



Original Article

Using DNA to Test the Utility of Pellet-Group Counts as an Index of Deer Counts

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ABSTRACT Despite widespread use of fecal pellet-group counts as an index of ungulate density, techniques used to convert pellet-group numbers to ungulate numbers rarely are based on counts of known individuals, seldom evaluated across spatial and temporal scales, and precision is infrequently quantified. Using DNA from fecal pellets to identify individual deer, we evaluated the relationship between pellet-group count and count of Sitka black-tailed deer (*Odocoileus hemionus sitkensis*) during a 3-year study (2006–2008) in 3 watersheds in southeast Alaska, USA. We surveyed 141,054 m² of transect, counted 10,569 pellet groups, and identified 737 unique deer. We used a multilevel mixed-effects generalized linear model to analyze expected deer count as a function of pellet-group count. Pellet-group count was a significant predictor of DNA-based index of deer count, but that relationship varied by transect, watershed, and year, indicating that extrapolation of a single linear relationship across space and time was not possible. More importantly, most of the variation in our models was residual and unexplained. Assuming that our DNA-based results were a more accurate and precise metric of true deer count, we do not support the use of pellet-group count to index deer count in southeast Alaska unless confounding factors are accounted for at fine spatial (e.g., habitat patch) scales. Because of the difficulty in routinely evaluating the influence of confounding variables in remote and unmanaged landscapes, we suggest that wildlife programs in these environments consider alternatives, such as DNA-based methods, for monitoring trends in ungulate populations. © 2013 The Wildlife Society.

KEY WORDS Alaska, DNA, fecal pellets, *Odocoileus hemionus sitkensis*, pellet-group counts, Sitka black-tailed deer.

For over a half-century, many monitoring programs of wildlife around the world have relied on fecal pellet-group counts to estimate size, trends, distribution, and habitat use of ungulate populations (Bennett et al. 1940, Neff 1968 [comprehensive review], Kirchhoff and Pitcher 1988, Koster and Hart 1988). In many cases, pellet-group counts were used because ungulate populations were living in densely forested environments and were difficult to monitor using other techniques requiring direct observation or live capture (Putman 1984, Ratcliffe 1987, Forsyth et al. 2007). Despite widespread use, the value of pellet-group counts as an index of ungulate numbers continues to be a contentious issue. Some authors reported that pellet-group counts index ungulate abundance well (Forsyth et al. 2007, Acevedo et al. 2010), whereas others suggested pellet-group counts

lack utility and reliability as an index (Ryel 1971, Fuller 1991, Campbell et al. 2004, Smart et al. 2004). Surprisingly, given the volume of literature on pellet-group survey techniques, there are few studies that compare pellet-group counts with ungulate populations of known density or even with estimates of ungulate density obtained through independent means.

Factors limiting the use of pellet-group counts as an index of population trends include human error (e.g., pellet detectability, observer experience), variation in pellet deposition rates and pellet persistence (e.g., influence of weather, insects), and the lack of uniformity in pellet-group distribution (Neff 1968, Jenkins and Manly 2008). Moreover, in many circumstances, procedures to convert pellet-group counts to numbers of animals are based on few empirical data, seldom evaluated over time, and precision is rarely quantified. Given the potential for combinations of those factors to confound or mask relationships between pellet-group counts and actual populations, researchers have sought alternative strategies to monitor ungulates.

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Non-invasive genetic techniques developed during the past decade now enable biologists to identify individuals within populations of rare and forest-dwelling wildlife (Waits and Paetkau 2005). These techniques have been applied successfully to ungulates using DNA extracted from hair and feces (Belant et al. 2007, Gebremedhin et al. 2009). If an adequate number of individuals are identified, then estimates of population size are possible (Kendall et al. 2008, White 2008). More recently, Brinkman et al. (2011) used DNA extracted from Sitka black-tailed deer (*Odocoileus hemionus sitkensis*), hereafter black-tailed deer, pellets and mark-recapture procedures to estimate abundance of a wild and unenclosed deer population with precision of $\pm 20\%$ (defined by 95% CIs). The number of individual animals identified represents a minimum number of animals known to be alive, which is a useful measure unencumbered by many of the assumptions associated with mark-recapture methods. However, researchers also should be aware that this approach has a tendency to negatively bias estimates and should be applied appropriately (Slade and Blair 2000).

