Balancing costs and confidence: volunteer-provided point observations, GPS telemetry and the genetic monitoring of Finland's wolves

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Abstract

Reliable and updated population estimates are a necessity for the successful conservation and management of endangered animal populations. Citizen science has become increasingly important in wildlife monitoring and is an attractive concept due to its low costs. However, the applicability of citizen science in the monitoring of large carnivore populations is questionable for various reasons, including the difficulties associated with species identification. In Finland, where estimates of the fragmentary wolf (*Canis lupus*) population have varied between 140 and 280 animals in the last 10 years, population monitoring has been based on volunteer-provided data and telemetry. To compensate for a recent decrease in the proportion of territories with boundaries mapped through telemetry, a non-invasive genetics project was launched in 2016. We evaluated the experiences from this project, in which non-invasive genetic techniques were, for the first time, widely used ($n = 22$ territories, 54% of the 41 apparent territories hosted by wolves in March 2017) to determine the post-hunting population estimate in early March 2017, before pack sizes began to decrease due to dispersal by sub-adult wolves. In territories where the non-invasive genetic monitoring was executed in the winter of 2016/2017, the pack sizes resulting from the volunteer-provided observations and the genetic analyses were highly correlated. By using the most typical variation in the proportion of non-residents in the wolf populations (6–20%, Fuller et al. 2003), we derived a population estimate of 150–178 wolves for early March 2016, and, by considering the known mortality during the study period, a minimum estimate of 204–234 wolves for early Aug. 2016. Despite its high costs, we recommend that non-invasive genetic monitoring should cover all known territories supporting Finland's small and exploited wolf population. This much costlier protocol may be unrealistic in Finland. In any case, there is a need for more genetic sampling to test the quality of volunteer-provided data.

Keywords Population monitoring · DNA · GPS · Volunteers · Observations · Costs · *Canis lupus*

Introduction

Adaptive conservation and the management of wild animal populations need reliable and updated population estimates. This viewpoint is highlighted with small populations, which are most vulnerable to stochastic mortality risks. Citizen

science has increasingly become important in wildlife monitoring (Silvertown 2009; Bonney et al. 2009; Chandler et al. 2017) for providing data, e.g. about road crossings by large mammals in the Canadian Rockies (Lee et al. 2006).

Citizen science is a process whereby citizens are involved in science as researchers (Kruger and Shannon 2000), but it is also known as voluntary biological monitoring (Conrad and Hilchey 2011). We consider citizen science by its traditional definition, namely, scientists using citizens as data collectors. Citizen science may be questionable as a data source for various reasons. Some people question the practice of citing citizen science because of concerns about the quality of data collected by volunteers (Bonney et al. 2014). Citizen reports about observations might be vulnerable to spatiotemporal stochastic variations, and it is difficult to correct for such variations because the effort is difficult to quantify.

Large carnivorous mammals, such as the grey wolf (*Canis lupus*), are colonising new areas (Chapron et al. 2014), but many populations, including Finland's wolf population, are still

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endangered (Liukko et al. 2015). Finland's wolf population is under lethal management, which additionally enhances the need for well-functioning monitoring schemes. Low population densities and large movement ranges make the monitoring of wolf populations a considerable challenge. One of the most common approaches for wolves has been the mapping of territory boundaries by radiotelemetry, and recently, non-invasive genetics has become an increasingly important monitoring tool (Kunkel et al. 2005; Echegaray and Vila 2009; Stenglein et al. 2010; Liberg et al. 2012; Ausband et al. 2014; Galaverni et al. 2014, 2016; Stansbury et al. 2014; Reinhardt et al. 2015; Nowak and Myslajek 2016).

In Finland, the monitoring of wolf populations has been based on volunteer-provided observations since 1978 (Kojola et al. 2011), and borderline crossings have been recorded by the frontier guard detachment since 1964 (Pulliainen 1980). Since 1990, the wildlife triangle network (12 km triangle-shaped transect lines) monitors approximately 10,000 km of transect lines each winter (Linden et al. 1996); however, for wolves, it provides information only about trends over years (Kojola et al. 2014). Volunteer-provided point observations are the primary data source for monitoring large carnivorous mammals (Kojola et al. 2014; Pellikka and Hiedanpää 2017). Other important monitoring data are collected through telemetry, but the estimated annual proportion of all territories mapped by telemetry has decreased over the last 15 years, from 30–40% to 15–20% (S. Heikkinen, unpublished data).

