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DEER SPECIALIST GROUP NEWS

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Editorial

Dear DSG members,

We start this year thanking for your continue commitment on deer management and conservation. We understand that for most of you the DSG work is done voluntarily on top of your day jobs, so your contribution is not taken for granted and we greatly appreciate it.

In this year we would like to advance, among others, the following targets and it would be great if you find those interesting and relevant to your areas of expertise and join us in our efforts:

- Establish a Climate Change Working Group
- Collect data on the currently known effects, and estimates possible ones, of global warming on cold-climate DSG species.
- Create protocols to mitigate human-deer conflict in general, and, more specifically in various South American habitats and regions, such as the Pampas, Cerrado, open grasslands, as well as in several forested regions
- Develop and publish deer conservation-translocation guidelines by the end of 2023.

We invite all of you to contact us to work and share your expertise in those targets. Noam is leading the Climate change Working Group Network and the translocation guidelines and Susana the work on the protocols to mitigate human-deer conflict.

Finally, but not less important, we ask you to identify young deer conservationists, especially from under-represented groups and regions, such as women and/or from areas such as south, south-east and east Asia, as potential DSG members who will become involved in our Network and work and in time introduce their fresh visions into our future strategic plan.

Lastly, we want to thank all those who contributed to this edition of the newsletter and invite all of you to submit manuscripts for the next issue by sending them to Dr. Patricia Black (black.patricia@gmail.com).

Our best wishes,

Susana González and Noam Werner,
Co-Chairs, IUCN/SSC Deer Specialist Group.

Evaluation of Body condition of two major cervids in a semi-arid landscape of Western India

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Abstract:

Body condition of an animal is a strong indicator of its fitness, thereby its survival, breeding success and reproductive potential. The body condition index (BCI) scoring, based on visual assessment of fat and muscle mass of different body and associated skeletal structures has been found useful in predicting total body fat in animals fairly accurately and is a non-invasive technique that has been replicated in the field for the assessment of wild ungulates. With the above rationale, we recorded the body condition of two major cervids viz. sambar (*Rusa unicolor*) and chital (*Axis axis*), in Sariska National Park, a semi-arid landscape of Western India, during the summer (March-June) and monsoon (July-October) of 2015, along 12 vehicle transects with a total effort of 293.7 km. We found that 100% of the sampled chital individuals during both summer (n=442) and monsoon (n=577) had good body condition; while in the case of sambar, ~94% of the sampled individuals during summer (n=108) and ~99% of the sampled individuals during monsoon (n=234), showed good body condition. Pearson's Chi-squared test showed that there was no significant difference in the BCI scores of the sampled chital (P=0.4604) and sambar (P=0.9942) individuals between seasons. The BCI scores of the evaluated individuals of chital and sambar in our study area during our study period indicated the presence of a healthy population of both cervids that can be attributed to the availability of adequate nutritious resources. Since both chital and sambar are preferred wild prey species of the reintroduced tiger population, the implications from our study will be crucial to the recovery and management of this endangered reintroduced apex predator in Sariska, which would depend on healthy wild prey populations for its long-term viability and sustenance.

Keywords: Body condition index, sambar, chital, re-introduced, tiger, principal prey

Resumen

La condición corporal de un animal es un fuerte indicador de su aptitud física y, por lo tanto, de su supervivencia, éxito y potencial reproductivo. La puntuación del índice de condición corporal, está basada en la evaluación visual de la masa grasa y muscular de diferentes estructuras corporales y esqueléticas asociadas. La misma resulta útil para predecir la grasa corporal total en animales con bastante precisión y es una técnica no invasiva que se ha replicado en el campo para la evaluación de ungulados salvajes. Con el razonamiento anterior, registramos la condición corporal de dos importantes cérvidos, sambar (*Rusa unicolor*) y chital (*Axis axis*), en el Parque Nacional Sariska. El mismo se encuentra en un paisaje semiárido del oeste de la India, durante el verano (marzo-junio) y el monzón (julio-octubre) de 2015, a lo largo de 12 transectos vehiculares con un esfuerzo total de 293,7 km. Encontramos que el 100% de los individuos chitales muestreados durante el verano (n=442) y el monzón (n=577) tenían una buena condición corporal; mientras que en el caso del sambar, ~94% de los individuos muestreados durante el verano (n=108) y ~99% de los individuos muestreados durante el monzón (n=234), mostraron buena condición corporal. La prueba de chi-cuadrado de Pearson mostró que no hubo una diferencia significativa de los individuos muestreados de chital (P = 0.4604) y sambar (P = 0.9942) entre temporadas. Los puntajes de los individuos evaluados de chital y sambar en nuestra área de estudio durante nuestro período de estudio indicaron la presencia de una población saludable de ambos cérvidos que puede atribuirse a la disponibilidad de recursos nutritivos adecuados. Dado que tanto el chital como el sambar son especies de presas silvestres preferidas de la población de tigres reintroducida, las implicaciones de nuestro estudio serán cruciales para la recuperación y el manejo de este depredador tope reintroducido en peligro de extinción en Sariska, que dependería de poblaciones de presas silvestres sanas para su viabilidad a largo plazo y sustento.

