



Science Newsletter

Updates on respiratory disease affecting desert bighorn sheep in and near Mojave National Preserve

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Desert bighorn sheep (*Ovis canadensis nelsoni*) are an iconic mammal of the desert southwest and are found in small mountain ranges scattered across Mojave National Preserve (Preserve) and nearby desert habitats in southeastern California. In many areas, they are the only large native herbivore that can persist, inhabiting places that are too hot, dry, and sparsely vegetated for deer. California is thought to be home to ~3000-5000 desert bighorn in total (1); desert bighorn sheep are uniquely adapted for the harsh environment of the southwest deserts and populations appear to be resilient in spite of threats from poaching, climate change, drought, and habitat fragmentation (2, 3). In the Mojave Desert, bighorn sheep populations are strongly fragmented by expanses of flat desert between mountain ranges, and in some cases, by behavioral and physical barriers such as interstate highways (4). Yet, southeastern California, including the Preserve, represents the largest intact “metapopulation” of naturally

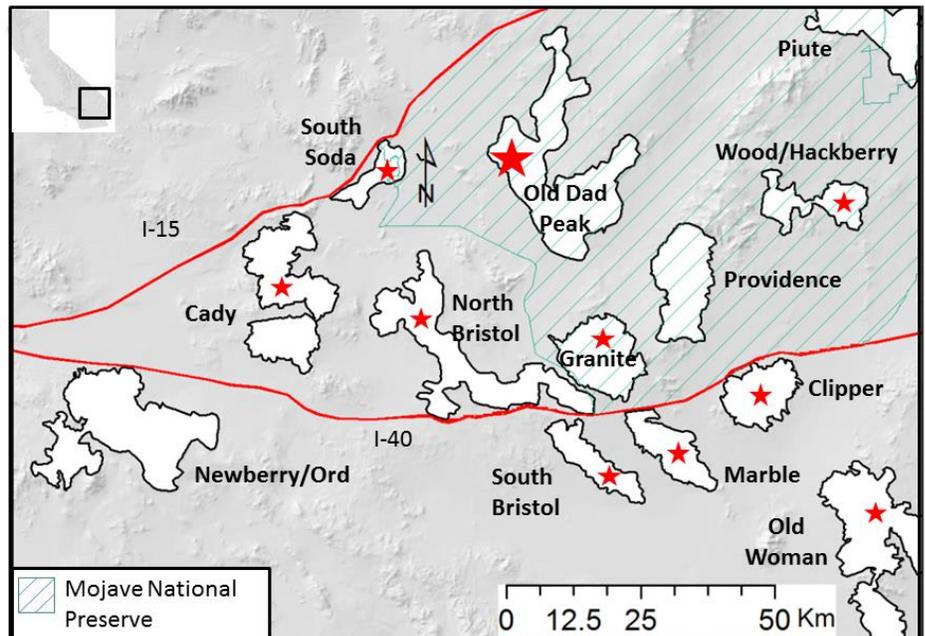


Figure 1. Map of Mojave National Preserve and nearby areas in southeastern California, showing mountain ranges (white polygons) where respiratory disease of bighorn sheep is being studied using GPS collars, remote cameras, disease screening of captured animals, fecal DNA, immunological and genetic measures, and other methods. The respiratory pathogen *Mycoplasma ovipneumoniae* was first reported at Old Dad Peak in spring of 2013 (large red star); current infection or past exposure has been confirmed at other red-starred ranges. Providence and Piute Mountain Ranges have not yet been tested; only four animals from the Newberry/Ord population were tested in 2014, but no definitive evidence of disease in those animals was found.

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persisting desert bighorn sheep – a system of small populations linked by intermountain movements and experiencing local extinctions (loss of entire populations) and recolonizations (populations reestablished in empty habitat by natural dispersal from other occupied populations) (2, 3, 5, 6). Although numerous population extinctions occurred in the 20th century, in recent decades desert bighorn sheep populations in the region appear to have expanded (1, 7), bolstered in part by human-made water developments and translocations (8), but also by natural recolonization (6).