During 2006–2008, we assessed concordance between pellet-group counts from free-ranging populations of black-tailed deer with concurrent DNA-based estimates of deer count. Our study took place in 3 separate watersheds on Prince of Wales Island, Alaska, USA, over 3 years. We modeled deer count as a function of pellet-group count, and explicitly tested for the effects of transect, watershed, and year to account for the influence of spatial and temporal changes in this relationship. Fortunately, we experienced 2 consecutive severe winters during the course of our study enabling us to observe changes in pellet-group count as deer numbers declined (Brinkman et al. 2011). We were able to test some key assumptions that should be evaluated to ensure that pellet-group surveys are reliable indices of deer population trends: 1) a strong, consistent, and positive correlation between pellet-group count and deer count; 2) the relationship must be consistent across landscapes with differing habitat composition; and 3) the relationship must be invariant across years.

Our study contributes to the body of knowledge concerning fecal indices of animal abundance, and it has implications for management of black-tailed deer, which are a key indicator of the effects of forest management in southeast Alaska (Hanley 1993). Over the past 3 decades, the Alaska Department of Fish and Game (ADFG) and the U.S. Forest Service (USFS) used pellet-group counts as the primary tool to monitor deer population trends (Kirchhoff and Pitcher 1988). Precise estimates of trends in deer abundance are needed because perceived fluctuations in the deer population size above or below a predetermined population objective set by ADFG results in changes in harvest regulations (Bethune 2009). Despite heavy reliance on these data, pellet-group counts of black-tailed deer were compared with an independent measure of population size only once (Kirchhoff 1990). In that study, 13 radiocollared deer were introduced to a small (approx. 40 ha) island in southeast Alaska. Researchers returned to the island 264 days later and surveyed 1.9% of the island for pellet groups. Data from that

study indicated that a pellet-group density of 0.05 pellet-groups/m² represented 12 deer/km² (95% CI = 10.7–13.8). This estimate assumed constant pellet persistence, detection, and deposition rates. Unfortunately, data were obtained only during a single year, which prevented any evaluation of how well counts of pellet groups deposited during winter tracked changes in deer population. Also, only 4 deer remained on the island (6 swam off and 3 died) when researchers returned to conduct pellet-group counts, which complicated the association between deer numbers and number of pellet groups encountered. Moreover, the island was much smaller than typical deer home ranges (which likely concentrated deer activity) and habitat diversity was low compared with typical deer ranges in southeast Alaska. Consequently, the usefulness of the study for evaluating the reliability of pellet-group surveys as conducted by ADFG and USFS personnel was limited. Deer managers in southeast Alaska need more information on the utility of pellet-group counts to monitor deer populations.

STUDY AREA

We conducted our research on Prince of Wales Island (approx. 55°N–136°W), near the south end of the southeastern panhandle of Alaska (Fig. 1). The topography included rugged mountains extending up to 1,160 m in elevation, with landscapes below 600 m dominated by temperate coniferous rainforest consisting primarily of Sitka spruce (*Picea sitchensis*) and western hemlock (*Tsuga heterophylla*; Alaback 1982). Annual precipitation varied from 130 cm to 400 cm, and mean monthly temperatures ranged from 1° C in January to 13° C in July. Between winters 1948–2008, mean annual snowfall at sea level was 115 cm (SE = 9.5) at the closest weather station on Annette Island (Alaska Climate Research Center 2009). Snowfall, snow depth, and snow persistence increased with elevation.

Our study areas included Maybeso, Upper Staney (hereafter, Staney), and Upper Steelhead (hereafter, Steelhead) watersheds, located within the north-central portion of Prince of Wales Island (Fig. 1). Each watershed represented a different mix of habitats that might affect deer use during winter and spring and the density of fecal pellets deposited (Brinkman et al. 2011). All watersheds were accessible by road and deer were actively hunted from August until January. Each watershed encompassed a mosaic of productive old-growth forest, unproductive forests on hydric soils, open muskeg heaths, and clearcut stands ranging from 5 years to 60 years old. Successional patterns of forest growth following disturbances such as logging are described comprehensively by Alaback (1982). In addition to hunting, deer were exposed to predation by wolves (*Canis lupus*) and black bears (*Ursus americanus*). No animals producing fecal pellets similar to deer occurred within the study areas.

