

## **Detection of farm fox genotypes among Swedish arctic foxes?**

**- Genetic screening and action plan**



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Cover Photo: Lars Liljemark

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## Sammanfattning på svenska

Föreliggande rapport har tillkommit efter att fjällrävar med en genetisk bakgrund avvikande från den naturliga Skandinaviska fjällräven upptäcktes på Hardangervidda i Norge. De avvikande fjällrävarna var hade rymt från pälsfarmer och avvek både genetiskt och morfologiskt från skandinaviska fjällrävar. I Hardangervidda-populationen konstaterades att hybridisering mellan farmade och vilda fjällrävar förekommit och idag finns inte längre några ursprungliga individer kvar i området. Hybridisering mellan farmade och vilda fjällrävar är ett allvarligt hot mot fjällrävens överlevnad genom att lokala anpassningar till den skandinaviska fjällkedjan förloras eller att sjukdomar och parasiter introduceras. Enligt Konventionen för biologisk mångfald (CDB) och The World Conservation Unit (IUCN) skall individer med avvikande geografisk eller genetiskt ursprung klassificeras som främmande art. Fjällrävar på skandinaviska pälsfarmer har sitt geografiska ursprung utanför Skandinavien och har varit under domesticering i ca 100 år, vilket har resulterat i genetiska skillnader mellan farmade och vilda skandinaviska fjällrävar. Detta innebär att förrymda farmade fjällrävar skall klassificeras som främmande art och åtgärder skall vidtas därefter.

I denna rapport har 165 spillningsprover och 125 vävnadsprover, insamlade i den svenska fjällkedjan, analyserats med genetiska metoder för att utvärdera huruvida fjällrävar från pälsfarmer finns i den svenska vilda populationen. Totalt identifierades fem individer med farmursprung, fyra utanför den naturliga utbredningen för fjällräv och en i direkt anslutning till kalfjället (Abisko, Norrbotten). Inga individer bland de vilda fjällrävarna identifierades som hybrider mellan vilda och farmad fjällrävar. I Sverige stängdes den sista rävfarmen 2001 beroende på införandet av en strängare djurhållningslagstiftning och därför är det troligt att de identifierade farmrävarna har invandrat från Norge eller Finland där pälsindustrin är aktiv. Två av farmrävarna identifierades längs kusten i Västerbotten vilka troligen invandrat över Bottenvikens is. Farmrävar i detta område utgör ett litet hot mot den vilda fjällrävsstammen då risken är låg att de kommer i kontakt med varandra är liten. De två andra farmrävarna identifierades i Härjedalen varav den ena förolyckades av en bil och den avlivades av länsstyrelsens personal. Dessa individer hade troligen invandrat från Norge, då flera pälsfarmer ligger nära den svenska gränsen. I detta område är det viktigt att identifierade farmrävar snabbt tas bort då risken föreligger att de når den vilda populationen i Helagsfjällen (Härjedalen/Jämtland).

För att undvika framtida hybridisering mellan vilda och farmade fjällrävar bör samtliga identifierade farmrävar tas bort, oberoende om de upptäcks i fjällområdet eller i skogslandet. Om en hybridkull upptäcks bör hela kullen fångas in för att minska risken att främmande gener sprids i den vilda populationen. Vi föreslår att en expertgrupp bildas för att snabbt kunna identifiera och bistå Naturvårdsverket och länsstyrelserna om åtgärder.

## Summary in English

Arctic foxes are farmed in large extent both in Norway and Finland for fur production. This report was initiated by the discovery of free-ranging arctic foxes (*Alopex lagopus*) with a genetic composition alien to the native Fennoscandian arctic foxes in the Hardangervidda area, south of Norway. The deviant arctic foxes were identified as farmed or hybrids between farmed and wild arctic foxes. Hybridisation between wild and escaped farmed arctic foxes is a threat to the persistence of the wild arctic fox population in Fennoscandia through introduction of diseases, parasites and loss of local adaptations through outbreeding depression. According to the Convention of Biological Diversity (CDB) and The World Conservation Unit (IUCN) animal individuals should be classified as an alien species if they have another genetic and/or geographical origin compared to the native population. Farmed arctic foxes originate from populations outside Fennoscandia and have been under domestication process for approximately 100 years and should therefore be classified as alien species.

To evaluate the impact of farm fox genotypes in Sweden, 165 faecal pellets and 125 tissue samples, mainly from the Swedish mountain range, have been screened on genetic basis to identify arctic foxes that are genetic influenced by farmed arctic foxes. Both new genetic data as well as data from previous studies regarding Swedish arctic foxes have been used in this report. The genetic screening has identified six individuals with farmed origin in Sweden. Four were identified in areas outside the regular distribution range and one in Abisko, Norrbotten, which is a potential breeding area for wild arctic foxes. However, no farmed or hybrid arctic fox has been detected among wild arctic foxes. A condition for a hybridisation event should occur between a wild and a farmed arctic fox is that a fugitive manage to reach the natural distribution range. Since arctic fox farming in Sweden is rare or absent, escaped farm foxes probably originate from farms in either Finland or Norway and have thereafter migrated into the Swedish mountain range.

