

A Review of the Conservation Genetics Issues Confronting the Lesser White-fronted Goose Recovery Program

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George Amato
Director, Sackler Institute for Comparative Genomics and
Center for Conservation Genetics
American Museum of Natural History
gamato@amnh.org

Executive Summary

This report was prepared at the request of Nina Mikander, Coordinator of the Lesser White-fronted goose and UNEP/AEWA Secretariat. It is based on a careful review of all the provided materials as indicated in the Terms of Reference for the Independent Expert Review of the Genetic Status of the Lesser White-fronted Geese in Fennoscandia. Previous to this review, I have not participated in any direct discussion or been involved in any primary genetics research related to this species. I have however conducted conservation genetics research, and managed and advised numerous, international, species conservation recovery efforts for more than twenty years. *A curriculum vitae* has been attached to detail what training and experiences helped to shape this review.

The genetics issues confronting a successful LWfG recovery program have been well articulated by the various stakeholders through a succession of international meetings, summary plans and scientific articles. In many ways the breadth of issues spans the broad hierarchical levels of conservation genetics – from uncertain taxonomy and metapopulation structure through the challenges of detailed individual genotyping necessary to detect multi-generation hybridization. In addition to a consideration of the various evolutionary and population genetics scales involved, there is also the various management scales from environmental degradation and control of illegal hunting to intensive *ex situ* breeding for population reinforcement or as a hedge against extinction. I have attempted to deal with each specific issue below, and then summarize a set of options to best accomplish the goal of reversing the steep decline of the LWfG in nature while maintaining a genetically and demographically robust species.

Before addressing the specific genetic threats and management implications it is important to again reiterate that the highest priority for successful conservation of the LWfG is a reduction in mortality in the wild from illegal hunting and protection of critical habitat across the species migration routes. Ultimately these efforts will determine if this species persists into the future. Genetic management may provide an important aid to this effort – and avoid some of the additional threats due to loss of genetic variation in small fragmented populations – or genetic introgression from interspecies hybridization. But those efforts will be moot if there is not a reduction of mortality and increase in recruitment in the wild populations.

LWfG meta-population structure

A review of the available molecular genetic data indicate that the three geographically separated breeding populations of the LWfG are part of a meta-population and not genetically distinct evolutionarily significant units. These populations are characterized by an amount of genetic discontinuity predicted by geographic distance with a distribution of mitochondrial haplotypes and microsatellite allele frequencies indicative of historical connectivity. This pattern, combined with our knowledge of the changing climactic periods over relatively recent evolutionary time, support treating all LWfG populations as sub-populations of the same species – and not as unique evolutionary units that are on separate evolutionary trajectories.

What is most important in these evaluations is that we place the patterns observed from the primary research into an evolutionary context. Any survey of mtDNA haplotypes or nuclear alleles is only a snapshot in evolutionary time. We know that frequencies of these genotypes are constantly changing due to selection as a response to changing environmental conditions, isolation and drift, and accumulation of new mutations. A pattern of fixed, diagnosable characters – similar to what is defined in the Phylogenetic Species Concept (PSC) would indicate significant evolutionary distinctiveness that could only have resulted from coalescence of a pattern due to reproductive separation over evolutionary time. This is the pattern we see in the closely related – but diagnosably distinct LWfG and GWfG species. The pattern for the geographically isolated populations of the LWfG is consistent with non-random, intraspecific variation, and this indicates the importance of historical connectivity.

Specifically, in terms of the genetic health of the species, this argues for more concern with the isolation and loss of genetic variation within the sub-populations than it does with concern for local, co-adapted gene complexes. Furthermore, it strongly supports the option of using individuals and/or their descendents from any one of the LWfG populations for translocations or reintroductions to another sub-population. Indications of a loss of genetic variation in a sub-population would support consideration of augmenting that population by “recreating” historical connectivity though translocations/reintroductions from other sub-populations if natural population size recovery is likely to be slow.

Captive breeding and population reinforcement for the LWfG

The use of intensive management techniques, including captive breeding and translocation for conservation has always been contentious. The reasons for this include concerns over the relative emphasis of efforts and resources allocated to *ex situ* and *in situ* efforts, perceived lack of successes historically for reintroductions, a disconnect between the *ex situ* efforts and the *in situ* efforts, concerns about disease

transmission to wild populations, and issues of genetically appropriate release candidates. And yet, such intensive efforts may be essential to the recovery or very survival of certain species. The IUCN provides valuable guidelines for appropriate and responsible use of these intensive management strategies, and this is well discussed within the May 2010 *Feasibility study for the re-introduction/supplementation programme for the Lesser White-fronted Goose Anser erythropus in Norway*.