METHODS

We counted pellet groups along transects that followed deer trails, a technique described by Brinkman et al. (2011). We designed trail transects to facilitate mark-recapture methods to estimate abundance of deer using DNA from fecal pellets

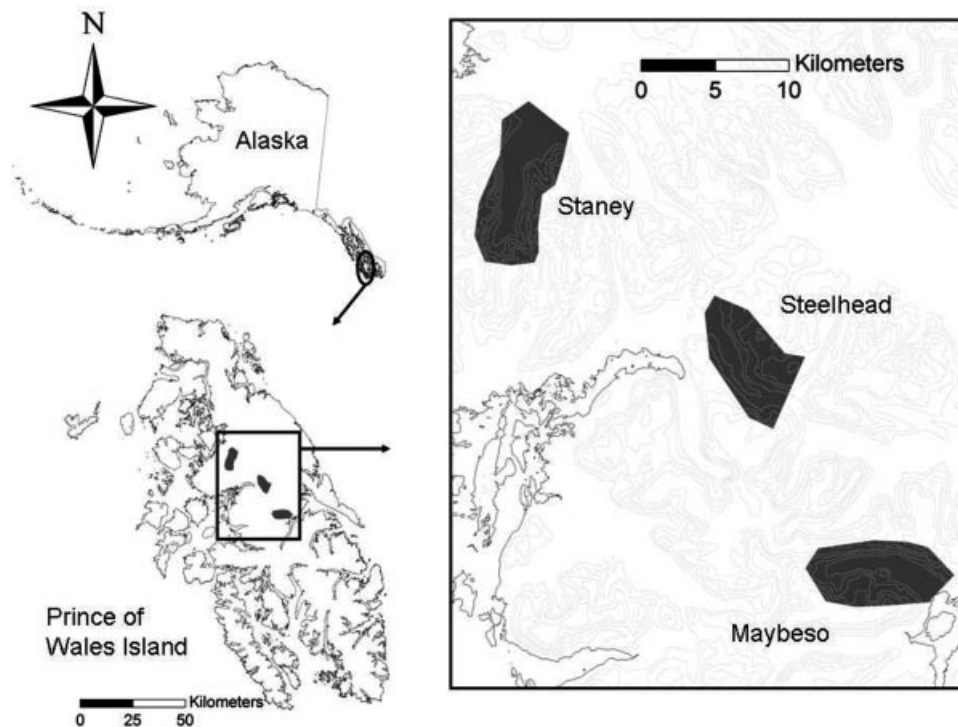


Figure 1. Location of study watersheds (Maybeso, Staney, Steelhead) on Prince of Wales Island in southeast Alaska, USA, where we tested the utility of pellet-group counts as an index of deer counts during 2006–2008.

(Brinkman et al. 2011). They have advantages over straight-line transects, including substantially higher encounter rates with pellet groups, applicability in all habitat types, better pellet-detection rates, easier travel through thickly vegetated habitats, and greater repeatability (Brinkman 2009).

In each watershed, we located transects to ensure they traversed a proportionally representative sample of 5 coarse vegetation and forest classification types (productive old-growth forest, unproductive forests on hydric soils, open muskeg heaths, clearcuts <30 years old, and clearcuts ≥30 yr old) that represent habitats available to deer during winter and early spring. Our transects encompassed variation in landscape features such as slope, elevation, aspect, and distance to roads. To reduce the probability of recapturing an individual deer along multiple transects, we separated adjacent transects by >500 m, which represented the circular radius of deer home ranges (0.78 km²) estimated from radio-collared deer in southeast Alaska (Farmer et al. 2006). Starting points for each transect were randomly selected between 1 m and 100 m from the edge of the habitat patch within which the transect began. Transects generally stayed within the habitat type in which they started. We used a predefined compass bearing to increase the likelihood that we were sampling habitat types proportionally to their representation within the watershed. We surveyed from the starting point along the predefined bearing until a deer trail was encountered. The deer trail was followed in the direction closest to the bearing until intersected by another deer trail. We then used a compass to determine which trail more closely paralleled the direction of the predetermined bearing and continued surveying along that trail. If the trail ended or

a trail could no longer be identified, we followed a straight-line path along our bearing until another deer trail was encountered. A pellet group was defined as >20 pellets of the same size, color, and shape that were positioned in a clumped distribution. We intensively marked the trail for subsequent surveys.