Farmed individuals detected along the coast in Västerbotten County constitute a low risk to the wild population since they are separated by distance and several geographical barriers e.g. roads and forests. Fugitives from northern Norway, close to the Swedish border, do have a greater chance of reaching the Rosto area, north of Norrbotten, which is an important migration corridor for arctic foxes from Kola Peninsula, Russia. The most likely scenario is getting a fugitive from farms in middle Norway population, where several farms are closely located to wild arctic fox population in Helagsfjällen.

To avoid future hybridisation between farmed and wild arctic foxes, all free ranging farmed foxes must be efficiently removed independently if detected in the mountain range or in the surrounding forest zone. If a hybrid litter is found, it is of great importance to immediately remove pups and the farmed adult. With a fast decision order in combination with effective removal actions of hybrids, spreading of farmed genes into the wild population can be prevented.

## **Conclusions**

The main conclusion of this report:

- Six individuals have been identified as individuals with farmed origin in Sweden between years 2003-2006.
- The genetic analyses have not revealed any farmed foxes or hybrids within the Swedish arctic fox population.
- Escaped farmed arctic foxes must be classified as alien species according to CDB article 8h (CDB, 2002) and the IUCN (IUCN, 1987).
- Free ranging arctic foxes with farmed origin should be removed to prevent alien genes to be spread among wild arctic foxes.
- All observations of farmed arctic must be reported and DNA samples should be collected if possible.
- A reference group should be established for identification of farmed arctic foxes and consultation in situations where farmed arctic foxes are identified.

# 1. Introduction

This report was initiated by the discovery of free-ranging arctic foxes (*Alopex lagopus*) with a genetic composition alien to the native Fennoscandian arctic foxes. Samples collected from arctic fox population in the Hardangervidda area, south of Norway, were identified as farmed foxes or hybrids between farmed and wild arctic foxes (Norén *et al.*, 2005). Hybridisation between wild arctic foxes and escaped farmed foxes is suggested to have changed the genetic structure in the Hardangervidda population (Norén *et al.*, unpubl.) and is a threat to the persistence of the local population. In this report, six individuals have been identified as individuals with farmed origin, located both in the mountain range and in the forest zone in Sweden.

Hybridisation between wild and escaped farmed arctic foxes is a threat to the persistence of the wild arctic fox population in Fennoscandia through introduction of diseases, parasites and loss of local adaptations through outbreeding depression (Angerbjörn, Hersteinsson & Tannerfeldt, 2004; Dalén *et al.*, 2002; Hersteinsson *et al.*, 1989; Linnell, 1999; Norén *et al.*, 2005). According to the Convention of Biological Diversity (CDB, 2002) and The World Conservation Unit (IUCN, 1987) animal individuals should be classified as an alien species if they have another genetic and/or geographical origin compared to the native population. Farmed arctic foxes originate from populations outside Fennoscandia (Konnerup-Madsen & Hansen, 1980; Nes, Einarsson & Lohi, 1987) that are genetic differentiated to Fennoscandian arctic foxes (Norén *et al.*, 2005) in combination with 100years of domestication process contributes to large differences between wild and farmed arctic foxes. Following the guidelines by CDB and IUCN, escaped farmed arctic foxes should be classified as alien species and should thus be handled as a serious threat to the Fennoscandian population.

This report aims to quantify and evaluate the existence of free ranging farmed arctic foxes and hybrids among the native arctic fox population in Sweden. The report was conducted within the framework of the EU-Life project SEFALO+ and was financed by the Swedish Environmental Protection Agency. Both new genetic data as well as data from previous studies regarding Swedish arctic foxes has been used in this report.

## 2 Alien/introduced species or genes

### 2.1 Definitions

Introduced and alien species is one of the major threats in the “The evil quartet” that list the main four threats to biological diversity (Moulton & Sanderson, 1998). The definition of alien species has been modified over time due to increased knowledge and comprehension in population genetics why there is no consensus definition. An alien species is defined by The Convention of Biological Diversity as (CDB, 2002): “A species alien to the geographical area or of genetically distinct populations found within species”. The International Union for Conservation of Nature and Natural Resources (IUCN) has the following definition of alien species: “A species, subspecies, or lower taxon occurring as a result of human agency in an area or ecosystem in which it is not native”. The North European and Baltic Network on

Invasive Alien Species (NOBANIS) has developed a network of common databases on alien and invasive species of the region to implement the CDB and defines alien species as; “a species, subspecies or lower taxon (such as a variety, race, provenance or stock), introduced outside its natural past or present distribution; includes any part, gametes, seeds, eggs, or propagules of such species that might survive and subsequently reproduce (CDB, 2002).

