Project information

Project title
ASSESSING THE GENETIC STRUCTURE AND THE MAIN DRIVERS OF DIVERGENCE IN SEMI-DOMESTIC REINDEER ACROSS FENNOSCANDIA

Year
2020

Project leader
Bård-Jørgen Bårdsen

Geographical localization of the research project in decimal degrees (max 5 per project, ex. 70,662°N and 23,707°E)
Locations for the outermost populations used in the current project (in decimal degrees): North (70.921, 27.886); South (60.833, 7.787); East (67.914, 70.369); and West (60.833, 7.787).

Participants

Project leader(s)/institutions:

- **Bård-Jørgen Bårdsen** (bjb@nina.no): Norwegian Institute for Nature Research (NINA; www.nina.no), Tromsø, Norway.

Project participants/institutions:

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- **Marius Warg Næss** (marius.naess@niku.no): Norwegian Institute for Cultural Heritage Research (NIKU; www.niku.no), Tromsø, Norway.

Administrative responsible:

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Flagship
Terrestrial

Funding Source

Summary of Results

One primary aim for the project was to test if the previously established relationship between population size (N) and genetic variation reported for Norwegian wild reindeer (Kvie et al. 2019[1]:Fig. 3), is valid for Fennoscandian semi-domestic reindeer as well. This assessment has substantial management implications as the presence of such a relationship document the importance of keeping herd size above a given threshold in order to conserve genetic variability. This is consistent with population genetic theory and represents a significant conservation concern as low levels of genetic variation is expected to limit to the ability for populations to deal with multiple, often co-occurring, stressors such as climate change, diseases, parasites and predation (Kvie et al. 2019 and references therein). Using the number of alleles (Na) and the plateau-model we documented a similar relationship for domestic reindeer as for wild reindeer (Fig. 1a): the estimated threshold population size for domestic reindeer of 2098 [95% Confidence Intervals (CI)=331,13296] was ~440 animals higher than the estimated threshold of 1560 (95% CI=279,2844) for wild reindeer (Kvie et al. 2019). As the 95 CIs for the two estimates are overlapping the difference between wild and semi-domestic reindeer is, however, not statistically significant. Nonetheless, the inference drawn from the plateau-model in the analyses of semi-domestic reindeer had some limitations as 1) None of the estimated coefficients, except the already reported threshold, were statistically significant at an α-level of 0.05; 2) Re-analyzing the relationship with a more flexible segmented-model resulted in a higher predictive power as this model explained ~17% of the variance in Na and statistically significant differences in slopes as well as a breakpoint of 2500 individuals (a population size comparable to the plateau model, but with a much higher precision: 95% CI=1050,5959); and 3) a positive relationship between genetic variance and N but varied significantly across-countries (Fig. 1b). Based on this, we plan to re-analyze both the data from wild and semi-domestic reindeer in order to produce comparable and more precise results than by using the plateau-model (Fig. 1c). Moreover, in the analyses of domestic reindeer, we will produce both pooled and separate estimates per country in order to see if the relationship between genetic variability [including more than just Na as discussed so far (but see Fig. 1c); with the difference between the models is even more promising in favour of the segmented model] and N are similar across the Fennoscandian countries or not.

The second aim for the current project was to look at the spatial genetic structure of domestic reindeer in the Nordic countries and to discuss possible main drivers behind the observed structure. To accomplish this, we analyzed the output of a clustering algorithm using microsatellite DNA as input from the program STRUCTURE. The analysis revealed an increase in the mean likelihood of the data for up to three populations (K=3): 1) one group dominated by Finnish reindeer; 2) one by southern Swedish- and Norwegian reindeer; and 3) one group that was dominated by reindeer from the Northern parts of Sweden and Norway. Further, by using K=3 (i.e. three ancestry coefficients), we documented that Language (i.e. a separation of herds into areas classified as Norwegian, Central Sami, South Sami and

Finnish) had by far the best support when compared to other geographical, ecological and cultural classifications (Røed et al. manuscript; details provided under point 7. below). Language also explained a surprisingly high amount of the variance in these models, indicating that traditional knowledge, cultural identities and herd migration have contributed significantly to the observed genetic structure. Moreover, ecological gradients were more pronounced within- than between-genetic clusters, and this provided even more evidence for the fact that historical and social-cultural processes are the most critical drivers for the genetic differentiation of domestic reindeer observed today.

