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## **EDITORIAL**

## Changing of the guard at the Caprinae News

Dear CSG members,

it's hard to believe that so many years have already passed since Sandro Lovari and Juan Herrero asked me, in 2018, to take over the reins of the editorial board of the Caprinae News, the official newsletter of the IUCN Caprinae Specialist Group. I accepted this challenge with enthusiasm, convinced that the newsletter could be an excellent opportunity to bring together the community of researchers, conservationists and practitioners working on mountain ungulates, and to preserve valuable information, including information that would have

had little chance of being published in peer-reviewed journals, but that it is nonetheless valuable and worth reporting. To achieve this, it was necessary to work on several fronts: on the one hand, to redesign the Bulletin's graphics to make them more appealing, while keeping an eye on the past. On the other hand, it was necessary to work effectively with a group that could support the entire editorial process: Steve Ross, Gerhard Damm, Sandro Lovari, Juan Herrero, Yash Veer Bhatnagar, in different capacities participated in this adventure, and each of them contributed to its success! I especially want to thank Steve Ross for all his help. After following this challenge for 8 years, I believe it is time to pass the baton, to renew the enthusiasm needed to continue on the path marked during these years. I am therefore delighted that Steve will be taking over the Bulletin himself, and I wish him and the entire Editorial Board every success!

Luca Corlatti

IUCN SSC Caprinae Specialist Group

Thanks to work and leadership of Luca, Caprinae News is in a great place. I'm excited to build on the work we've done and explore new ways to expand our reach. The Caprinae newsletter fulfills a special function in our community. As researchers, we strive to publish in peer-reviewed journals, but many conservation insights, observations, and experiences go unpublished. These may include novel behaviors, conservation or restoration actions, lesserknown species information, red listing insights and more. The Caprinae newsletter is a place to share this information and get exposure, both with and beyond our community.

The editorial board is here to offer support, through feedback, editing, and language assistance if needed. We hope this support encourages more contributions from all our members, fostering a rich exchange of knowledge. I've personally learned a lot from reviewing previous submissions and look forward to continuing this journey. If you have any ideas, observations, or contributions to share, we'd love to hear from you.

## **HEADLINE NEWS**

## Asir J.T. Johnsingh Obituary

Dr. Asir Jawahar Thomas Johnsingh who pioneered wildlife research in India and inspired generations of wildlife professionals expired on 07 June 2024 after a brief illness.



Figure 1: Dr. Asir Jawahar Thomas Johnsingh

Born in 1944 in Nanguneri, a village close to the Western Ghats in the southern tip of India, Dr. Johnsingh inherited his passion for wildlife from his father and became a good naturalist. After his schooling, he did his Bachelors in Zoology from St. Xaviers College and Master's degree in Zoology from Madras Christian College. He worked as a lecturer at Ayya Nadar Janaki Ammal College in Sivakasi and began his field observations on wildlife in the Western Ghats. He conducted the first-ever study on the dhole or Indian wild dog in Bandipur for his Ph.D. and later received a post-doctoral fellowship from the Smithsonian Institute, USA.

Since then, he conducted various research projects on large mammals such as the elephant, tiger, lion, bears, and ungulates including mountain ungulates such as Nilgiri tahr, goral and ibex.

He had served in the Bombay Natural History Society briefly before joining the Wildlife Institute of India in 1986. He retired as Dean, Faculty of Wildlife Sciences at the Wildlife Institute of India in October 2005. Later, he served in advisory positions at WWF-India, Wildlife Trust of India and Nature Conservation Foundation, Mysuru.

At a very young age, Dr. Johnsingh got inspired by Jim Corbett's adventure and narration about wildlife of the foot hills of the Himalaya while hunting man-eating tigers and leopards. After joining WII, Dr. Johnsingh explored the shiwalik hills in the neighbouring Rajaji National Park and discovered the presence of goral in the area. He began his research on goral and continued that for many years and had shared some of his research findings during the 1st and 2nd WCMUs. Later, he was supervisor of projects in the Trans Himalaya and Greater Himalaya in which Dr. Yash Veer Bhatnagar and I worked and obtained our Ph.Ds.

He has truly been a doyen of modern wildlife biology and conservation in India, and equally wellknown and highly respected for his work globally. With over 70 scientific papers and over 80 popular articles on wildlife conservation, his legacy is huge. He was awarded the Carl Zeiss Wildlife Conservation Award 2004 for lifetime service to Indian wildlife, 2004 Distinguished Service Award from the Society for Conservation Biology, and the ABN AMRO Sanctuary Lifetime Wildlife Service Award in 2005. Recently, he received the Lifetime Achievement Award from the GTI Council.

His passing away leaves a void and marks the end of an era of deep-rooted naturalists, taking a grass-roots field-based approach to enable practical conservation across India and beyond. He was a stalwart who influenced generations of wildlife managers, field biologists, conservationists, and policymakers. Many of the accomplished wildlifers in the country today have been trained first-hand by Dr. Johnsingh (including me) and they imbibed his philosophies and deep-rooted commitment towards protecting a range of threatened species spanning across landscapes from the heights of the Himalaya to the coastal plains of his hometown Kanyakumari. His students say "He brings the jungle into the classroom and makes a classroom out of the jungle".

What made him a unique personality was his love for the wilderness and even at the age of 79 he was an avid trekker, and possibly yearned for being in the outdoors some more even when physically his body was failing him.

His family wrote "We can't hear his voice anymore but we can hear him in the chirp of every bird, the roar of every tiger and the trumpet of every elephant".