A review of the published molecular genetic data on the current *ex situ* populations, however, indicate that only one is appropriate for use for augmentation of the wild populations of the LWfG. The *ex situ* group maintained at Nordens Ark in Sweden are of known provenance, and represent a subsample of the Western Main population from Russia. MtDNA analysis and surveys of microsatellite loci demonstrate significant interspecific hybridization between the LWfG, GWfG and Greylag goose for the older, widespread captive populations. Beyond first generation F1 hybrids, it is difficult to assess the degree of hybridization for individual geese. Even though we now possess the ability to sequence whole genomes – the detailed molecular analyses necessary to differentiate the pedigrees of individual geese in these hybrid populations precludes their use for responsible population augmentation of the declining wild population. Any analyses would only confidently exclude known hybrids – but it would not preclude type I errors of including some individuals of hybrid origin that do not contain common, foreign genes.

The captive population maintained at the Nordens Ark represents the best option for captive breeding for population augmentation. The population was started with wild caught birds of known provenance. They also are a subsample of the LWfG subpopulation that is demographically larger and more genetically variable than the Fennoscandian subpopulation. This captive bred population should be managed to retain maximum genetic diversity and to meet demographic goals. This will also minimize some of the risks of selection for domestication. Managing for minimizing mean kinship with accurate pedigree information is the standard tool for accomplishing these goals. It is also important that the population be monitored for any infectious diseases, and be maintained only in range countries and, if possible, isolated from other captive wildlife and domestic animals.

At this point, starting new captive breeding populations from wild caught individuals – especially from the Fennoscandian subpopulation presents too great a risk to the demographic health of these declining populations. While there are methods to minimize the impact, the potential disturbance is not worth the risk. The exception might be very limited additions from the wild for the Western Main population. These individuals could be added to a satellite population of the Nordens Ark birds. Even a very few individuals, added over time would prevent selection for domestication and would help meet genetic retention goals for a captive bred population that would be available for multi-generational supplementation of the wild populations.

Genetic variation in the Fennoscandian subpopulation and use of captive bred birds for population augmentation

The Fennoscandian subpopulation breeding in Norway has declined precipitously and is not showing signs of recovery. Available molecular data support two hypotheses relevant to guiding an active recovery program. The first, as stated previously, is that historically there was connectivity between LWfG subpopulations. Even at low levels, this connectivity may have played an important role in the persistence of subpopulations – but minimally is indicative of the “natural” evolutionary trajectory of this species. Therefore, lack of connectivity currently is an anthropogenic factor – and one that ideally should be ameliorated. If conservation efforts had resulted in a rapid increase in this subpopulation, then natural connectivity through migrants might have been reestablished without more intensive management.

Which brings us to the second hypothesis that is supported by the available molecular data. Genetic data from the Fennoscandian subpopulation indicates that this subpopulation has lost some degree of genetic variation due to the loss of connectivity to other subpopulations, and due to the drastic decline in population size. This is exacerbated by the lack of recovery to date. The effective (breeding) population is small and likely to remain small for a long enough time that the subpopulation is at significant risk of extinction. While the most important efforts remain reducing the mortality of the wild individuals from this subpopulation across their migration routes --- conservation genetics theory would support the augmentation of this endangered subpopulation with captive bred individuals from the Nordens Ark *ex situ* population. The benefits of this strategy would be an immediate improvement in the demographics of this subpopulation, but perhaps more importantly – would bring a halt to the decline of genetic variation in the subpopulation.

Any conservation strategy has potential risks and benefits that need to be carefully examined and weighed. Typically, when there is a lack of consensus, taking no action is the default decision – with the notion that this is somehow more conservative and less threatening to the species. This, however, is an incorrect assumption. Doing nothing often has as many serious and significant implications as more active management. And, no action can sometimes reduce future opportunities. This is especially true for genetic and evolutionary conservation management when the local extinction of a subpopulation may represent a significant, long-term threat to the species.

Specifically, the Fennoscandian population is at high risk of local extinction. A review of viability analysis modeling indicates that current levels of mortality and recruitment will result in the extinction of this sub-population. Population reinforcement through the release of captive bred individuals would reduce this risk. Protocols that would reduce the potential of disease transmission and

disturbance of wild breeding pairs would be important as part of this effort. Starting a new *ex situ* population from the current, small subpopulation in Norway would involve too great a risk to this endangered subpopulation. Evolutionary biology theory and a review of the available molecular genetic data support the use of captive bred birds from the Western Main subpopulation as appropriate release candidates for this effort.

Importantly, there are two compelling reasons to do this as soon as possible. First, the more quickly this is done, the greater the opportunity to retain the genetic variation present in the Fennoscandian subpopulation. That is, the longer it is isolated and small, the greater the risk of loss of more genetic variation – possibly including important local adaptive genes and gene combinations. This is why waiting until the subpopulation declines further – or is extirpated – is an irreversible genetic and evolutionary decision for this species. While the example of a release of hybrid, captive bred individuals in Sweden demonstrates the risks of moving ahead with insufficient data – there is currently sufficient data and theory to support the addition of Western Main/Nordens Ark birds to help rescue this subpopulation.

Dr. Robert Lacy commented in 2005 that the small size and reduced genetic variation of the Fennoscandian subpopulation did not require genetic rescue, and that there were examples of very small populations of long-lived animals rebounding. Five years later, however, I think the weight of evidence suggests that this subpopulation may require demographic and genetic “rescue” in addition to the mitigation of the continued low levels of natural recruitment.

