

Final report: Distribution, Prevalence, and Feeding Patterns for Tabanid Flies, the Vector of the Arterial Worm of Sheep and Cervids

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Grant money for this project was received in 2013 to hire one of the two summer field technicians that collected horse flies in four Wyoming mountain ranges. Having an independent field team allowed for simultaneous data collection and sample testing. This was beneficial in that it reduced the time samples awaited processing and testing, maintaining sample integrity.

Two of the main goals of this research were to document the species of horse flies found in moose hunt areas with differing levels of prevalence of *E. schneideri*, and to determine the host preferences of those horse flies. By examining the distribution and relative abundance of horse flies, we can hypothesize how individual species may be affecting *E. schneideri* prevalence. Two species of horse flies made up the majority of the collection of horse flies, and it is likely that one of these two species is driving *E. schneideri* prevalence. The Bighorn's horse fly assemblage stands apart from the other study sites. This unique grouping and the relative abundance of those species of horse flies may be keeping parasite prevalence in the Bighorns low. In contrast, the other low prevalence site, Upper Green, has many species in common with the high prevalence sites, Greys River and Snowy Range. This overlap in species indicates that it likely does have the right vector, but some other factor is contributing to the low prevalence of *E. schneideri*.

We found a lack of host specificity among species of horse flies indicating these species are more opportunistic, feeding on easily available targets. If horse flies are more opportunistic in their host selection, livestock species such as cattle and sheep may offer a dilution effect by increasing available hosts and potentially protecting wildlife by offering non-competent hosts for horse flies to feed on. However, this does not explain *E. schneideri* prevalence in all areas. Some moose herd units have a high density of livestock grazing, and a high prevalence of *E. schneideri*. Increases in hosts, even non-competent hosts, can increase the abundance of horse flies enough that while the ratio of infected to non-infected flies doesn't change, it can be enough to increase or amplify the infective burden and increase *E. schneideri* prevalence.

The effectiveness of this project can be measured by the number of horse flies trapped and our ability to test them. Almost 2,000 horse flies were trapped, identified, and tested. Horse flies not tested will be added to the University of Wyoming arthropod collections to bolster their numbers and to add new species to the collections. New diagnostic tests were successfully developed for this project giving future researchers a relatively fast and reliable way to identify DNA from moose, elk, deer, cattle, sheep, and horses. This project was able to build a foundation which

with continued research, can be used to research wildlife populations by connecting field and laboratory methods.