## **2.2 Possible effects of alien species on biological diversity**

Introduction of alien species represents one of the primary threats to biological diversity (CDB, 2002; Keane & Crawley, 2002). Several populations have gone to extinction due to introduction of alien species due to increased resource competition, hybridisation and introduced diseases (Allendorf *et al.*, 2001; Rhymer & Simberloff, 1996). Introgression of alien genes can lower the fitness of the hybrid offspring by loss of local adaptations or disruptions of coadapted gene complexes (Edmands & Timmerman, 2003; Lynch, 1991; Templeton., 1986). Hybridisation between divergent species or populations has been described for several carnivore species *e. g.* Florida panther (Fergus, 1991), European mink (Rozhnov, 1993), grey wolf and coyotes (Lehman *et al.*, 1991), red wolves and coyotes (Adams, Kelly & Waits, 2003). Hybridisations have also been detected between domesticated individuals and their wild progenitors like grey wolf and domesticated dog (Hope, 1994; Vila & Wayne, 1999), Scottish wildcat and house cat (Beaumont *et al.*, 2001), European wildcat and house cat (Hubbard *et al.*, 1992), polecat and domestic ferrets (Davison *et al.*, 1999). In Sweden, hybridisation between a female grey wolf and male domesticated dog has been recorded (Vila *et al.*, 2003).

The most common group of alien species released in Sweden are fish such as Atlantic salmon, brown trout, arctic char (Laikre & Palmé, 2005). Atlantic salmon is globally farmed in a large extent and several millions of individuals escape yearly. A large part of the escaped farmed salmon survive and breed in the wild but are genetic differentiated to the wild as a result of geographic origin, founder effects, directional selection and genetic drift during the domestication process (McGinnity *et al.*, 2003). The escaped salmons hybridize with wild strains of salmon which may change the natural gene pool. Hybrids between farmed and wild salmons have been shown to have a lowered fitness compared to pure wild salmons, which is a potential threat to the population (McGinnity *et al.*, 2003).

The effects of hybridisation on the population level depend on several factors such as population size, fitness of hybrids and the overall genetic divergence between the species. A small population is more vulnerable for hybridisation than a large population due to a lower mixing effect (Wolf, Takebayashi & Rieseberg, 2001).

## **3 The arctic fox – brief background**

### **3.1 The arctic fox - Background**

The arctic fox, *Alopex lagopus*, is a small carnivore with a circumpolar distribution, living in the tundra habitats (Angerbjörn *et al.*, 2004; Audet, Ribbins & Larivière, 2002). An adult arctic fox male is typically 271mm high and have a weight about 3-4 kg (Angerbjörn *et al.*, 2004). Two different colour morphs exist in the wild: blue and white. The blue fox is dark black/blue all year while the white fox is white during winter and brown coloured during summer (Angerbjörn *et al.*, 2004). It becomes



sexually mature in their first year and seldom lives longer than 7 years (Angerbjörn *et al.*, 2004). The female can give birth every year but the reproductive output is controlled by the prey dynamics (Tannerfeldt & Angerbjörn, 1998). The litter size is highly variable and locally adapted to the prey dynamics i.e. lemming cycles (Tannerfeldt *et al.*, 1998). Arctic foxes in coastal areas rely on stable food resources such as bird colonies and usually give birth every year with a stable moderate litter size. Arctic foxes in Fennoscandia have a highly variable reproductive output that depends on the population dynamics of small rodents (Tannerfeldt *et al.*, 1998). Juveniles are usually fairly stationary at the den during the first summer but can migrate long distances as yearlings or sub adults (Tannerfeldt & Angerbjörn, 1996).



Figure 1. Three arctic foxes in winter fur (white morph), Helagsfjällen, Jämtland county, Sweden. Photo: Tomas Meijer

### 3.2 Population status and distribution in Fennoscandia

The wild arctic fox in Fennoscandia is classified as critically endangered (Angerbjörn *et al.*, 2004; Gärdenfors, 2005) and has been protected from hunting in Sweden since 1928. Before legal protection, the arctic fox was extensively hunted for their valuable fur (Zetterberg, 1927). Over harvest caused a severe population decline and with a persistent demographic bottleneck as consequence with a great loss of genetic variation (Nyström, Angerbjörn & Dalén, 2006). Despite legal protection and conservation actions has the population not yet recovered (Angerbjörn *et al.*, 2004). There are several combining factors affecting the population recovery (Hersteinsson *et al.*, 1989) such as changes in prey dynamics (Angerbjörn, Tannerfeldt & Lundberg, 2001), increased competition with red foxes (*Vulpes vulpes*) (Elmhagen, Tannerfeldt & Angerbjörn, 2002; Hersteinsson *et al.*, 1989; Tannerfeldt, Elmhagen & Angerbjörn, 2002) and possible effects of climate change (Moen *et al.*, 2004). Today the Fennoscandian population is subdivided in four areas; Hardangervidda, Helagsfjällen, Borgafjäll and Vindelfjällen-Varanger (Dalén *et al.*, 2006) (Fig 2). The gene flow between the subpopulations is low or absent, which cause a great risk of inbreeding depression, genetic drift and demographic stochasticity (Dalén *et al.*, 2006). The total population size in Fennoscandia is estimated to about 105 individuals, approximately