Conservation genetics of the hybrid LWfG population breeding in Sweden

A review of the molecular genetic data indicates that the LWfG subpopulation breeding in Sweden and wintering in the Netherlands has some level of introgression of genes from hybridization that took place in the captive flocks before individuals were released in nature. From the published data it is not possible to get an accurate estimate of the original levels of hybridization, or of the current persistence of introgressed genes. Capturing wild birds and attempting to quantify this more accurately would not be a priority for the recovery of the LWfG. Even with more detailed genotyping methods available, the logistics and resources necessary to try to purge this population of introgressed genes is unwarranted. Specifically, the threat of a small, subpopulation of LWfG containing some introgressed genes from closely related species seems quite low in terms of their possible impact on other recovering subpopulations. We would predict that if the genes make individuals less fit then they will be selected against in nature. If they are neutral, they will remain at current levels or decline through drift. Natural introgression is not uncommon in many closely related species but seems to be controlled mostly by positive assortative mating within species. While an unfortunate experiment, no specific management actions seem warranted for this subpopulation.

- Considering the lack of empirical molecular genetic data available to guide many endangered species recovery efforts, the assembled literature for the LWfG is reasonably sufficient to guide the management decisions under consideration. That does not mean that there are not multiple interpretations of both the data, in terms of what they tell us unambiguously about the evolutionary history of this species, or the certainty of the implications of the data. In some cases the questions are simple. Evidence of hybridization in the captive populations is clear. Will there be a lowered fitness due to loss of genetic variation in the Fennoscandian subpopulation without active management? This is likely but not yet certain – and difficult to measure. When evaluating scientific data to make decisions, it is unlikely that every single scientist or stakeholder will be in agreement. But the information available for this recovery program is sufficient to draw a broad consensus among conservation geneticists.
- You can quantify the genetic differences between closely related species by a number of objective measures. Most simply it can be estimated as a numerical distance value based on percent DNA sequence divergence across the whole genome or some subsample of the genome. It is, however, difficult to generalize exactly what that means in terms of hybridization or threats due to introgression. Within biology there is an enormous body of literature that suggests that it is difficult to generalize about this. Knowing the exact amount of DNA sequence divergence between LWfG and GWfG provides no additional information on the affects of introgressed genes. What is most important is that the molecular data support the taxonomy of these as good species that do not naturally hybridize in nature – so that should be avoided in our management programs.
- The published scientific results represent reasonable approaches to the questions that they examined based on the time the research was conducted. Almost all published research would benefit from larger sample sizes, and in this case more detailed genotyping. That said, in the current papers it is unlikely that these additions would change the basic conclusions. The LWfG recovery program would benefit from ongoing surveys of genetic variation, primarily to empirically measure the impact of management strategies. More genetic markers could be constructed or may be available. Single nucleotide polymorphisms (SNPs), in addition to more microsatellite loci may be useful tools for reconstructing past population structure or even past natural hybridization events. Techniques have now been optimized for using less-invasively collected samples – such as molted feathers. I would emphasize again, however, that there is sufficient information of sufficient quality to make the important, necessary management decisions to guide the LWfG recovery program.

- As stated previously, beyond first generation hybridization events, it is very difficult and research intensive to try to identify individuals that have no hybrid ancestry. The more genes and gene regions analyzed, the better the process gets – but with tens of thousands of genes and gene combinations – and with the remaining uncertainty even after such an exercise – this would not be a sensible use of technology for guiding an endangered species recover program.
- Most simply put, research on the occurrence of hybridization and introgression on other related species is not particularly relevant to the LWfG recovery program. There is no evidence that hybridization or introgression is naturally occurring in this species. For this reason it should be avoided as part of any responsible recovery strategies for this species. Evolutionary biology teaches us that the implications may be significant but they are impossible to predict with certainty. At a certain point it is an esoteric argument to debate the exact likelihood of levels of reduced fitness or threat. The captive populations of LWfG, other than the Western Main/Nordens Ark, should not be used for reintroductions. The free-ranging LWfG subpopulation in Sweden, however, does not pose a significant threat to the recovery of the other subpopulations. For this reason no action needs to be initiated in terms of screening wild birds for evidence of hybrid genes or in removing birds from the ecosystem where they currently fill an ecological role. If additions are made to this population from captive individuals of the Western Main/Nordens Ark birds it will reduce even further any concerns about the initial release of birds with introgressed genes since this will help “swamp them out” with LWfG genotypes.
- The Fennoscandian subpopulation in Norway is highly threatened by continuing low recruitment, and is highly vulnerable to stochastic disasters. As one of three geographically separated subpopulations, its loss would be a significant loss, and possibly endanger the LWfG species. Genetic data supports the hypothesis that these subpopulations have maintained connectivity in recent evolutionary history. For all of these reasons, a synthesis of conservation genetic research and theory would argue for the population augmentation of this subpopulation with individuals from the Western Main/Nordens Ark captive population.