Translocation Plan for Sierra Nevada Bighorn Sheep

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Executive Summary

Translocations are integral to achieving a distribution of Sierra bighorn that will ensure long-term viability of the population (USFWS 2007). This plan considers many concerns: logistics, habitat, predation, population viability of source and reintroduced herds, genetic variability, disease, and recent capture activity. Translocations planned for spring 2013 include a reintroduction to the currently unoccupied herd unit at Olancha Peak and augmentations to increase genetic variability at Mt. Gibbs. Additional augmentations to increase the size of herds at Convict Creek and Mt. Warren may occur if logistical constraints allow.

Currently, four herd units (Taboose Creek, Olancha Peak, Big Arroyo, and Laurel Creek) considered essential for recovery are not inhabited by ewes (Figure 1). One of those, the Taboose Creek herd unit, is occupied by rams and occasionally ewes have explored the habitat there. It is also immediately adjacent to the larger Sawmill Canyon herd and is relatively likely to be colonized by ewes from this herd. Consequently, we will allow time for colonization to occur as we proceed with reintroduction to the 3 remaining herds. Olancha Peak was selected for reintroduction in March 2013. Although, it is close to an occupied herd at Mt. Langley, the two herd units are separated by forest and less contiguous escape terrain making it unlikely that natural colonization will occur. A reintroduction at Olancha Peak has a high potential for success because the extensive low-elevation winter range in the herd unit provides for an abundance of high-quality winter forage with virtually no concern about the negative effects of severe winters with deep snow. Abundant rugged lambing habitat is upslope of the winter range and en route to the summer range. The alpine summer range, while not extensive, provides adequate forage and is supplemented by high quality subalpine summer range that includes numerous springs and seeps with associated forage. Risks associated with predation and disease transmission in the Olancha Peak herd unit are of minimal concern and are discussed in further detail. Finally, good road access to the base of the winter range facilitates easy release of Sierra bighorn during translocations and provides for ease of monitoring following reintroduction. Monitoring of this newly established herd will be important to evaluate its success and to inform future translocations. The 2 remaining herds, Big Arroyo and Laurel Creek, are in the Kern Recovery Unit that lies within Sequoia and Kings Canyon National Parks. Those 2 herd units are in remote wilderness and are about 20 miles from the nearest road access. Reintroductions to the Kern Recovery Unit require greater resources and expense for helicopter time and monitoring to

evaluate the success of the action. Those resources could not be gathered in time for a translocation in spring 2013 but planning is occurring to facilitate reintroduction in the near future.

Population viability analyses indicate that 2 populations, Mt. Langley and Sawmill Canyon, can sustain removals of ewes for translocations at this time. The Mt. Langley herd unit is adjacent to the Olancha Peak herd unit; thus, Sierra bighorn from the Mt. Langley herd unit will not be used for reintroductions to Olancha Peak to reduce the probability of individuals returning to their neighboring home-range. Ten ewes and 5 rams from Sawmill Canyon will be placed in the Olancha Peak herd unit, and up to 10 ewes from Mt. Langley will be used for augmentations to existing herds at Mt. Gibbs, Convict Creek, and Mt. Warren.

Genetic analyses indicate that the genetic variability in source populations can be maintained in re-introduced populations by selecting founding individuals with high heterozygosity levels from multiple source populations. Thus collared ewes from Sawmill Canyon and rams from multiple source populations will be selected for reintroduction based on their individual heterozygosity levels. To prevent depletion of genetic variability in Sawmill Canyon, an important source herd, a maximum of 7 high-heterozygosity previously collared ewes will be targeted for translocation. At least 3 additional unmarked ewes will be selected.. Genetic diversity in the new Olancha Peak herd can be further enhanced by minimizing the probability of rams breeding their offspring. To reduce the possibility of a single ram maintaining dominance for multiple years and breeding his offspring, rams will be selected with a staggered age structure, and future supplemental translocations to this new population may replace rams.

The highest priority augmentation is at Mt. Gibbs. Within Sierra bighorn, the Mt. Gibbs herd unit stands out in showing clear signs of declining genetic diversity, which is consistent with its demographic history and substantial isolation. We plan to supplement this population with 2-3 ewes of high heterozygosity from Mt. Langley.

This initial reintroduction to the Olancha Peak herd will be supplemented by augmentations from other source herds, besides Sawmill Canyon, within 2 years. This will add genetic diversity and minimize impacts to source herds.

Introduction

Sierra Nevada bighorn sheep (hereafter Sierra bighorn) are a subspecies of wild sheep that is native to the mountain range for which they are named. In 1999, the U.S. Fish and Wildlife Service granted emergency endangered status to Sierra bighorn sheep inhabiting the central and southern Sierra Nevada of California as a distinct population segment (USFWS 1999a, 1999b). The final rule granting endangered status to the population was published in 2000 (USFWS 2000). While the population has grown to 500 in recent years, the current size and geographic distribution does not meet recovery objectives; thus, the population is still under threat from factors such as disease, predation, and weather..

Recovery goals for Sierra bighorn include recovery unit size thresholds and distribution criteria. Specifically, the goals stipulate that 305 adult and yearling females be distributed among 12 of 16 geographic areas, referred to as herd units. Each recovery unit contains 2 - 6 herd units. Meeting these goals will ensure long-term viability of this genetically unique subspecies. The 12 herd units needed for recovery are also designated as critical habitat. Currently, 8 of these 12 herd units are occupied. One of the delisting criteria identified in the Recovery Plan for Sierra bighorn (Recovery Plan; USFWS 2007) recommends that Sierra bighorn persist in these 12 herd units without intervention for at least 7 years.

Translocations to reoccupy historic habitat and to meet recovery goals are identified as a priority level 1 task in the Recovery Plan. This translocation plan analyzes reintroductions into currently-unoccupied herd units and augmentations to supplement existing subpopulations of Sierra bighorn. Using a hierarchical decision-making framework, we evaluate the conservation potential of translocation of Sierra bighorn. The 4 tiers addressed in the hierarchy are necessity, risk, likelihood of restoration, and feasibility.

Necessity of translocation

The complex topography and the vegetation structure of the southern and central Sierra landscape, coupled with the intrinsic biology and behavior of these bighorn sheep, has resulted in a naturally fragmented distribution of animals, a metapopulation (Bleich *et al*. 1990). Conservative philopatric behaviors (reluctance to disperse from their home range) make bighorn slow to colonize unoccupied habitat (Geist 1967, 1971). Since the 1950s, translocation of bighorn sheep has been the primary means of reestablishing populations in historical and unoccupied habitat and of supplementing dwindling populations. Many transplants in the western U.S. have consisted of groups of 12 to 40 animals (Singer et al. 2001). The minimum number suggested for direct release is 20 (Wilson and Douglas, 1982). Limited numbers of Sierra bighorn are available for translocations. It will be important to utilize them in a way that maximizes recovery in the shortest period while minimizing risk to source populations.

Risk Evaluation

This analysis addresses impacts to source populations of Sierra bighorn and considers potential effects to other sensitive species and the ecosystem as a whole.

Helicopter Net-Gun Captures

The U.S. Fish and Wildlife Service issued a biological opinion analyzing the effects of activities listed under the California Department of Fish and Wildlife’s Federal Fish and Wildlife Permit (i.e., recovery permit) and determined that these activities , and the methods used to carry out these activities, namely helicopter net-gun captures, would not jeopardize the continued existence of Sierra bighorn (USDI 2011). Guidelines provided by the Northern Wild Sheep and Goat Council and the Desert Bighorn Council describe the steps necessary for a successful capture and state that helicopter net-gunning is the most commonly used capture technique, followed by drop-nets, drive-nets, and darting (Foster 2005). Kock et al. (1987) compared the success rate of 4 capture methods (drop-net, drive-net, net-gun, and darting) on 644 bighorn sheep in the western United States. The net-gun was found to have considerable advantages over the use of ground nets and chemical immobilization, and the net-gun method had the lowest proportion of injured or killed bighorn sheep, had no capture myopathy (CM) mortality, and resulted in 2% (2/137) accidental mortality. Other studies (Jessup et al. 1988) and captures of Sierra bighorn have had similar results. Over the past 10 years the average capture-related mortality rate for Sierra bighorn was 3.33% (less than 1 individual per year; Stephenson et al. 2012). This mortality rate falls below the amount of take (3 bighorn / year) authorized under the Federal Fish and Wildlife Permit issued by the U.S. Fish and Wildlife Service. As mentioned previously, the U.S. Fish and Wildlife Service determined that this amount of take would not jeopardize the continued existence of the Sierra bighorn. Additionally, CDFW should cease any operations that may result in take the exceeds the amount identified in the U.S Fish and Wildlife Service's biological opinion and Federal Fish and Wildlife Permit pending reinitiation with the Service.