50 individuals in Sweden, 50 in Norway and 5 in Finland (Anderssen *et al.*, 2004; Angerbjörn *et al.*, 2004)

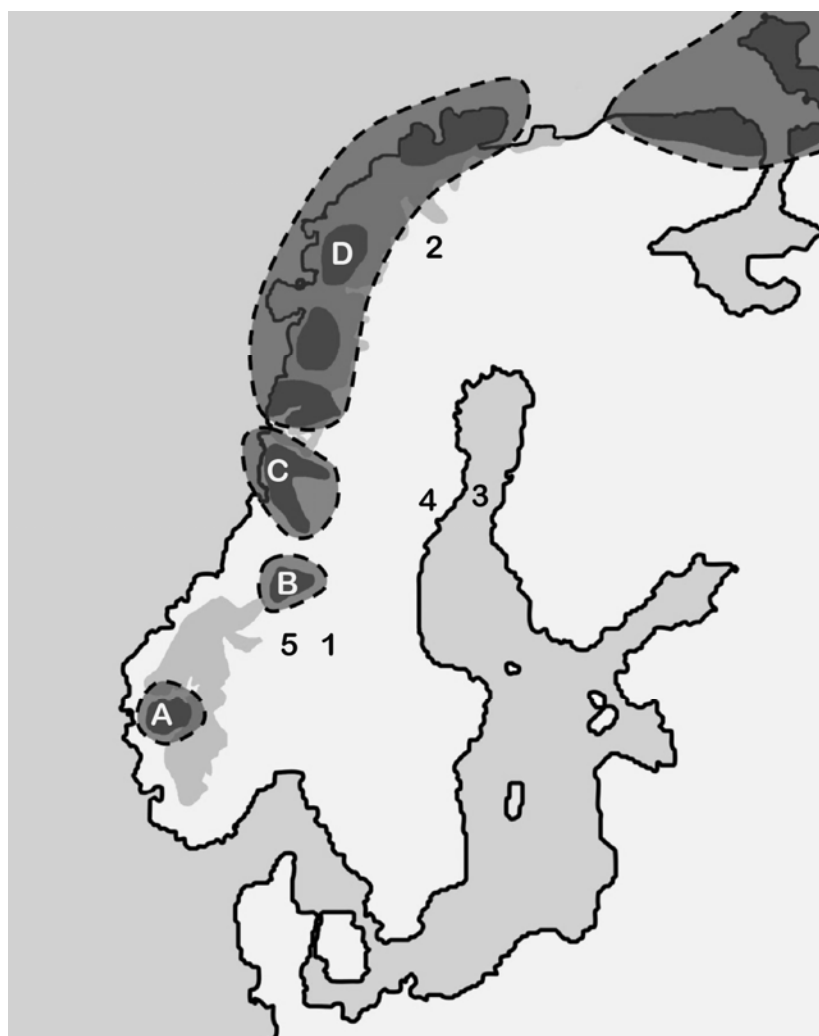


Figure 2. Distribution (grey) of arctic foxes in Fennoscandia (Dalén *et al.*, 2006). Area A; Hardangervidda, B; Helagsfjällen, C; Borgafjäll, D; Vindelfjällen-Varanger. Numbers show the location of identified farmed arctic foxes; 1 Sveg (Härjedalen) 2 Abisko (Norrbotten), 3 Holmön (Västerbotten), 4 Mickelträsk (Västerbotten), 5 Slagavallen (Härjedalen).

## 4. Status of farmed arctic foxes

### 4.1 Fur farms – Background

The population decline in the early 19<sup>th</sup> century caused by over harvest, opened up for commercial farming and production of arctic fox fur. The first Scandinavian attempts of arctic foxes farming started on islands outside the Norwegian coastline using native arctic foxes in the beginning of the 20<sup>th</sup> century. In the 1930s, arctic fox farming had expanded to a profitable industry by successful breeding of individuals originating from farms in Alaska, Greenland, Jan Mayen and Svalbard (Konnerup-Madsen *et al.*, 1980; Nes *et al.*, 1987). Farming of arctic foxes is today a large industry in e.g. Finland, Norway and Estonia.

## 4.2 Morphology of farmed arctic foxes and the domestication process

The geographic origin and domestication are most likely the two major factors that contribute to both the morphological and genetic differences between farmed and wild Fennoscandian arctic foxes (Norén *et al.*, 2005). Arctic foxes have been under domestication process for about one hundred years of captivity (Konnerup-Madsen *et al.*, 1980) with strong selective breeding towards goals like high reproductive performance, good fur quality and large body size (Nordrum, 1994). There has also been a selection of “docile” and “tame” individuals to improve the progress of domestication (Nordrum, 1994; Price, 1999). Even though the arctic fox only has been under domestication process for a relatively short period and has become weakly domesticated (Braastad, 1988) it has several deviations compared to wild foxes (Eide *et al.*, 2005). The selective breeding during the domestication process have contributed to both morphological and behavioural differences between farmed and wild Fennoscandian foxes, see Table 1. (Eide *et al.*, 2005).