Sambandam Sathyakumar<sup>1\*</sup>

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## IV Rupicapra Symposium

#### Haritakis Papaioannou<sup>1,2\*</sup>, Luca Corlatti<sup>3</sup>

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The University of Ioannina and the Balkan Chamois Society are pleased to invite you to the IV International *Rupicapra* Symposium, to be held on September 25-27, 2025 in Konitsa, North-West Greece, close to the largest chamois population in the country. The aim of the Symposium is to promote the exchange of ideas among chamois experts from around the world, to encourage the sharing of the latest knowledge on different chamois species and subspecies, and to promote the research, conservation and sustainable management of chamois.



Figure 1: Balkan chamois. Photo Haritakis Papaioannou.

The symposium is open to researchers, experts, managers and anyone interested in the species, and we aim to bridge the gap between science and practice. The two-day scientific program will cover topics related to genetics and systematics, physiology and disease, behavior and ecology, and management and conservation.

The conference encourages the participation of early career researchers and aims for inclusive collaboration with good gender balance and broad geographical representation.

The symposium is held with the endorsement of the IUCN SSC Caprinae Specialist Group.

The meeting will be held at the Event Hall of the Municipality of Konitsa. For more information, please follow us on our Twitter and Facebook pages while we set up the symposium website. We look forward to seeing you in Konitsa!

#### https://www.facebook.com/RupicapraSymp/ https://x.com/RupicapraSymp

#### The organizing committee:

Haritakis Papaioannou, Luca Corlatti, Laura Iacolina, Vassiliki Kati, Konstantinos Papakostas, Toni Safner, Nikica Šprem

## **CONSERVATION AND MANAGEMENT**

# New information on Bukhara urial *Ovis vignei* bochariensis in Baljuvon, Tajikistan

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## Introduction

The Bukhara urial Ovis vignei bochariensis is a subspecies of the urial sheep native to Afghanistan, Tajikistan, and Uzbekistan. Over the past 35 years, it has faced significant population decline throughout its range due to poaching and competition with livestock. As a result, it is currently classified as Endangered on the IUCN Red List (Michel & Ghoddousi 2020). In Tajikistan, fewer than 500 individuals may survive in isolated populations (Michel & Ghoddousi 2020). The Vakhsh mountain range in central-south Tajikistan was known before World War II as one of main urial strongholds (Village hunters, pers. comm.). However, poaching and livestock overgrazing of preferred habitat has reduced their numbers (Kholmatov et al. 2024), and in the early 2010's urials in the region were considered rare (Michel 2010). In 2017, Oxus Holding, a Tajik limited liability company, leased for 10 years 'Miron', a concession covering approximately 250 km<sup>2</sup> of Vakhsh mountain range in Baljuvon district, with the primary goal to restore the Bukhara urial population for sustainable trophy hunting. The Miron concession has been implementing measures to control poaching and livestock numbers and provide jobs to local community members (e.g., cook, rangers, household keeping, guiding) to offset the reduced landuse by communities. In 2020 the national NGO Taiikistan Nature Foundation (TNF) engaged in a collaboration with Miron to pilot private-public natural resource management and support training of rangers in standard operational procedures, in wildlife monitoring methodology, and the development of a five-year management plan (Miron 2024). The paper presents the results of five urial population monitoring counts conducted by Miron rangers and TNF ecologists. The 2020-2024 surveys aimed to assess urial population trends as an indication of the effectiveness of implemented conservation measures. It is the first monitoring effort of this scale and duration carried out for the Bukhara urial across its range.

## Methods

Counts

Counts took two to four days and were conducted between April 7-19 by two to four teams of 3 - 5 surveyors (Table 1). and so we performed a non-parametric Kruskal-Wallis test to identify significant differences in the RAI values across years. Significance between specific years was set at  $\alpha$ =0.05 and tested with Wilcoxon rank-sum test.

Survey sequence	0	1	2	3	4
Year	2020	2021	2022	2023	2024
Day.month	10.04-12.04	10.04-12.04	12.04-16.04	7.04-8.04	17.04-19.04
Number of days	3	3	5	2	3
Number of teams	2	4	4	5	4
Number of surveyors	11	15	12	10	12
Weather/visibility Average		Good	Average	Poor	Average to
					Poor

Table 1. Information on urial counts carried out in Miron, Baljuvon, Tajikistan (2020-2024).

Each team included a primary surveyor who took notes and recorded GPS locations, and several observers using10x42 binoculars and one 20-60x spotting scope to scan for urial. Teams conducted surveys along the same pre-defined routes in the concession during the five counts, from dawn till dusk (6:00am to 6:00pm). All observations were made from points with good visibility, following the recommendations and methodology used in previous mountain ungulate surveys in Tajikistan (Saidov et al. 2011; Michel et al. 2015; Kholmatov et al. 2024). Each record included the date/time, GPS coordinates of the surveyors, elevation, estimated distance, azimuth, vertical angle to the observed urials, slope, steepness, aspect, the substrate of the habitat, behavior of animals, age, and sex composition. Before each survey, TNF biologists provided a refresher training on urial age and sex identification to the rangers and in each team, one experienced ranger was included to assist with these determinations. In cases where two teams were surveying adjacent areas, they used radio communication to avoid counting the same animals. Additionally, after reuniting, the teams discussed their observations to rule out duplicate records of animals based on location, time, group size, sex, and age composition.

