Genetic Characteristics of Restored Elk Populations in Kentucky

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ABSTRACT Translocations are a common management practice to restore or augment populations. Understanding the genetic consequences of translocation efforts is important for the long-term health of restored populations. The restoration of elk (Cervus canadensis) to Kentucky, USA, included source stocks from 6 western states, which were released at 8 sites in southeastern Kentucky during 1997–2002. We assessed genetic diversity in restored herds and compared genetic similarity to source stocks based on 15 microsatellite DNA loci. Genetic variation in the restored populations was comparable to source stocks (\(\bar{x}\) allelic richness = 3.52 and 3.50; \(\bar{x}\) expected heterozygosity = 0.665 and 0.661 for restored and source, respectively). Genetic differentiation among all source and restored populations ranged from 0.000 to 0.065 for pairwise F\(_{ST}\) and 0.034 to 0.161 for pairwise Nei’s D\(_{A}\). Pairwise genetic differentiation and Bayesian clustering revealed that stocks from Utah and North Dakota, USA, contributed most to restored populations. Other western stocks appeared less successful and were not detected with our data, though our sampling was not exhaustive. We also inferred natural movements of elk among release sites by the presence of multiple genetic stocks. The success of the elk restoration effort in Kentucky may be due, in part, to the large number of elk (\(n = 1,548\)), repeated releases, and use of diverse source stocks. Future restoration efforts for elk in the eastern United States should consider the use of multiple stock sources and a large number of individuals. In addition, preservation of genetic samples of founder stock will enable detailed monitoring in the future. © 2020 The Authors. The Journal of Wildlife Management published by Wiley Periodicals, Inc. on behalf of The Wildlife Society.

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Humans have transplanted animals and plants outside their native ranges for millennia (Hofman and Rick 2018). In modern times, the translocation of individuals is one of the most widely employed and successful management techniques for wildlife populations. Translocations have been used for the restoration or augmentation of extirpated populations, to relocate nuisance individuals, to establish new populations of economically desirable animals, to establish additional populations of threatened or endangered species, and to relieve overabundance (Nielsen 1988). Early translocations often experienced mixed success due to primitive capture, handling, and transport methods. As transplantation techniques improved, issues involving animal behavior, adaptive genetic variation, and long-term effects became apparent. For instance, captive stocks are unsuitable for restoration of many species of upland birds because they lack appropriate predator avoidance and foraging behaviors (Leopold 1944). The restoration of white-tailed deer (Odocoileus virginianus) to the southeastern United States was one of the most successful wildlife management actions in history, yet the use of diverse source stocks has left a legacy of altered breeding dates throughout the region (Sumners et al. 2015). Furthermore, not all source stocks were successful, possibly because of differences in adaptive genetic variation between the source populations and the new environment (DeYoung et al. 2003). Similarly, restoration of wild turkey (Meleagris gallopavo) using wild stocks has been successful, yet restored stocks have expanded and introgressed into unique gene pools (Latch et al. 2006, Seidel et al. 2013). Although the long-term success of translocations is ultimately dictated by availability of habitat (Bouzat et al. 2009), understanding the success or failure of active management remains a primary concern.
Translocations are commonly used to augment low-density populations or, in wildlife restoration efforts, to return populations to their historical ranges (Griffith et al. 1989). Unless carefully planned, translocations can reduce population viability through loss of genetic variation. Small populations are prone to losing genetic diversity via a process termed genetic drift because of stochastic differences in reproduction and survival among individuals (Wright 1931). Founder events occur when few individuals initiate a population, thus causing a reduction in overall genetic diversity (Tarr et al. 1998, Broders et al. 1999, Hedrick et al. 2001, Cardoso et al. 2009). Serial bottlenecks occur through the use of restored populations as source stocks for later restoration efforts, where genetic diversity may be lost in each successive restoration event step via the founder effect or genetic drift (Clegg et al. 2002, Gautschi et al. 2002, Lambert et al. 2005).