We collected 4–6 pellets for DNA analysis from each pellet group encountered on deer-trail transects. We followed sampling, DNA extraction, genotyping, and analysis protocols described in Brinkman et al. (2010, 2011). We re-sampled transects 2–8 times/annual field season (approx. Feb–May) at 10-day intervals. During poor conditions (warm summer months with abundant rainfall), Brinkman et al. (2010) found that pellets should be collected ≤10 days following deposition to yield sufficient DNA. Starting and ending date of sampling occasions was dependent on date of snowmelt and green-up. Starting pellet-group counts after snowmelt reduced the likelihood of missing pellets covered with snow. Ending pellet-group counts in May likely reduced potentially confounding effects of seasonal migration and change in habitat selection during vegetation green-up. After recording location, date, and time for each pellet group sampled, all remaining pellets were removed to avoid re-counting and re-sampling the same pellet group during subsequent sampling occasions. During the first sampling effort each year, we sampled pellets only from pellet groups with characteristics of recent deposition (pellets intact, surface with a glossy sheen, and a detectable coating of mucus). Brinkman et al. (2010) noted that pellet appearance was an adequate indicator of genotyping potential. Using appearance as a collection filter meant that a small percentage of the

total pellet groups encountered were sampled for DNA. However, because we used the same protocol on all samples encountered, each pellet group encountered had the same chance of being genotyped. We sampled all pellet groups detected during subsequent surveys except those submerged or too decomposed by rain to enable collection of intact pellets (<10%).

We extracted, amplified, and sequenced DNA from pellets and identified multi-locus microsatellite genotypes for individual deer (Brinkman et al. 2010). We divided the total number of individual deer identified each year on each transect by the length of the transect to compute minimum number of deer per km of transect known to be alive as a measure of count, which we considered as an index of true deer abundance. We chose “deer/km of transect,” rather than deer/km², because it represented a meaningful value that corresponded to count of deer but did not require estimation of the effective sampling area (Efford et al. 2004).

We counted all pellet groups within 1 m of the center of trail transects in addition to collecting pellets for DNA extraction. We tallied both “standing” and “clearance” crops of pellet groups (Staines and Ratcliffe 1987). Standing crop consisted of all pellet groups deposited during the spring field season and all pellet groups that persisted over winter (Staines and Ratcliffe 1987). It represented the sample of pellet groups typically counted by management agencies in southeast Alaska during routine spring pellet surveys (Kirchhoff and Pitcher 1988). Clearance crop consisted only of those pellets deposited during our spring field season by excluding pellet groups encountered during the first sampling occasion (Staines and Ratcliffe 1987, Campbell et al. 2004, Smart et al. 2004). Clearance-crop data represented the deposition of pellets from deer known to be alive at the beginning of pellet-group surveys. In contrast, pellet groups deposited during winter and counted as standing crop may have represented deer that died or moved out of the sampling area before spring pellet-group surveys. Clearance pellet-group counts reduced the confounding influence of variation in pellet persistence (Harestad and Bunnell 1987, Jenkins and Manly 2008). However, like standing-crop counts, clearance pellet-group counts still suffered from biases associated with variability in defecation rates, which may vary over time and among individuals (Mitchell et al. 1985, Harestad and Bunnell 1987).

We then modeled deer count as a function of pellet-group count on each sampling occasion to evaluate the relation between the 2 indices of deer abundance and explicitly to test for effects of transect, year, and watershed. We used a multilevel, mixed-effects, generalized linear model with a Poisson regression. For both standing and clearance crops, our model included pellet-group count as a fixed effect, and transect, watershed (Maybeso, Staney, Steelhead), and year (2006, 2007, 2008) as random effects. We used the glmmPQL (generalized linear mixed model with penalized quasi-likelihood) function of the MASS Package for R (R Development Core Team 2009) to nest sampling occasion within transect, within watershed, and within year to account for reduced replications (effective sampling size) due to

repeated measures on individual transects. One limitation of the glmmPQL function of the MASS Package was that Akaike's Information Criterion values were not computed. However, model comparisons were not needed because we fit our data to the single and most sensible model given the nature of our data. With our approach, the importance of a particular nested random effect will still be evident by the effect of variance and a lack of contribution to the widening of confidence intervals around deer count estimates. Data were coded and analyzed using the statistical computer programs SPSS 12.0.1 (SPSS, Inc., Chicago, IL) and R.