## Data analysis

Although survey routes and periods were consistent between counts, it was not possible to achieve consistency in detection effort because of variable levels of engagement of rangers (in numbers and experience). Therefore, to avoid the effect of this methodological bias we used Relative Abundance Indices (RAIs) to assess the population trend rather than population size. To compute the RAIs the total counts per observation point for every surveyed year were divided by the overall mean of counted urial per observation point among all surveyed years and multiplied by 100. A RAI >100 indicates that the urial population was above the average level, and an RAI <100 indicates it was below average. The small sample sizes obtained did not always meet the assumption of a normal distribution We produced a kernel density map using the Kernel Density Estimation tool from the Density Analysis plugin (Hamilton 2024) in QGIS (QGIS Development Team, 2024, 3.34.0-Prizren) to examine the spatial distribution of detected urial groups within the surveyed area (Map 1). The pixel dimensions were set to 0.01 and the kernel radius was set to 2 km to focus on the spatial patterns within the concession area. A continuous mode and a discrete interpolation were applied to enhance the visualization of the distribution.

## Results

The total number of urial tallied during each count varied between 179 and 353 and the median group size varied between 5 and 9.5 (Table 2). The largest groups varied between 21 and 45 individuals in 2022 and 2020, respectively. When pulling the data from the five surveys the average male-to-female ratio was 0.96 ( $\pm$  0.179), and the average female to lambs and yearlings (pulled together) ratio was 1.46 ( $\pm$  0.135).

The RÅI in 2020 was 121% and in 2021 129%, then it declined to 79% in 2022, and increased again to 81% in 2023 and 88% in 2024 (Table 2). However, the changes between all years were non-significant (p=0.4). The notable decline of RAI from 2021 to 2022 was also not statistically significant.

We excluded a few observations located farther from the Miron concession from the calculation for the kernel density map, resulting in 146 recorded urial group observations. Most urial observations were taken in the core of Miron concession, along the central mountain ridge from south to north (Fig. 1). The range stretches along the left bank of the Vakhsh river, where over 50% of all recorded observations were made during the morning hours. We mainly observed urial walking (33% of the groups) or feeding (30%). Observed urial used habitats including forested areas (23%), scattered high shrubs (24%), and barren areas (22%) usually on medium slopes with inclines of 30° - 40° noted in 33% of observations.

Survey Year	Total tallied	Lambs	Yearlings	Adult females	Subadult males	Adult males	Unidentified	Mean group size	Median group size	RAI
2020	197	2	33	54	15	75	18	12.3 ± 2.39	9.5	121.08
2021	335	59	39	130	25	66	16	9.85 ± 1.45	7	129.65
2022	353	0	91	121	36	63	42	7.06 ± 0.70	6	79.46
2023	179	17	27	51	10	32	42	11.2 ± 1.69	9	81.35
2024	258	24	28	101	16	63	26	6.79 ± 0.82	5	88.46
Overall	1322	102	218	457	102	299	144	8.58 ± 0.55	7	



Figure 1: Kernel density distribution of urial in Miron concession, based on the results of five surveys carried out between 2020-2024, Baljuvon, Tajikistan.

#### Discussion

The urial population of Baljuvon remained stable between 2020 to 2024, a likely result of better protection, control of livestock numbers and improved general land management. The main objective of Oxus Holding is to restore the population of urial and implement sustainable trophy hunting. Notably two male urial were hunted for trophies between 2020 – 2023 without discernible effects on the population trend. Count results revealed high variability between years with a particularly noticeable decline in the RAIs from 2021 to 2022. The origin of these fluctuations could result from random unknown environmental factors, and/or sampling effort which could both influence population dynamics and/or detection probability.

We encountered several difficulties during the surveys that affected the quality of results, among them the very rugged and remote terrain did not allow teams to survey the different areas with the same exhaustivity. Also, despite dedicated efforts the risk of double counting the same animals by several teams (and overestimating counts) remained because surveys extended over several days and the urial is a very mobile species. The weather conditions also affected results as the visibility was sometimes limited by dense dust and fog, or heavy rains which hampered surveys that had to be either shortened or rescheduled. For example, in 2023, due to constant fog and dust storms, there was poor visibility, which made it impossible for surveyors to observe animals at distances greater than 500 meters. Similarly, in 2024, due to the fear that surveyors would get caught in the rain, they were in a hurry and spent less time at each viewpoint, which may have affected their ability to detect animals or to count all individuals of detected animal groups. Survey quality was also affected by the variable level of experience of rangers. A lack of experience was at times noticeable in the determination of the sex and age of observed animals.

The observed patterns of urial distribution in Miron concession can be compared to findings by Sokolov (1959) who described habitat preferences among urial in the Sarsarak mountains and Vakhsh Ridge and reported that urial migrated between upper mountain areas with rich, diverse vegetation near springs in summer and lower elevations with semi-desert vegetation in winter while some remained at mid-elevations if there was no presence of domestic sheep. Our surveys, conducted during spring in Miron, confirmed that in the absence of livestock urial use medium slopes with rich vegetation at mid elevations.



Figure 2: The core habitat of urial in Miron concession in the Vakhsh mountain range, Baljuvon, Tajikistan. Photo: TNF, 2020.

#### Conclusion

Although the study did not allow accurate estimates of urial population size in Miron, we counted an average of 265 individuals per survey, which to our knowledge makes it the largest free-ranging population of Bukhara urials recorded to date across its entire range. Further research and better standardization of methods are essential to ensure more effective monitoring of this population and better long-term management (Moheb *et al.* 2023). Oxus Holding has committed to a positive management path in Miron by implementing effective threat mitigation measures, developing a data-informed management plan, and including monitoring efforts (Miron 2024). However, many challenges remain to urial conservation including frequent staff turnover, associated capacity deficits, continued low management capacity at the local level, and the difficult balance between improving services and access, and maintaining the wilderness and pristine environment enjoyed by tourists and hunters.