A previously underestimated threat to desert bighorn sheep in the Preserve has recently emerged. Potentially fatal respiratory disease,

originally contracted by direct contact with domestic sheep or goats but then presumably spread by natural movements of bighorn sheep across wide areas (9-11), appeared in the Mojave Desert in 2013. Across western North America, domestic ovine (sheep) and caprine (goat) respiratory pathogens have been identified as one of the major threats to persistence of bighorn sheep (9, 12). Until recently, outbreaks were more commonly reported in the Rocky Mountain subspecies (*O. c. canadensis*) (13, 14), with major outbreaks occurring in nearly every state where that subspecies is found. However, in recent years, scientists in the Southwest have observed respiratory disease outbreaks in many desert bighorn sheep populations, including Arizona, Nevada, Utah, and California (15). One

such outbreak was reported in the Preserve in spring of 2013, when sick and dying bighorn sheep were reported in the Old Dad Peak population (16) (Figure 1). Because of the relative isolation of this population (4, 17), biologists responding to the initial outbreak were hopeful that it might be contained to that mountain range. Two months later, however, sick bighorn were reported over 30 km away in the Marble Mountains south of Interstate 40 (Figure 1), and it was clear that a widespread epidemic was underway.

The National Park Service (NPS) and California Department of Fish and Wildlife (CDFW), in collaboration with researchers at Oregon State University and volunteers from the Society for the Conservation of Bighorn Sheep and the California Chapter for the Foundation for Wild Sheep, initiated monitoring and research immediately after the detection of the disease to determine: 1) the extent of the current disease outbreak, 2) likely patterns of spread among bighorn sheep populations in different mountain ranges, and 3) consequences for the bighorn sheep population at Old Dad Peak and other affected areas, in terms of survival of adults and lambs. Here, we describe what we have learned after the first two years of work to diagnose the disease, establish its extent and understand the potential for spread, and track its impacts on this unique species.

Detecting the disease—Establishing the extent of the disease was the first challenge. Infectious pneumonia in bighorn sheep is a respiratory disease complex with multiple pathogens, often acting concurrently, but disagreement persists as to the exact role played by different pathogens and parasites (11). A variety of pathogens have been associated with pneumonia in bighorn sheep, including *Mannheimia haemolytica* and *Biberstera trehelosi* (11), species from the Pasteurellaceae family of bacteria. In recent years, another bacterium, *Mycoplasma ovipneumoniae* (*Movi*), has been recognized as an important pathogen capable of causing bighorn pneumonia or possibly acting in concert with other bacteria to greatly worsen their effects (11, 14, 18, 19). Indeed, *Movi* has been implicated in most recent outbreaks of bighorn pneumonia throughout the West (11, 12). When a

bighorn sheep has severe pneumonia – marked loss of functional lung tissue due to bacterial infection, inflammation, and fluid accumulation – death can occur very quickly. However, before that point, a sick animal may show few obvious symptoms. Coughing and nasal discharge are the first telltale signs, but are not entirely specific to pneumonia, and even with pneumonia may only be present when the animal exerts itself. Therefore, identifying potentially diseased animals in the field requires close observation of bighorn sheep for long periods of time; reliable detection of the disease and identification of the pathogens involved requires prompt necropsy of dead animals (i.e., by opening the carcass and examining the lungs) before rapid deterioration in the desert environment, or collection of blood and other samples from captured animals, followed in both cases by laboratory testing for pathogens.

Two basic laboratory tests are used to detect *Movi*, and those tests give different information: the first, ELISA (enzyme-linked immunosorbent assay), screens for antibodies to respiratory pathogens in the animal's blood. This serological test, if positive, indicates that the animal was infected by that pathogen some time in the past, creating a response in its immune system specific to that pathogen. The ELISA test is advantageous because it can be conducted on fresh or archived samples, such as blood serum samples collected in previous decades and stored in freezers. However, from a single sample, this test cannot distinguish animals that are currently infected and shedding pathogens from animals exposed to the pathogen in the past and now less likely to be contagious. The second test, PCR (polymerase chain reaction) is a newer diagnostic tool with significant advantages over older, slower culture-based methods (methods that require growing bacteria), which are less sensitive for many bacteria that do not grow readily in the laboratory. PCR identifies pathogen DNA currently present in the host, which indicates that the animal is actively or recently infected. During capture operations, or on recently-dead carcasses, biologists swab a bighorn sheep's nose, throat, or ear canal, where the pathogens are likely to be present in an infected animal. The swab is tested for DNA specific to the pathogens of interest by amplifying bits of DNA and matching sequences to a

pathogen library. That DNA sequence can be compared to other known strains, which helps determine whether outbreaks in different places come from the same initial source. Although *Movi* testing is increasingly used, additional tests are often used to screen for some of the other bacteria associated with bighorn pneumonia, such as the Pasteurella-type bacteria mentioned previously.