Population Viability Analysis: Source Populations

We performed population viability analyses to determine the effects of harvesting ewes for translocation from selected populations. Each of these scenarios was performed parametrically to demonstrate the relative effects of varying the number of removals. We constructed a stochastic, discrete time, stage-structured matrix model (Cahn 2011) and based estimates of demographic rates on data collected from 1999–2011. Because bighorn sheep are polygynous (Geist 1971), their populations are sensitive to adult female survival ; therefore, we restricted the model to females (Morris and Doak 2002). The model was based on 4 approximate life stages: 2 juvenile and 2 adult stage classes (Cahn 2011 and Johnson et al. 2010). We incorporated a ceiling model of density dependence only in the survival of the youngest class and used 100 bighorn sheep for carrying capacity (Cahn 2011). To incorporate environmental variation, we generated random values of vital rates by parametric bootstrapping. We also incorporated demographic stochasticity in survival and reproduction (Mills and Smouse, 1994). For each model we ran 1,000 iterations and calculated probabilities for the following outcomes: 1) 5 ewes as a quasi-extinction threshold, 2) 15 ewes as the number of animals below which demographic stochasticity and genetic stochasticity may contribute to an extinction vortex (Morris and Doak 2002), 3) 25 ewes as the Recovery Plan target for each population, and 4) 25 ewes for more than 7 years to represent realization of delisting goals.

We modeled harvesting scenarios from source populations based on the underlying demographics. Lambda reported for these populations represents the growth rate over the 5 years following removals. For the Mt. Langley (λ =1.045) and Sawmill Canyon (λ =1.052) populations, we modeled 3 different cases: 1) removing 10 ewes in year 1, 2) removing 10 ewes in year 1 and 5 ewes in year 2, and 3) removing 10 ewes in year 1 and 5 ewes in year 3. For the Mt Baxter (λ =1.032) herd we modeled removing 5 ewes in year 2 only. For Wheeler Ridge (λ =0.985) the observed demographic rates do not support removals; thus, we did not analyze harvesting scenarios.

Table 1 shows the projected effects of removal on the source populations over a 5-year, 10-year and 20-year time span. At Sawmill Canyon the probability of achieving delisting goals in 20 years after removing 10 ewes in year 1 and 5 ewes in year 3 is *0.83*. At Mt. Langley the same harvesting strategy had a negligible effect on the probability of achieving delisting goals in 20 years (Pr =*0.95*). Compared to scenarios with no removals, the third scenario (10 animals in year 1 and 5 animals in year 3) leads to a 7% (Sawmill Canyon) and 4% (Mt. Langley) reduction in the probability of achieving delisting goals in 20 years (Table 1). At Mt. Baxter the probability of achieving delisting goals with a single harvest of 5 animals is *0.93*. This represents a 3% decline in the probability of achieving delisting goals in 20 years compared to the scenario with no removals. We did not model a harvesting strategy at Wheeler Ridge because the probability of achieving delisting goals in the absence of removals is *0.81*. Only populations with a lambda greater than 1 were considered as sources for translocation stock. Figure 2 shows the population trajectories for the Mt. Langley, Sawmill Canyon and Mt. Baxter herds with harvesting regimes that have the greatest impact on the probability of achieving delisting goals. The translocations will be sourced from a variety of herds so that the removals are sustainable based on population demographic rates. This suggests that Sawmill Canyon and Mt. Langley, using demographic rates from the past decade, will be the primary sources of translocation stock, supplemented by Mt. Baxter. Further reintroductions will be initiated as the source populations are able to support additional removals.

The modeled variability in survival rates incorporated predation to the extent predation occurred during the data-collection period (1999-2011). During this period, mountain lions were responsible for 90% of the known predator kills of bighorn ewes (26 of 29). Consequently, predator management focused on removing specific mountain lions documented to have killed Sierra bighorn. Removing mountain lions may have resulted in depressed predation rates of Sierra bighorn. If, in the future, mountain lion predation is not controlled in a similar manner, demographic rates for the underlying populations may decline. Simulating additional additive mortality at Mt. Baxter and Sawmill Canyon at a rate of 2 ewes per year resulted in a decline of lambda(λ) of 3.5% and 2.2% respectively. Additive mortality was not modeled at Mt. Langley because the documented predator kills of ewes in that population were less than 50% of that observed at either Mt. Baxter or Sawmill Canyon. If such declines were to occur, the population growth rate at Mt. Baxter (lambda <1) would not support removals for translocation, and the number of animals available for removals at Sawmill Canyon (lambda>1) would decrease. Together these circumstances could prolong the time needed to reach downlisting goals because lower rates of population growth and fewer source herds would produce fewer surplus animals to support reintroductions and augmentations. Predicting precisely how much delay in downlisting may result from potential additive predation is not feasible because of the variability in estimating growth rates beyond the next decade..

Sensitive Species

Sierra bighorn will be captured for translocation by a net-gun deployed from a helicopter, a standard practice for bighorn captures throughout the west (Kock et al. 1987). Once captured Sierra bighorn will be transported to a nearby processing site with road access, handled, and transported by truck for release at Olancha Peak, Mt. Warren, Mt. Gibbs, and Convict Creek. Bighorn intended for release at Mt. Gibbs and Convict Creek will be transported from a vehicle near the base of the herd unit onto the mountain by helicopter due to the inability to drive to a release with immediate access to bighorn habitat.

All of the herd units identified for translocation are located within the Inyo National Forest. Therefore, the U.S. Forest Service evaluated the potential impacts of translocations on Forest Service Pacific Southwest Region sensitive aquatic, plant, and wildlife species (Murphy and Sims 2011 and Weis 2011). This analysis identified potential habitat for 2 sensitive wildlife species, Sierra Nevada red fox (*Vulpes vulpes necator*) and wolverine (*Gulo gulo*) (Murphy and Sims 2011). The U.S. Forest Service determined that translocation activities would have negligible effects at the species level because of the short duration of potential impacts from noise and the presence of a helicopter (Murphy and Sims 2011). The U.S. Forest Service also determined that translocations of Sierra bighorn may impact individuals but would not lead toward federal listing or a loss of viability for the following special status plant species: *Arabis tiehmii, Astragalus ravenii, Botrychium lineare, Botrychium lunaria, Botrychium minganense, Carex tiogana, Cordylanthus eremicus var. olanchense, Draba asterophora var. asterophora, Eriogonum wrightii var. olanchense, Lupinus padre-crowleyi, Monardella beneolens, Streptanthus gracilis, Trifolium dedeckerae,* and *Draba sharsmithii*. Specifically, the U.S. Forest Service concluded that the timing of the helicopter capture flights, the limited number of landings, the short duration of the activities, the small number of animals to be translocated, and the normal use patterns of the sheep (Weis 2011) would result in minimal potential impacts.

Likelihood of Restoration

To determine the likelihood of establishing a viable population, we conducted population viability analyses, modeled habitat characteristics, simulated genetic founder effects, and analyzed threats caused by disease and predation.

Population Viability Analysis: Recipient populations

We performed population viability analyses to determine the probability of successful reintroduction with varying augmentation regimes. Similar to the models presented for the source populations, the recipient models are based on females only. For recipient populations we modeled 3 different cases: 1) a single translocation consisting of 10 pregnant ewes and 5 rams (not in model), 2) additional augmentation of 5 pregnant ewes at year 3, and 3) additional augmentation of 10 pregnant ewes at year 3. Two demographic rates were modeled, representing the best and worst case scenarios based on observed demographic patterns of Sierra bighorn: positive growth (λ =1.018) using demographic rates from Mt. Langley and negative growth (λ =0.991) using demographic rates from the Mono Basin (Mt. Warren and Mt. Gibbs). Lambda for reintroduced (i.e., recipient) populations was calculated based on these population growths rates and projected for 20 years.

In Table 2 the results show that for positive growth with a single translocation the probability of achieving delisting goals in 20 years is *0.76*. This increases by 16% with a second translocation of 10 ewes to augment the first reintroduction (Pr =*0.92*). If the reintroduced population were to experience negative growth, an augmentation of 10 ewes would increase the probability of achieving delisting goals by 33%; however, the probability of reaching delisting goals in 20 years is *0.54*. This scenario, of negative population growth, presents a dilemma. If the long-term trends are truly negative, the population would be a sink and require periodic influxes to stay viable. Under this scenario larger-scale (Sierra wide) meta-population dynamics, not modeled here, would be required to support long-term population viability. Based on our population viability analyses, we have determined that the most successful strategy for reintroducing Sierra bighorn would be to introduce bighorn sheep to new source populations using 10 ewes as an initial population followed by 10 additional ewes within the next two years as an augmentation.

Genetic Variability

Because Sierra bighorn are recognized for their genetic uniqueness as a subspecies, recovery efforts for this taxon are ultimately about conserving and enhancing this unique gene pool. Genetic drift erodes gene pool diversity over time when, by chance, alleles drift to lower frequencies and then disappear. The populations most vulnerable to erosion of gene pool diversity by genetic drift are those that are smaller and with higher isolation (less gene flow). From the standpoint of population management, the greatest influence on the diversity of gene pools within herds will occur at the founding stage for reintroductions, or through augmentations when populations are small. Careful genetic planning for translocations can maximize genetic diversity within small herds. This is especially the case for Sierra bighorn because of the limited sources of translocation stock. Current technology provides the means for identifying specific individuals for translocation.. Helicopter net-gunning allows selective captures of individual sheep, and modern methods of genetic analysis allow relative levels of heterozygosity to be measured for individual bighorn. Additionally, because numerous bighorn are captured and collared on a regular basis within the Sierra Nevada, we have a pool of Sierra bighorn with known genetic profiles. This analysis is separated into 2 topics: augmentation of existing herds for genetic rescue and translocations for reintroductions.

