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Research Report

The day of the jackal was over: the first golden jackal (Canis aureus) collected in Finland

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Keywords: Arctic Circle, Canidae, diet, genetics, skull measurements.

Abstract

In recent decades, the golden jackal (*Canis aureus*) has expanded its range westwards and northwards in Europe. In this study, we present genetic and morphological data on the first golden jackal collected north of the Arctic Circle. An adult male was shot after having been captured in a leg snare set for foxes near Sodankylä in Finland. It was a large-sized animal in good body condition, showing no signs of hybridization with other canids. The stomach contents included fish bones, likely obtained from an anthropogenic source, as well as remains of a galliform bird. This finding suggests that golden jackals are able to survive harsh winters, allowing them to extend their distribution range to the northernmost parts of Europe.

Introduction

The golden jackal (*Canis aureus*) is a newcomer to the European carnivore community. There is some evidence suggesting that the species may have lived in eastern Europe during the early Holocene (Kurtén 1968, Spassov and Acosta-Panko 2019), but the earliest confirmed records of the species date back to the Middle Ages in the regions along the European Black Sea coast, the Aegean Sea, and southern Greece. Small, isolated populations also existed in Hungary and Romania (Tóth et al. 2009). However, these Central European populations went extinct in the 1960s, likely due to persecution. Meanwhile, the populations in southeastern Europe remained small. In most Balkan countries, the use of poisoned bait was prohibited in the late 20th Century, and the golden jackal was granted legal protection. As a result, populations began to recover, and the distribution expanded to Central and Western Europe (Spassov and Acosta-Panko 2019). Currently, the new range includes for example Hungary, Ukraine, Slovakia, Czechia, Austria, Switzerland, France, northern Italy, Germany, Poland, and the Baltic countries, while vagrants have been recorded in the Netherlands, Belgium, and Denmark (Bauer and Suchentrunk 1989, Hoi-Leitner and Kraus 1989, Zedrosser 1995, Koubek and Červený 2007, Plass 2007, Herzig-Straschil 2007, Lapini et al. 2009, 2011, Szabó et al. 2009, Fabbri et al. 2014, Zagorodniuk 2014, Slamka et al. 2017, Jirků et al. 2018, Stoyanov 2020, Böcker et al. 2023).

The golden jackal has also expanded northwards. The northernmost known breeding population is in Estonia, where the first successful reproduction was reported in 2013 (Männil and Ranc 2022). The Estonian and other Baltic populations probably have multiple origins, with genetic similarities to the populations in Hungary and the Caucasus with ongoing gene flow (Rutkowski et al. 2015). The northernmost sightings of golden jackal so far have been in the Norwegian Arctic (69°50’ N, 20°61’ E) (Sørensen and Lindsø 2021), followed by three individuals killed in the Russian subarctic region. These were a male killed near St. Petersburg in 2007, a female killed in 2016 in the Moscow region, and a male caught in a leg-hold trap set for wolves (*C. lupus*) in Arkhangelsk Oblast (64°40′20″N, 43°22′56″E) in the winter of 2021 (Rykov et al. 2022). Skull measurements and mtDNA analysis of the control region confirmed that the male from Arkhangelsk Oblast had typical European golden jackal body and cranial dimensions, and genetically clustered with European, Caucasian, and Turkish populations (Rykov et al. 2022).

Among the northernmost records are those from Finland, where camera footage and tracks have revealed five different individuals (Kojola et al. 2023). The sixth record is an adult male golden jackal which was accidentally caught in a fox leg-hold trap and killed in Sodankylä, a locality in northern Finland, north of the Arctic Circle (67°25’27 N, 27°70’87” E) in March 2022. After a routine examination by the Finnish Food Authority officials, the male was sent to the University of Oulu (Ecology and Genetics Research Unit) for a closer study. Here, we report the results of this study.