What is the extent of the disease?—In the Preserve outbreak, pneumonia was first confirmed at Old Dad Peak by examining bighorn sheep found dying or dead; subsequent laboratory tests found that *Movi* was present. Later that summer, when animals were reported coughing in the large Marble Mountains population to the south (Figure 1), sick animals were collected and tested, once again confirming *Movi*. Subsequently, this strain was found to be identical both to the one detected in the Old Dad Peak population as well as to a strain of *Movi* detected in a 2013 outbreak in western Nevada. At this point, the pathogen appeared to have widespread distribution in the region.

Efficient testing for disease detection requires capturing multiple bighorn sheep in each population, at which point swabs and blood samples can be taken for PCR and ELISA diagnostics. Therefore, we captured bighorn sheep in most of the populations across the Preserve in November of 2013 (70 females, 2 males, Figure 1), expanded to other more distant areas in November 2014 (33 females, 11 males, Figure 1), and captured an additional 60 animals in the study area in November of 2015 (43 females, 17 males). Although the captures serve other research purposes (survival, movement, and immunogenetic studies; Figure 2) they have also provided us with a relatively comprehensive picture of the current extent of *Movi* in the Preserve and other parts of California's Mojave and Sonoran Deserts.

We detected bighorn sheep with active *Movi* infection (PCR) or evidence of past *Movi* infection (ELISA) in all 9 populations tested in 2013 (Figure 1); all infections were the same *Movi* strain as first detected at Old Dad Peak (20). Despite varying levels of population isolation in the various mountain ranges, *Movi* seemed to be

infectious enough to invade the entire study region. In 2014, captures over a wider area returned mixed results. Two bighorn sheep captured in southern Death Valley National Park showed no evidence of current or past *Movi* infection, nor did 4 bighorn sheep captured in the Newberry Mountains south of I-40 but well to the west of the initial outbreak (Figure 1); however, these sample sizes were too small to confidently determine that these populations were not affected (9). Nevertheless, *Movi* was verified in several different populations including the Old Woman, Cady, and Orocopia Mountains (Figure 1), although the *Movi* in the Orocopia Mountains appears to be a different strain than the 2013 outbreak. In summer 2015, sick bighorn sheep were reported in Joshua Tree National Park, and recent lab tests on a dead bighorn recovered for testing have confirmed that yet another strain of *Movi* is present. Recent tests have confirmed that the *Movi* strain found in the Preserve is now present in a bighorn sheep population in Arizona, suggesting transmission via bighorn sheep that reportedly occasionally cross the Colorado River along the California-Arizona border (21). As information on distribution of *Movi* strains improves, biologists in the affected states will be able to ask questions about whether different *Movi* strains affect populations in different ways.

What are the consequences of the disease?—Although ovine pneumonia has been observed and studied for decades in Rocky Mountain bighorn sheep (e.g., 13, 22, 23), we still know little about how the disease affects desert bighorn sheep, or whether the disease is likely to persist once a metapopulation is exposed. The initial investigation at Old Dad Peak showed that this outbreak was capable of killing adult bighorn sheep, as dozens of dead rams and several sick and dying ewes were found in spring and summer of 2013, including all four radio-collared ewes present before the outbreak. Therefore, the second important goal for the 2013 collaring was to get real-time information on survival of adult bighorn sheep around the Preserve. Unlike earlier studies in the region, we now have the opportunity to deploy modern GPS collars designed for large animals that are capable of providing 1-12 precise locations per day, uploaded by satellite link and then observable by computer. Each collar also contains a “mortality



Figure 2. Bighorn sheep are captured by skilled teams using a helicopter, and in some cases are transported to a base camp for examination by veterinarians (Photo by B. Dugovich).

alert”, which sends a special message when the collar does not move for a predetermined length of time. Thus, we can now monitor movement, understand habitat use, and track survival for more than 150 bighorn sheep in or near the Preserve.