Genetic Rescue

Microsatellite analyses and bottleneck tests of Sierra bighorn indicate that a considerable amount of genetic diversity has been lost (J. D. Wehausen, unpublished data). Further, Johnson et al. (2011) found a heterozygosity-fitness correlation suggesting that genetic diversity has declined far enough that Sierra bighorn at the lower end of the heterozygosity spectrum may be less fit. This presents the challenge of whether it might be possible to increase heterozygosity levels in small and reintroduced populations to enhance their population fitness and success. Bringing in animals from outside populations, such as desert or Rocky Mountain bighorn, is not an option because of the uniqueness of the Sierra bighorn gene pool and the risk of outbreeding depression for sheep that appear to be adapted to very different habitats.

The first question relative to genetic rescue is what population might need it and why. To address that question, recent microsatellite data were compiled for Sierra bighorn herds that have been sampled, as well as for a variety of populations of desert bighorn sheep for comparison (Table 3). A number of noteworthy patterns emerged. First, for the average number of alleles per locus (A), Sierra bighorn have the lowest genetic diversity levels of the populations sampled. When the frequency distribution of those alleles is also considered, Sierra bighorn are joined at the bottom by the Pilares and Red Rock captive herds relative to effective number of alleles (A_E) and expected heterozygosity (H_E -- heterozygosity expected at Hardy Weinberg equilibrium; Table 3). Second, within Sierra bighorn, the Mt. Gibbs herd unit stands out in showing clear signs of declining genetic diversity, which is consistent with its demographic history and substantial isolation. According to the data in Table 3, this is the 1 herd that currently shows a clear need for genetic management.

Since the mid-1990s, the population at Mt. Gibbs has grown from a reproductive base of just 1 ewe to 7 ewes, but in recent years it has not increased further because of low reproductive rates One hypothesis is that this population has reached the carrying capacity population size that its habitat can support. This appears to be unsupported given the particularly fat condition of Sierra bighorn in this herd that have been measured by ultrasound, suggesting that Sierra bighorn have sufficient forage. However, we cannot explain why some of these ewes were not pregnant in spring. An alternative to the carrying capacity hypothesis is that inbreeding is limiting growth of this population through inadequate reproduction. A well-planned genetic augmentation of this herd unit should be able to distinguish between these 2 hypotheses.

There are two strategies for augmenting the Mt. Gibbs population. The first strategy is translocate 1-3 rams of high heterozygosity into this herd. This could radically change the reproductive output of the resident ewes. However, there is great uncertainty whether those rams would be reproductively successful or even remain with that herd. The current Mt. Gibbs rams are large in body and horn size, and socially might greatly outrank introduced rams for some years. Consequently, there is a risk genetic diversity would decline until the introduced rams establish themselves in the herd. The second strategy for genetic management would be initially to translocate 2-3 pregnant ewes of high heterozygosity into this herd. Because Sierra bighorn are polygynous, the introduction of additional ewes into the herd unit would be the most effective approach to increase genetic diversity. If inbreeding is limiting the current herd, such an augmentation should trigger an increase in reproductive output and a population increase. If this appears to be the case, additional ewes can be translocated to this population in 2-4 years to accelerate population growth, add additional genetic diversity, and increase the sample size for comparisons. Ram lambs born to the translocated sheep will likely add further genetic diversity when they reach breeding age. This second approach is consistent with the recommendations of Hedrick and Fredrickson (2010) and is the preferred approach.

Genetics and Reintroductions

Olancha Peak, Big Arroyo, and Laurel Creek are 3 vacant herd units that need reintroductions of Sierra bighorn. Each of these herd units will likely be peripheral populations with limited sources of gene flow. This and the potential for faster growth because of higher fitness of females are reasons to initiate herds with the highest genetic diversity in these areas. The ability to selectively capture individuals with known levels of heterozygosity opens the door to potentially initiate herds with higher genetic diversity than existing herds. Various authors have recommended that large numbers of bighorn sheep be used in reintroductions to maximize the sampling of genetic diversity in the new herd. However, Sierra bighorn have limited genetic diversity that needs to be maximized in the founding animals. With a selective approach it may be possible to initiate herds with fewer animals in such a way that increases genetic diversity by making allele frequencies in the founding gene pool more even.

There are currently 4 herd units (Mt. Langley, Mt. Baxter, Sawmill Canyon, and Wheeler Ridge) that contain surplus animals for translocation, or soon will be contain enough animals for such use. Genetically these sources of translocation stock can be considered 3 populations because the Mt. Baxter and Sawmill Canyon herds have contiguous habitat and consequently represent 1 gene pool. The Mt. Langley and Wheeler Ridge herd units stem from reintroductions in 1979-86 from the Mt. Baxter/Sawmill Canyon gene pool. Variation in observed heterozygosity in each herd is high (Table 3) and an ANOVA of those heterozygosity values found no difference among samples from these 3 gene pools ($F = 0.787$; $P = 0.458$), suggesting that individuals from all 3 gene pool could be used for translocation stock. However, expected heterozygosity indicates that at Hardy Weinberg equilibrium the herds (Wheeler Ridge, Mt. Langley, and Mt. Warren) created through translocations from the Baxter/Sawmill gene pool all will have lower levels of genetic variation than the source gene pool (Table 3). This is also evident in the effective number of alleles (Table 3, 4). These differences are most obvious in alleles present in the sampling of the Baxter/Sawmill gene pool that are missing in these reintroduced herds. For the potential sources of translocation stock, Mt. Langley is the most extreme, missing 4 alleles in 19 loci (1 each in 4 loci), or 4 out of 53 total alleles (7.5%). In contrast, Wheeler Ridge is missing only 1 allele (1.9%) in the current sampling. If 1 of these reintroduced herds were used unselectively to create new herds, there is the risk of further reducing genetic diversity.

Consequently, 19 variable microsatellite loci were used to investigate the genetic consequences of potential translocation approaches.

This investigation considered 2 ends of a spectrum of potential uses of these 3 gene pools of translocation stock. One was to catch animals without any regard to genetic constitution, as was done in the past. Six of the currently sampled Sierra bighorn from each of the 3 gene pools were randomly selected without replacement to make a total of 18 Sierra bighorn used to initiate a population. This random sampling was carried out 10 times and population genetic measures were obtained for each sampling. At the other end of the spectrum, 3 founding populations of 5, 11, and 18 Sierra bighorn were selected, constituting individuals with the highest heterozygosity levels for the 19 loci measured. Multiple individuals had the same heterozygosity levels and the number of individuals used in this exercise reflected natural breaks in the heterozygosity data.

Results for both of these samplings are presented in Table 4 along with statistics for each of the 3 translocation source gene pools. When a biased population is created with individuals of highest H_O values, the result is a population with a large heterozygosity excess relative to H_E (Table 4). However, the numbers of alleles in the Sierra bighorn population limit what the heterozygosity level will be at Hardy Weinberg equilibrium, which is reflected in the H_E values. To the extent that more heterozygous individuals may have a higher fitness, this might be advantageous in maximizing early population growth. Faster initial population growth is desirable for both demographic and genetic reasons. However, it needs to be recognized that the population will not maintain that initial level of heterozygosity when equilibrium is reached. Nevertheless, this approach does produce a founding population with a higher H_E than any of the source populations (Table 4).

At the other end of the spectrum, the 10 random draws from the 3 gene pools provide a glimpse at what the genetic structure of a founding population might look like with no selectivity. As might be expected, the average H_O is very close to the average of the 3 gene pools sampled. However, this is not the case for H_E. Instead, the lowest value obtained equals the average of the 3 gene pools sampled, and the highest exceeds any of those of the source gene pools (Table 4). This reflects the advantage of mixing samples from 3 different gene pools that have drifted apart, resulting in different allele frequencies that complement each other when combined. Thus, a strategy of sampling equally from these 3 gene pools produces populations biased toward greater genetic diversity. Even so, the average H_E from these 10 random samples is lower than that of the Baxter/Sawmill gene pool.

Given an already-compromised genetic diversity in Sierra bighorn, the goal for reintroductions is to create herds with H_E values at least as high as the Baxter/Sawmill gene pool. Between the 2 extreme approaches to reintroductions presented in Table 4 lie many possible strategies. Greater selectivity in the individuals used to initiate a population should allow for fewer animals to be used to represent the gene pool variation, but the downside of a smaller founding population is that matings between close relatives are more likely to occur, and such inbreeding can negate the advantages of the initial selectivity. This problem could be countered by allowing the founding rams to breed for only 2 years and then catching, removing, and replacing them every 2 years for at least the first generation (6 years), at which time there will be breeding-age rams that were born in that population. Another possible strategy would involve being minimally selective for the females caught and released, but being very selective in the heterozygosity levels of the rams for the first generation. We would expect this strategy to produce a population about midway between the 2 extremes presented in Table 4. If multiple populations are initiated within a short time period, rams of high heterozygosity might be used sequentially in multiple herds.

A further issue is the potential effect on each source population gene pool of selectively removing individuals of highest heterozygosity. The Mt. Langley and Wheeler Ridge herds number or have numbered about 100 sheep. The Mt. Baxter/Sawmill Canyon gene pool is close to 200 and growing. If sheep are selectively removed from all 3 herds, the effect on each of the source herds will be minimized; however, those animals removed might be ones that would have contributed more genes because of higher fitness. This might be a reason to adopt a hybrid strategy that does not selectively remove too many sheep. Based on the combination of factors discussed above including capture logistics, the focus for the initial reintroduction will be that of selecting largely uncollared females from a herd with high heterzygosity (e.g., Sawmill) and males of known genotypes with high heterzygosity from various herds (Appendix 1).