Herein, we consider the usability of citizen-provided data in wolf population monitoring by using non-invasive genetics as a reference. Additionally, we consider prospects and concerns in the combination of observations, non-invasive genetics and small-scale telemetry and discuss potential concrete actions to tackle weaknesses (Andren et al. 2016) in a cost-effective way.

Methods

Study area

The coniferous boreal forest zone is predominant in Finland (land area 336,000 km²), with a small alpine region in the northernmost segment of the country. The mean human population density is 15 people km². The mean length of the snow-covered season in 1981–2010 ranged from 123 days in the south coast (Helsinki) to 210 days in Mid-Lapland (Sodankylä) in the north (<http://ilmatieteenlaitos.fi/lumitilastot>).

The grey wolf is classified as a game species in Finnish legislation. In the reindeer husbandry area (covers 38% of the land area of Finland), the wolf belongs to Appendix V of the EU habitat directive, and south of the reindeer husbandry area, it belongs to the Appendix IV in EU habitat directive (Habitats directive, Council Directive 92/43/EEC). Thus, the wolf is formally a strictly protected species in 62% of Finland's land area.

Hunting, based on either special licences to remove certain individuals, e.g. for human safety and decreasing livestock depredations, or a management hunting quota, is governed by the Ministry of Agriculture and Forestry (MAF). Hunters form approximately 7% of Finns older than 15 years. For the hunting years of 2016–2017 and 2017–2018, the maximum yearly wolf mortality quota was set to 53 individuals outside the reindeer husbandry area (MAF), including special licences.

Volunteer-provided point observations

The voluntary network consists of approximately 2000 large carnivore contact persons (abbreviated as LCCP hereafter) who record wolf observations into a digital large carnivore observation system, “Tassu” (the Paw), specifying, for example, the observation type (sighting, track, prey kill site, livestock depredation), date, geographic location, age status and number of animals and front paw print dimensions. Contact persons are nominated by the local game management associations. These persons are educated about the biology, ecology and movement behaviour of wolves and footprint identification, but there are no formal exams used for the LCCP nomination process. Contact details of LCCPs are publicly available and are known in local rural societies (Pellikka and Hiedanpää 2017).

Our monitoring scheme started on the first day of the hunting year 2016 (1 August) and ended in mid-March 2017, before the peak of natal dispersal (Kojola et al. 2006). In total, 8047 wolf observations were recorded by LCCPs during our study period. Out of these observations, 69% ($n = 5559$) were estimated to be done within the apparent territory boundaries (see “Territorial analysis”) and thereby concern territorial wolves. The majority (60%) of observations made within territories and concerned twosomes or groups of wolves (Fig. 1), whereas loners predominated (83%) in observations ($n = 2488$) made outside the estimated territories.

Based on the spatial distribution of twosomes and groups, we delineated rough territorial boundaries for potential family packs and territory-marking pairs on digital maps (55 potential territories). We evaluated the rough location of territory boundaries by comparing the density of observations within apparent territories to the 10-km-wide buffer zone surrounding the territory.

DNA

Non-invasive genetic monitoring was based on two types of collection schemes. A volunteer network collected material in 10 territories in southwestern Finland, and professional personnel collected material in 12 territories in east-central Finland (Fig. 1). The voluntary scheme was established to opportunistically collect faecal samples (Granroth-Widing et al. 2017). In the east-central territories, 10 professionals snow-tracked wolves for 2 months in Jan–Feb 2017 and collected scat and urine samples for the genetic analyses. The genetic analyses

Fig. 1 Observations concerning packs and twosome wolves (a), territories with at least one GPS-collared wolf (b), genetic analyses (c) and dead wolves (d) from August 1, 2016, to March 15, 2017, Finland

were conducted in the Center of Evolutionary Applications (CEA), University of Turku, Finland. A detailed description of the genetic analyses is given by Granroth-Widing et al. (2017) and Jansson et al. (2012). All samples were genotyped at 17 established canid microsatellite loci.