Palabras clave: Índice de condición corporal, sambar, chital, tigre reintroducido, presa principal

Introduction

The body condition of an animal in any given habitat is a strong indicator of its fitness, which in turn determines the chance of its survival, breeding success and reproductive potential (Flydal & Reimers 2001, Tavecchia et al. 2005, Ezenwa et al. 2009, Courturier et al. 2009). Body condition has been found to be dependent on environmental factors, which are influenced by climatic variations and nutritional factors, which are in turn influenced by the abundance and availability of food resources, acting independently, or via a string of complex interactions with one another (Courturier et al. 2009, Ramesh et al. 2011). In other words, adverse climatic conditions might have both direct and indirect effects on the health of an animal. The direct effects include changes in the physiological functions of an animal, e.g., thermoregulation, while the indirect effects may include adverse change in the food resource availability in a given habitat (Courturier et al. 2009). Such an impact might manifest poor body condition in animals that are dependent on the resources. Consequently, individuals become more susceptible to infectious parasites, which could have a disproportionately negative impact on the population.

We recorded the body condition of two major cervids (sambar and chital) (Fig. 1), in Sariska National Park, a semi-arid landscape of Western India, during summer (March-June) and monsoon (July-October) of 2015. The study was conducted during summer since it is considered as a pinch period in a semi-arid dry deciduous forest (Dave 2008). To elaborate, during summer the major vegetation in a dry deciduous forest sheds its leaves and the natural water bodies, and ephemeral streams dry up, thus creating a scarcity of forage and water in contrast to monsoon when the resources are abundant (Sankar 1994). Therefore, we hypothesized that the difference in natural conditions between these two seasons might affect in the body condition of our study species.


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Figure 1. Left Chital (*Axis axis*), and right Sambar (*Rusa unicolor*).

Tigers were locally extinct from Sariska due to poaching by 2004 and subsequently eight individuals were reintroduced from nearby Ranthambore Tiger Reserve, Rajasthan, from 2008 till 2012 (Sankar et al. 2013a). The present population of tigers in Sariska stands at 23 individuals. Ensuring the long-term sustenance of this reintroduced endangered felid would require the availability of a healthy prey population. This further justifies our study since both sambar and chital have been found to be the two major prey species of the re-introduced tiger population in our study area (Sankar et al. 2013a, Qureshi et al. 2017), and information from our study would be a crucial component in the management and conservation of the predator and habitat of Sariska, since the ungulates act as a bridge between these two trophic levels.

Materials and Methods

Study Area

The study area, Sariska Tiger Reserve (STR), a protected area in Western India, falls between 27°05’ N to 27˚45’ N and 76˚15’ E to 76˚35’ E, latitude and longitude respectively, with an altitude ranging from 540 to 777 m a.s.l.) (Fig. 2). It is situated in the Aravalli Hill Range of a semi-arid part of the Indian state of Rajasthan (Rodgers & Panwar 1988). It became a Wildlife Sanctuary in 1955 and a Tiger Reserve in 1982. The total area of the Tiger Reserve is ~1200 km^2; of which 400.14 km^2 area is the official National Park.