In 2014, we initiated a graduate research project to determine how environmental factors such as rainfall and nutrition interact with the disease to influence bighorn populations in the Preserve. Besides tracking adult survival and movement, we are also working to characterize another likely consequence of the disease: poor lamb recruitment. After the first contact of a population with respiratory pathogens, an all-ages die-off may occur. However, unless new strains of pathogens are introduced, adult bighorn appear to gain some resistance to *Movi*, and less often die from pneumonia after that initial period of high mortality. Unfortunately, low lamb survival may persist for many years (22). This ongoing lamb mortality may be caused by persistent chronic infection in at least some of the ewes that “shed” the pathogen to their lambs (24). Lamb survival can vary widely depending on rainfall and forage quality (25), therefore another key piece of information for this study will be separating effects of disease and environmental variation, especially the effects of rainfall on forage and the subsequent impact on lamb recruitment (i.e.,

surviving to the yearling stage) (26). This is being attempted both spatially, by studying 9 bighorn populations, and temporally, by taking advantage of many years of remote camera data collected by Dr. John Wehausen of White Mountain Research Center in several key populations predating the disease outbreak. Lamb survival can be difficult to monitor on large landscapes: while radio-collaring individual lambs would give the best information, finding and capturing new lambs is extremely difficult among the cliffs and remote mountainsides favored by desert bighorn ewes in early spring. Therefore, we are using remote cameras to capture images of bighorn sheep at water sources during the summer (Figure 3), allowing us to estimate lamb to ewe ratios (a typical index of how many lambs survive over the course of the year). In some cases, we supplement those estimates with direct lamb and ewe counts collected by ground observers in several key populations. We are also collecting fecal samples for diet quality analysis (25), linking current conditions to more than 30 years of diet quality data collected in several mountain ranges, as well as remotely-sensed measures of vegetation growth (27). Combining those data will help us determine whether lamb to ewe ratios diverge from those expected given pre-outbreak relationships with precipitation and diet quality, how they vary across the study area with environmental conditions after the start of the

outbreak, and whether the seasonal timing of lamb mortality has changed because of the disease.

Although formal analysis is just beginning, the GPS collar and camera data have demonstrated two important conclusions about the current course of the disease: Firstly, we have not observed large numbers of adult bighorn dying from the disease since the first collars were placed in November 2013, either in Old Dad Peak or in other affected ranges. Secondly, we are seeing few lambs accompanying ewes by the end of the summer in many ranges. In combination with field observations of ewe groups and reports of coughing lambs from field personnel, this suggests that the disease is curtailing lamb recruitment and therefore could have significant effects on population dynamics. However, precise conclusions will require collecting several years' more data and completing formal analysis.

How does the disease spread?—Pneumonia-causing pathogens such as *Mov* are spread by contact, probably including indirect contact via airborne particles over short distances (28). Because bighorn sheep associate loosely in small groups throughout the year (29), and because rams actively pursue ewes in different groups for several months during the rut, individual contacts among bighorn appear to be sufficient to spread the disease rapidly both within and among populations. However, the pattern of such contacts among bighorn sheep probably varies widely across different ecosystems. For instance, in this region, large numbers of animals congregate at the few available water sources (natural and man-made) from late spring through fall, unlike many more northern bighorn habitats where water is less restricted. Thus, contact among desert bighorn at water sources may play an important role in disease transmission. For instance, the 2013 Old Dad Peak die-off appeared to begin early in the season of water use, and many bighorn sheep died near water sources.

With the unprecedented volume and quality of data now available from GPS collars, we hope to learn much more about how bighorn sheep move within populations - as well as, occasionally,



Figure 3. Remote cameras can provide detailed information on survival, reproduction, and physical condition of bighorn sheep during summer months when they use surface water frequently (Photo by D. Dekelaita).

between them. Our current understanding of how bighorn sheep move between mountain ranges in the Preserve is largely derived from genetic data collected and analyzed in the early 2000s (4, 30), as well as occasional movements observed using radio telemetry (reviewed in 17). That work suggested that the rates of movement among ranges varied widely depending on distance and topography (17); in some instances, little or no movement was suspected, such as across Interstate 40. Gene flow and infectious disease spread can both result from movements between the disparate populations. However, gene flow is a different process than a disease outbreak: for gene flow, animals must move, then stay and reproduce in the new area. Infectious disease, on the other hand, could be transmitted by even a very brief visit by a single animal. Therefore, the combination of genetic data and GPS collar data may provide the best picture of short and long-term movement patterns across the region. The GPS collar data collected to date have revealed some surprising movements by individual bighorn sheep, including very short-term forays into different populations, movements by females of >65 km, and in several cases, movement by males and one female across Interstate 40. GPS collar data will also help us to determine how

environmental conditions and availability of water sources influence seasonal movements and distribution of bighorn sheep.