GPS collars

We closed data collection based on the dates at which 36 GPS-collared sub-adults departed their natal territory (see Kojola et al. 2006) in 2003–2016. During winter 2016/2017, a total of seven territories hosted 1–2 collared wolves. The collars were manufactured at Vectronics GHMP, Berlin, Germany. The collaring of wolves was done by darting from helicopter or looping from snowmobile in January–March. Details about the capture and immobilisation procedures are provided

elsewhere (Kojola et al. 2006, Wabakken et al. 2007). The interval between consecutive locations was 1 h. Territory boundaries were assessed by calculating 100% multiple convex polygons (MCPs) using Home Range Tools for ArcGIS.

Known wolf mortality

In total, there were 58 recorded wolf deaths during the study period (from Aug. 1 to 15 Mar.) with attributed geographic location (Fig. 1), date, cause of death, sex, age and individual genetic identification data. These known mortalities were taken into account when assessing the pack size and estimating the population size in August. We monitored known mortalities to get a comparable number of wolves based on both the observations and the DNA results.

Territorial analysis

To properly evaluate how well observations indicated the presence of wolves within delineated territories, we created a time window for daily observations for each territory. We considered a territory to be actually empty of wolves (due to poaching or false observations) whenever observations were recorded in 2016 but not in 2017. Seven of 55 roughly delineated potential wolf territories fulfilled these criteria and were ignored when the population estimate for early March was calculated. Furthermore, six more territories were excluded based on the known loss of one or both wolves in territories hosted by twosomes. From observations recorded from 1 Jan to 15 Mar, we chose (1) the observations where the number of wolves per observation was highest for each territory and (2) the observations where the number of wolves per observation was the second highest (if these observations were more

common than those in which the number of wolves was highest). In one Finnish-Russian territory hosting two wolves, no volunteer-provided observations were recorded in 2017; in this case, our data were based only on the genetic analysis.

We estimated the number of wolves both in the beginning and at the end of the study period. To determine whether the proportion of non-resident wolves varied temporally, we calculated the monthly proportions of observations concerning (1) single wolves and (2) ≥ 2 wolves outside and inside the apparent territory boundaries. The estimated proportion of non-resident animals varies from 6 to 20% in different wolf populations (Fuller et al. 2003). Because the proportion is not known for the Finnish wolf population, we used this range in the population estimation. When creating the population estimate, we summed up (1) the number of wolves profiled in the DNA analysis and (2) the total number of wolves living within the territories where sampling for genetic material was not executed. We back-counted the

Fig. 2 The timing of the departure by sub-adult wolves from their natal territory in mid-March. Based on wolves that were GPS-collared in Finland 2003–2017

minimum estimate for August 2016 by considering the known mortality during the study period ($n = 54$ wolves).

We conducted the statistical analyses by using linear models, and a two-tailed $p < 0.05$ was considered statistically significant. Akaike's information criteria (AIC) were used for the model comparison, to determine the most supported model. All statistical analyses were conducted with SYSTAT (version 13) software.

Results

We delineated a total of 41 territories hosted by packs or twosomes in February–March 2017. Of these, 11 territories were estimated to be transboundary, shared by both Finland and Russia. For the 23 Finnish territories that seemed to be hosted by packs or pairs in early March based on point observations, the mean territory size (MCP 100%) was 901 km^2 (range $340\text{--}1700 \text{ km}^2$). The mean territory size based on the locations of GPS-collared wolves in February–March 2017 was 923 km^2 ($n = 7$ territories, range $480\text{--}1490 \text{ km}^2$). The mean density of observations within the delineated territory was $7.8/100 \text{ km}^2$ ($\text{SE} = 1.2$), and the mean density of observations was $1.1/100 \text{ km}^2$ ($\text{SE} = 0.2$) within the 10-km buffer zone around the territory boundaries (Figs. 2 and 3). In some cases, in territories with a low density of observations, the density was higher within the buffer zone than within the delineated territory (Fig. 3), probably because observations in the area were

Fig. 3 Density of observations per 100 km^2 within Finland's wolf territories and within the 10-km-wide buffer zone around the delineated territory MCPs. Territories are ranked by increasing observation density

more actively recorded for the neighbouring territory. The size of the delineated, completely Finnish territories was related to the number of observations, indicating that there is a risk that the wrong conclusions may be drawn about the number within neighbouring territories, especially when only a few observations were recorded (territories without transmitters, occupied by wolves in March 2017; $y = 605 \text{ km}^2 + 3.5 \times \text{observations}$, adjusted $r^2 = 0.38$, $F = 17.43$, $n = 23$, $p < 0.001$).