Table .1 Morphological and behavioural differences between wild and farmed arctic foxes.

Character	Wild arctic fox	Farmed arctic fox
Weight	Wild foxes weight about 3-5 kg depending on sex and age.	A grown up farmed female weights 6-7 kg and a male 8-9 kg. In the autumn can the weight be up to 20 kg.
Body form		The body is hunched. larger cranium, shorter legs and different feet angle compared to wild foxes.
Fur	Two colour morphs; white and blue/dark. The white morph change colour during summer to brown.	Thicker fur and more/longer fur in the neck than wild. Farmed white foxes does not change fur colour in summer time. There is a large variation of different fur colour races among farmed arctic foxes.
Behaviour		Less reserved to humans and can often be intrusive.
Geographical distribution	Rarely observed in the forest zone.	Most common in the forest zone in areas with farms.

Farmed arctic foxes have their geographic origin from populations outside Fennoscandia e.g. Alaska, Greenland, Jan Mayen and Svalbard (Konnerup-Madsen *et al.*, 1980; Nes *et al.*, 1987). Arctic foxes in these areas are geographically isolated from foxes in the Fennoscandian population (Dalén *et al.*, 2006) and inhabit both “lemming foxes” and “coastal foxes”. The difference between highly fluctuating food resource in “lemming fox” populations and the more stable food source in coastal areas has led to a number of different life-history strategies among the different populations (Angerbjörn *et al.*, 2001). “Lemming foxes” undergo an enormous reproductive output during lemming peaks with up to 18 cubs, compared to coastal foxes which have a stable reproductive output with typically five cubs (Tannerfeldt *et al.*, 1998). There are also differences in migration pattern were lemming foxes migrate further than coastal foxes (Angerbjörn *et al.*, 2004).



Figure 3. (a) Escaped farmed fox observed in Bjuröklubb, Västerbotten. (b) Farmed fox observed in Abisko, Norrbotten.

### 4.3 Possible effects of intraspecific competition and hybridisation

Free ranging arctic foxes with genetic origin in farms have survived and reproduced in the Hardangervidda area, south Norway (Norén *et al.* unpubl) (Eide *et al.*, 2006; Landa *et al.*, 2006). However, the geographical origin in combination with strong selective breeding might contribute to that adaptation for life on the Fennoscandian mountain tundra may be lacking. Due to the larger body size of farmed arctic foxes, they may compete with native arctic foxes during small rodent peak years, while suffering a higher mortality during years with low prey density. Hybridisation between native and farmed arctic foxes can lead to outbreeding depression with loss of local adaptations as litter size (Tannerfeldt *et al.*, 1998) and migration patterns (Angerbjörn *et al.*, 2004). Hybrids in the Hardangervidda population also seem to be less reserved to humans than native foxes, a factor that might increase mortality by e.g. car accidents. The loss of local adaptations and behavioural alterations is a serious threat to the long term persistence of the Fennoscandian arctic fox population.

### 4.4 Legal status of farmed arctic foxes

According to the definitions of alien species by CDB in article 8 (CDB, 2002) and IUCN (1987), individuals from other populations or with other distinct genotypes should be classified as alien species if released, with direct purpose or by accident, into a foreign ecosystem. Arctic foxes in Scandinavian fur farms have their geographical origin outside Fennoscandia (Konnerup-Madsen *et al.*, 1980; Nes *et al.*, 1987) and have been under domestication process during the last decade (Nordrum, 1994). These factors in combination contributes both to morphological and a strong genetic difference between farmed and wild Fennoscandian arctic foxes. The differentiation between farmed and wild arctic foxes makes that individuals from farms must be classified as alien species if they are released in wild.

## 5. Situation in Sweden

### 5.1 Arctic fox fur farms in Sweden

In Sweden, all arctic fox farms were terminated after year 2000 when a more strict legislation was introduced (Jordbruksverket, 2003). The new legislation introduced more specific requirements on how to enrich animal environment which made fox farming unprofitable. The only holders of arctic foxes in Sweden today are zoo's that keep arctic foxes with farmed origin for exhibition purposes. Due to the low number of arctic fox farms in Sweden, free ranging farmed arctic foxes are assumed to be fugitives from farms in Norway or Finland. The amplitude of escaped farmed foxes

from Swedish farms before year 2000 is difficult to estimate due to lack of registration.