When the outbreak at Old Dad Peak was first detected, we were initially hopeful that the disease might not spread to other ranges - assuming it originated at Old Dad Peak in the first place - because gene flow maps created in the early 2000s suggested this population was relatively isolated. However, in the dynamic Mojave metapopulation, even 12 years (two bighorn generations) can see substantial change. In that time, some populations appear to have grown (1), habitat in the North Bristol Mountains that had previously apparently only received occasional ram use became home to a reproducing population, and bighorn sheep appear to have discovered new ways to move around the landscape. During 2013-2015, we have resampled populations across the Preserve and the surrounding region to reanalyze genetic structure and learn whether new gene flow maps correspond with the spread of disease. Our preliminary results suggest that they do. For instance, we can now see that Old Dad Peak is clearly linked to the North Bristol Mountains by gene flow; bighorn in the North Bristol Mountains,

in turn, are clearly linked to populations in the Cady Mountains and the Granite Mountains (Figure 4) (31). In most cases, these links are being verified by movements we detect from GPS-collared ewes or rams. Thus, the rapid spread of *Movi* to both Old Dad Peak and the Marble Mountains population in a short time period conforms to our new understanding of bighorn sheep movements across the study area.

Why are some individuals or populations of bighorn sheep more susceptible to disease?—Respiratory disease mortality differs among individual bighorn sheep. Habitat fragmentation and fluctuating levels of connectivity have led to desert bighorn sheep populations with varying levels of genetic diversity from altered gene flow and inbreeding (30, 32). Therefore, even within the Preserve, detectable genetic differences exist between populations (Figure 4, 4), raising the likelihood that individuals and populations may have different variants of immune system genes related to genetic diversity. Thus, population responses to pneumonia may differ, and some of those differences may have a genetic basis influenced by habitat fragmentation and connectivity.

Researchers at Oregon State University (OSU) have taken advantage of the bighorn sheep captures in the Preserve to investigate “ecoimmunology” of desert bighorn sheep, a growing field of inquiry in which researchers attempt to relate immune system function to the ecology of the study animal and the disease (33). Goals for this part of the study include evaluating whether bighorn sheep immune system function varies among populations, and to explore the possible role of major histocompatibility complex (MHC) genes in determining how bighorn sheep experience respiratory disease. MHC genes are a key component of mammalian immune systems and influence how they fight pathogens such as harmful bacteria. MHC diversity is commonly studied in wildlife populations, because high diversity of MHC genes is thought to decrease disease susceptibility (34). In addition, “immunophenotype” - a characterization of how strongly an individual’s immune system reacts to pathogens - is being measured for bighorn sheep across the study area by counting immune system cells in blood samples from captured