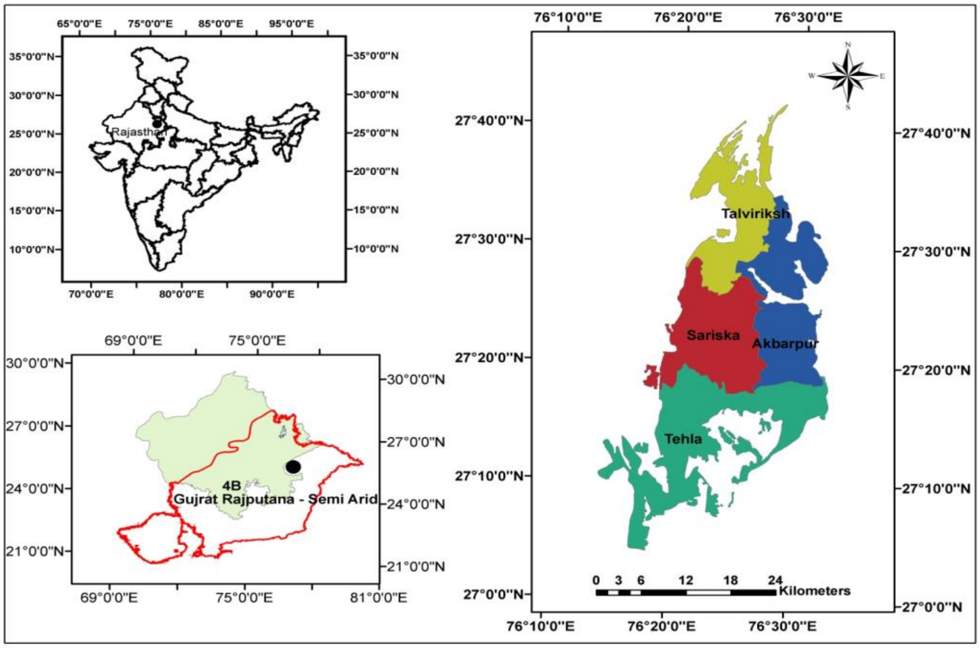

Figure 2. Location and Administrative Boundary of Sariska Tiger Reserve (Sankar et al. 2013a).

The terrain is undulating to hilly with numerous narrow valleys. The climate is subtropical, with a distinct summer, monsoon, post monsoon and winter. The vegetation corresponds to Northern Tropical Dry Deciduous Forest and Northern Tropical Thorn Forest (Champion & Seth 1968). Apart from leopard and a re-introduced tiger population, other carnivores present are striped hyena (*Hyaena hyaena*), jackal (*Canis aureus*), jungle cat (*Felis chaus*), desert cat (*Felis silvestris*), common mongoose (*Herpestes edwardsi*), small Indian mongoose (*H. auropunctatus*), ruddy mongoose (*H. smithi*) palm civet (*Paradoxurus hermaphroditus*), small Indian civet (*Viverricula indica*) and ratel (*Mellivora capensis*) (Gupta 2011). Prey species include chital (*Axis axis*), sambar (*Rusa unicolor*), nilgai (*Boselaphus tragocamelus*), common langur (*Semnopithecus entellus*), wild pig (*Sus scrofa*), rhesus macaque (*Macaca mulatta*), porcupine (*Hystrix indica*), rufous tailed hare (*Lepus nigricollis ruficaudatus*) and Indian peafowl (*Pavo cristatus*) (Sankar et al. 2013a). The predominant domestic livestock found inside the reserve are buffaloes (*Bubalis bubalis*), cow (*Bos indicus*) and goats (*Capra hircus*) (Sankar et al. 2013a). There are eight villages located inside the National Park area which have been due for relocation since 1984. The human population is over 1700 in the villages of the National Park with a population of 10,000 livestock (Sankar et al. 2009). There are 19 villages located outside the National Park but within the Tiger Reserve, with a human population of around 6000 and a livestock population of more than 20,000 (Sankar et al. 2009).

The present study was conducted mainly in a 274 sq. km. area, (Figure 3a) which falls under the National Park area of STR, for the entire study period.