## 5.2 DNA based inventory of farmed arctic foxes

For evaluation of the present number of free-ranging farmed arctic foxes and their possible impact on the wild Swedish arctic fox population, we have screened for individuals with farmed origin on a molecular basis. DNA was obtained from both non-invasively collected faecal and tissue samples from juveniles that has been trapped, weighted, measured and ear tagged (Dalén *et al.*, 2006; Norén, Unpubl.). In total, 165 faecal pellets and 125 tissue samples (see Table 2.) from juveniles have been collected and analyzed between years 2004-2006. All samples have been screened for mitochondrial haplotype H9, which is a unique haplotype for farmed foxes and does not exist among wild arctic foxes (Norén *et al.*, 2005). For identification of hybrids between wild and farmed foxes, tissue samples from juveniles and faecal samples have been genotyped and genetically been compared to farmed foxes (see methods). All samples with haplotype H9 were genotyped for 10 microsatellite-loci and compared with wild Swedish arctic foxes (Norén *et al.*, 2005).

Table 2 . Summary of faecal samples and species origin.

Area	Arctic fox (n)	Red fox/ wolverine (n)	Empty (n)	Total (n)
Helagsfjällen (B)	65	20	8	93
Borgafjäll (C)	14	7	11	32
Vindelfjällen and Northern Sweden (D)	11	17	12	40
Total	90	44	31	165

## 5.3 Results

Six individuals were identified as arctic foxes with origin in fur farms, three by genetic identification and two by photos combined with descriptions by the observer. Four of the findings were located outside the regular distribution range for arctic foxes and the fifth individual was found in the Abisko area, Norrbotten County, which is a potential arctic fox breeding area. The identified farmed arctic foxes are all assumed to have migrated into Sweden from either Finland or Norway. The findings of escaped farmed arctic foxes in Sweden are all located close to areas in Norway or Finland with extensive farming (Norén).

Table 3. Identified arctic foxes with genetic origin in farms.

	Year	Haplotype	Sex	Weight	Comment
Mickelträsk, Västerbotten	2006	H9	Female		.
Holmön, Västerbotten	2006	H9	Female		Assumed to have escaped from Finland and crossed the Bottnian bay on the ice.
Abisko, Norrbotten	2006	unknown	unknown	>6000g	Identified by behavior and morphology (se picture). Killed by train (Malmbanan). Assumed to have escaped from Norway.
Vemdalen, Härjedalen	2006	H9	unknown		Identified and removed by the county administration in Jämtland county. Assumed to have escaped from a Norwegian farm. Weight > 6000g
Bjuröklubb, Västerbotten	2005	unknown			Identified by behavior and morphology via picture. Assumed to have escaped from Finland and crossed the ice on the Bottnian bay. No tissue samples were collected.

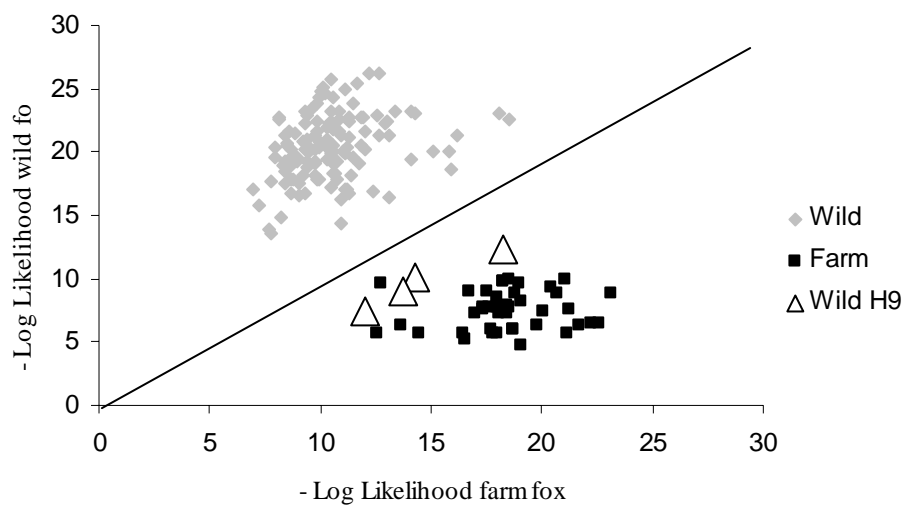


Figure 4. Population assignment test between wild arctic foxes from Sweden assigned vs. farmed foxes and wild H9 individuals. The assignment test shows that the wild H9 have their origin from the farmed arctic fox gene pool. No wild collected samples seem to be influenced by farmed arctic foxes.