Elk (Cervus canadensis) were once widespread in the eastern United States but were extirpated by the late 1700s to mid-1800s because of habitat loss and overhunting (Bryant and Maser 1982). Highly valued as a game animal, elk have been the subject of numerous restoration efforts in North America since the twentieth century. Early reintroduction efforts began in the western United States using remnant populations of elk from the Greater Yellowstone Ecosystem. These recovery efforts were largely successful in that restored populations exhibited high genetic diversity and low differentiation, indicating rapid growth and gene flow after initial establishment (Hicks et al. 2007).

Efforts to restock elk to the eastern United States, including the Midwest and within the Appalachians, have resulted in mixed success, often due to post-introduction mortality through hunting, poaching, disease, and vehicle collisions (Popp et al. 2014, Keller et al. 2015). Limited population growth over time has resulted in cases where reintroduced elk exhibit low genetic diversity many years after restoration (Conard et al. 2010). For example, current populations of restored elk in Pennsylvania, USA, exhibit comparatively low levels of genetic variation, attributed to serial bottlenecks and genetic drift (Williams et al. 2002). Pennsylvania’s elk herd is also highly differentiated from western populations, including its stock source, probably because of founder effect and genetic drift.

Genetic researchers have reported a correlation between genetic variation and the health and survival of wildlife populations (Honecutt 2000). Unlike historical management actions, modern restoration programs have the ability to assess the genetic effects of translocations as part of post-release monitoring of restoration efforts. During the late 1990s, the Kentucky Department of Fish and Wildlife Resources (KDFWWR) embarked on an elk restoration project using stock sources from western states. Overall, 1,548 elk were translocated from source populations in Arizona, Kansas, New Mexico, North Dakota, Oregon, and Utah, USA (G. S. W. Jenkins, KDFWWR, personal communication). Reintroduced elk expanded rapidly and the elk population in Kentucky presently numbers about 11,000 animals, by far the largest herd east of the Mississippi River (KDFWWR 2016). To date, no analysis of genetic structure has been conducted, and the relative influence of the different stock sources on the current population is unknown.

We analyzed genetic variation and structure in the recently restored elk herd in Kentucky and compared genetic variation in the restoration area to 5 of the stock sources. Specific objectives were to determine genetic diversity and differentiation among stock sources, to examine the genetic structure within the Kentucky population, to determine the relative influence of different stock sources, and to examine gene flow between release sites.

**STUDY AREA**

Elk were released in southeastern Kentucky within a 16-county, 1.2 million-ha restoration zone. The restoration zone is located next to the Cumberland Plateau and is comprised of 79% mixed-deciduous forest (Braun 1950), 10% surface mines, 9% agriculture, and 2% urban (Olsson et al. 2007). Within this zone, there were 8 release sites: Blue Diamond, in southern Perry County; Starfire, in Knott County; the Orr Property, located on the Bell–Harlan County line; Letcher, in Letcher County; Pike, in Pike County; Czar-Martin, in southern Martin County; Raven, in Floyd County; and Redbird Wildlife Management Area, in Leslie County (Fig. 1). The climate in the restoration zone was temperate humid continental (Overstreet 1984), with an average winter temperature of 4°C and an average summer temperature of 24°C (McDonald and Blevins 1965).

Six different Western states served as sources for translocated elk to Kentucky (Table 1). Utah was the largest source and contributed 1,027 elk from the Ensign Ranch (near Castle Rock, UT), the Deseret Ranch (northwest of Evanston, WY), Mount Nebo, Ogden Valley, and near the towns of Echo, Henefer, Morgan, and Nephi. Elsewhere, stocks were obtained from Theodore Roosevelt National Park, North Dakota, the Maxwell Refuge near Canton, Kansas, Flagstaff, Arizona, Ute Mountain and the Uracca

![Figure 1](image-url)
Wildlife Management Area, New Mexico, and from Mount Emily, the Ladd Marsh Wildlife Area, and Baker County, Oregon.