[1]Kvie et al. 2019. Cons Genet 20:1405 https://doi.org/10.1007/s10592-019-01225-w.
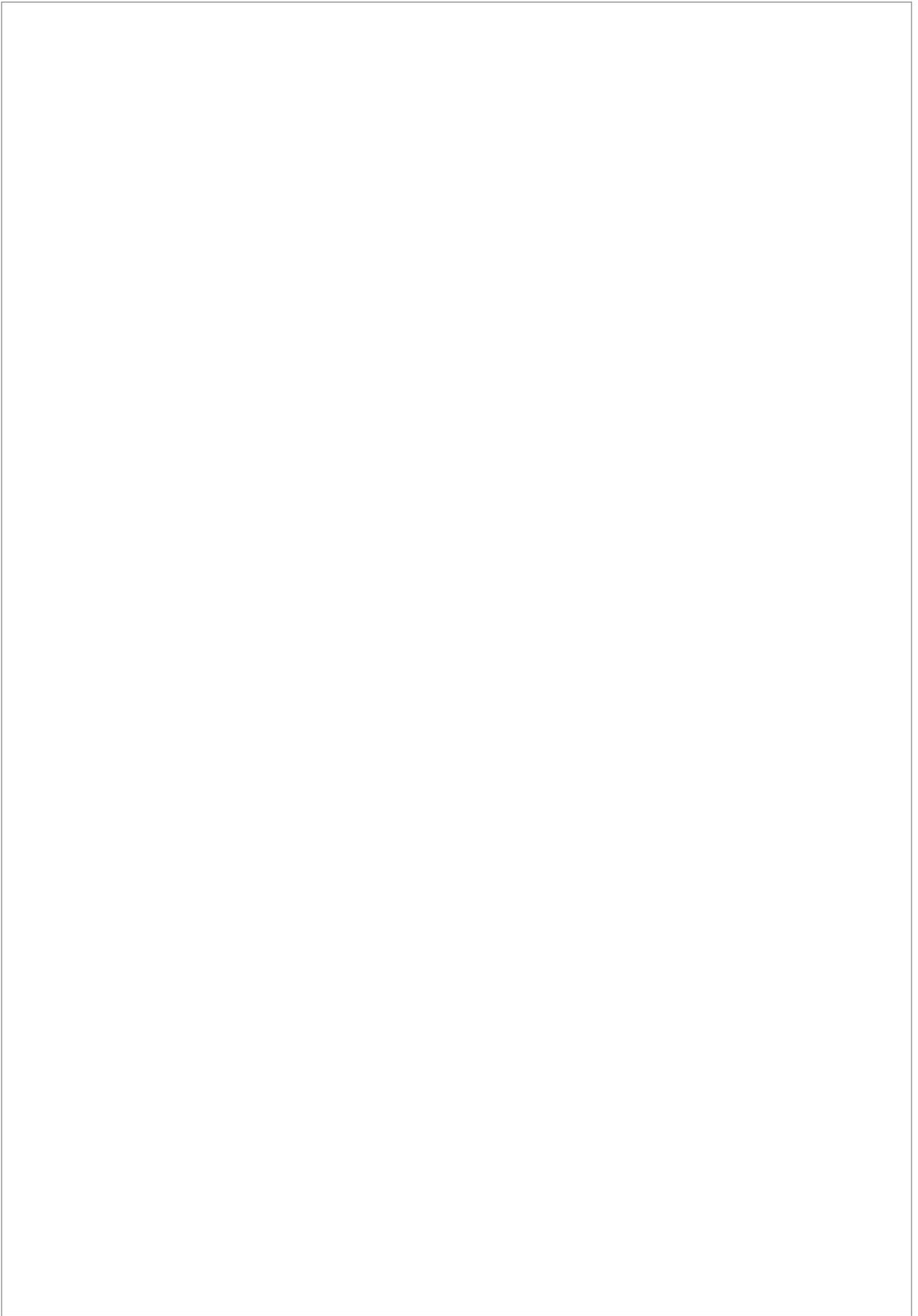
Master and PhD-students involved in the project

Not relevant.

