The future is now; science in a spoonful of snow.

Using *e*DNA to monitor a polar bear (*Ursus maritimus*) population in the Chukchi Sea

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Objective

Develop, test, and optimize a novel genetic method that uses the rare and degraded nuclear *e*DNA present in the snow tracks of a polar bear to identify the individual that has left the tracks.

Background

1. Polar bear conservation and management relies upon scientific knowledge about their populations including genetic, demographic, and population parameters (Regehr et al. 2010).
2. However, monitoring polar bear populations is challenging due to their enormous home ranges, remote settings, and extreme climatic conditions.
3. Methods that require physically handling polar bears (e.g., chemical immobilization from a helicopter) are costly, dangerous, and there are concerns among stakeholders about stress to the bears.
4. Minimally invasive methods, such as hair-DNA (using barb wire snags) and fecal-DNA have been used, but face limitations to sample size and spatial extent.
5. Polar bear trails are very abundant along Alaska's Arctic coasts, and are readily accessible by local community members.

Methods

1. Sampling occurred near Utqiaġvik, Alaska (Fig. 1).
2. Fresh polar bear trails were located on the sea ice. Snow was sampled from a minimum of 10 tracks per trail (Fig. 2) and stored in plastic bags.
3. Snow was slowly melted and filtered through Sterivex filters (Fig. 3). Filtrate was stored and shipped to the lab in a buffered preservative.
4. Nuclear DNA was extracted and genotyped using High Throughput Sequencing (HTS) of 13 microsatellite markers (De Barba et al. 2016).
5. Genotyping of the *e*DNA was validated by using the same methods of amplification and sequencing to genotype a separate DNA source (e.g., hair) from known individuals that left the tracks (Figs. 4, 5).
6. Two of the trails consisted of "artificial" tracks that were made by pressing the foot of a harvested polar bear into the snow. These tracks represented ideal conditions and were sampled & processed using the same methods as the other tracks.
7. Ambient conditions including temperature, wind, and snow characteristics were recorded.

Figure 1. Sampling area near Utqiaġvik, AK (71.4° N, 156.5° W)

Figure 2. To sample polar bear tracks, a clean steel spatula was used to cut the snow around & below the track. At least 10 tracks were collected.

Results

- Matched samples consisting of snow tracks and hair (n = 9) were collected on the sea ice at hair sampling stations in 2015-16.
- All hair samples (n = 9) were successfully genotyped.
- Genotypes from "artificial" snow tracks (n = 2) perfectly matched the corresponding skin and hair genotypes.
- The *e*DNA from the remaining snow tracks (n = 7) could not be genotyped.

Discussion

- Under "ideal" conditions, HTS genotyping can identify individual polar bears from their tracks in the snow.
- Less than ideal conditions warrant further methodological refinements through a controlled experimental approach that considers:
  - UV light damage to cells (e.g. track freshness and/or season of collection)
  - Weathering of cells by freeze-thaw cycles, desiccation, & physical abrasion
  - Snow texture vs. the likelihood that epidermal cells are abraded from the foot pads of the polar bears
  - Collection methods for both cellular and extra-cellular DNA

Conclusion

Polar bear genetic identification using nuclear *e*DNA from snow tracks is possible. However, several technical challenges remain unresolved. Nevertheless, upon refinement of these methods, polar bear conservation will gain an invaluable new tool that will help reduce costs, increase sample size, and reduce controversy associated with invasive sampling methods. This method also enables local residents to participate in citizen-science based monitoring (Biggs et al. 2015).

Figure 5. Typical scene when a hair trap was visited by a polar bear. Samples of both the snow and hair were collected to compare both sources of DNA.

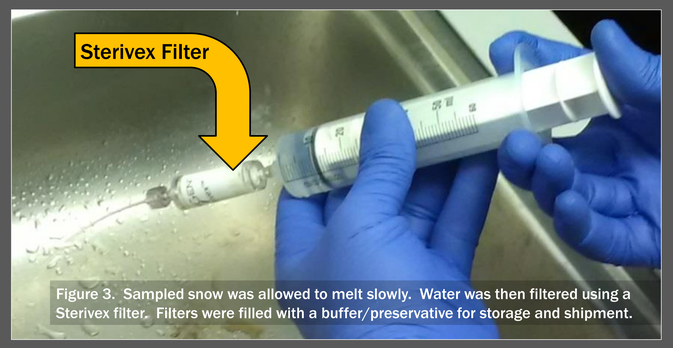

Figure 3. Sampled snow was allowed to melt slowly. Water was then filtered using a Sterivex filter. Filters were filled with a buffer/preservative for storage and shipment.

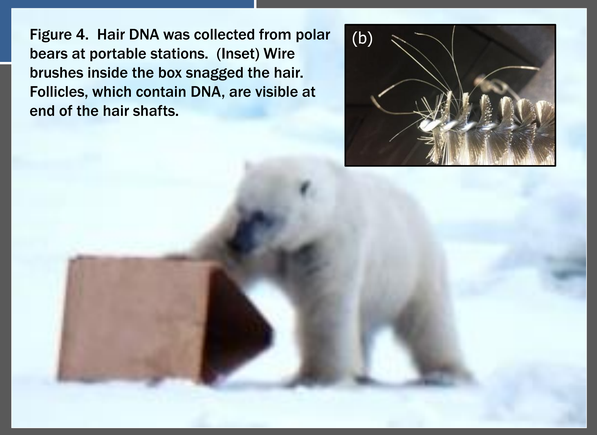

Figure 4. Hair DNA was collected from polar bears at portable stations. (Inset) Wire brushes inside the box snagged the hair. Follicles, which contain DNA, are visible at end of the hair shafts.

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Acknowledgements

- U.S. Fish and Wildlife Service – Polar Bear Program
- Native Village of Utqiaġvik
- Barrow Whaling Captains' Association
- Alaska Eskimo Whaling Commission
- Alaska Native hunters and stakeholders

USFWS Permit No. MA80164B-0
CITES Permit No. 16US89997 B/9