RESULTS

We averaged 154 (SE = 12.2) sampling occasions/year along 31 transects in Maybeso, Staney, and Steelhead watersheds during 2006, 2007, and 2008. We sampled each transect a mean of 5.0 (SE = 0.12) times/year. Across watersheds, mean transect length was 666 m (SE = 15.9), encompassing 13,372 m², 17,796 m², and 9,970 m² of area within Maybeso, Staney, and Steelhead watersheds, respectively.

During 2006–2008, we counted 10,569 pellet groups, collected fecal-pellet samples from 2,248 pellet groups for DNA analysis, successfully genotyped 1,156 (51% of collection) samples, and identified 737 unique deer. Genotyping success on individual transects was similar among watersheds ($\chi^2 = 0.136$, $P = 0.934$), but different across years ($\chi^2 = 48.14$, $P < 0.001$). This difference across years occurred because we improved our ability to identify and collect pellets suitable for DNA extraction during the initial sampling effort each year, which was when pellets deposited during winter were encountered along with freshly deposited pellet groups. As a result, the number of samples collected each year declined and the proportion of those successfully genotyped increased. Although we became more selective of pellets for DNA extraction, the opportunity to identify deer from all pellets encountered did not change. For instance, the mean percentage of pellet groups genotyped (10.7%, SE = 0.88) relative to pellet-group number encountered was similar across years ($n = 3$, $F = 1.17$, $P = 0.31$), despite differences in proportion sampled. This indicates that DNA quality (rather than proportion of pellet groups sampled) determined minimum deer count and the appearance criteria used to filter pellets was effective.

Mean standing pellet-group density was 0.10 pellet groups/m² of transect ($n = 93$, SE = 0.006) and the mean clearance pellet-group density was 0.02 pellet groups/m² of transect ($n = 93$, SE = 0.002) when all watersheds and years were pooled. Standing pellet-group counts were correlated with clearance pellet-group counts ($r = 0.631$, $P < 0.001$). Mean deer count was 13 deer/km of transect ($n = 93$, SE = 0.964) when transects were pooled across watersheds and years. Our multilevel, mixed-effects generalized linear models indicated that both standing ($P < 0.001$) and clearance ($P < 0.001$) pellet-group counts were significant predictors of deer count (Table 1). However, this result should be interpreted with caution because high levels of variation in the model

Table 1. Output summary of the generalized linear mixed model used to estimate deer count as a function of clearance and standing pellet-group count (fixed effect) during each sampling occasion (n), while estimating variance introduced by residual error and the random effects of transect, year, and watershed. Data were collected during a 3-year study (2006–2008) in 3 watersheds in Prince of Wales Island, Alaska, USA.

Clearance crop ($n = 370$)						Standing crop ($n = 93$)					
Fixed effect	Est.	SE	df	t -value	P -value	Fixed effect	Est.	SE	df	t -Value	P -value
Intercept	0.147	0.084	276	1.75	0.08	Intercept	0.698	0.120	83	3.49	<0.01
Pellet-group count	0.018	0.002	276	7.47	<0.01	Pellet-group count	0.008	0.002	83	4.53	<0.01

Clearance crop ($n = 370$)			Standing crop ($n = 93$)		
Random effects	Variance	% of total variance	Random effects	Variance	% of total variance
Residual	1.164	79.7	Residual	1.450	91.8
Transect	0.297	20.3	Transect	0.061	3.9
Site	<0.001	<0.1	Site	0.036	2.2
Year	<0.001	<0.1	Year	0.033	2.1

produced estimates of deer count with poor precision (Table 2). For example, because of residual variance alone, a hypothetical clearance pellet-group count of 100 on a 1-km trail transect would result in a minimum count of 7 deer (Lower 95% CI = 1, Upper 95% CI = 56) over the same area (Table 2). If the random effect of transect were included, confidence intervals expand to a lower of 1 and an upper of 72 deer (Table 2). These results occur because 80% of the variation in the model was residual (variation that could not be attributed to a specific cause) and 20% of the variation was explained by the random effect of transect. The random effects of watershed and year on the clearance crop were negligible (Table 2). For the standing crop, 92% of the variation in the model was residual, with the random effects of transect, watershed, and year explaining 4%, 2%, and 2%, respectively. Clearly, there are confounding factors affecting the relationship between pellet-group count and deer count that were not accounted for in our model.