**METHODS**

**Sample Collection and Amplification**

We obtained muscle tissue samples from hunter-harvested elk during the 2008 and 2009 male and female hunts in the 8 southeastern Kentucky restoration zones. Samples of released stocks were not available, so we also obtained hunter-harvested tissues from the source states during 2008–2009 from the same herd units as the founding individuals. We froze and stored all samples at −20°C until DNA extraction. We isolated DNA from tissue samples using the Qiagen® DNeasy™ Tissue Kit (QIAGEN Genomics, Germantown, MD, USA). We amplified 15 microsatellite DNA loci for all samples. All loci were tetranucleotide repeats, and included C01, T107, C143, C180, and C273 (Meredith et al. 2005), and T123, T156, T172, T193, T268, T108, C217, T26, T501, and T507 (Jones et al. 2002). We amplified loci in 4 multiplex reactions, as described by Meredith et al. (2007), and loaded the resulting products onto an automated genetic analyzer for separation and detection (3130xl, Applied Biosystems, Foster City, CA, USA). We determined allele size calls for each locus using GeneMapper 4.0 (Applied Biosystems). We implemented several different quality control procedures during the genotyping of the samples. First, we modified all reverse primers with a 5′-GTGTCTTT sequence to reduce split peaks and encourage +A addition (Meredith et al. 2007). This resulted in almost no detectable stutter peaks. Because the markers amplified only tetranucleotide repeats, all allele bins were separated by 4 base pairs; combined with the lack of stutter, the potential for allele calling errors was greatly reduced. We included a standard reference DNA sample in every polymerase chain reaction run to confirm consistency of electrophoretic mobility of fragments among runs. We called only alleles that were ≥100 on the fluorescence intensity scale; if allele-like peaks were <100 units, we scored the allele as missing. Finally, we re-amplified and re-scored ≥10% of samples to assess consistency of allele calls.

**Data Analysis**

We indexed genetic diversity based on allelic richness (A; El Mousadik and Petit 1996), computed in HP-RARE (Kalinowski et al. 2007), to facilitate comparisons among samples. We calculated observed heterozygosity (H₀) and expected heterozygosity (Hₑ) using ARLEQUIN 3.1 (Excoffier et al. 2005). We computed the inbreeding coefficient (Fᵢₛ) using ARLEQUIN 3.1 to evaluate departures from equilibrium within samples and computed 95% confidence intervals to determine significant differences from zero. Linkage disequilibrium within restored populations may indicate admixture between stock sources; we tested for linkage disequilibrium within and among samples using ARLEQUIN 3.1.

We assessed genetic structure using genetic distances and Bayesian clustering. First, we computed pairwise Fₛₘ using the Reynolds et al. (1983) coancestry coefficient among all sites using ARLEQUIN 3.1 (Excoffier et al. 2005); we assessed statistical significance based on 100 permutations of genotypes between populations. Genetic distances such as Fₛₘ rely on an underlying evolutionary model (Nei and Kumar 2000) and may not perform as expected in the presence of admixture. Therefore, we also computed Nei’s Dₐ (Nei et al. 1983), which does not assume an evolutionary model and is more efficient at recovering simulated population relationships than many other genetic distances (Takezaki and Nei 1996); we computed pairwise Dₐ values using ADEGENET (Jombart 2008). Next, we evaluated contribution of source stocks to restored populations using the Bayesian clustering algorithm STRUCTURE 2.3.

**Table 1.** The number of female (F) and male (M) elk translocated from stocking source states of Arizona, Kansas, North Dakota, New Mexico, Oregon, and Utah, USA. Translocated elk were used for stocking 8 restoration zones in southeastern Kentucky, USA, from 1997 to 2002.