#### Acknowledgments

This project was implemented by Tajikistan Nature Foundation (TNF) and the Wildlife Conservation Society (WCS) thanks to grants awarded by the Critical Ecosystem Partnership Fund (CEPF) which is a joint initiative of l'Agence Française de Development, Conservation International, the European Union, the Global Environment Facility, the Government of Japan, and the World Bank. We extend our gratitude to Oxus Holding who actively engaged in the project and Miron concession staff for their efforts and assistance. We would like to acknowledge the support of the Committee for Environmental Protection under the Government of the Republic of Tajikistan and the National Academy of Sciences of Tajikistan which was instrumental in involving field experts during the surveys. Finally, we thank all conservationists who supported the project from its inception to its completion, and particularly Dan Rothberg, CEPF.

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## RESEARCH

Genetic origin of four Alpine ibex *Capra ibex* units recently appeared in Écrins National Park, France

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#### Introduction

Analysing and monitoring population genetics has become a fundamental tool for the effective conservation and management of wild species (Frankham et al. 2014). The genetic structure of populations depends mainly on the ecological characteristics of the species and on the environmental changes that have occurred during its evolution. However, part of what we observe today is also the result of the recent history of species, their movements, and their interaction with human activities. Although common guidelines are still lacking (Frankham et al. 2014), the maintenance or restoration of genetic variation is widely accepted as an essential tool for long-term species conservation. Knowing the origin and genetic characteristics of different populations is therefore a pivotal tool in improving the genetic conservation of wildlife.

The Alpine ibex Capra ibex is a wild ungulate endemic to the European Alps. In the Middle Ages, the species was widespread throughout the Alpine region, but intensive hunting following the spread of firearms brought the species to the brink of extinction (Grodinsky & Stüwe 1987). The first protection measures date back to 1821, when a ban on hunting ibex was enacted in Italy. The number of individuals began to increase again only following the declaration of the area surrounding Gran Paradiso, where few individuals were left, as a royal hunting reserve by Vittorio Emanuele II in 1856. Repopulation in the Alps, initially through captive breeding and then through translocations, began in the first half of the 19th century and left an imprint on the genetic makeup of present-day populations (Biebach & Keller 2009).

Thanks to reintroduction efforts, Alpine ibex are again present throughout the Alpine region. To date (2008-2017) there are an estimated 180 ibex populations in the Alps, for a total of about 52,000 individuals (Brambilla *et al.* 2020). However, Alpine ibex distribution is still fragmented, and not all suitable areas are occupied. Ibex can be found in France (about 9,450 individuals), Italy (16,400 individuals), Switzerland (18,000 individuals), Germany (about 500 individuals), Austria (about 7,400 individuals), and Slovenia (about 300 individuals).

In Écrins National Park (France, Fig.1) there are three main populations of Alpine ibex, namely those of Oisans, Champsaur, and Cerces, that were founded between 1959 and 1994 with individuals from Haute Maurienne (France), Peisey-Champagny (France), and Pleureur (Switzerland), respectively. Preliminary analyses (unpublished data) carried out by the authors in 2017 (EU Interreg Alcotra LEMED-IBEX Project, hereafter referred to as LEMED-IBEX project) revealed some level of genetic differentiation among the populations.

Recently, following the expansion of Alpine ibex into suitable habitat, the establishment of four new isolated small ibex colonies (hereafter referred to as units, without implying any specific social relationship between the individuals), composed by few (≈10-15) individuals each, were observed in Écrins National Park. Their geographic location is placed between or adjacent to the three older populations (Fig. 1). The aim of this study was to identify, through non-invasive DNA sampling, the population of origin of the individuals composing the new units recently observed in the Écrins National Park.

#### **Data collection**

#### Sampling

Sample collection from individuals belonging to the newly identified units was carried out by the Écrins National Park staff during late summer 2023 and 2024. Sample collection was performed by collecting faecal samples as fresh as possible and rubbing them with cotton swabs (Ramón-Laca et al. 2015). Swabs were then placed in Longmire buffer and stored at room temperature. In total, N=17 samples were collected from the four new Alpine ibex units (Fig.1): Tête de Gaulent (sector Vallouise, 3 samples); Villar d'Arène (sector Briançonnais, 4 samples); Réallon (sector Embrunais, 3 samples); Vallon de la Selle (sector Oisans, 7 samples). An additional 51 blood samples were previously collected from the three populations identified in the Écrins National Park during the Alcotra LEMED-IBEX Project in 2017 (19 samples from Champsaur, 20 from Cerces and 12 from Oisans population) were included as references in the sample set.



Figure 1. Representation of the genetic clusters of Alpine ibex populations and localization of the samples collected for this study in the Écrins National Park. The four units analysed are (clockwise from top left): Vallon de la Selle (sector Oisans, PNE\_OI, N=7 samples), Villar d'Arène (sector Briançonnais, PNE\_BR, N= 4 samples), Tête de Gaulent (sector Vallouise, PNE\_VA, N=3 samples), Réallon (sector Embrunais, PNE\_EM, N=3 samples).

#### DNA extraction

DNA extraction from the 17 faecal swabs was carried out using the DNeasy QIAgen kit tissue protocol modified as suggested by Ramón-Laca et al. (2015) to increase yield of endogenous DNA from faecal samples preserved in Longmire buffer. Final DNA elution was done in 100ul buffer AE and 100ul H<sub>2</sub>0. DNA extraction from the 51 blood samples was carried out in 2017 as part of the LEMED-IBEX Project using the DNeasy QIAgen kit blood protocol.