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Methods

The golden jackal cadaver from Sodankylä was deposited at the University of Oulu where its skin and skeleton were assigned the collection number OV.35824. Prior to dissection, the animal's body mass was recorded. We measured the skull with digital calipers and the skin using a measuring tape. Both the skin and the skull were photographed. We compared the measurements with those in Hatlauf et al. (2021b) and Srinivas and Jhala (2021). We assessed the body condition based on the amount of visceral and subcutaneous fat, and the stomach contents were examined to identify the remains of the animal's last meal.

DNA was extracted from muscle tissue with E.Z.N.A. ®Tissue DNA kit (Omega Bio-tek) according to the manufacturer's protocol. A part of the cytochrome oxidase I (COI) gene was amplified by polymerase chain reaction (PCR), using primers BC -F2, BC-F3 and BC-R2 (Chaves et al. 2012). The PCR amplification was conducted in 10 µl volumes containing about 20 ng of template DNA, 0.2 mM of each dNTP, 0.5 µM of both primers, 2 µl of reaction buffer (5X), 5 mM MgCl2, and 0.02 U of Phusion ® DNA-polymerase (Thermo Scientific). The PCR profile in Piko Thermal Cycler included an initial denaturation at 98°C for 1 min 10 sec followed by 40 cycles of 98 °C for 1 sec, 57 °C for 10 sec and 72 °C for 40 sec and a final extension at 72 °C for 1 min. The PCR-product was sequenced using all three primers with the BigDye Terminator v.3.1 ® Kit and run on an ABI3730 (Applied Biosystems) sequencer. The obtained sequence was used in a Blast search against the NCBI Genbank database.

In addition, a microsatellite panel including 28 canid loci was applied. Amplification was conducted in five multiplex PCRs, each using a 10 µl total reaction volume containing 3 µl template DNA, 1x Qiagen multiplex PCR master mix ® (QMP), and 0.1–0.4 µM of each primer (Appendix 1). All reactions used the same PCR programme: initial denaturation at 95 °C for 15 min, 40 amplification cycles of denaturation at 94 °C for 30 sec, annealing at 60 °C for 90 sec, extension at 72 °C for 60 sec, and a final extension step at 60 °C for 30 min. Alleles were run with ABI3730 (Applied Biosystems) and scored in GeneMapper (v. 5.0). The obtained genotype was studied by a factorial correspondence analysis in Genetix v. 4.05 (Belkhir 2004), with reference data of dogs and wolves that included 17 of the 28 microsatellite loci.

Results

We obtained a 200 bp sequence of the COI. The similarity search in GenBank resulted in 100% identity matches (e-value 5 x 10^{-98}) to six COI sequences of golden jackals. These sequences originated from samples collected in Turkey, Israel, and India. The microsatellite genotype was clearly distinct from both wolves and dogs as demonstrated by the factorial correspondence analysis (Figure 1).

The mass of OV.35824 without the skin was at 10.4 kg. Body mass was was estimated at around 11 kg (Marja Isomursu, pers comm.). The skull was slightly larger than typical, but still within the size range of the Eurasian golden jackal (Table 1, Appendix 2).

The pelage of OV.35824 displayed a mix of white and black hairs from the base of the neck to the tail. The hair was long and fluffy. The limbs were covered with short rufous hair. The head, including the ears, was also covered in short rufous hair, with a median stripe of short black hair running from the nose to the base of the neck (Figure 2).

Based on the dental wear, we estimated the age of OV.35824 to be older than 3 years. The animal also exhibited signs of physical injuries sustained during its life. He had lost the third lower right premolar (p3 dex) with the alveolus completely occluded by the time of death. Both ears showed scars on their lateral margins (Figure 2), possibly resulting from fights with conspecifics or with other animals.

The animal's body condition had been good at the time of death, with a fair amount of visceral and subcutaneous fat. The muscles were also well-developed. The stomach was full, and among the identifiable animal remains were the foot skin of a black grouse (*Lyrurus tetrix*) (Figure 3) and feather shafts, likely from the same individual. Additionally, numerous fish bones of varying sizes belonging to whitefish (*Coregonus* indet.) were found.