| Release site          | Sex | AZ | KS | ND | NM | OR | UT | Sex ratio (F:M) | Total |
|-----------------------|-----|----|----|----|----|----|----|----------------|-------|
| Blue Diamond          | F   |    |    | 144| 88 |    |    | 1.64           | 232   |
|                       | M   |    |    |    |    | 72 |    | 3.37           | 250   |
| Czar-Martin County    | F   |    | 120|    | 12 |    |    | 1              | 54    |
|                       | M   |    |    |    | 45 |    |    | 2.60           | 54    |
| Letcher County        | F   |    |    | 39 |    |    |    | 1.5            | 54    |
|                       | M   |    |    |    |    | 15 |    | 3              | 54    |
| Orr Property          | F   |    |    | 38 |    | 205|    | 3.08           | 322   |
|                       | M   |    |    |    | 18 | 61 |    | 4.07           | 143   |
| Pike County           | F   |    |    | 19 |    | 55 |    | 4.07           | 143   |
|                       | M   |    |    | 11 |    | 3 |    | 1.64           | 143   |
| Starfire              | F   |    |    |    |    | 1 |    | 3.39           | 145   |
|                       | M   |    |    | 33 |    |    |    | 4.00           | 145   |
| Raven                 | F   |    | 112|    |    |    |    | 1.64           | 145   |
|                       | M   |    | 33 |    |    |    |    | 4.00           | 145   |
| Redbird               | F   |    |    | 48 |    | 40 |    | 4.07           | 143   |
|                       | M   |    |    |    | 14 | 8  |    | 4.07           | 143   |
| Total                 |     | 29 | 39 | 145| 190| 118| 1,027| 1,548         |       |
We used the admixture model and assumed correlated allele frequencies. We used the LOCprior designation for source stocks, where sampling location acts as a weak prior to inform clustering (Hubisz et al. 2009), and modeled the Kentucky samples as unknowns. We modeled the assumed number of genetic clusters (K) from 1–10, with an initial burn-in of 50,000 Markov chain Monte Carlo (MCMC) repetitions, followed by 150,000 MCMC repetitions for data collection. We repeated the runs for each K 5 times. We determined the most likely number of clusters based on the change in the likelihood function between each successive cluster (ΔK; Evanno et al. 2005) using the online software program STRUCTURE HARVESTER (Earl and vonHoldt 2012). We performed an additional series of runs at the most likely K, K−1 and K+1, to ensure model convergence. The additional runs consisted of a 100,000 MCMC burn-in followed by 200,000 MCMC repetitions of data collection, with 10 iterations at K, K−1, and K+1.

RESULTS

We collected 421 samples from Kentucky and 5 of the 6 states that provided stock sources: Arizona, New Mexico, North Dakota, Oregon, and Utah. We were unable to procure samples from Kansas. Mean proportion of loci typed was 91% and no monomorphic loci were present in any population. Although there were private alleles at 5 loci (C01, C180, T107, T193, and T128), all were at low frequency, present in only 1 or 2 copies, and uninformative for assignment purposes. Allelic richness and observed heterozygosity were similar among all populations, and ranged from 3.3–3.7 and 0.643–0.682, respectively (Table 2; Table S1, available online in Supporting Information). Oregon had the highest number of locus pairs that displayed linkage disequilibrium (27), followed by the Raven restoration zone with 23; the Letcher County restoration zone had the least with only 1 pair of loci in linkage disequilibrium. Estimates of FIS ranged from −0.038 to 0.048, with a slight excess of heterozygotes in 3 of 5 source stocks and 4 of 8 release populations, although all 95% confidence intervals overlapped 0.

Statistically significant pairwise FST ranged from 0.012 to 0.065, with the lowest differentiation between New Mexico and the Pike County restoration site in Kentucky and the highest between the Raven and Redbird WMA restoration sites in Kentucky (Table 3). Regardless of statistical significance, pairwise FST values showed low levels of differentiation between Utah and Kentucky populations (0.000–0.019) except with the Raven site (0.054) and Letcher County (0.030). Conversely, North Dakota had higher levels of differentiation with all Kentucky and source populations (0.039–0.057) except for restoration sites Czar-Martin, Letcher County, Raven, and Starfire (0.000–0.016). Pairwise differentiation of Nei’s D_{A} ranged from 0.034 to 0.161. Similar to FST, pairwise Nei’s D_{A} showed low differentiation between Utah and Kentucky populations (0.037–0.090) except with the Raven site (0.103). North Dakota was more differentiated from Kentucky populations (0.104–0.146) except for restoration sites Letcher County, Pike County, Starfire, and Raven (0.034–0.083).