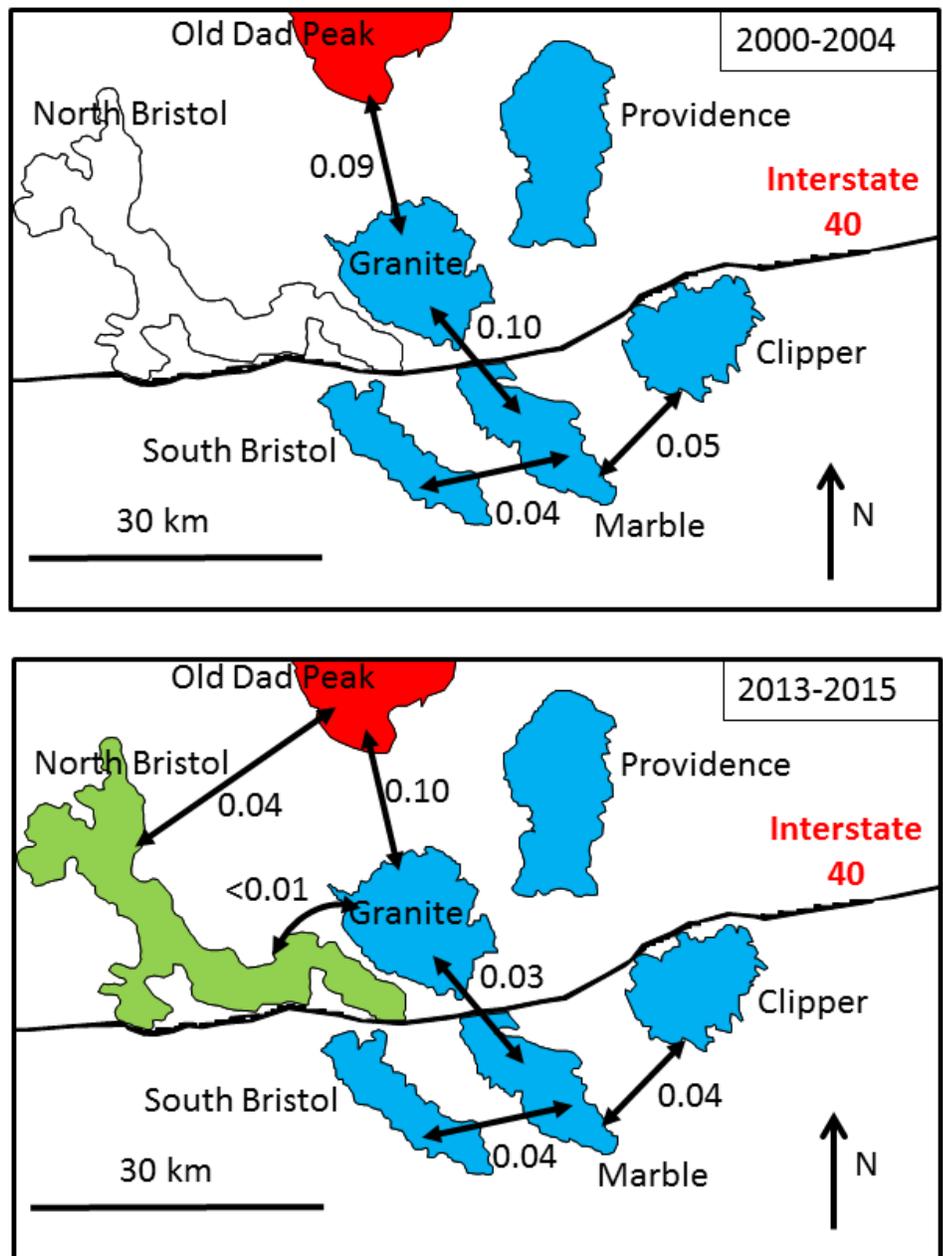


Figure 4. Preliminary analysis of recent nuclear DNA (16 microsatellites) recovered from fecal pellets of bighorn sheep and captured animals 2013-2015 suggests that movement of bighorn sheep among populations (colored polygons) has changed significantly since the first systematic characterization of gene flow conducted in 2000-2004 (39). Here, we show preliminary estimates of genetic structure (F_{ST} , numbers next to arrows) between selected ranges. F_{ST} is a measure of genetic distance, in this case, among pairs of populations; F_{ST} values range from 0 (complete mixing of individuals among populations) to a theoretical maximum of 1 (no shared genetic variation). In this system, F_{ST} values ≤ 0.05 are associated with frequent interpopulation movements (6), and maximum values do not exceed 0.40 (4). In 2000-2004, genetic structure suggested that bighorn did not move across Interstate 40, e.g. between the Marble and Granite Mountains, the North Bristol Mountains apparently lacked a resident population, and Old Dad Peak (red polygon) was relatively isolated. Both the new genetic data and observations of collared animals from 2013-2015 show that bighorn sheep now move across Interstate 40 between the Marble and Granite Mountains, and that strong gene flow and movements of collared animals link the Granite Mountains with the recently established North Bristol Mountains (green polygon) and the North Bristol Mountains with Old Dad Peak. Thus, the rapid spread of respiratory disease to both Old Dad Peak and Marble Mountains conforms to our new understanding of movements of bighorn sheep in the study area. Not all comparisons among populations are shown.

animals, as well as other tests such as the bacterial killing assay (BKA) (33). The BKA examines how well blood plasma and its associated anti-microbial components can kill test bacteria, in this case, *E. coli*, under laboratory conditions (Figure 6). In 2013, the OSU research team set up a temporary laboratory at the University of California's Sweeney Granite Mountains Desert Research Center to process blood samples and initiated laboratory analyses. Subsequent captures have also relied on a temporary mobile laboratory set up in a truck-towed trailer (Figure 5) or large tent.

