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## GENOMICS OF BRUCellosIS IN WILDLIFE AND LIVESTOCK OF THE GREATER YELLOWSTONE ECOSYSTEM

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Brucellosis, a disease caused by the bacterium *Brucella abortus*, has recently been expanding its distribution in the Greater Yellowstone Ecosystem (GYE), with increased outbreaks in cattle and rising seroprevalence in elk (*Cervus elaphus*) over the past decade. Genetic studies suggest elk are a primary source of recent transmission to cattle. However, these studies are based on Variable Number Tandem Repeat (VNTR) data, which are limited in assessing and quantifying transmission among species. The goal of this study was to (i) investigate the introduction history of *B. abortus* in the GYE, (ii) identify *B. abortus* lineages associated with host species and/or geographic localities, and (iii) quantify transmission across wildlife and livestock host species and populations. We sequenced *B. abortus* whole genomes ( $n=207$ ) derived from isolates collected from three host species (bison, elk, cattle) over the past 30 years, throughout the GYE. We identified genetic variation among isolates, and applied a spatial diffusion phylogeographic modeling approach that incorporated temporal information from sampling. Based on these data, our results suggest four divergent *Brucella* lineages, with a time to most recent common ancestor of ~130 years ago, possibly representing a minimum of four brucellosis introductions into the GYE. Two *Brucella* lineages were generally clustered by geography. Evidence for cross-species transmission was detected among all species, though most events occur within species and herds. Understanding transmission dynamics is imperative for implementing effective control measures and may assist in identifying source populations responsible for past and future brucellosis infections in wildlife and outbreaks in livestock.