Habitat Models

GPS locations of Sierra bighorn have been used to develop resource selection functions (RSFs) to identify new potential summer and winter habitat for females (Johnson et al. 2006). Habitat predictor variables included in the models were elevation, elevation^2, slope, hillshade, distance to escape terrain, aspect, ruggedness, and forested/non-forested. Explanatory models were applied across the landscape to predict summer and winter habitat in currently unoccupied herd units. The largest expanse of predicted winter range (38 km) was found along the eastern slopes of the currently-unoccupied Olancha Peak herd unit. The largest winter range of currently-occupied herd units is 15.7 km at Wheeler Ridge. Other currently-unoccupied herd units that are candidates for reintroduction, Laurel Creek and Big Arroyo, have much less predicted winter range, 3.9 km and 3.8 km respectively. Because the amount of winter range predicted appeared to be an indicator of the number of reproductive females in that herd unit (Johnson et al. 2006), a reintroduction at Olancha Peak is likely to produce a persistent subpopulation.

The size of summer range, generally characterized by high-elevation alpine habitat, when predicted by an explanatory RSF varied within currently-occupied herd units from 5.9 km to 13.6 km (Johnson et al. 2006). Smaller amounts of summer range were predicted for herd units that are candidates for reintroduction with summer range varying between 3.8 km and 5 km; Olancha Peak has 4 km of predicted summer range. The small summer range is expected to support a population size needed to meet recovery goals at Olancha Peak; furthermore, the abundance of winter habitat and historic locations suggest that summer habitat is sufficient for this population to persist.

Altitudinal migration from summer alpine habitat to lower-elevation winter ranges maximizes nutrient intake. Connectivity between summer and winter ranges was estimated by calculating the average minimum distance from predicted patches of summer and winter ranges within a herd unit (Johnson et al. 2006). The average minimum distance between summer and winter ranges at Olancha Peak was 1.2 km. Average minimum distances between summer and winter ranges in currently-occupied herd units is smaller, varying between 0.37 km to 1.1 km. Some of the most productive herds, Sawmill Canyon and Wheeler Ridge, have average connectivity distances of approximately 1 km. Other currently-unoccupied herd units that are candidates for reintroduction, Laurel Creek and Big Arroyo, have larger distances between summer and winter ranges, >1.7 km.

In addition to connectivity between summer and winter ranges, connectivity between adjacent herds is important for gene flow to mitigate impacts of genetic drift in small isolated herds. Olancha Peak would be a peripheral herd, having gene flow from 1 adjacent herd unit at most. The winter RSF identified potential habitat between the Mt. Langley and Olancha Peak herds (Johnson et al. 2006). These patches of winter range may provide a path for gene flow from Mt. Langley. A single herd in the Kern Recovery Unit, either Laurel Creek or Big Arroyo, would probably be completely isolated until an additional herd is established in the Kern Recovery Unit because the Kern River and the adjacent forested habitat would likely act as a movement barrier.

The RSFs discussed in this translocation analysis were created using data from GPS collars deployed between 2002 and 2004. Data collected during this period largely represent habitat use in the Southern and Central Recovery Units. Subsequent to this analysis GPS collars have been deployed on females utilizing habitat west of the crest in the Bubbs Creek herd unit. Habitat use in this area is remarkably different than that seen east of the crest. Bubbs Creek females spend significant time in areas of dense shrubs such as manzanita, chinquapin, and ceanothus, particularly in winter. Additional habitat analyses are needed to incorporate GPS locations west of the crest and data from satellite imagery which represent snow cover and vegetation as habitat variables. When these analyses are completed, they will help better inform subsequent translocation efforts to west side habitat.

With the current habitat models, Olancha Peak stands out among currently unoccupied herd units as prime Sierra bighorn habitat. Although this population may be limited by the size of its summer range, the abundance of low elevation winter habitat, connectivity between summer and winter ranges, and opportunity for gene flow from an adjacent herd unit make Olancha Peak the recommended site for initial reintroductions.

Threatening Factors: Disease

Herds of Sierra bighorn that are used as source populations were sampled for disease during captures in October 2012 prior to implementation of translocations in March. Surveillance of respiratory pathogens was of considerable interest and included analyses for Pateurellaceae and Mycoplasma. No pathogens of concern were detected.

Respiratory disease is widely recognized as one of the greatest threats to the persistence of bighorn sheep throughout the western United States (Wehausen et al. 2011). The Recovery Plan for Sierra bighorn identifies respiratory disease from domestic sheep as one of the primary threats to recovery and stipulates that contact with domestic sheep must be prevented in order to meet recovery goals (USFWS 2007). When the Recovery Plan was finalized in 2007 there remained more than 31 domestic sheep allotments totaling more than 350,000 acres on public land within 20 km of habitat occupied by Sierra bighorn. Most of the allotments recommended for closure in the Recovery Plan were vacated by 2011.

Baumer et al. (2009) outline a process that identifies criteria to assess the threat of disease transmission from domestic sheep grazing adjacent to Sierra bighorn habitat. Risk of contact is quantified using a model of inverse weighted distances that may be interpreted as risk values. GPS locations of Sierra bighorn identify core use areas and are plotted on a resistance surface that is the inverse of a habitat suitability model. The inverse weighted distances characterize the cost of movement across a landscape in terms of the likelihood of where Sierra bighorn will travel given their habitat preferences.

One public land grazing allotment for domestic sheep exists in proximity to the Olancha Peak herd unit. The Tunawee allotment is located on BLM land 15 km south of the perimeter of the Olancha Peak herd unit. In addition to the Tunawee allotment, domestic sheep are grazed on private land east of Highway 395 on the western edge of Owens Dry Lake in the community of Olancha.

Baumer et al. (2009) outline steps for implementing an assessment of risk of contact between bighorn and domestic sheep; they advise the user to rely on the spatial model described above and also to consider the behavior of bighorn sheep and the management practices of grazing permittees. Croft et al. (2010) further establish, based on the movement of rams in the recovery area, that a mean inverse weighted distance (MIWD) of 0.833 represents a threshold above which the risk of contact between the 2 species is unacceptable. Croft et al. (2010) also establish criteria to mitigate a high risk of contact that include natural and man-made barriers to prevent movement by either or both species. The Tunawee allotment has an MIWD value of 0.199 which corresponds to a very low risk of contact. Furthermore, the permitted dates are March 1 – May 31; hence, grazing occurs at a time when there are unlikely to be rams making forays in search of females. The domestic sheep grazing on private land in the community of Olancha is not considered a significant risk because of the location of the LA aqueduct. The aqueduct passes between the community of Olancha and the Olancha Peak herd unit (Figure 3).

The aqueduct represents an impassible barrier because it has an 8 foot chain link fence topped with angled barbed wire along its entire length (Figure 4).

Threatening Factors: Predation

There is a moderate risk of predation to any Sierra bighorn translocated to the Olancha Peak area. Densities of mule deer (*Odocoileus hemionus*) are not as high, on average, as those on the winter ranges adjacent to Wheeler Ridge or Goodale Peak. However, estimates of approximately 1500 to 2200 animals (Thompson, 2008) in recent years are sufficient to support some mountain lions (*Puma concolor*). In fact, mountain lions have been confirmed to use this herd unit area on both their winter and summer ranges (Thompson 2008, personal observation). The release of bighorn to an area that overlaps with mule deer habitat increases the probability of apparent competition (Cooley et al. 2007, Johnson et al. 2012). Apparent competition can occur with a generalist predator like the mountain lion when the presence of a primary prey species, like deer, results in a disproportionately high level of predator activity on a sympatric and relatively rare secondary prey species such as Sierra bighorn. Therefore, it is likely that mountain lions will inhabit areas occupied by Sierra bighorn sheep in the Olancha Peak area and occasionally prey upon them.

Like most of the mule deer herds that inhabit winter ranges in the eastern Sierra Nevada, the Monache deer herd, located southwest of the Olancha Peak herd unit, is migratory, moving to winter ranges at lower elevations between October and April and returning to higher elevations during the summer. The primary risk of predation on Sierra bighorn will occur during the winter when bighorn winter range overlaps with deer habitat. During the summer, the deer occupy ranges at lower elevations than bighorn, typically below tree line, and there will be very little overlap between the species.

The greatest risk of predation on Sierra bighorn in the Olancha area is that of a mountain lion that becomes a specialist at preying on Sierra bighorn (Ross et al. 1997). Despite relatively low deer densities in the areas adjacent to Mt. Langley, a number of predation events by mountain lions on the bighorn population have occurred. Fortunately, the mountain lions responsible for that predation either left the area or were quickly removed. Therefore, the impact of mountain lion predation on Sierra bighorn that may have occurred in the Mt. Langley area, had it not been monitored and managed, is unknown. Predation on the Mt. Langley herd may have been higher than what we would expect for Sierra bighorn in the Olancha Peak herd unit simply because there will be a limited number of animals translocated. Given the density of deer in this area, it is unlikely that mountain lions will cease focusing on deer as their primary prey until the availability of Sierra bighorn increases.