## 6. Situation in Norway

Norway is the second largest producer of arctic fox fur in Scandinavia and free ranging individuals of farm origin are observed yearly (Eide *et al.*, 2005). Arctic fox farms are distributed in a large part of Norway with a higher density in south and middle Norway (Norén) Genetic analyses have also revealed the existence of free-ranging individuals with farm origin within the wild arctic fox population in Hardangervidda, south Norway (Norén *et al.*, 2005). Both arctic foxes with pure farm-origin and individuals suggested as hybrids, between wild and farmed individuals,

have been detected in this area (Norén, Unpubl.; Norén *et al.*, 2005). According to the Norwegian monitoring program, all identified foxes in south Norway 2006 were genetically influenced by farmed arctic foxes (Eide *et al.*, 2006). However, in the northern part of Norway, no influence of farmed arctic foxes has so far been detected (Eide *et al.*, 2006). The status of arctic foxes and the spread of farmed foxes in Norway is fully described in Bevaringsbiologi-Fjellrev i NINA 2006 (Landa *et al.*, 2006) and Fjellrev i Norge 2006 (Eide *et al.*, 2006).

## **7. Situation in Finland**

Finland is the single largest producer of arctic foxes in Scandinavia with a yearly production of 1.5 million arctic fox pups (Finlands Pälsdjursuppfödarens Förbund). The farming industry is mainly located in the Österbotten region, middle of Finland. Reproduction between escaped farmed foxes has earlier been recorded in wild, as well as established populations on islands in the Bottnian bay. The number of free living farmed arctic foxes is however assumed to have been reduced the last years due to a more strict legislation, where farms should be fenced or have equally protection from escapes (Jord- och skogsbruksministeriet., 1999). Escaped farmed arctic foxes are classified as wild animals and belong to the landowner (Jaktlag 28.6.1993/615., 1993). Hunting is allowed all year except for females with pups, which are protected between 1/5-31/7. Hybrids between wild and farmed arctic foxes have not been observed, despite the long history of fur farming. This can be explained by the long distance between the farming areas and the sub arctic tundra in Finland.

## **8. Risk assessment and Action plan**

### **8.1 Risk assessment**

There are two separated aspects to take in account when quantifying the problem and the potential risk of getting farmed foxes mixed with wild arctic foxes; 1) the risk of getting fugitives from farms in contact with wild arctic foxes. 2) The effects of introducing alien species/genes into the arctic fox population. A condition for a hybridisation event should occur between a wild and a farmed arctic fox is that a fugitive manage to reach wild arctic foxes natural distribution range. Since arctic fox farming is winded up in Sweden, escaped farm foxes probably originate from farms in either Finland or Norway and thereafter migrated into the Swedish mountain range.

Farmed individuals detected along the coast line in Västerbotten County constitute a low risk to the wild population since they are separated by distance and several geographical barriers e.g. roads and forests. Fugitives from northern Norway, close to the Swedish border, do have a greater risk of reaching the Rosto area, north of Norrbotten, which is an important migration corridor to and from arctic foxes on the Kola Peninsula, Russia. The most likely scenario is getting a fugitive from farms in middle Norway into the Helags population where several farms are located close to wild arctic fox populations. Despite the long history of arctic fox farming both in Sweden and Norway, hybridisation does not seem to have occurred except for the population in Hardangervidda, which implies that the risk of getting farmed individuals into Swedish arctic fox population is limited. Even though the risk of getting a fox with farm ancestry into the wild population is low, would a hybridisation event between wild and farmed arctic foxes get a severe effect on the population.

Since the Fennoscandian arctic fox population are fragmented into several small and genetically differentiated populations (Dalén *et al.*, 2006) can even a single farmed individual change the local genetic structure and induce loss of local adaptations *e.g.* Greig (1979). The only way to prevent and stop the spread of alien genes in the Swedish population would be to remove the farmed fox and possible offspring.

## 8.2 Action plan

According to article 8h in CDB(CDB, 2002), alien species should be controlled or eradicated if it threatens ecosystems, habitats or species. The IUCN states that legal actions should be taken in order to avoid hybridisation between individuals escaping from captivity and their wild progenitors (IUCN, 1987). To avoid future hybridisation between farmed and wild arctic foxes, all free ranging farmed foxes must be efficiently removed independently if detected in the mountain range or in the surrounding forest zone. If a hybrid litter is found, despite removal of the farmed parent, it is of great importance to immediately remove pups and the farmed adult. With a fast decision order in combination with effective removal actions of hybrids, diffusion of farmed genes into the wild population can be prevented.

Since the arctic fox is a threatened species (Gärdenfors, 2005) and placed under protection, removal decisions have to be taken by the environmental protection agency. To facilitate removal decision and identification of farmed arctic foxes we recommend the use of a three step identification order and that the removal decision is delegated to the county borders;