#### Genetic data generation

All samples were genotyped using a microfluidics-based amplicon sequencing assay (Juno system, Fluidigm) designed by Kessler *et al.* (2022). The assay was designed to cover 1'265 amplicons and includes 744 neutral SNPs markers that were used for this study.

Sample preparation and PCR amplification was carried out at the GDC (Genetic Diversity Centre) and performed according to the manufacturer's protocol. Input DNA concentration was normalized to 50 ng/µl or kept lower when this concentration could not be reached. Libraries were sequenced by the FGCZ (Functional Genomic Centre Zurich) on a NextSeq 500 system (Illumina, San Diego Ca, USA) for the samples analysed in 2023 and on an AVITI platform (Element Biosciences, San Diego, Ca. USA) for the samples analysed in 2024. Amplicon sequencing was repeated at least twice for each faecal sample to increase the number of genotypes. For samples analysed in 2023 that had low genotyping rate, Amplicon sequencing was repeated in 2024. Each sample was finally analysed up to 5 times. Reads of the same sample were then pooled based on sample ID to increase genotyping rate.

The sequenced reads were demultiplexed with default settings using Bcl2fastq v2.19 (Illumina®, 2019) and resulting fastq files of different repeats of the same sample were catenated. The sequences were trimmed with Trimmomatic v0.36. Forward and reverse reads were merged with Flash v1.2.11 and mapped to the domestic goat reference genome ARS1 using bwa mem 0.7.13.

We called SNPs using haplotypecaller, combinegvcfs and genotypegvcfs from gatk version 4.0.1 (McKenna et al., 2010; Van der Auwera et al., 2013). Variant sites were excluded if matching any of the following conditions: QD < 5, MQ < 20, -3 >ReadPosRankSum > 3, -3 > MQRankSum > 3, -3 >BaseQRankSum > 3. Vcftools (Danecek et al., 2011) was used to convert to vcf format, set the minimal genotype quality to 20 (minGQ=20).

Finally, two datasets were produced. We removed individuals with missingness rate >50% and only kept bi-allelic SNPs with a genotype rate of at least 90% to produce the main dataset (dataset 1). However, as less than 50% of the samples of the new units were retained in the main dataset, we also created a second datasets with less stringent filter (dataset 2, mid-stringent filtering: missing rate < 20%, genotyping rate > 90%).

### Data analysis

#### Principal Component Analysis

An analysis of the principal components (PCA) was carried out to visualise how the individuals of the newly established units clustered with the putative origin populations within R version 4.4.1 (R Core Team, 2022). PCAs were carried out on the two different datasets described that included different number of samples retained after filtering. In addition to the samples collected in the new units, the PCAs included the reference samples from the three putative origin populations established in the Écrins National Park (see above for details about reference samples). As the Cerces population was genetically well differentiated from both the other two reference populations as well as from individuals of the newly established units, to better visualize the clustering between individuals of the new units and reference populations, PCAs were repeated including only Champsaur and Oisans as putative origin populations.

#### Population structure analysis

A structure analysis was run to assign samples of the individuals of the newly established ibex units to the putative origin populations. Structure analysis was carried out on the two datasets using the software Structure 2.3.4 (Pritchard et al., 2002) with the following parameters: Running length: Length of Burnin Period: 10,000; Number of MCMC reps after Burnin: 100,000; Ancestry model: Admixture model; infer Alpha (initial value: 1.0, max value: 10.0); Frequency model: Allele frequencies correlated among populations (assume different values of Fst for different Subpopulations).

K=3 was chosen to maximise the difference between the three putative origin populations. For each analysis, we run 10 repetitions and averaged them with Clumpak: Cluster Markov Packager Across K (Kopelman *et al.* 2015).

Consistent with the earlier description, as Cerces population was shown to be genetically very different from the other two source populations as well as from the individuals of the newly established units, we repeated structure analysis removing the samples collected in the Cerces population and setting K=2.

#### Results

After filtering for minimal genotype quality and genotyping rate, dataset 1 comprised 56 samples genotyped at 487 neutral loci (including 6 samples out of the 17 collected in the new units of interest for this research). Dataset 2 comprised 62 samples (including 11/17 samples from the new units) genotyped at 284 loci.



Figure 2. Visualization of the Principal Component Analysis (PCA) based on dataset 1. a) shows the PCA on the full dataset including reference samples from Cerces. b) shows the PCA run on the same dataset but excluding samples from the Cerces population. Colours represent the different putative origin populations and the sampled new units as shown in the legend. c) shows the PCA run on dataset 2 (without reference individuals from Cerces).

#### Principal Component Analysis

Results of the PCA analysis performed on dataset 1 are presented in Figure 2a (PC1, 21.4% variance explained). Figure 2b shows the results of the PCA analysis performed on the same dataset excluding individuals from Cerces. Individuals from the new ibex units included in the dataset seem to cluster with individuals of Champsaur, which suggests that the new units were established by individuals migrating from the Champsaur population. Particularly, this seems quite clear for two samples collected in Réallon (Embrunais sector) and two of the samples from Villar d'Arène (Briançonnais sector). In addition, the third sample collected in Villar d'Arène and the sample from Vallon de la Selle (Oisans sector) are included in the same cluster despite the seemingly higher overlap with the Oisans population. The additional PCA analysis on dataset 2 (Fig. 2c) seems to confirm the results obtained with the more stringently filtered dataset. Our analysis indicates that there is a greater overlap of all samples collected in the new ibex units with Champsaur than with Oisans even if a sample from Villar d'Arène and the sample from Vallon de la Selle (Oisans sector) also overlap with the Oisans cluster. However, the results obtained with dataset 2 must be interpreted with caution due to the higher number of missing genotypes obtained with less stringent filtering for genotyping rate.