Based on the initial Bayesian clustering runs, we determined that 3 clusters showed the greatest change in likelihood values (Fig. 2). The additional runs at K = 3 revealed clear assignment of the North Dakota population and Utah population to distinct, separate clusters (Fig. 3). The Arizona and Oregon populations grouped together into a third cluster, whereas the New Mexico population had nearly equal membership proportions between all 3 clusters. Overall, elk in Kentucky displayed high levels of admixture at the individual and site level, with most membership proportion assigned to clusters representing Utah and North Dakota. The Blue Diamond, the Orr Property, Redbird Wildlife Management Area, and Czar-Martin County restoration sites clustered with Utah, whereas the Raven site clustered with North Dakota. Letcher and Pike counties, and the Starfire site were admixed between the Utah and North Dakota clusters. Although the ΔK method suggested best fit at K = 3 clusters, we also interpreted K = 4 clusters.

Table 2. Summary statistics of genetic diversity including sample size (n), mean number of alleles (a), mean allelic richness (A), alleles under linkage disequilibrium (LD), inbreeding coefficient (FIS), standard deviation of FIS, observed heterozygosity (H0), and expected heterozygosity (HE) across elk populations where samples were collected in 2008–2009 at the 8 restocking sites in Kentucky, USA, and the 5 western United States stock source states used for elk restoration in Kentucky, 1997–2002.

| Population       | n    | a    | A (10 genes) | LD (P ≤ 0.05) | FIS      | SDa | H0    | HE    |
|------------------|------|------|--------------|---------------|----------|-----|-------|-------|
| Blue Diamond     | 19   | 5.1  | 3.7          | 8             | 0.038    | 0.144 | 0.643 | 0.674 |
| Letcher County   | 10   | 3.9  | 3.4          | 1             | −0.009   | 0.356 | 0.650 | 0.652 |
| Pike County      | 29   | 4.9  | 3.5          | 19            | −0.038   | 0.116 | 0.673 | 0.656 |
| Starfire         | 38   | 5.4  | 3.5          | 17            | 0.018    | 0.080 | 0.646 | 0.657 |
| Orr Property     | 27   | 5.1  | 3.6          | 7             | 0.033    | 0.143 | 0.650 | 0.672 |
| Redbird          | 8    | 4.1  | 3.7          | 6             | 0.048    | 0.209 | 0.653 | 0.682 |
| Czar-Martin      | 16   | 4.3  | 3.5          | 11            | −0.017   | 0.266 | 0.671 | 0.666 |
| Raven            | 29   | 4.2  | 3.3          | 23            | −0.033   | 0.173 | 0.682 | 0.660 |
| ND               | 39   | 4.6  | 3.3          | 17            | −0.018   | 0.106 | 0.658 | 0.642 |
| AZ               | 31   | 4.5  | 3.4          | 17            | −0.014   | 0.166 | 0.652 | 0.649 |
| OR               | 65   | 5.5  | 3.6          | 27            | −0.020   | 0.080 | 0.682 | 0.669 |
| UT               | 88   | 5.7  | 3.6          | 15            | 0.027    | 0.064 | 0.656 | 0.673 |
| NM               | 22   | 4.7  | 3.6          | 12            | 0.018    | 0.245 | 0.656 | 0.673 |

*a All 95% confidence intervals overlapped 0.
because Arizona and Oregon populations formed 2 distinct groups at K = 4. We found no further differentiation within Kentucky populations.

