Microbial Community Assessment of Lone Star Ticks from Athens, GA
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Introduction
Amblyomma americanum (Lone Star) ticks are an important vector in the spread of disease, and cause millions in damage per year to livestock in Mexico. Lone Star ticks prefer mammalian hosts and spread several diseases including ehrlichiosis, babesiosis, Q fever, and rickettsial diseases (Goddard and Varela-Stokes 2008). These diseases pose a significant risk in terms of difficulty of diagnosis and treatment protocol.

Methods
Ticks were collected by dragging a white sheet through a wooded property on Simonton Bridge Road on two days in June, one week apart. Collected ticks were kept in ethanol for preservation. Ticks were identified with a dissecting microscope.

DNA was extracted using QIAGEN Tissue & Blood kits (Method 1 of Halos et al. 2004). The amplified DNA was sequenced using Illumina MiSeq Hotstart and broad spectrum 16S primers (Klindworth et al. 2013). The amplified DNA was sequenced using Illumina MiSeq v3 600 cycle kits to obtain paired-end 300 base reads. DNA sequences were analyzed using Geneious R8. Reads were paired, trimmed, merged using FLASH, the community described via the 16S BioDiversity tool (Figs 2-4), then assembled if ≥98% similar and identified to species via BLAST.

Results
- Four types of pathogenic bacteria were found in Lone Star Ticks: Coxiella, Rickettsia, Ehrlichia chaffeensis, and Ehrlichia canis.
- Robust and HiFi Taq Polymerase amplified comparable microbial communities (Figure 3 and 4).
- Males and females were found to have similar levels of Rickettsia infection.
- Female lone star ticks had higher Coxiella infection rates than males.

Further Directions
- Develop an assay to cheaply and easily screen ticks for human pathogens to determine if someone who was bitten is at risk.
- Look at the sequence variation among different pathogen types.

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References
3. http://bugguide.net/node/view/51997