## Population structure

Structure analysis run on dataset 1 supports the result of the PCA confirming that the population of Cerces is genetically distinct from both the other two previously known populations (Oisans and Champsaur) as well as from the individuals from the newly established units (Fig. 3).

population. This seems to hold also for dataset 2 (Fig. 4b) which included more samples from all four newly formed units: Villar d'Arène (Briançonnais sector, 4 samples), Rèallon (Embrunais sector, 2 samples), Vallon de la Selle (Oisans sector, 2 sample), Tête de Gaulent (Vallouise sector, 3 samples). The structure analysis repeated on dataset 2 (Fig.4b), with less stringent filtering and more individuals but fewer SNPs, confirms the results of the first analysis. Furthermore, it suggests that the individuals sampled in Tête de Gaulent (Vallouise sector) also belong to the Champsaur cluster, as already suggested by the PCA.

However, it should be noted that individuals from Champsaur and Oisans are also very similar to each other and show a partial overlap due to their founding history (or perhaps also due to gene flow between the two populations, but no data are available to test this hypothesis). Therefore, even if this scenario is not very likely, it is not possible to completely exclude the possibility that some of the individuals from the new units (namely PNE\_OI\_06, collected in Vallon de la Selle) may also come from the current Oisans population.

## **Discussion and perspectives**

Of the 17 samples collected in the newly established ibex units, 6 samples were successfully genotyped at 487 SNPs (with stringent filtering) and 11 samples were genotyped at 284 SNPs (with midstringent filtering). PCA analysis support the hypothesis that the 6 individuals retained in dataset 1, sampled in Villar d'Arène (Briançonnais), Vallon de la Selle (Oisans) and Réallon (Embrunais), genetically originate from the Champsaur population, suggesting that the new ibex units were founded by individuals originating from this population.



Figure 3. Visualization of the averaged Structure analysis for k=3 on dataset 1. New units include the 6 individuals retained in dataset 1. Sectors abbreviations: BR: Briançonnais; EM: Embrunais, OI: Oisans.

The alternative structure analysis run on dataset 1 without Cerces and with K=2 (Fig.4a) also shows similar results to the PCA, i.e., that the 6 individuals from the newly established units retained in dataset 1 and collected in Villar d'Arène (Briançonnais sector, 3 samples), Réallon (Embrunais sector, 2 samples) and Vallon de la Selle (Oisans sector, 1 sample) are more similar to individuals of the Champsaur population than to those of the Oisans The same seems true for the other individuals, including those sampled in Tête de Gaulent (Vallouise), although the lower quality of the samples requires interpreting this result with caution.

The genetic similarity and partial overlap between Champsaur and Oisans, evident in previous genetic and structure analysis (Alcotra LEMED-IBEX), does not rule out the possibility that some of them may originate from Oisans.



Figure 4. Visualization of the averaged Structure analysis for k=2. a) results obtained with dataset 1. New units represent the 6 individuals retained in dataset 1. b) results obtained with dataset 2. New units represent the 11 individuals retained in dataset 2. Sectors abbreviations in sample names: BR: Briançonnais; EM: Embrunais, OI: Oisans; VA: Vallouise.

Indeed, microsatellite analyses and observations of animal movements with GPS collars carried out in the LEMED-IBEX project did not detect nor exclude gene flow between the three main populations. In particular, the Champsaur and Oisans populations were found to be genetically very similar. Despite having been founded by individuals from different sources (Haute Maurienne and Peisey-Champagny), the genetic similarity of the source populations themselves made it difficult to clearly distinguish whether the observed similarities in the current populations were due to the founding history or to gene flow. However, this scenario is less likely than that presented above, i.e., that the new units originated from Champsaur.

Our sample methods, where we collected fresh faecal samples using cotton swabs preserved in Longmire buffer was confirmed as a successful method, suitable for non-invasive genomic analysis for population structure in areas where other sampling methods are not possible. However, the sampling and extraction method could be improved by testing different options and developing a specific protocol for the target species. Finally, the relatively low genotyping success (6 samples out of 17 discarded after mid-stringent filtering), shows that a larger number of samples should be collected to ensure the target number of genotyped individuals is reached when using such non-invasive sampling techniques.

#### Acknowledgements

We are grateful to all the staff of the Ecrins National Park for their contribution to this study. Special thanks go to those who took part in collecting the samples, whose involvement was essential to the completion of this work. Their scientific curiosity and their involvement during the sample collection phases in the field made this study possible and are therefore at the origin of the results presented here. We also acknowledge Daniela Grob from the University of Zurich for her help in DNA extraction.

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## **SPOTLIGHTS**

### Camera-trap record of Himalayan Serow *Capricornis sumatraensis thar* in Himachal Pradesh, India.

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The Himalayan serow *Capricornis sumatraensis thar* is a sub-species of mainland serow *Capricornis sumatraensis* with a distribution restricted to the Himalayan range (Mori *et al.* 2019; Phan *et al.*2020). It is known to occur at altitudes between 300m and 3,000 m asl in all the Himalayan states (Green 1987; Menon 2014; Mishra & Johnsingh 2015; Phan *et al.* 2020). Based upon population size, distribution and habitat declines the Mainland serow is currently listed as Vulnerable by the IUCN (Phan et al. 2020). Himalayan serow are considered a Schedule-I species according to the Indian Wildlife Protection Act, 1972 (Amendenment 2022). This article reports a new camera-trap record of Himalayan Serow in Himachal Pradesh, India.