DISCUSSION

The variability in the relationship between deer abundance and pellet-group count casts doubt on the reliability of pellet-group survey data to monitor population trends in free-ranging deer, at least within the densely forested environment of southeast Alaska. Although theoretically possible, the utility of pellet-group counts to index deer numbers becomes impractical if site-specific functions must be derived on an annual basis for each transect being surveyed. Accounting for sources of residual variation would require additional research focusing on interactions among several plausible confounding variables, such as weather, pellet-

group distribution, rate of deposition, pellet-group persistence, and detectability across relevant spatial and temporal scales. For decades, several of these confounding factors have prevented researchers from achieving a solution that is applicable in all circumstances (Neff 1968).

Because DNA estimates of minimum deer count are based on known individual deer, and others using this technique have found reasonable precision ($\pm 20\%$) using mark-recapture analysis on the same data set (Brinkman et al. 2011), we hypothesized that a comparison between the 2 indices would advance understanding of the utility of pellet-group counts. If we assume our DNA-based technique in this study tracks deer numbers with precision similar to that reported by Brinkman et al. (2011), then we would conclude that the utility of pellet-group counts to track deer trends in southeast Alaska may be insufficient for management purposes. However, it is possible that the residual error in the relationship between pellet-group counts and deer counts also may have been influenced by uncertainty in the DNA-based technique. DNA-based estimates of deer count allowed genotyping of a consistent but small subset (10.6%) of pellet-groups encountered each year in each watershed. Further experimentation with DNA-based techniques may provide improved estimates of deer counts for comparison with pellet-group counts. Other DNA-based approaches that allow inclusion of some degree of genotyping uncertainty (Miller et al. 2002, Lukacs and Burnham 2005, Wright et al. 2009) may increase sample size of known individuals for comparison with pellet-group data. The only way to conduct a credible test of the performance of both pellet-group and DNA-based counts is to compare each index with known

Table 2. Predictions of minimum deer count as a function of a hypothetical standing and clearance crop of 100 pellet groups. Predictions are based on proportion of model variation (component variance/total variance) caused by residual error and the random effects of transect, watershed, and year for a study conducted in 3 watersheds on Prince of Wales Island, Alaska, during 2006–2008.

	Pellet-group count	Deer count	Residual			+Transect			+Watershed			+Year		
			% ^a	L ^b	U ^c	% ^a	L ^b	U ^c	% ^a	L ^b	U ^c	% ^a	L ^b	U ^c
Standing crop	100	4	92	0	45	4	0	48	2	0	49	2	0	50
Clearance crop	100	7	80	1	56	20	1	72	<0.1	1	72	<0.1	1	72

^a Percentage of total variance from individual component (component variance/total variance).

^b Lower bounds of the 95% CI.

^c Upper bounds of the 95% CI.

deer density in a wild, unenclosed, and representative environment. For pellet-group counts, this comparison needs to be conducted across multiple years to account for temporal variability in confounding factors (e.g., deposition rates, pellet-group persistence).

Of the random effects accounted for in our model, most of the variation was explained by transect (20% in clearance crop, 4% in the standing crop). Although insignificant compared with residual variance, the effects of transect may be caused by the wide range of landscape characteristics traversed by transects and the disproportionate use of certain habitat types by deer. For instance, black-tailed deer exhibit seasonal differences in habitat selection (Wallmo and Schoen 1980, Schoen and Kirchhoff 1990, Doerr et al. 2005). Moreover, habitat selection during winter is strongly influenced by snow depth, which varies annually. During snowy winters, deer are forced into old-growth forest stands with relatively lower snow depths. We speculate that the patchy use of a heterogeneous environment by deer in Alaska leads to additional variability in pellet-group counts. Therefore, disproportionate sampling of habitat types would likely bias pellet-group counts and the influence of this bias would change with deer population dynamics and seasonal conditions. For instance, standing pellet-group densities were <0.02 pellet groups/m² in each year of our study for transects that mainly traversed muskeg and forest that had been logged >30 years ago; whereas, some transects that traversed young clearcuts (logged <20 yr ago) consistently supported standing-crop densities >0.2 pellet groups/m² of transect. Although we sampled deer habitat types proportionally to their representation within each watershed, proportions of each habitat type sampled were not consistent across the watersheds we evaluated, which potentially contributed to spatial variation in relationships between pellet-group count and deer count.

