

Is there a genetic basis for plague resistance in Gunnison's prairie dogs?

David M. Wagner, Ph.D., Associate Professor, [Center for Microbial Genetics and Genomics, Northern Arizona University](#), Flagstaff, AZ, 86011. Dave.Wagner@nau.edu, **Joseph Busch, Ph.D.**, Assistant Director, [Center for Microbial Genetics and Genomics, Joseph.Busch@nau.edu](#)

The Current Situation: Prairie dogs are keystone species that increase the biological diversity of grassland communities. Unfortunately, all five prairie dog species have experienced large reductions in the past 100 years from poisoning campaigns, habitat loss due to human development, and outbreaks of plague, which is caused by the bacterium *Yersinia pestis*. Plague is one of the most significant problems for prairie dogs because outbreaks can often result in >99% mortality within affected colonies. Importantly, continued plague outbreaks also prevent the formation of large prairie dog complexes that were common prior to European settlement and the introduction of plague in North America and it is these large, stable complexes that are critical for black-footed ferrets, an endangered predator that is dependent of prairie dogs as a food source. Oral plague vaccinations and flea control measures show promise for controlling plague outbreaks in prairie dog colonies. However, these measures are expensive and must be reapplied every year, making them unrealistic for large-scale and long-term application.

A Possible Solution: In previous experimental studies, we and our collaborators have demonstrated that some individual prairie dogs (both [Gunnison's](#) and [black-tailed](#)) are resistant to *Y. pestis* when infected with the pathogen under controlled laboratory conditions. What is unknown is whether or not this observed resistance to plague in prairie dogs has a genetic basis. It is possible that other factors that are not under genetic control account for these differences. For example, prairie dogs that survived our plague infection experiment may have been previously exposed to other pathogens that “primed” their immune systems and allowed them to mount more robust immune responses to the plague infection. However, it may also be the case that there is a genetic basis to their resistance to plague. If so, this would provide valuable new management tools that could decrease the impact of this disease on prairie dogs and associated species over time. For instance, it would be possible to screen prairie dogs for genetic markers associated with resistance to plague – a “resistant fingerprint” – and then use only prairie dogs with the resistant fingerprint to establish new colonies that may then be more resistant to plague. But the first step is to determine if there is indeed a genetic basis for resistance to plague in prairie dogs.

Experimental Approach: We propose to compare the genomes of Gunnison's prairie dogs that died in our previous laboratory infection [experiment](#) to those that survived, which will provide key information on genetic differences between these two groups. Specifically, we will test the hypothesis that there is a genetic basis for plague resistance in Gunnison's prairie dogs via a genome wide association scan using existing DNA from the 60 animals from our previous challenge experiment. The results of this study will provide genome-wide data for identification of specific mutations and genes that may play a role in prairie dog resistance to plague.

Required Funding: \$100,000 in direct costs.

Timeframe: This project will be completed in one year from the receipt of funding.

Dissemination of Results: The results of this research will be disseminated via publication in a peer-reviewed scientific journal.