During our biodiversity survey (February, 2023 to March, 2023) in Gobind Sagar Lake and surrounding hills in Bilaspur, Himachal Pradesh (Fig.1). We placed 10 Cuddeback (20MP Long Range IR) camera traps were deployed in the study area to detect mammal presence. Despite a short 5 trap night assessment we captured 3 photographs of a single individual Himalayan serow within a pine *Pinus sp.* forest patch close to mandwa bridge (31.36579 076.61283; 656 m asl) near Jhandhuta. The location was very close to ghat road and nearby villages (Fig. 2).

According to Phan *et al.* (2020) the Himalayan serow of Himachal Pradesh are facing serious population decline due to disease transmission from domestic livestock, especially sheep. Detailed study is needed to understand the current distribution and status of Himalayan serow and key recovery steps for the species in Himachal Pradesh and adjacent states in the Himalayas.



Figure 1: Sighting location of Himalayan Serow (yellow asterisk) in Bilaspur, Himachal Pradesh.



Figure 2: Himalayan Serow in Bilaspur, Himachal Pradesh.

#### Acknowledgements

The study was financially supported by the Ministry of Environment, Forest and Climate Change under the scheme National Mission on Himalayan Studies. The authors are thankful to Ankush of Hamirpur Wildlife Division.

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# Research and monitoring framework for Caprinae

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Wildlife professionals put considerable effort into monitoring Caprinae populations, especially those threatened with extinction. But sometimes our monitoring programs aren't SMART - Specific, Measurable, Achievable, Results oriented, or Time-fixed. This outcome risks wasting resources and producing unhelpful data. Using a SMART framework when monitoring can help projects remain sustainable and produce results that directly inform Caprinae research and management activities.

Data describing the population sizes and demographics of many Caprinae populations remain unknown (Shackleton 1997). Resolving these gaps in our understanding is a priority and recent development of inexpensive, simple and logistically tractable sampling techniques show promise in addressing them (e.g., Corlatti *et al.* 2020; Harris *et al.* 2020; Pal *et al.* 2021; Harris *et al.* 2024). Yet before any monitoring starts, it is important to clearly identify the survey intent. Namely the type of information required, along with justification and description for how data will be used.

Sometimes our enthusiasm to start a new project overshadows the time spent critically thinking about the information being collected. Stepping back and taking a holistic perspective can better ensure that the data produced meets project purposes. In this regard, we share a strategy for building more informative and fiscally sustainable projects, intended to help our Caprinae community improve data collection for research and management.

Framing research, monitoring and management needs as SMART objectives forms a productive way to start (USFWS 2013). The acronym stands for Specific, Measurable, Achievable, Results-oriented and Time-fixed. This step could be the most important piece of the monitoring process, as it guides and informs subsequent actions. While completing this step may appear simple, in practice it can be challenging.

Imagine biologists seeking population estimates and trends of desert bighorn sheep *Ovis canadensis nelsoni* inhabiting San Andres National Wildlife Refuge (SANWR). If development of the monitoring objective ends here, then the specific, measurable outcomes of such a survey remain open to interpretation, hindering the ability to determine survey frequency, precision, amount of effort and costs (Stewart *et al.* 2024). Such ambiguity can generate mismatches between survey expectations and the data the survey produces.

Relevant questions that facilitate building good monitoring objectives include: "why do I require this

information?" and "how will this information change or affect my decisions?" These questions force us to think critically about the purpose of our work (Gitzen *et al.* 2012). Sometimes the answers indicate that the project would not produce data for informing decision making. In these cases, it may be prudent to abandon the work and focus resources on more pressing, applied projects.

Other responses may be: "we want to ensure that hunting only removes a sustainable number of rams" or "if the population falls below a given number or by a certain percentage, then we plan to investigate cause (like disease or predation)." This information helps build SMART objectives by aligning a project's design with management needs.

If managers want to ensure a sustainable hunt, then a SMART objective might be: "Annually estimate if enough rams (> 50) exist in the population of desert bighorn sheep at SANWR to identify the number of rams to harvest, provided the harvested number is < 15% of rams and < 5% of the total population". The objective is Specific: by providing numerical criteria for harvestable rams; Measurable: evaluated by if the survey was conducted or not; Results oriented: The objective will produce data identifying a count of rams to inform hunting quotas; and Time fixed: the survey occurs annually. Is the work Achievable? Perhaps, but remaining questions involve cost and effort, such as: "how to survey", "should the same areas be surveyed each year?" and "should the counting approach and amount of sampling effort be consistent across years?" etc.

Alternatively, managers may be concerned about predation or disease outbreaks. Then the SMART objective could be: "Annually estimate the population size of bighorn sheep at SANWR using a survey design with enough statistical power to measure a 10% population change between years". The objective is SMART, but the sampling costs to achieve this level of confidence in population change may be prohibitive. If so, a revision could be "Estimate the population size of bighorn sheep at SANWR with enough statistical power to measure a 20% population change with surveys occurring every 3 years." In this case, the biologists have reduced the threshold for detecting changes and survey costs, to obtain achievable estimates (within budget) that they consider relevant.

Once the SMART objectives are developed, identifying methods to acquire such data become simpler. The first example seeks a count or rams which could be pursued with a ground-based approach (minimum count). For the second example, if aerial surveys are possible, animal visibility high (low vegetation cover and uncomplicated terrain), and budget sufficient, transect techniques like double observer and distance sampling should work (e.g., Buckland *et al.* 2010; Lubow & Ransom 2016; Conroy *et al.* 2018; Thapa *et al.* 2021). If vegetation is thick, flying is not possible, budgets low, and/or terrain complex, then possibilities include groundbased methods with camera traps using relative abundance indices (designed to correlate with overall abundance), or techniques like distance sampling and N-mixture that produce abundance estimates (e.g., Keever *et al.* 2017; Palmer *et al.* 2018; Harris *et al.* 2020; Pal *et al.* 2021; Harris *et al.* 2024).