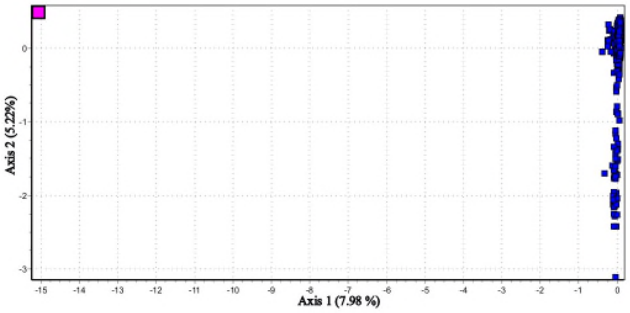

Figure 1. Factorial correspondence analysis of the OV.35824 genotype (pink) with wolves and dogs (blue).

Figure 2. The skin of OV.35824 (golden jackal caught in Sodankylä, Finland). Length of metal ruler 100 cm.

Figure 3. The foot skin of a black grouse (*Lyrurus tetrix*) from the stomach of OV.35824, golden jackal caught in Sodankylä, Finland.

Discussion

In March 2022, a male golden jackal in good body condition was killed near a water reservoir in Sodankylä, Arctic Lapland, Finland. The fact that a

golden jackal thrived in such a northern location in winter is surprising, although the species has recently been expanding its distribution range into areas with seasonal thick snow cover (e.g., Shakarasvili et al. 2020).

While golden jackals are often independent of human-modified environments and may even avoid them (Torreta et al. 2022), anthropogenic food sources play an important role in many parts of their Eurasian range and may be crucial for their survival (Ćirović et al. 2016, Lanszki et al. 2022).

The male golden jackal in Sodankylä, living in the harsh environment of northern Lapland, likely relied at least partly on human-provided food. The fish remains found in his stomach most likely came from leftovers discarded by local fishers, as it is unlikely for a golden jackal catch fish from an ice-covered reservoir. The reservoir is home to two introduced whitefish species, native *Coregonus lavaretus* and non-native *C. peled*. Although it was not possible to identify to which of these two species the stomach contents belonged, no *Coregonus* species has previously been reported as a food item of the golden jackal in the literature (Supporting information in Lanszki et al. 2022).

Table 1. Metric data of golden jackal specimen OV.35824, compared with data from the literature. The data from Srinivas and Jhala (2021) are combined for both sexes; the data from Hatlauf et al. (2021b) are for males only. All measurements are in millimeters (mm).

Measurement	Range	Mean	source
Head and body length	436 – 926	712.5	Srinivas and Jhala 2021
	900	N/A	OV.35824
Tail length	104 – 314	235.4	
	320	N/A	OV.35824
Hind foot length	130	N/A	OV.35824
Ear length	33.0 – 90.0	6.96	
	80.0	N/A	OV.35824
Condylobasal length	129.1 – 166.39	153.8	Hatlauf et al. 2021b
	109.1 – 155.7	143.68	Srinivas and Jhala 2021
	ca. 150	N/A	OV.35824
Palatine length	68.1 – 84.78	78.0	Hatlauf et al. 2021b
	55.54 – 79.86	73.8	
	77.5	N/A	OV.35824
Rostral width over canines	22.56 – 31.24	29.48	Hatlauf et al. 2021b
	17.54 – 29.4	26.27	Srinivas and Jhala 2021
	31.4	N/A	OV.35824
Upper carnassial (p4) length	10.83 – 17.77	16.27	Srinivas and Jhala 2021
	17.0	N/A	OV.35824
Lower carnassial (m1) length	11.05 – 19.36	17.7	Srinivas and Jhala 2021
	20.0	N/A	OV.35824

In addition to fish bones, remains of a black grouse were identified in the stomach. The black grouse is a widespread species across northern Eurasia (BirdLife International 2016). However, like *Coregonus* spp., it has so far not been recorded in the diet of the Eurasian golden jackal (Supporting information in Lanszki et al. 2022).

