
MODELING MANAGEMENT STRATEGIES FOR THE CONTROL OF BIGHORN SHEEP RESPIRATORY DISEASE

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Infectious pneumonia has plagued bighorn sheep populations and stymied recovery efforts across the western United States for decades. Here we present a simple, non-spatial, stochastic, discrete-time model that captures basic bighorn sheep demographics and in which we simulate the dynamics of *Mycoplasma ovipneumoniae*, the suspected primary causative agent in bighorn sheep respiratory disease. We then use the model to explore the impacts of

management approaches, including augmentation, depopulation and reintroduction, density reduction, and test-and-cull, aimed at reducing or eliminating the pathogen, its transmission, or associated infection costs. Results suggest that test-and-cull (testing 95% of a herd and removing PCR-positive individuals) and depopulation and reintroduction (assuming ability to only depopulate 95% of the herd) offer the best probability of eliminating the pathogen, although neither are expected to be 100% successful. Augmentation (adding 30 adult ewes) does not increase the probability of pathogen extinction, and in some cases may prolong pathogen persistence and diminish herd recovery. Density reduction (randomly removing 25-50% of the herd) only modestly increases the probability of stochastic pathogen extinction and herd recovery. Stochastic pathogen extinction and herd recovery is predicted to occur on occasion without any management intervention. Ultimately, decisions to manage respiratory disease in wild sheep must weigh the predicted success of the management tool against financial, logistical, ethical, and value-based considerations. Here, we aim to supply mechanistic-based predictions of the relative efficacy of currently employed or proposed tools, as well as characterize the sensitivity of these predictions to our assumptions about how the disease process works.