DISCUSSION

Overall, the elk reintroduction in Kentucky appears to be the most successful restoration effort for elk in the eastern United States, as evidenced by rate of population growth, total population size, and our genetic assessment of the herd. Growth of the elk herd in Kentucky from a release of 1,548 animals to the current estimate of 11,000 individuals suggests that the population rapidly expanded post-introduction (KDFWR 2016). Rapid growth of introduced populations and use of diverse source stocks can alleviate loss of genetic diversity via founder effects and genetic drift (DeYoung et al. 2003, Conard et al. 2010). Furthermore, the size and diversity of founding stock is associated with success of restoration efforts (Smith et al. 1976; Leberg 1990, 1993). We were unable to directly address the factors that contributed to the success of the Kentucky restoration effort compared to other cases (Popp et al. 2014). Popp et al. (2014) reported that across all eastern elk restorations, stock size and diversity were not associated with translocation success; however, they indicated that Kentucky was an exception to this rule. Additionally, Conrad et al. (2010) reported that the Kentucky population had little effect on the population of elk in the eastern United States (Popp et al. 2014). Although previous researchers of elk restoration reported that both of these factors had little effect on the success of translocation efforts, stock size and diversity were not associated with stock size and diversity in eastern elk restorations. Overall, the elk reintroduction in Kentucky appears to be the most successful restoration effort for elk in the eastern United States, as evidenced by rate of population growth, total population size, and our genetic assessment of the herd.

| Area                | Blue Diamond, KY | Letcher County, KY | Pike County, KY | Starfire, KY | Orr Property, KY | Redbird WMA, KY | Czar-Martín, KY | Raven, KY | ND | AZ | OR | UT | NM |
|---------------------|------------------|--------------------|-----------------|--------------|-----------------|-----------------|-----------------|------------|----|----|----|----|----|
| Blue Diamond, KY    | 0.107            | 0.076              | 0.058           | 0.078        | 0.118           | 0.077           | 0.110           | 0.104     | 0.076| 0.077| 0.037| 0.109 | 0.091|
| Letcher County, KY  | 0.039*           | 0.093              | 0.051           | 0.113        | 0.136           | 0.114           | 0.061           | 0.060     | 0.112| 0.110| 0.090| 0.116| 0.091|
| Pike County, KY     | 0.040*           | 0.025*             | 0.059           | 0.066        | 0.081           | 0.078           | 0.099           | 0.083     | 0.077| 0.073| 0.044| 0.060| 0.060|
| Starfire, KY        | 0.031*           | 0.000              | 0.036*          | 0.067        | 0.105           | 0.079           | 0.056           | 0.051     | 0.067| 0.064| 0.043| 0.069| 0.069|
| Orr Property, KY    | 0.035*           | 0.035*             | 0.025*          | 0.038*       | 0.054           | 0.085           | 0.109           | 0.107     | 0.086| 0.056| 0.045| 0.075| 0.075|
| Redbird WMA, KY     | 0.052*           | 0.040*             | 0.008           | 0.047*       | 0.000           | 0.000           | 0.161           | 0.146     | 0.111| 0.085| 0.075| 0.105| 0.105|
| Czar-Martín, KY     | 0.000            | 0.000              | 0.000           | 0.000        | 0.000           | 0.000           | 0.120           | 0.110     | 0.092| 0.103| 0.100| 0.100| 0.100|
| Raven, KY           | 0.051*           | 0.000              | 0.055*          | 0.016*       | 0.055*          | 0.065*          | 0.005           | 0.034     | 0.092| 0.093| 0.103| 0.100| 0.100|
| ND                  | 0.049*           | 0.000              | 0.042*          | 0.000        | 0.039*          | 0.057*          | 0.016*          | 0.000     | 0.091| 0.102| 0.091| 0.091| 0.091|
| AZ                  | 0.040*           | 0.024*             | 0.029*          | 0.019*       | 0.013*          | 0.012           | 0.001           | 0.040*    | 0.044*| 0.062| 0.056| 0.088| 0.088|
| OR                  | 0.038*           | 0.039*             | 0.045*          | 0.032*       | 0.018*          | 0.022*          | 0.000           | 0.038*    | 0.046*| 0.041| 0.062| 0.062| 0.062|
| UT                  | 0.005            | 0.030*             | 0.015*          | 0.019*       | 0.015*          | 0.017           | 0.000           | 0.054*    | 0.053*| 0.027*| 0.027*| 0.057| 0.057|
| NM                  | 0.045*           | 0.029*             | 0.012*          | 0.030*       | 0.025*          | 0.031*          | 0.003           | 0.045*    | 0.032*| 0.028*| 0.028*| 0.022*| 0.022*|
explained genetic diversity in restocked elk populations, instead stable or increasing post-introduction populations played an important role. Kentucky restoration efforts were conducted over half a decade with each successive cohort of translocated elk providing large numbers of new individuals. By using more individuals and stocks than other states and substantially augmenting stock each year, Kentucky established a viable elk population that was able to quickly grow.