1. Identification by Field personnel - The major part of detected farm foxes can easily be identified on morphological and behavioural characters se Eide *et al.* (2005). Fur colour and body form in combination with behaviour are often so characteristic for farmed arctic foxes that a reliable identification can be performed. The geographical location can also be taken in account when identifying farmed foxes, wild foxes are today rarely observed outside the mountain range. We recommend that arctic foxes found outside the natural distribution range and is identified as farmed by field personnel should be removed on this basis. If there is any concern about origin of the observed fox should the reference group be contacted (se point 2.)
2. Reference group – If there are any concerns about the origin of a fox or if a suspected farm fox is observed within the natural distribution range of wild arctic foxes, should the reference group be consulted. The observation should be presented for the reference group with descriptions of morphological characters, if possible with pictures, behavioural observation and other complementing information. If a farmed fox or hybridisation event is detected within the natural distribution range of wild arctic foxes should the reference group evaluate the situation and suggest appropriate methods for removal. The reference group should consist of personnel from the environmental protection agency, the county administration from Jämtland, Västerbotten and Norrbotten county and active arctic fox scientists.
3. DNA analysis – DNA methods have been shown to be a reliable method to identify both farmed and hybrids between wild and farmed arctic foxes (Norén, Unpubl.; Norén *et al.*, 2005);. When a suspected farm fox is observed it is a great demand of fast handling and action. DNA analyses have the



disadvantage of being time consuming and might not stand up to the demands of fast handling. We recommend using DNA analysis only in cases when the origin of the suspected fox not can be determined by behaviour and/or morphological characters. Possible hybrids between wild and farmed arctic foxes should however always be DNA determined to minimize the risk of removing pure wild arctic foxes. Further we recommend that DNA samples always should be collected afterwards from all suspected individuals for evaluation purposes. DNA analysis is also recommended for remote monitoring using non-invasively collected faecal pellets.

Removal of farmed or hybrid arctic foxes can either be by capture or euthanasia. Further, we recommend to officially classifying farmed arctic foxes as an alien species and including it in the work for implementing the CDB.

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# Appendix

## 1. Methods

### 1.1 Field methods- Sample collection

Faecal samples were collected along the Swedish mountain range during summer and winter inventories by volunteers and county administration personnel in Jämtland, Västerbotten and Norrbotten county between year 2004 and 2006. All known dens, marking scent points (stones, hills) and supplemental feeding stations were surveyed for faecal droppings during each field period. The geographical position for all faecal samples was geo-referenced using a Global Positioning System (GPS) unit. In total 165 samples were collected. Tissue samples were collected and genotyped from individuals that had been trapped, weighted, measured and ear tagged (Dalén *et al.*, 2006); Norén unpubl.data) between year 2004 to 2006. Arctic fox samples of suspected origin reported to the Natural history museum (NRM) was also included in the report.

### 1.2 DNA identification of arctic foxes with farmed origin

Farmed arctic foxes can often be identified and separated from wild foxes by behaviour and morphological characters caused by the selective breeding towards greater size and fur quality. However, individuals in wild can be difficult to identify why the use of genetic methods is an additional tool for identification. DNA identification also gives the opportunity of using non-invasive samples as faecal pellets or fur samples for identification of species, farmed foxes, hybrids and geographical origin (Dalén, Götherström & Angerbjörn, 2004; Dalén *et al.*, 2006; Norén *et al.*, 2005).

In this report, two different methods were used to identify arctic foxes with farmed origin; analysis of mtDNA haplotypes (Norén *et al.*, 2005) and genotyping using microsatellite analysis (Dalén *et al.*, 2004; Norén *et al.*, 2005). (Norén *et al.*, 2005) showed that all farm foxes in Scandinavia and Finland share the mitochondrial haplotype H9, which now days not is present in the wild Fennoscandian population (Dalén *et al.*, 2004; Strand *et al.*, 1998). The longest fragment in haplotype H9 is shorter than in the wild haplotypes, why identification of farmed foxes can be conducted by the use of agarose gel electrophoresis (Norén *et al.*, 2005). The identification method using haplotype H9 and agarose gel electrophoresis is a relatively cheap and quick method to identify foxes with farmed origin.

The second method to identify individuals with farmed origin is the usage of nuclear microsatellite DNA for genotyping. For genotyping are nine different microsatellite loci used (CPH3, CPH9, CPH15, CXX20, CXX140, CXX173, CXX 250, 377, 771) (Fredholm & Wintero, 1995; Ostrander *et al.*, 1995; Ostrander, Sprague & Rine, 1993). The PCR protocol follows Dalén *et al.*(2006), with the nine loci arranged in five different multiplexes. Arctic foxes can after genotyping be identified to origin by comparing the gene frequencies between wild and farmed foxes (Norén *et al.*, 2005). By genotyping individuals, hybrids between wild and farmed foxes can be detected.

All faecal samples were screened for species origin using the Rapid Classificatory Protocol PCR (RCP-PCR) as described in Dalén *et al.*(2004) before it was tested for

haplotype or genotyped. The RCP-PCR protocol is developed for separating faeces samples from arctic fox, red fox and wolverine using mitochondrial DNA. The method is based on a multiple primer system with a general mammal primer and specific species primers. The species primer will bind at different distance from the general primer depending on the sample origin. The fragment sizes are visualized by gel electrophoresis compared with samples with known origin. The fragment sizes are 100 base pairs (red fox), 242 base pairs (wolverine) and 332 base pairs (arctic fox).