In total, 970 samples were analysed for DNA, with an overall success rate of 56%. For the samples collected by professionals in eastern Finland, the overall success rate was 57%, with rates of 72% for scat samples ($n = 288$) and 43% for urine samples ($n = 454$). The difference between the maximum number of wolves of the observations and the number of wolves found by the genetic analysis averaged at zero and varied from -3 to $+2$ wolves. This difference was neither related to the number of successful DNA analyses per wolf (Pearson's $r = -0.119$, $\text{df} = 20$, $p = 0.618$) nor correlated with the number of recorded observations ($r = 0.059$, $p = 0.812$) or wolves in the territories (three categories, see “Methods”; Kruskal-Wallis test statistic 5.57 , $\text{df} = 2$, $p = 0.062$). Three of the 36 GPS-collared wolves that dispersed in 2003–2016 left their natal territory before Mar 15 (Fig. 2).

The results yielded by the genetic analyses in the 21 territories with both DNA and observational data were significantly related to the maximum number of wolves in the point observations (Figs. 4 and 5 and Table 1). This model was better than the model in which the second highest number of wolves per observation was selected as an independent variable (for cases when such observations were more common than the highest number; $\Delta \text{AIC} = 7.161$, see Burnham and Anderson 2006). The relationship between the highest number of wolves in observations and the number of wolves yielded in genetic analyses was slightly stronger in territories ($n = 11$) where volunteers collected samples for DNA analyses (the adjusted $r^2 = 0.829$) than in territories ($n = 10$) where samples were collected by paid persons ($r^2 = 0.591$).

The mean proportion of observations of lone wolves outside the delineated territory boundaries was 27%, without any clear trend, while within territories, the proportion of observations of loners decreased and the proportion of twosomes and packs increased during the study period (Fig. 6). The monthly percentages of twosomes and packs observed outside delineated territories ranged between 4 and 6%.

Out of the 99 wolves profiled in genetic analyses, 86 were estimated to be alive in early March 2017.

The mean number of DNA samples and successful genetic analyses per each genetically profiled wolf was higher in territories where samples were collected by paid personnel (analyses per wolf; Student's $t = 2.76$, $\text{df} = 10.43$, $p =$

Fig. 4 Delineated wolf territories based on observations (empty), observations and genetic analyses (green), positions of GPS-collared wolves (red) and both genetic analyses and GPS data (blue), with the number of estimated wolves hosted by the territories in early March 2017. West of the red line, DNA samples were collected by volunteers, and east of the line, the samples were collected by professionals

0.019, means (and ranges) 8.6 (2.5–22.3) and 2.7 (1.2–4.5)). The estimated number of wolves occupying the delineated territories for which only point observations were available was 55 animals. Thus, the sum of territorial wolves was 141, and these wolves occupied 41 territories, of which 23 hosted packs and 18 hosted twosomes (Fig. 4). Using the range for the proportion of non-residents in North American wolf populations (6–20%, Fuller et al. 2003), we derived a post-hunting population size of 150–178 wolves in March 2017. By taking into account the known mortality during our study period (58 wolves), we determined a minimum estimate of 208–236 wolves for early August 2016.

Fig. 5 Relationship between the maximum number of wolves in the observations and the number of wolves profiled in the genetic analyses from 21 wolf territories in Finland during 2016–2017

Discussion

The costs and the availability of experts to collect data do not scale readily to broad spatial scales (Hochachka et al. 2012). This problem is highlighted with large carnivorous mammals that are rare, elusive and highly mobile. Discussions about quality control and methods of handling of inevitable observational biases in citizen-collected observations are key concerns, e.g. when scientists just map distributions with data provided by volunteers (Hochachka et al. 2012; Bonney et al. 2014). When most of the used observations are provided by volunteers and direct population control is among the key motivations of recording the observations, such as in the population control of brown bear (*Ursus arctos*; Mykrä et al. 2017), data quality is likely to be a major issue that must be addressed.