We observed levels of genetic diversity in the restored Kentucky populations comparable to that of the stock sources used for restoration. Although levels of heterozygosity based on different genetic loci are not directly comparable across studies, our findings were similar to western elk populations reported by Hicks et al. (2007), where expected heterozygosity ranged from 0.51–0.60. Heterozygosity found in the Kentucky population was substantially higher than other restored populations of elk east of the Mississippi River; for example, expected heterozygosity in the elk herd in Pennsylvania was 0.254 (Williams et al. 2002). This result is consistent with the demographic history and number and source of stocks used (1,548 in Kentucky compared to 177 in Pennsylvania). Additionally, the elk population in Kentucky has rapidly grown since stocking in the late 1990s, whereas the population in Pennsylvania only grew to an estimated 833 by 2013 from the original population in the early 1900s (Popp et al. 2014).

We documented clear genetic structure within the Kentucky herd as a result of stock sources, specifically the North Dakota and Utah stocks. North Dakota was used to stock only the Raven restoration site in Kentucky, and our STRUCTURE analysis showed clear evidence of this. Utah, on the other hand, provided the largest percentage of elk to the restoration effort and provided elk to all but one (Raven) restoration site. Other than those individuals that grouped with North Dakota, all but 2 elk in Kentucky were predominately assigned to the Utah cluster.

The clear distinction between North Dakota and all other populations except for Kentucky was not reported in previous comparisons of restocked western populations where North Dakota, specifically Theodore Roosevelt National Park, was included (Hicks et al. 2007). One explanation for the genetic distance between North Dakota and other populations is that North Dakota’s elk population was stocked from the intermediate location of Wind Cave National Park in South Dakota (Anderson 1958). This additional step may have contributed to the differentiation between North Dakota and the other stocking sites, all of which were founded with stocks from Yellowstone National Park.
Understanding how species respond to restoration efforts through translocations helps biologists learn from past mistakes and prepare for future conservation efforts. Leberg (1990) calls for careful consideration to be taken with regard to genetic variation in species targeted for restoration efforts. To this end, we have seen translocation success stories across North America with rapid population growth and high genetic variation in white-tailed deer (DeYoung et al. 2003), wild turkeys (Seidel et al. 2013), and western populations of elk (Hicks et al. 2007). The continued growth and success of the elk herd in Kentucky after restocking in the late 1990s further demonstrates the importance of using multiple stock sources and translocating large numbers of individuals repeatedly over several years. Genetic variation within the Kentucky herd can be attributed to ≥2 stock sources, and they exhibit high levels of genetic diversity. Wildlife managers should look to the elk model in Kentucky as a blueprint for future translocation efforts.

MANAGEMENT IMPLICATIONS

The effort, time, and expense of restoring populations of large game animals makes it imperative to use every tool to ensure success. In the case of the elk restoration project in Kentucky, the Kentucky Department of Fish and Wildlife Resources used a large number of translocated stock from 6 sources to combat chances of inbreeding, founder’s effect, and serial bottlenecking. These efforts resulted in a robust elk herd that rapidly grew despite hunting and presence of meningeal worm. Kentucky elk display high genetic diversity, with genetic contributions of ≥2 stock sources still apparent. When resources allow, state agencies should attempt to diversify their stock sources and work to ensure rapid initial growth. Furthermore, preservation of tissues from the founding individuals will enable more precise tracking of the contribution of founding individuals and stocks to restored populations.

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