Irrespective of the sampling technique, projects should enact the methods with a preliminary (pilot) effort. This pilot could be a complete or partial survey. Subsequent analysis of pilot data would reveal the amount of variability in survey data (e.g., counts of rams across transects or cameras), manifested as the precision (variance) generated by the survey. Power analyses incorporating the pilot data would identify the ideal sampling effort required to obtain the precision goals needed for detecting meaningful and relevant trends (or effect sizes). In practice, we typically increase sampling effort slightly above the power analysis results.

As a final consideration, imagine an agency designed survey to monitor trends in a Caprinae population, and that any population decline > 20% over 3 years should trigger an investigation into cause (e.g., disease, predation). Suppose that after 6 years of surveys, analysis indicates a 25% decline over the past 3 years, but this decline is not statistically significant (using a 90% CI). What should be done?

If nothing is done, and the decline is real and continues unabated, then it could reflect poorly on the agency. If this result triggers an expensive response, and the decline is not real, the agency could also look bad. Like most challenging situations, the best answer is context dependent. If the population in question is valuable, then being proactive could be the better choice. If higher priorities are competing for limited funding, then letting things play out could be advisable.

In application, biologists should take a hard look at the survey. If the survey was based on pilot data and designed to have sufficient power to detect > 20% decline in 3 years but has not, then clearly something odd happened. Maybe a third of the Caprinae population didn't occur in the sampling frame (i.e., unavailable for detection, perhaps from a weather anomaly), creating high variance in animal counts between sampling units (transects, cameras) unseen during survey design. In this case the result may be real, as the survey may have lacked power due to natural changes in the population distribution or survey conditions that affected results.

In summary, a framework for improving research and monitoring programs involves clearly articulating project intent. We suggest that SMART techniques can assist in framing project objectives. Using pilot studies to test methods and ensure adequate sample sizes for accomplishing the SMART objective is important to achieve monitoring goals. This framework helps align resource expenditure with on-the-ground implementation and information gain. Ultimately, the framework focuses our approaches, helping us channel our enthusiasm toward building better, more applicable projects for improving management of harvestable Caprinae populations and the recovery of those imperiled species.

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#### Results of the 9th World Conference on Mountain Ungulates, Dushanbe 2024

Khurshed Shamsiddinov<sup>1\*</sup> & the Organising and Scientific Committees of the 9WCMU

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The 9th World Conference on Mountain Ungulates (9WCMU) sought to bring together a diverse group of scientists, conservationists, policymakers, and stakeholders to exchange knowledge, research findings, and strategies aimed at the conservation and sustainable management of mountain ungulates and their habitats. More than 100 participants from 17 countries presented the results of their research on 21 species of Caprinae and other ungulates living in mountain environments.

Mountain ungulates were highlighted as essential components of mountain ecosystems, playing a crucial role in maintaining ecological balance. Despite their importance, they were noted to face a multitude of threats, including habitat loss, climate change, poaching, and escalating human-wildlife conflict. The conference served as a platform for addressing these challenges, providing a space where innovative ideas were shared and collaborative solutions developed.

The conference facilitated the sharing of scientific research and practical experiences related to the ecology, behavior, and conservation of mountain ungulates. By fostering international collaboration among researchers, conservationists, and policymakers, it aimed to develop effective conservation strategies that could be applied globally. Additionally, it raised awareness about the critical role of mountain ungulates and the pressing need for their conservation.

A wide range of themes were explored during the conference. Sessions delved into topics such as the interactions between mountain ungulates and their environments, their behavior and evolution, and the impacts of rapid environmental changes. Experts shared insights into the effects of predator recovery, changes in life history, population dynamics, spatial behavior, diet adaptations, and the interactions between ungulates, humans, and livestock.

Genetics was another major focus of the conference, with discussions centered around the latest advances in molecular techniques. Presentations covered conservation genetics, hybridization, immunogenetics, and genomics, offering new perspectives on the genetic diversity and resilience of mountain ungulates. Systematics and paleontology also took center stage, with new discoveries and insights presented on the systematics of mountain ungulates, integrating both paleontological and molecular data.

The health and disease session addressed the emerging threats to mountain ungulate populations, such as new pathogens and the impacts of zoonotic diseases, while also highlighting climate change as a significant factor in population health. Conservation and management practices were thoroughly examined through case studies that explored the role of indigenous knowledge, human-wildlife interaction, and the direct impacts of various management strategies.

The importance of effective monitoring methods was a recurring theme throughout the conference, as participants shared and developed best practices for estimating and monitoring mountain ungulate populations. Additionally, there were discussions on the application of new technologies in wildlife research and conservation, including the use of drones, remote sensing, camera traps, and machine learning to enhance conservation efforts.

By the conclusion of the conference, several key outcomes were achieved. Participants gained an enriched understanding of mountain ungulate ecology and behavior, as well as the challenges they face. The conference also helped to strengthen international networks, fostering collaborations that will benefit future conservation efforts. Furthermore, policy recommendations were developed to enhance the protection and management of mountain ungulates, and awareness of the urgent need for their conservation was heightened among both the public and relevant stakeholders.

This gathering of minds and ideas was a vital step in ensuring the long-term survival of mountain ungulates, helping to secure their place within the ecosystems they support.

The abstract's booklet is available at <u>www.tajna-</u> ture.tj

Next WCMU will be held in India in 2026. Keep in touch!

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