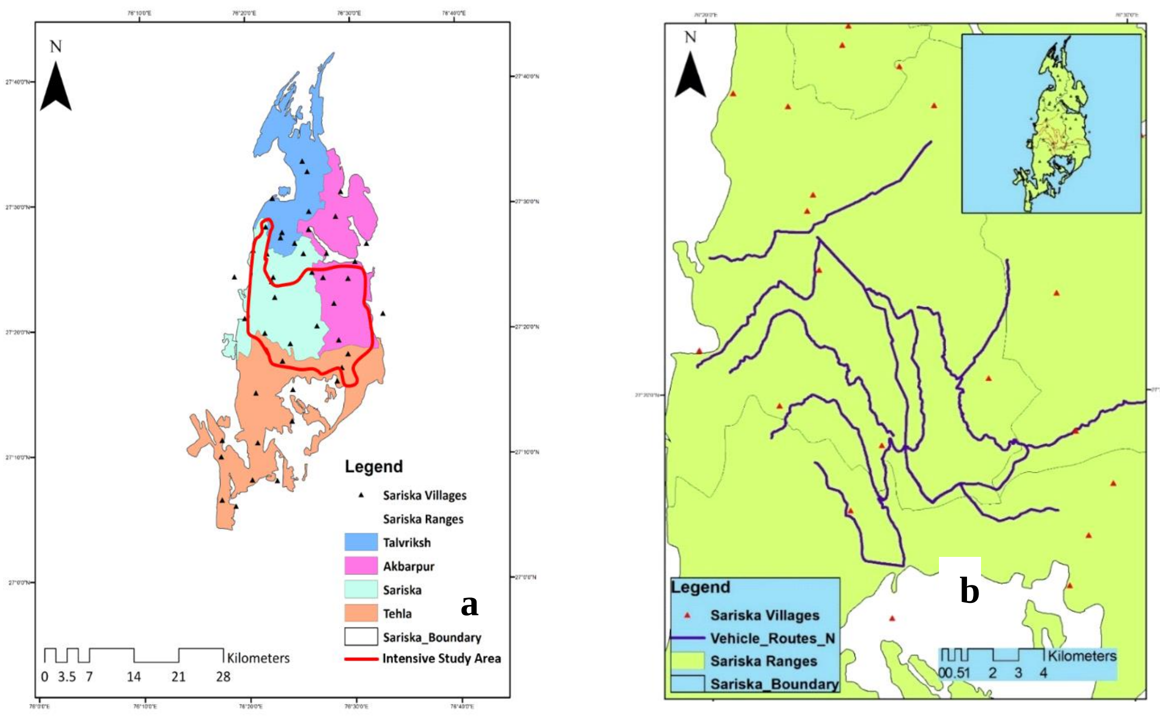

Figure 3: (a) Intensive study area. (b) Vehicular Transects traversed for the study

Methods

The body condition of chital and sambar individuals was determined through direct observation, employing a body condition index/score (Riney 1960), using vehicle transects (Varman & Sukumar 1993, Ramesh et al. 2011). For this purpose, 12 vehicle transects were traversed once during the mmer and once during the monsoon, with roads each varying in length from 9.1 to 15.2 kms, in the intensive study area (Figure 3b). We assessed all the individuals of each group of chital (no. of individuals ranged in a group from 1 to 15 individuals) and sambar (no. of individuals in a group ranged from 1 to 7 individuals) encountered during sampling. Body condition index (BCI) consists of individually scoring five different regions of an ungulate body, *viz.* flank, ribs, pelvic girdle, vertebral column, and lumbar shelf, between 0-2 with a numerically higher value corresponding to poor body condition (0-good, 1-fair and 2-poor) (Table 1).

Table 1: Table showing the criteria on which individual body parts are scored to evaluate the Body Condition Index.

BODY PART	SCORE=0	SCORE=1	SCORE=2
FLANK AREA	Depression barely visible. Flank area outline is indistinct	Flank area slightly concave & outline visible	Depression concave and tucked in
RIBS	Thoracic surface is smooth and ribs are difficult to see	Ribs are visible but not all can be counted with ease	Ribs prominent with distinct inter-costal depressions
PELVIC GIRDLE	Bony projections of pelvic girdle are barely visible	Pelvic girdle outline slightly visible	Bony projections of pelvic girdle are clearly visible
VERTEBRAL COLUMN	When seen laterally, it runs smooth without any breaks. Lumbar process visible	Lateral processes of lumbar vertebrae are visible but not prominent	Lateral processes of lumbar vertebrae very prominent. Dorsal processes of vertebrae seen
LUMBAR SHELF	No depression in shelf. Appears almost round from behind	Slight depression on either side	Depression deep and concave

Finally, these score values were added up for each individual to calculate the BCI of that particular individual and interpreted as good (BCI score: 0-5), fair (BCI score: 6-8) and poor (BCI score: 9-10), accordingly (Riney 1960). Description of the body parts observed, and the scoring system are as follows: *Interpretation of summed up score of five body parts: 0-5= 'Good'; 6-8= 'Fair'; 9-10= 'Poor' (Riney 1960).*

The age class ungulate sighting was grouped based on previous studies (Schaller 1967, Johnsingh 1983, Sankar 1994, Bagchi et al. 2008, Ramesh et al. 2012, Majumdar et al. 2013) as adult female (individuals more than two years of age and greater than 70 kilograms in case of sambar and greater than 30 kilograms in case of chital); sub-adult female (characterized by height of individuals above mother's belly and weight less than or equal to 70 kilograms in case of sambar and less than or equal to 30 kilograms in case of chital); sub-adult male (characterized by spike or antlers less than 1 feet long; height and body weight as described in case of sub-adult female of respective species), fawn (characterized by individuals with height below mother's belly); adult males (characterized by antler size greater than one feet in case of sambar and chital; body weight same as mentioned in above in the case of adult females of respective species). We used Pearson's chi-squared test (Greenwood & Nikulin 1996) to check if there was a significant difference in the BCI scores of our study species between summer and monsoon in our study area (Ramesh et al. 2011).