At present, Finnish Lapland is devoid of large carnivores, including the wolf, due to human-wildlife conflict. Wolves are heavily persecuted in reindeer (*Rangifer tarandus*) management areas (Kojola et al. 2009, Suutarinen and Kojola 2018). In other parts of Finland, wolves are legally protected and better tolerated, which has facilitated the recovery of the species (Mäntyniemi et al. 2022). The presence of wolves or other large carnivores may benefit the golden jackal, as wolves provide them with carcasses (Shakarsvili et al. 2020, Guimarães et al. 2021). On the other hand, golden jackals have also been shown to avoid wolf territories (Krofel et al. 2017, Männil and Ranc 2022, Karamanlidis et al. 2023).

Our genetic analysis confirmed that the Sodankylä animal is a pure golden jackal, with a 100% match with other golden jackals in the GenBank database and a clear distinction from wolves and dogs (*C. familiaris*). The expansion of the golden jackal's range in Europe is a result of the long-distance dispersal of both young males and females, indicating the potential for rapid dispersion (Rutkowski et al. 2015, Lanszki et al. 2018). The northern European populations likely have origins in at least two regions; southeastern Europe and the Caucasus (Rutkowski et al. 2015). However, without population genetic data from other golden jackal populations for comparison, we were not able to determine the geographical origin of the Sodankylä individual.

The golden jackal is listed in the European Union habitat directive Annex V (https://ec.europa.eu/environment/nature/legislation/habitatsdirective/index_en.html). The Convention on Biological Diversity and the Bern Convention on the Conservation of European Wildlife and Natural Habitats also apply to the golden jackal in Europe (Hatlauf et al. 2021a). Finland's legislation aligns with these directives; monitoring is required, and hunting of golden jackals will be prohibited in Finland until the population reaches sustainable numbers. However, as the present case demonstrates, being caught in legal traps intended for game species can still pose a threat to golden jackals on their way to northern Europe.

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Biographical sketch

Suvi Viranta is an anatomist and taxonomist working on both living and fossil carnivores. Her main interest is in canids. Suvi is a member of the IUCN SSC Canid Specialist Group.

Henry Pihlström is a researcher at the University of Helsinki, Finland. He is interested in mammals in general, and especially in carnivores, ungulates, primates, and afrotherians.

Laura Kvist is a geneticist with an interest in wildlife population genetics and genomics, conservation genetics, molecular ecology, phylogeography, and domestication, and in applications using eDNA and aDNA.

Jenni Harmoinen is a large carnivore researcher who has lately focused on population genetic monitoring, and more broadly in conservation genetic/genomic issues. She has also experience in forensics and aDNA.

Jouni Aspi is a conservation geneticist interested in evolutionary processes, particularly in heavily exploited or domesticated animals. He uses present-day and ancient DNA to construct comprehensive evolutionary histories.

Appendix 1. Microsatellite loci used for genotyping.