In southeast Alaska, ADFG and USFS monitor deer population trends using pellet-group plots established along straight-line transects that only traverse productive old-growth forest, which is considered winter range for deer. Surveys of pellet groups are conducted in mid-late spring and standing pellet groups are counted (Kirchhoff and Pitcher 1988). Data from individual transects surveyed by ADFG and USFS are compiled within watersheds and inference is made at that scale rather than evaluating pellet-group densities for individual transects. The variation we reported between estimates of pellet-group counts and deer counts at the transect level do not support the use of pellet-group count surveys to reliably monitor trends in deer populations at larger spatial scales. Indeed, during our study, pellet-group data aggregated within watersheds did not reflect the decline in deer count within those watersheds. For instance, in the Staney watershed, DNA results indicated a 24% decline in minimum deer count from 2006 to 2008, whereas pellet-group counts indicated a 17% increase over the same years.

Although some studies support the use of pellet-group counts for indexing deer abundance (Forsyth et al. 2007, Acevedo et al. 2010), it is evident from our findings that the utility of this index requires relatively intensive surveys with a

location-specific sampling design. In southeast Alaska, Kirchhoff (1990) determined that a density of 0.05 pellet groups/m² corresponded to use by 12 deer/km² (95% CI = 10.7–13.8). Although our findings are not directly comparable because of different methodologies, our standing-crop model suggests that a similar pellet-group density over a 1-km transect represents a minimum deer count of 2.9 deer (95% CI = 0.4–24.3). The important difference between our study and Kirchhoff's (1990) were estimates of precision rather than deer count. Previous pellet-group count studies outside of Alaska that demonstrated the usefulness of pellet-group counts were conducted under conditions that may be difficult to replicate with unenclosed populations of deer in unmanaged landscapes. For instance, Forsyth et al. (2007) validated the utility of pellet-group counts with known numbers of deer in intensively managed hunting enclosures in New Zealand. Acevedo et al. (2010) conducted their study in an intensively managed area (e.g., artificial feeding, water provisioning) in Mediterranean habitat in Spain; this is a dry, open, and accessible landscape relative to a coastal temperate rainforest in Alaska. Budgetary constraints, accessibility of survey areas, ruggedness of terrain, density of understory vegetation, and weather severity are all factors in southeast Alaska that may exacerbate common confounding variables (e.g., pellet distribution, deposition, persistence, and detection) that limit the feasibility of using pellet-group counts as population indices other than for confined populations.

Recent pellet-group count studies focused on strategies to quantify or limit the variability introduced by confounding variables (Jenkins and Manly 2008), determine whether return justifies effort (Campbell et al. 2004), test collection strategies (e.g., standing vs. clearance crop; Staines and Ratcliffe [1987]), and to compare performance with alternatives (Acevedo et al. 2010) and known numbers (Forsyth et al. 2007). We have added to each of those discussions by comparing pellet-group counts with a count estimate derived from known individuals identified using DNA from fecal pellets. Despite our use of trail transects to reduce observer error and application of clearance-crop methods to reduce the influence of variability in pellet persistence and deposition rates, our findings indicated that enough variability remained to question the utility of pellet-group surveys for monitoring free-ranging ungulates.

MANAGEMENT IMPLICATIONS

We recommend that wildlife managers interpret pellet-group count data untested against known population numbers with caution. Also, we suggest that additional research should evaluate the influence of finer scale spatial and temporal variables (e.g., season, deer behavior, and habitat heterogeneity) on confounding factors (pellet-group distribution, deposition rates, and persistence). Nonetheless, we suspect that even if many confounding factors can be modeled and the reliability of inference from pellet-group surveys was improved, it will not be feasible to obtain the data required on a routine and cost-effective basis. In environments where direct observation of ungulates is impractical, such as southeast

Alaska, we recommend that management agencies invest scarce resources in further development of alternatives such as DNA-based methods. We believe that pellet-group surveys conducted in a manner similar to those routinely applied in southeast Alaska produce unreliable indices of deer population trends and have the potential to be misleading.

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