical maps. This is one of the greatest impediments to the translation of genome data into solutions for tick-borne disease control. The advent of high throughput sequencing (HTS) technologies provides the first realistic opportunity to overcome this hurdle. We focus our attention on the Lyme disease tick, *I. scapularis*, which is the most important arthropod vector of human disease in North America. *Ixodes scapularis* is the only tick for which a genome assembly is available, a valuable resource that our research will exploit and then improve for the scientific community, as we develop new genetic resources for tick and mite research. We propose the first use of genome-wide single nucleotide polymorphism (SNP) discovery in *I. scapularis* in order to (1) create the first densely populated tick genetic map, (2) launch the first population genomics studies for any tick species, and (3) produce an integrated sequence, genetic and physical map of the *I. scapularis* genome. We will utilize the cost-effective Restriction-Site-Associated DNA sequencing (RADseq) technique (Miller et al., 2007a) featuring the Illumina sequencing platform for SNP discovery. SNPs are the most abundant genetic markers that, when paired with HTS approaches, provide novel opportunities for vastly expanding genome resources needed to address central genetic and evolutionary questions underlying tick and mite vector biology. The genomic data and resources proposed on this DBP are shown in Table 1.

Table 1. Summary of proposed *I. scapularis* genomic data & biological resources

Genomic Data	**Number**	**Database**	**Aim**
Illumina reads	Billions	SRA	1, 2
SNP markers	Thousands	VB/dbSNP	1, 2
Genetic maps	1-2 (W x W, W x I maps)	VB	1
FISH images/physical map	~ 100 mapped BAC clones/one map	VB	3
Biological Resources	**Number**	**Institution**	**Aim**
I. scapularis colonies	≤ 10 (CT, GA, IN, MA, MD, MN, SC, WI, ON, QU)	Purdue, MR4	1, 2
F1 Mapping Populations	1-2 (W x W, W x I crosses)	Purdue, MR4	1

BAC, Bacterial Artificial Chromosome; dbSNP, SNP database; I, Indiana strain; MR4; NIH Malaria Research Repository; ON, Ontario; QU, Quebec; SRA, Short Read Archive; W, Wikel strain

Impact on VB and Scientific Communities: We anticipate the following impact on the scientific communities served by VB. Firstly, the project will provide for an improved *I. scapularis* genome assembly that will facilitate expanded research on this vector and underpin genome initiatives for other tick and mite vectors. Secondly, project resources will facilitate much needed population gemomics research (e.g., genotyping and association mapping) on *I. scapularis*. This DBP will enable our team to make progress toward our long-term goal of generating the first high-density linkage map for *I. scapularis*. The laboratory lines we establish on this project will be assessed for quantifiable traits such as host preference and vector competence and used to create mapping populations to map genes influencing these traits. Lastly, our proposed integrated sequence, genetic and physical map will provide a community tool for analysis of genome organization among *I. scapularis* populations, and comparative analyses between acarine species.