Genetic data, even collected opportunistically by volunteers, increases the validity of population estimates. They provide a less ambiguous basis for estimations than observations; therefore, results from DNA analyses should be treated independently of observational data when such data are available. Our finding that volunteer-provided observations seemingly delivered a reliable range of estimates for the number of wolves occupying the studied territories, which were similar to those revealed by the DNA results, indicates that hunters can collect relevant information about pack sizes. However, these two datasets (observations and DNA analyses) are unlikely to be totally independent from each other. For example, in territories where volunteers collected scat for genetic

Table 1 Linear regression models testing how good the maximum number of observed wolves within the 21 territories in Finland is related to the number of wolves profiled in the DNA analyses

Independent variable	Constant	Coefficient	Adjusted r^2	p value	AIC (corrected)
Maximum	−0.478	1.133	0.703	< 0.001	71.504
Corrected maximum*	−0.057	0.926	0.590	< 0.001	78.665

*The results show the maximum and the second highest number of wolves (corrected maximum) for the observations, whenever the corrected maximum was more common than the maximum

analyses, the observational data might possess a higher than average quality level, as there probably was more overall interest and observational activities for the wolves in these territories.

The territories that were simple delineations based solely on observations produced more uncertainties related to the population estimation process and the final wolf numbers. Without genetic monitoring or systematic snow tracking, it is questionable whether we know how well the delineated territory boundaries represent the real situation, especially when the number of observations is low. This uncertainty represents one of the explicit challenges for data collected by voluntary networks, the unavoidable spatial variations in data coverage (Hochacka et al. 2012). The second challenge is due to temporal variations in the observational activities. For example, the ability to identify so-called apparent territories is questionable when packs were reported in autumn and early winter but no observations were recorded after the turn of the year. The type of uncertainty concerns species identification; there are > 2500 Eurasian lynxes (*Lynx lynx*) in Finland (Chapron et al. 2014, supplementary material), and their tracks in soft snow are sometimes difficult to distinguish from wolf tracks. In some cases, in territories with a low density of observations, the density was higher within the buffer zone than within the delineated territory (Fig. 3), probably because observations in the area were more actively recorded for the neighbouring territory.

The proportion of non-resident wolves did not appear to change over our Aug–Mar study period, which is consistent with the finding that only a few sub-adults depart

their natal territory before mid-March. The decreased proportion of observations of loners and the increased proportion of at least two wolves per observation from autumn towards winter might be due to the snow layer, as it is less costly to move as a group in snow because wolves usually step on the tracks of forerunners when moving in the snow. Another reason for this observation may be that, in winter, pups more frequently move with the other pack members.

To tackle these different types of uncertainties in the observational volunteer-provided data, we recommend that non-invasive genetic monitoring should be conducted in all wolf territories in Finland, despite the increased costs of monitoring. However, this may prove unrealistic because of the high costs. Even if all samples were collected by volunteers, the extra costs would be considerable. The genetic analyses for the samples in our study cost approximately 110 Euros per sample and 106,000 Euros in total (K. Holmala, unpublished). To ensure a stable and sufficient quantity of DNA samples in the long term, sampling solely by volunteers may yield too much unpredictability temporally and spatially, although it may work well for a few consecutive years, as demonstrated in southeastern Finland (Granroth-Wilding et al. 2017). There is, however, a declining tendency in the number of samples provided by volunteers from the same areas over time. The balancing of sample sizes across territories could enable more cost-efficient genetic monitoring. Another area that requires development is the extraction of DNA from other types of DNA samples. The success rate for the easily detectable urine samples was low compared to that of the faecal samples,

Fig. 6 The monthly proportions of observations concerning single wolves (a) and at least two wolves (b) inside (solid line) and outside (dashed line) delineated territory boundaries in Finland during 2016–2017

indicating that the methodology needs urgent development before it can be useful for monitoring purposes.

Citizen science and community-based monitoring have been traditionally integrated with large carnivore monitoring in Finland. This method is associated with low costs, but, for conflicting and vulnerable species such as wolves, concurrent genetic monitoring and a constant readiness to conduct non-invasive sampling by professional personnel is needed for reliable population size estimates. Whenever the monetary resources permit it, for Finland, the ideal monitoring method is the implementation of the Scandinavian model where approximately two persons per territory are paid for 2 months of fieldwork to perform systematic snow tracking and sampling for scat and urine for DNA analyses (Liberg et al. 2012). This much costlier protocol may be unrealistic in Finland. If this is the case, we still need more genetic sampling to test the quality of volunteer-provided data.

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