Feasibility

Monitoring

Successful implementation of translocations requires continued monitoring of both the source and recipient herds. The source herds must be followed to determine whether surplus animals are available for removal and how the herd responds to removals.

Herds that are being actively managed receive intensive monitoring. A high level of monitoring includes annual surveys to estimate population size and production and recruitment of young. In addition, telemetry is used to evaluate survival and cause-specific mortality. During captures to deploy collars, Sierra bighorn may be examined to determine nutritional condition and reproductive status and to conduct surveillance for disease. Finally, GPS collars will be deployed to help us understand patterns of habitat use and migration for newly established herds.

Ground surveys of herds has depended on knowing seasonal habitat use patterns and attempting to interact spatially and temporally with those patterns in a way that maximizes the probability of finding the most females and associated Sierra bighorn. Persistence and some luck have often been critically important to success. Habitat use patterns in the Sierra Nevada have shown notable changes over the past 30 years. It is necessary for monitoring efforts to recognize this potential and respond to such changes. A fixed monitoring protocol has the potential to produce data that may be misinterpreted as population dynamics when they instead reflect changing Sierra bighorn behavior.

Annual monitoring of all herds is desired and is generally attempted, yet may not be successful every year for every herd depending upon weather, personnel constraints, and luck. The intensity of monitoring applied to the various bighorn herds in the Sierra Nevada will depend on a variety of factors including herd size, risk of decline (e.g., from disease, predation, or severe weather), use as translocation stock, personnel, and financial resources. As long as a population remains small, monitoring will remain intensive so that immediate action may be taken to mitigate population declines. Until recovery goals are met, larger herds (>25 animals) are likely to be considered as translocation stock and will be monitored closely to assess their ability to provide removals.

Future Economic and Human Resources

We evaluate whether adequate resources will be available to complete the translocation efforts needed to meet the downlisting goals outlined in the Recovery Plan, including monitoring and future augmentations. Achieving downlisting goals for Sierra bighorn involves 3 significant cost areas that need to be specifically addressed: 1) capture costs, 2) collaring costs, and 3) human monitoring costs.

Capture costs

In order to maintain adequate numbers of collars in the population to facilitate effective monitoring and to create and augment subpopulations in accordance with the Recovery Plan, varying numbers of Sierra bighorn will need to be captured during the next 10 years. Projected capture numbers vary from 30 per year to 60 per year. This number of captures will cost $50,000 to $100,000 per year.

Collaring costs

Satellite collars currently deployed on Sierra bighorn aid in efficient population monitoring and allow for identification of suitable habitat through habitat modeling. We anticipate continuing to deploy VHF collars ($250 per animal) on all captures and GPS collars ($3000 per animal) on >50% of the animals. Collaring costs are expected to be about $90,000 per year.

Human monitoring costs

As subpopulations are created, some significantly more remote than the current subpopulations east of the crest, on-the-ground field monitoring will become more complex and thus more expensive. Current on-the-ground field monitoring requires approximately 4 full-time field technicians each year. The cost of this monitoring is approximately $100,000. As more populations require monitoring, additional funds may be necessary to support increased monitoring. Through a combination of satellite collars and flight monitoring of VHF collars, population surveys can be completed more efficiently to ensure adequate insight into population dynamics for each herd.

In order to meet the anticipated capture and monitoring goals for the program, we will need to solicit additional funding above the current levels of State budgeting, particularly in the years when large translocations are anticipated. This is consistent with the funding levels the State has been able to provide and solicit from outside sources in the last 12 years of operation.

Stakeholder Support

The Recovery Plan was developed with the assistance of a recovery team that included scientific experts in the biology of Sierra bighorn as well as stakeholders representing diverse interests, including ranchers, conservation, and recreation groups. The Recovery Plan recognized the reintroduction of Sierra bighorn to vacant herds as essential for recovery (USFWS 2007). The Olancha Peak herd is 1 of 4 remaining vacant herd units needed to meet recovery goals. The more recent Science Subteam, a subteam of the Recovery Implementation Team, recognizes that reintroductions are essential to meet geographic recovery goals.

Multiple government agencies including the National Park Service, the U.S. Forest Service, the Bureau of Land Management, and the Los Angeles Department of Water and Power support the recovery effort. Yosemite National Park and Sequoia and Kings Canyon National Parks are very interested in restoring native wildlife throughout their land and Sierra bighorn represent the only federally-listed endangered species to inhabit the Parks. The recovery area for Sierra bighorn also encompasses 4 National Forests (Inyo, Humbold-Toiyabe, Sierra, and Sequoia) and 2 Bureau of Land Management districts (Bishop and Ridgecrest), and those agencies support the recovery effort. Environmental Assessments by Sequoia and Kings Canyon National Parks and the Inyo National Forest were completed in 2011 and 2012, respectively, and demonstrate the commitment of those agencies to recovery and reintroductions.

Long-Term Operational Guidelines:

1. Removals for translocations will occur when source populations exceed a minimum of 40 adult and yearling ewes.
2. Removals for translocations will not reduce source herds to less than 30 adult and yearling ewes.
3. The goal for reintroductions is to release a minimum of 10 ewes.
4. Augmentations will follow after reintroductions within 2 years.
5. Augmentations of small existing herds will consider genetics of founding individuals and allow for genetic rescue if necessary.
6. Sierra Bighorn in source populations will not be captured on low-elevation winter range within a particular subpopulation in consecutive years. Captures at high elevation are acceptable in consecutive years within a subpopulation.Translocations will be implemented using an adaptive management approach; postponed if exceptionally difficult winter or drought conditions exist.
7. All translocated individuals will be released with VHF collars at a minimum. More typically we expect to fit most animals with GPS collars as well.
8. Herds containing newly-translocated individuals will be closely monitored and surveyed annually.
9. A predator action plan is being developed to enable a response to increased predation that will minimize such effects on bighorn population growth.
10. Adaptive management will be applied to all translocations of Sierra bighorn with population viability analyses, genetic simulations, and habitat models contributing to the science based conservation decisions for this rare subspecies.

Literature Cited

Baumer, A., N. East, J. Echenique, M. Haworth, M. Leinassar, C. Papouchis, T. Stephenson, D. Weaver, and G. Wilson. 2009. A Process for Identifying and Managing Risk of Contact between Sierra Nevada Bighorn Sheep and Domestic Sheep. U.S. Fish and Wildlife Service, Ventura, CA

Bleich, V. C., J. D. Wehausen, and S. A. Holl. 1990. Desert-dwelling mountain sheep: Conservation implications of a naturally fragmented distribution. Conservation Biology 4:383-390.

Cahn, M. L., Conner, M. M., Schmitz, O. J., Stephenson, T. R., Wehausen, J. D. and Johnson, H. E. (2011), Disease, population viability, and recovery of endangered Sierra Nevada bighorn sheep. The Journal of Wildlife Management, 75: 1753–1766.

Cooley, H. S., H. S. Robinson, R. B Wielgus, and C. S. Lambert. 2008. Cougar prey selection in a White-Tailed Deer and Mule Deer community. Journal of Wildlife Management 72: 99-106.

Croft, B., A. Fesnock, M. Haworth, R. Mazur, L. Murphy, S. Nelson, R. Perloff, and T. Stephenson. 2010. Application of the Document Entitled *A Process for Identifying and Managing Risk of Contact between Sierra Nevada Bighorn Sheep and Domestic Sheep*. U.S. Fish and Wildlife Service, Ventura, CA

Francis J. Singer, J.F., Bleich, V.C., and Gudorf, M.A. 2001. Restoration of Bighorn Sheep Metapopulations in and Near Western National Parks. Restoration Ecology, 8:14-24.Geist, V. 1967. A consequence of togetherness. Natural History 76:24, 29-30.

Geist, V. 1971. Mountain sheep: a study in behavior and evolution. University of Chicago Press, Chicago, IL.

Kock, M.D., D.A. Jessup, R.K. Clark, C.E. Franti, and R. A. Weaver. 1987. Capture Methods in Five Subspecies of Free-Ranging Bighorn Sheep: An Evaluation of Drop-Net, Drive-Net, Chemical Immobilization and the Net-Gun. Journal of Wildlife Diseases 23(4): 634-340.

Hedrick, P. W., and R. Fredrickson. 2010. Genetic rescue guidelines with examples from Mexican wolves and Florida panthers. Conservation Genetics 11:615-626.

Johnson, H., V.C. Bleich, T.R. Stephenson. 2006. Habitat selection by mountain sheep and mule deer – a step toward understanding ecosystem health from the desert to the alpine. U.C. Davis Wildlife Health Center. California Department of Fish and Game Resource Assessment Program.

Johnson, H. E., L. S. Mills, T. R. Stephenson, and J. D. Wehausen. 2010.Population-specific vital rate contributions influence management of an endangered ungulate. Ecological Applications 20:1753–1765.

Johnson, H. E., L. S. Mills, J. D. Wehausen, T. R. Stephenson, and G. Luikart. 2011. Translating effects of inbreeding depression on component vital rates to overall population growth in endangered bighorn sheep. Conservation Biology 25:1240-1249.