Multiplex-group	Locus		Primer sequence	PCR product size	Fluorescent label	Reference
Group 1	C20.253	F	AATGGCAGGATTTTCTTTTGC	90-130	PET	Ostrander et al. (1993)
		R	GTTTATCTTTGGACGAATGGATAAGG			
	CPH4	F	ACTGGAGATGAAAACTGAAGATTATA	130-160	FAM	Fredholm and Winterø (1995)
		R	GTTTACAGGGGAAAGCCTCATT			
	CPH8	F	AGGCTCACAATCCCTCTCATA	190-230	VIC	Fredholm and Winterø (1995)
		R	GTTTAGATTTGATACCTCCCTGAGTCC			
Group 2	C2001	F	TCCTCCTCTTCTTTCCATTGG	120-164	PET	Francisco et al. (1996)
		R	GTTTGAACAGAGTTAAGGATAGACACG			
	C2088	F	CCTCTGCCTACATCTCGC	90-150	FAM	Francisco et al. (1996)
		R	GTTTAGGGCATGCATATAAGGAGC			
	CPH2	F	TTCTGTTGTTATCGGCACCA	86-110	NED	Fredholm and Winterø (1995)
		R	GTTTCTTGAGAACAGTGTCCTTCG			
Group 3	C2096	F	CCGTCTAAGAGCCTCCCAG	80-120	VIC	Francisco et al. (1996)
		R	GTTTGACAAGGTTTCCTGGTTCCA			
	C09.173	F	ATCCAGGTCTGGAATACCCC	93-129	PET	Ostrander et al. (1993)
		R	GTTTCCTTTGAATTAGCACTTGGC			
	CXX.225	F	AGCGACTATTATATGCCAGCG	149-171	FAM	Ostrander et al. (1993)
		R	GTTTCTCATTGGTGTAAAGTGGCG			
	CPH12	F	GGCATTACTTGGAGGGAGGAA	185-217	NED	Fredholm and Winterø (1995)
		R	GTTTGATGATTCCTATGCTTCTTTGAG			
Group 4	REN169O18	F	CACCCAACCTGTCTGTTCCT	154-170	NED	ISAG Canine Marker Panel (2019)
		R	GTTTACTGTGTGAGCCAATCCCTT			
	AHT137	F	TACAGAGCTCTTAACTGGGTCC	126-156	VIC	ISAG Canine Marker Panel (2019)
		R	GTTTCCTTGCAAAGTGTCATTGCT			
	AHT121	F	TATTGCGAATGTCACTGCTT	68-118	FAM	ISAG Canine Marker Panel (2019)
		R	GTTTATAGATACACTCTCTCTCCG			
Group 5	CXX279	F	TGCTCAATGAAATAAGCCAGG	109-133	NED	ISAG Canine Marker Panel (2019)
	(C22.279)	R	GTTTGGCGACCTTCATTCTCTGAC			
	INRA21	F	ATGTAGTTGAGATTTCTCCTACGG	87-111	PET	ISAG Canine Marker Panel (2019)
		R	GTTTTTAATGGCTGATTTATTTGGTGG			
	AHTk211	F	TTAGCAGCCGAGAAATACGC	83-101	VIC	ISAG Canine Marker Panel (2019)
		R	GTTTATTCGCCCGACTTTGGCA			
Group 6	AHTh260	F	CGCTATACCCACACCAGGAC	200-300	FAM	ISAG Canine Marker Panel (2019)
		R	CCACAGAGGAAGGGATGC			
	PEZ1	F	GGCTGTCACTTTTCCCTTTC	80-146	PET	Halverson et al. (1999)
		R	CACCACAATCTCTCTCATAAATAC			
	AHTH130	F	GTTTCTCTCCCTTCGGGTTC	111-141	FAM	ISAG Canine Marker Panel (2019)
		R	GTTTGACGTGTGTTCACGCCAG			
Group 7	AHT111	F	CCATACCCAGGATAGTTGAT	60-105	FAM	ISAG Canine Marker Panel (2019)
		R	CCATCCTGAGGCTAGCTGTG			
	PEZ3	F	CACTTCTCATACCCAGACTC	90-160	NED	Halverson et al. (1999)
		R	CAATATGTCAACTATACTTC			
	PEZ8	F	TATCGACTTTATCACTGTGG	180-270	VIC	Halverson et al. (1999)
		R	ATGGAGCCTCATGTCTCATC			
	FH2054	F	GCCTTATTCATTGCAGTTAGGG	105-195	FAM	Francisco et al. (1996)
		R	ATGCTGAGTTTTGAACTTTCCC			
	REN162C04	F	TTCCCTTTGCTTTAGTAGGTTTTG	175-230	NED	ISAG Canine Marker Panel (2019)
		R	TGGCTGTATTCTTTGGCACA			
Group 8	C08.410	F	GAGGAAAACCAAGTGATTTTGG	80-140	VIC	Breen et al. (2001)
		R	ACCTGCAAGTGACCCTCTCT			
	AHTh171	F	CTCACCAGGCATAGACACTCAG	215-239	PET	ISAG Canine Marker Panel (2019)
		R	CTCATTTGTTCACGCACCC			
	REN247M23	F	TGGTAACACCAAGGCTTTCC	258-282	NED	ISAG Canine Marker Panel (2019)
		R	TGTCTTTTCCATGGTGGTGA			

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Appendix 2. Comparisons of craniodental measurements.