HADEN FINCHAM, MELANIE SAL, & KIM BJORGO. Department of Biology and Environmental Sciences, West Virginia Wesleyan College, 59 College Avenue, Buckhannon, WV. Surveilling hard tick diversity and Spotted Fever *Rickettsia* Group prevalence in North-Central WV throughout 2023

The Spotted Fever *Rickettsia* Group (SFRG) causes dangerous, albeit rare, infections in West Virginia, with an untreated mortality rate of approximately 25% in the United States. The bacterial causes of SFRG are gram-negative, obligate intracellular *Rickettsia* species that infect human vascular endothelial cells. They are transmitted primarily during the blood meal of a colonized American Dog tick (*Dermacentor variabilis*) but can also be transmitted by Asian Longhorn (*Haemaphysalis longicornis*), Lone Star (*Amblyomma americanum*), and other less frequently detected ticks. The aim of this project is to survey hard tick (*Ixodidae*) diversity and SFRG incidence rates in collected *D. variabilis* samples. Tick samples were collected year-round from veterinarian clinic donations and throughout May, June, and July by tick drags conducted across Upshur and Lincoln Counties, WV. Of 563 ticks collected in 2023, *Ixodes* species were most prevalent (48.8%), followed by *Dermacentor* (25.6%) and *Haemaphysalis* (24.9%), and only 0.5% of the collection consisted of *Amblyomma* specimen. Following identification and photography, ticks were cut in half for cryopreservation at -80ºC and DNA extraction. 145 *D. variabilis* total-DNA samples were analyzed via quantitative real-time Polymerase Chain Reaction (qPCR) for a conserved *Rickettsia* genus gene (17kDa Outer Membrane Antigen). Preliminary results suggest an infection rate of 5.52%. Ongoing investigation includes confirming positive samples through gel electrophoresis and species-specific sequencing. Overall, these data underscore the importance of understanding the diversity and pathogen colonization rate of West Virginia hard ticks to predict and map vector-borne disease trends.

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