Johnson, H. E., M. Hebblewhite, T. R. Stephenson, D. W. German, B. M. Pierce, and V. C. Bleich. 2012. Evaluating apparent competition in limiting the recovery of an endangered ungulate. Oecologia 171:295-307.

Luikart, G, and J.-M. Cornuet. 1998. Empirical evaluation of a test for identifying recently bottlenecked populations from allele frequency data. Conservation Biology 12:228-237.

Mills, L. S., and P. E. Smouse. 1994. Demographic consequences of inbreeding in remnant populations. American Naturalist 144:412–431.

Morris, W. F., and D. F. Doak. 2002. Quantitative conservation biology: theory and practice of population viability analysis. Sinauer Associates, Inc., Sunderland, Massachusetts, USA.

Murphy, Leeann and Lisa Sims. 2011. Terrestrial and Aquatic Wildlife Biological Evaluation and Management Indicator Species Report. Signed May 11, 2011. USDA U.S. Forest Service, Inyo National Forest.

Ross, P. I., M. G. Jalkotzy, and M. Festa-Bianchet. 1997. Cougar predation on bighorn sheep in southwestern Alberta during winter. Canadian Journal of Zoology 75:771-775.

Thompson, R. 2008. Monache deer plan. California Department of Fish and Game.

U.S. Fish and Wildlife Service 1999a. Endangered and threatened wildlife and plants: Emergency rule to list the Sierra Nevada distinct population segment of California bighorn sheep as endangered. Federal Register 64:19300-19309. April 20, 1999.

U.S. Fish and Wildlife Service. 1999b. Endangered and threatened wildlife and plants: Proposed rule to list the Sierra Nevada distinct population segment of California bighorn sheep as endangered. Federal Register 64:19333-19334. April 20, 1999.

U.S. Fish and Wildlife Service. 2000. Endangered and threatened wildlife and plants: Final rule to list the Sierra Nevada distinct population segment of the California bighorn sheep as endangered. Federal Register 65:20-30. January 3, 2000.

U.S. Fish and Wildlife Service. 2007. Recovery Plan for the Sierra Nevada Bighorn Sheep. Sacramento, California.

USDI, U. S. Fish and Wildlife Service. 2011. Federal Fish and Wildlife Permit No. TE050122-4.

Wehausen, J. D., S. T. Kelley, and R. R. Ramey II. 2011. Domestic sheep, bighorn sheep, and respiratory disease: a review of the experimental evidence. California Fish and Game 97:7-24.

Weis, Sue 2011. Biological Evaluation Sensitive Plan Species Sierra Nevada Bighorn Sheep Helicopter Landings, Inyo National Forest. Signed April, 20, 2011. USDA U.S. Forest Service, Inyo National Forest.

Wilson, L. O., and C. L. Douglas. 1982. Revised guidelines for capturing and reestablishing desert bighorns. Transactions of the Desert Bighorn Council 26:1-7.

Wehausen, J.D. 1999. Effects of mountain lion predation on bighorn sheep in the Sierra Nevada and Granite Mountains of California. Wildlife Society Bulletin 24: 471-479.

Figure 1. Map illustrating currently occupied herd units and vacant herd units that need to be inhabited to meet recovery goals.

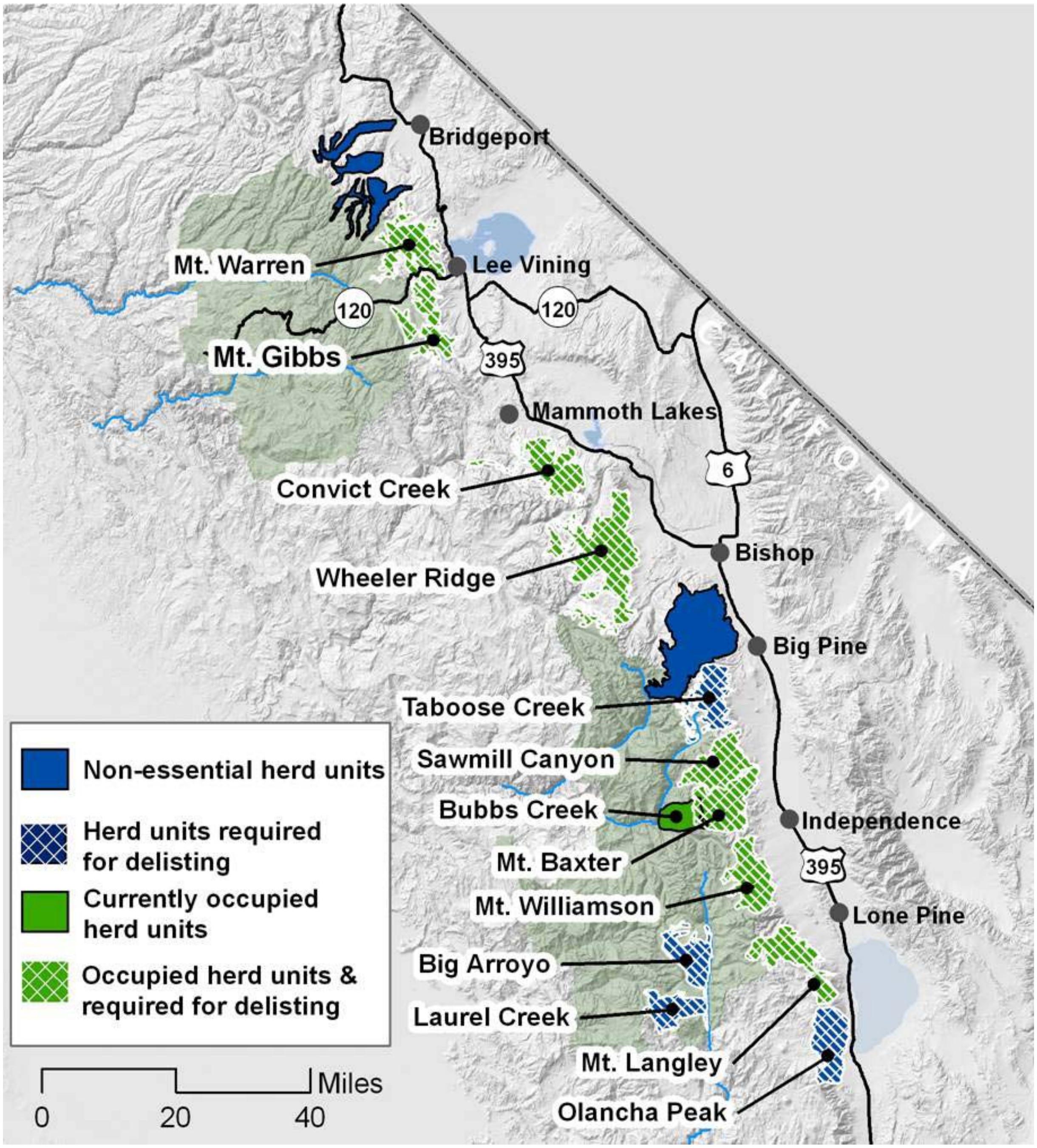
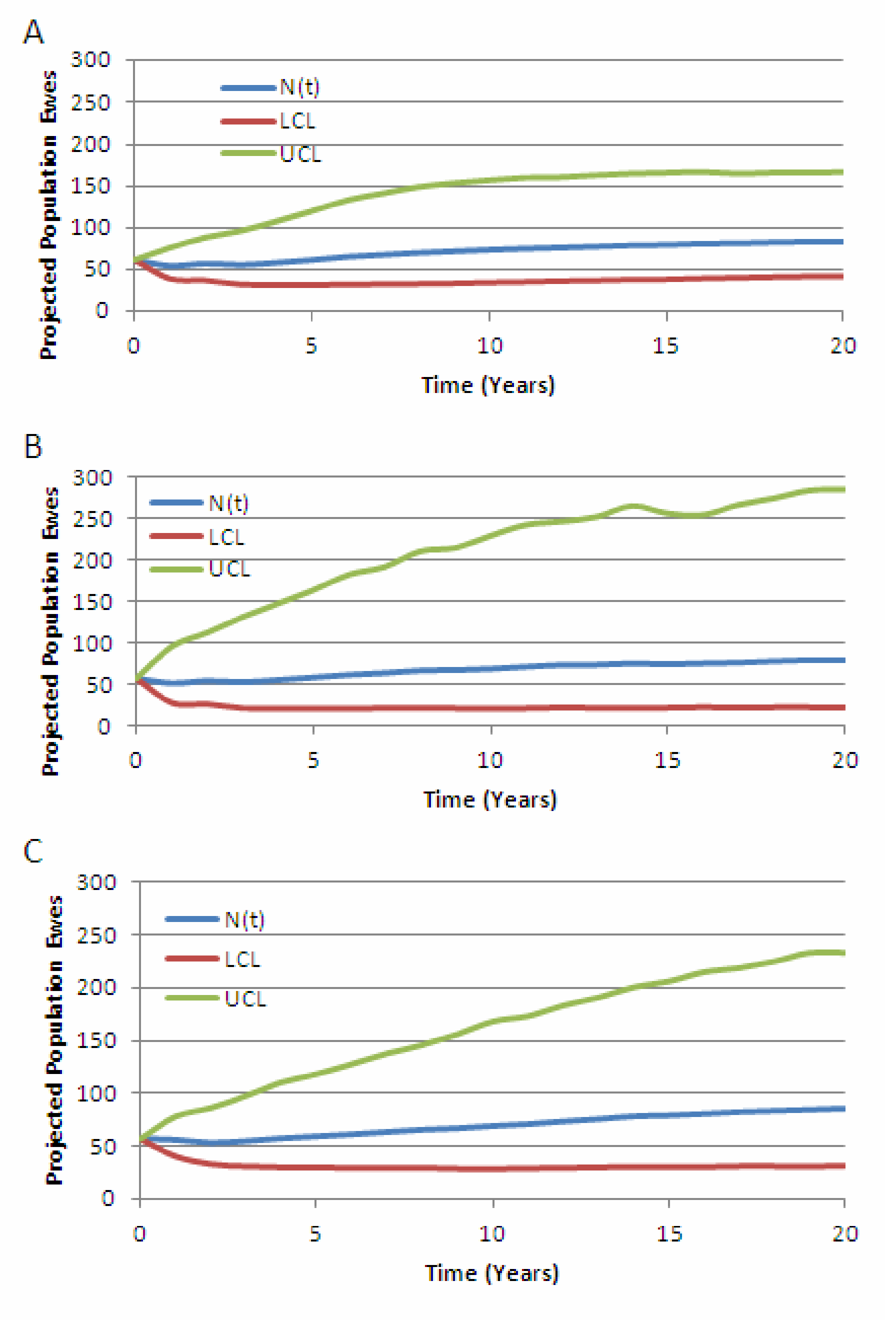