For the Management

The knowledge generated from this multidisciplinary project will be relevant for informing national/regional policymakers and reindeer herders, and for developing an sustainable reindeer husbandry, which is essential for the Norwegian Government. Our project also fits well within the objectives of the Terrestrial Flagship's Science Plan as it will shed new light on the relative importance of climatic- and anthropologic-factors on genetic variation in Fennoscandian semi-domestic populations. In particular, the project fits nicely into the flagship's aims to: "improve the predictability of climate-related changes of boreal-Arctic ecosystems (…), also concerning the effects on the society" (WP2); "develop models that incorporate the social, cultural and environmental dimensions since most models of the management of natural resources focus on ecological factors only" (WP3); achieve adaptive management of harvestable populations (WP4); and generate quality data at spatiotemporal scales appropriate for climate impact studies (WP5). Our project also strengthens the flagship's overall aim of achieving a broad multidisciplinary approach, and WP3's aim to facilitate projects where social and environmental scientists work together.

Published Results/Planned Publications
- Røed, K. H., K. S. Kvie, B.-J. Bårdsen et al. (manuscript). Historical and social-ecologic processes as drivers for genetic structure in Nordic domestic reindeer.
- Røed, K. H. et al. (in prep). Chapter 2 (Genetic structure and origin of semi-domestic reindeer) in a forthcoming book "Pastoralism in a changing Arctic - Complex challenges for people, reindeer and landscapes" (eds. Ø. Holand et al.).

Communicated Results

As stated in the project descriptions, we plan to post fortcoming results (i.e. publications and other output) on team members' blogs and social media accounts (e.g. Twitter and Research Gate) to ensure that that results become available to reindeer herders and the public in general as well as to relevant governmental institutions and other scientists.

Interdisciplinary Cooperation

The project consisted of three biologists (two geneticists and one ecologist) and one anthropologist, and the topics covered in the project covered for the following scientific fields:

- Population genetics;
- Ecology;
- Evolution;
- Anthropology; and
- Environmental science.

Budget in accordance to results

The budget was spent in accordance with the proposal (see point "4. Amount of funding from the Fram Centre, …" and project description for details). Our proposed project took advantage of historical data on climate change, human presence and official statistics combined with elaborate datasets on genetic structure and variability, and thus truly represents an extension of the research already included by ReiGN. The collaboration between the geneticist in ReiGN's Work Package (WP) 1 ('Genetic resources, biodiversity & breeding'; lead by NMBU) and the two WPs lead by Fram Centre institutions would not have been feasible within ReiGN's budget framework.

Could results from the project be subject for any commercial utilization
    No
Conclusions

This was the first of a two-year project, and it was organized in tasks as follows:

- Task 1: Data collection and genetic analyses;
- Task 2: Official statistics (Norway: accomplished; other countries: 2020);
- Task 3: Analyses of genetic data (2020);
- Task 4: Analyses of genetic variability (2020-2021); and
- Task 5: Dissemination & outreach (2021).

Even though Task 4-5 originally was planned to be finalized in 2021, we have accomplished all tasks except Task 3. In this task, we proposed to run an Approximate Bayesian Computation (ABC) to identify the most likely scenario for historical divergence for Fennoscandian semi-domestic reindeer. This has, however, been postponed as we have focused on the writing of results produced within the project so far. Finding additional support for our hypothesis, that genetic variability is explained by population size (Task 4), is highly relevant for the management authorities in all Nordic countries, as it is a common goal to have future viable herds. We thus plan to expand our collaboration regarding this topic around a comparative approach. The latter will both compare wild and domestic reindeer as well as the different countries (with a potential to include herds further east than what we have done so far).