Preliminary analysis of combining these ecoimmunology results with the disease testing results and previous genetic work (32, 35, 36) has revealed some intriguing patterns. During the initial 2013 *Movi* outbreak, we observed more actively-infected individual bighorn sheep in populations with lower genetic diversity at genetic markers linked to immune-system genes (37), although the different timing of disease spread to different populations may offer a counter explanation. Expression (essentially, whether the gene is "turned on" or not) of MHC genes also differs markedly among populations in the study area, as does the ability of blood plasma of bighorn sheep in those populations to kill bacteria (BKA, Figure 6) (38). These early analyses suggest that different populations could experience different impacts from the disease based on their genetic makeup, and reinforce the possibility that the natural and human-caused fragmentation of desert bighorn sheep populations in the Mojave may contribute to varied responses of bighorn sheep to respiratory pathogens in different mountain ranges.

Where next?—In fall of 2015, 60 additional bighorn sheep were collared to augment sample sizes in the movement and demography study in the Preserve, as well as to further contribute to the study of immunogenetic variation and immune system function. Field work to assess lamb survival, adult survival, and disease impacts will continue. Ultimately, we hope that these interlocking research efforts in the Preserve will contribute to new fundamental knowledge about the impact of habitat fragmentation, disease, and evolutionary processes on desert bighorn sheep. Our aim is to strengthen the ability of the NPS,



Figure 5. Initial laboratory analysis of blood and fecal samples collected during bighorn sheep captures takes place in temporary laboratory facilities set up in the field (Photo by B. Dugovich).

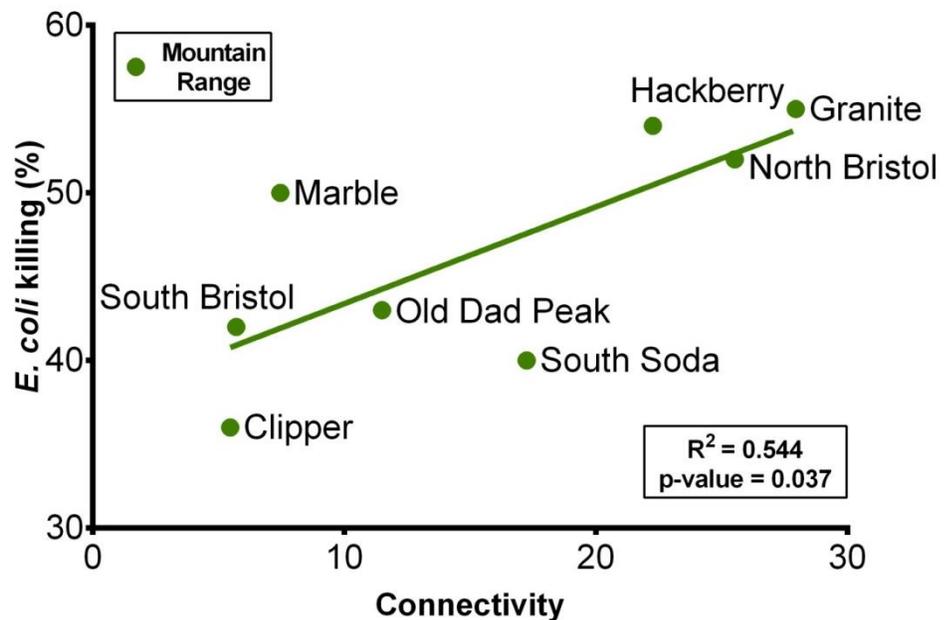


Figure 6. The percentage of test bacteria (*E. coli*) killed by plasma from bighorn sheep blood samples (bacteria killing assay [BKA]) from 8 populations in the Mojave study area increases significantly in populations with higher connectivity (Demographic Weighted Closeness, (35)). Connectivity of each population is determined from the number and proximity of nearby bighorn sheep populations, based on a dispersal model derived from genetic data (35). The BKA test provides a measure of immune system function. Genetic diversity of desert bighorn sheep populations also increases strongly with population connectivity (30, 32); thus, one hypothesis to explain this relationship between immune system function and connectivity is that populations with higher genetic diversity have immune systems better equipped to kill certain pathogens (40).

CDFW, and others to manage this iconic species in the face of new threats and contribute to a better appreciation of the unique ecosystems found in the Mojave Desert.

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Ovis canadensis drawing by Pat Hansen.