Figure 2: Projected population size of female Sierra Nevada bighorn sheep from stochastic simulations for the (A) Mt. Langley (10 removed year 1, 5 removed year 3), (B) Sawmill Canyon (10 removed year 1, 5 removed year 3), and (C) Mt. Baxter (5 removed year 2) populations and the 95% confidence intervals while each heard is being harvested for translocation animals. We based the population projections on data collected 1999-2011 in the Sierra Nevada Mountains, California. Sawmill Canyon yearling survival rate was adjusted upwards to reflect apparent misclassification of stage classes during surveys.



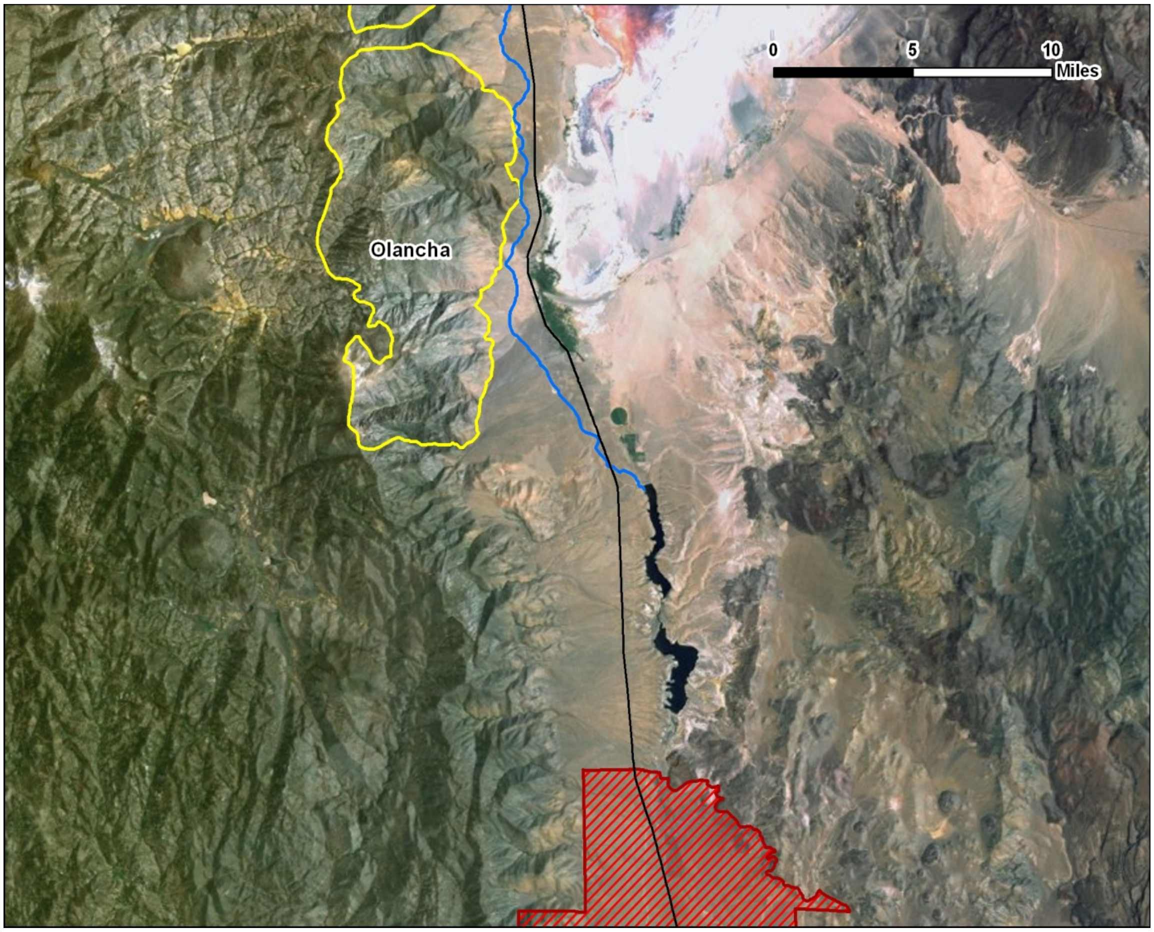


Figure 3. The Olancha Peak herd unit (yellow), the Tunawee allotment (red), and the Los Angeles aqueduct (blue) in proximity to one another along Highway 395 in the eastern Sierra Nevada.

Figure 4. Photos of the Los Angeles aqueduct adjacent to Olancha, California.

Table 1: Estimated probabilities of attaining various levels of females in source populations after harvesting stock for translocations over the next 3 years. Population projections from stage-class matrix models of females are based on demographic data collected 1999-2011 and projected for up to 20 years. Sawmill Canyon yearling survival rate was adjusted upwards to reflect apparent misclassification of stage classes during surveys. Probabilities listed represent: 1) 5 ewes as a quasi-extinction threshold, 2) 15 ewes as the number of animals below which demographic stochasticity and genetic stochasticity may contribute to an extinction vortex (Morris and Doak 2002), 3) 25 ewes as the Recovery Plan target for each population, and 4) 25 ewes for more than 7 years to represent realization of delisting goals.

Source Population and Translocation Details	**Yr**	**Pr (N<5)**	**Pr (N>15)**	**Pr(N>25)**	**Pr (N>25 for >7 consecutive yr)**
Sawmill Canyon					
no removals	5	0.01	0.95	0.90	
	10	0.03	0.91	0.83	0.84
	20	0.07	0.87	0.81	0.90
10 ewes removed year 1	5	0.01	0.93	0.85	
	10	0.03	0.90	0.81	0.77
	20	0.07	0.85	0.79	0.88
10 ewes removed year 1, 5 year 2	5	0.02	0.91	0.82	
	10	0.04	0.85	0.77	0.73
	20	0.10	0.83	0.75	0.84
10 ewes removed year 1, 5 year 3	5	0.03	0.89	0.81	
	10	0.06	0.86	0.76	0.73
	20	0.09	0.86	0.77	0.83
Mt. Langley					
no removals	5	0.00	1.00	0.98	
	10	0.00	1.00	0.98	0.97
	20	0.00	0.99	0.98	0.99
10 ewes removed year 1	5	0.00	0.99	0.96	
	10	0.00	0.99	0.94	0.92
	20	0.00	0.98	0.94	0.97
10 ewes removed year 1, 5 year 2	5	0.00	0.98	0.94	
	10	0.00	0.99	0.93	0.90
	20	0.00	0.98	0.95	0.97
10 ewes removed year 1, 5 year 3	5	0.00	0.98	0.93	
	10	0.01	0.97	0.92	0.89
	20	0.01	0.98	0.94	0.95
Mt. Baxter					
no removals	5	0.00	0.99	0.95	
	10	0.00	0.97	0.91	0.90
	20	0.01	0.96	0.90	0.96
5 animals removed year 2	5	0.00	0.98	0.91	
	10	0.00	0.97	0.88	0.83
	20	0.01	0.96	0.89	0.93
Wheeler Ridge					
no removals	5	0.00	0.98	0.85	
	10	0.00	0.91	0.74	0.74
	20	0.03	0.78	0.59	0.81

Table 2: Estimated probabilities of attaining various levels of females in a new population created by translocations (Olancha, Big Arroyo, and Laurel Canyon). Population projections are based on demographic data collected 1999-2011 in the Sierra Nevada Mountains. Positive growth is based on demographics from the Mt. Langley population and negative growth is based on the Mono Basin population. Probabilities listed represent: 1) 5 ewes as a quasi-extinction threshold, 2) 15 ewes as the number of animals below which demographic stochasticity and genetic stochasticity may contribute to an extinction vortex (Morris and Doak 2002), 3) 25 ewes as the Recovery Plan target for each population, and 4) 25 ewes for more than 7 years to represent realization of delisting goals.

Demographic Rates and Translocation Details	Yr	Pr (N<5)	Pr (N>15)	Pr(N>25)	Pr (N>25 for >7 consecutive yr)
Positive Growth					
10 ewes start, no augmentation	5.00	0.00	0.91	0.56	
	10.00	0.01	0.90	0.71	0.36
	20.00	0.02	0.92	0.81	0.76
10 ewes start, +5 year 3	5.00	0.00	0.95	0.76	
	10.00	0.00	0.94	0.79	0.58
	20.00	0.01	0.94	0.86	0.83
10 ewes start, +10 year 3	5.00	0.00	0.99	0.88	
	10.00	0.00	0.98	0.88	0.74
	20.00	0.00	0.97	0.91	0.92
Negative Growth					
10 ewes start, no augmentation	5.00	0.01	0.72	0.23	
	10.00	0.03	0.58	0.24	0.08
	20.00	0.14	0.45	0.21	0.21
10 ewes start, +5 year 3	5.00	0.00	0.89	0.48	
	10.00	0.01	0.76	0.41	0.24
	20.00	0.08	0.58	0.33	0.39
10 ewes start, +10 year 3	5.00	0.00	0.95	0.69	
	10.00	0.01	0.82	0.54	0.42
	20.00	0.05	0.65	0.39	0.54

Table 3. Population genetic statistics for Sierra bighorn and desert bighorn populations. N = sample size, H_O = average observed heterozygosity, H_O Range = range of individual observed heterozygosities, CV = the coefficient of variation of individual heterozygosities, H_E = expected heterozygosity (at Hardy Weinberg equilibrium; Nei 1983), A = average number of alleles per locus, A_E = effective number of alleles (number of alleles at equal frequency that would produce the observed homozygosity), Fixed = the number of invariant loci.

Herd/loci	**ST**	**N**	**H_O Range**	**H_O**	**CV**	**H_E**	**A**	**A_E**	**Fixed**
17 loci									
Sierra Nevada									
Gibbs	CA	12	0.059-0.588	0.363	41.3	0.316	1.9	1.6	4
Langley	CA	21	0.235-0.706	0.443	25.5	0.422	2.4	1.9	1
Wheeler Ridge	CA	52	0.235-0.765	0.480	24.9	0.467	2.6	2.0	1
Warren	CA	22	0.235-0.765	0.479	24.7	0.436	2.5	2.0	1
Baxter/Sawmill	CA	26	0.294-0.706	0.489	24.5	0.484	2.6	2.1	1
Williamson	CA	20	0.412-0.765	0.556	17.9	0.476	2.6	2.1	1
Desert									
Pilares (captive)	MX	10	0.235-0.529	0.412	27.1	0.436	2.9	2.0	1
Red Rock (captive)	NM	27	0.235-0.824	0.616	24.9	0.482	3.5	2.1	0
Upper San Juan River Cyn.	UT	12	0.529-0.823	0.651	16.9	0.578	3.1	2.5	0
Different 17 loci									
Sierra Nevada									
Gibbs	CA	12	0.176-0.588	0.353	46.1	0.303	1.9	1.5	4
Langley	CA	21	0.235-0.647	0.451	25.9	0.439	2.4	1.9	1
Warren	CA	22	0.235-0.765	0.500	25.3	0.445	2.5	2.0	1
Wheeler Ridge	CA	52	0.235-0.765	0.490	24.4	0.472	2.6	2.0	1
Baxter/Sawmill	CA	26	0.294-0.765	0.491	23.5	0.474	2.6	2.1	1
Desert									
Pilares (captive)	MX	10	0.235-0.588	0.453	27.9	0.469	3.1	2.2	1
Red Rock (captive)	NM	27	0.353-0.823	0.521	25.5	0.493	3.7	2.2	0
Spring Range, Brownstone Bas.	NV	17	0.412-0.824	0.578	23.5	0.608	4.3	2.8	0
Spring Range, Little Devil Pk.	NV	19	0.353-0.941	0.622	22.2	0.580	4.3	2.7	0
River Mts.	NV	46	0.353-0.882	0.639	23.1	0.635	4.8	3.0	0
Castle Mts.	CA	19	0.471-0.882	0.656	18.9	0.614	4.4	3.0	0
Highland Range	NV	20	0.412-0.941	0.685	18.3	0.659	4.5	3.1	0
Eldorado Mts., Goldstrike Cyn.	NV	20	0.529-0.882	0.674	18.2	0.638	4.6	3.0	0
McCullough Range	NV	23	0.471-0.882	0.683	18.1	0.661	4.6	3.1	0
Muddy Mts.	NV	34	0.353-0.824	0.623	16.9	0.591	4.4	2.8	0
Black Mts.	AZ	38	0.471-0.824	0.636	16.3	0.641	4.4	3.0	0
Upper San Juan River	UT	12	0.471-0.823	0.670	14.1	0.588	3.2	2.6	0
Newberry Mts.	NV	15	0.529-0.882	0.718	13.8	0.663	4.7	3.2	0
Eldorado Mts., Black Cyn.	NV	20	0.529-0.765	0.653	10.2	0.659	4.6	3.2	0

Table 4. Population genetic statistics for 3 populations (gene pools) available as sources of translocation stock and varying samples drawn from them. The 10 random samples of 18 Sierra bighorn? included 6 from each of the available gene pools.

Herd or Subsample	N	H_O Range	H_O	H_E	A	A_E
19 variable loci						
Sierra Nevada Source Herd						
Langley	21	0.210-0.737	0.471	0.457	2.5	2.0
Baxter/Sawmill	26	0.263-0.737	0.504	0.508	2.7	2.1
Wheeler	52	0.263-0.789	0.511	0.495	2.7	2.1
Averages			0.495	0.487		
Subsamples						
5 highest heterozygosities	5	0.737-0.789	0.758	0.526	2.6	2.2
11 highest heterozygosities	11	0.684-0.789	0.718	0.536	2.7	2.3
18 highest heterozygosities	18	0.623-0.789	0.684	0.537	2.7	2.3
Random draws of 18 sheep (6 ea.)	10	Averages:	0.496	0.497	2.65	2.1
		Lowest	0.436	0.487	2.6	2.0
		Highest	0.529	0.520	2.7	2.2

Appendix 1: ADDENDUM

To 11 February 2013 Report on Sierra Bighorn Genetic Questions

Since I wrote the February report providing comparative genetic microsatellite data and raising questions about potential strategies to incorporate genetic diversity into translocation strategies, I have genotyped another 84 Sierra Nevada bighorn sheep (SNBS) from frozen blood samples for 17 loci. Most of these sheep are live collared sheep that might be used for translocations. New and already existing data were compiled in a spreadsheet that was provided recently for use in potentially choosing sheep for translocation on the basis of their heterozygosity levels.

Those compiled data also were used to explore via random data sampling another approach to choosing translocation stock. This is an approach discussed in the February report of focusing heterozygosity selection on rams. In that report I discussed the potential desirability of manipulating genetic contributions from the ram side of the founding gene pool by removing and replacing rams on a regular basis. My new sampling approach simply chose 7 rams of higher heterozygosity from those currently existing, specifically including as many rams as possible from outside of the population from which the ewes will be captured (Sawmill Canyon herd). It also specifically chose two rams that are 10 years old that would be desirable because they are likely to die before needing to be removed to preclude potential father-daughter matings; and, it included some young rams that might be added in later years. These 7 ram genotypes were included in every sampling run. Added to those 7 genotypes were 8 additional genotypes chosen randomly from 51 recorded Baxter/Sawmill genotypes to represent founding ewes chosen unselectively from the Sawmill herd. For each of 10 such samplings, population genetic statistics were developed for the 15 sheep, and results are summarized in Table 3.

Table 3. Population genetic statistics for three populations (gene pools) available as sources of translocation stock and 10 random samples representing 8 ewes caught unselectively and 7 rams of known genotypes from 3 populations (Wheeler: S72, S112, S233 S234; Langley: S212; Baxter: S197, S202).

Herd or Subsample	**N**	**H_O Range**	**H_O**	**H_E**	**A**	**A_E**
17 variable loci						
Sierra Nevada Source Herds						
Langley	37	0.235-0.765	0.474	0.453	2.53	1.95
Baxter/Sawmill	51	0.294-0.765	0.529	0.514	2.82	2.16
Wheeler	52	0.235-0.765	0.510	0.498	2.76	2.09
Averages			0.504	0.488		
Results of 10 random samples		Averages:	0.594	0.526	2.72	2.22
		Lowest:	0.572	0.505	2.65	2.14
		Highest:	0.624	0.552	2.76	2.34

The results indicate that this approach can work. Even the sampling with the lowest average observed heterozygosity (H_O) substantially exceeded that of any existing herd, while the lowest expected heterozygosity (H_E) and effective number of alleles (A_E) were each only slightly lower than the Baxter/Sawmill gene pool (Table 3). In short, this approach should give a sufficient upward heterozygosity bias to a founding population. This allows uncollared ewes to be captured, which conserves collared ewes for use in population monitoring. It will be important to capture and collar rams, perhaps especially somewhat younger rams, at every opportunity to keep an adequate pool that can be genotyped. It will also be important to use fecal DNA to monitor genotypes of lambs born in newly created herds to allow an adaptive management approach to genetics questions.

John Wehausen, 18 March 2013