Results

The total effort of the vehicle transects for estimating BCI of the ungulates (sambar and chital) was 293.7 kms (144.4 km during summer and 149.3 km during the monsoon), in the intensive study area. The percentage of good, fair and poor body condition of the observed individuals per season were:

Chital

During summer and monsoon, 2015, body conditions of 442 and 577 chital individuals were evaluated respectively, in our study area and we found that, in both seasons, all the individuals (100%) were in good body condition. Pearson's chi-squared test showed that there was no significant difference in the body condition of chital between summer and monsoon (P=0.4604). Numbers for different Age/Sex classes and overall percentage of body condition of chital in our study area during our study period are shown in Table 2.

Table 2: Details of observed body condition of sambar in the study area classified as good, fair and poor according to the BCI score, during the summer and monsoon in 2015.

Season	**Age/Sex Class**	**Number of Observations**	**Body Condition**		
			% Good	**% Fair**	**% Poor**
Summer	Adult Female	223	100.00	0.00	0.00
	Adult Male	69	100.00	0.00	0.00
	Sub-adult Female	87	100.00	0.00	0.00
	Sub-adult Male	23	100.00	0.00	0.00
	Fawn	40	100.00	0.00	0.00
	Overall	**442**	**100.00**	**0.00**	**0.00**
Monsoon	Adult Female	272	100.00	0.00	0.00
	Adult Male	79	100.00	0.00	0.00
	Sub-adult Female	125	100.00	0.00	0.00
	Sub-adult Male	52	100.00	0.00	0.00
	Fawn	49	100.00	0.00	0.00
	Overall	**577**	**100.00**	**0.00**	**0.00**

Sambar

During summer, 2015, body conditions of 108 sambar individuals were evaluated in our study area and we found that 93.5% of the total individuals were in good body condition, while 2.8% of the observed individuals had fair body condition and 3.7% were in poor body condition. During the monsoon, 2015, we assessed the body condition of 234 individuals, 99.2% of which showed good condition, while fair and poor body conditions were observed in the case of 0.4% of the total individuals respectively in each category. Using the Pearson's chi-squared test we found that there was no significant difference in the body condition of sambar between summer and monsoon (P=0.9942). Age/Sex classes and overall percentage of body condition of sambar in our study area during our study period are shown in Table 3.

Table 3: Details of observed body condition of sambar in the study area classified as good, fair and poor according to the BCI score, during the summer and monsoon in 2015.

Season	Age/Sex Class	Number of Observations	Body Condition		
			% Good	% Fair	% Poor
Summer	Adult Female	63	93.65	3.17	3.17
	Adult Male	10	80.00	10.00	10.00
	Sub-adult Female	16	100.00	0.00	0.00
	Sub-adult Male	8	87.50	0.00	12.50
	Fawn	11	100.00	0.00	0.00
	Overall	**108**	**93.52**	**2.78**	**3.70**
Monsoon	Adult Female	117	99.15	0.00	0.85
	Adult Male	28	96.43	3.57	0.00
	Sub-adult Female	45	100.00	0.00	0.00
	Sub-adult Male	22	100.00	0.00	0.00
	Fawn	22	100.00	0.00	0.00
	Overall	**234**	**99.15**	**0.43**	**0.43**

Discussion:

The BCI score of chital and sambar showed that the observed individuals exhibited an overall good body condition during summer and monsoon in our study area. Such findings might be attributed to the presence of adequate resources that fulfil the nutritional requirements of both species (Ramesh et al. 2011), possibly leading to a healthy population of the two cervids in Sariska National Park (SNP). Contrary to our expectation, we found good body condition of chital and sambar during summer as well as monsoon. The study was conducted in the National Park (part of the core area), an area comprised of the least disturbed habitat, devoid of anthropogenic activities and limited interspecific competition with livestock (Sankar 1994, Sankar, 2013b). Poor habitat quality and high competition with livestock could cause poor health conditions for wild ungulates (Foley et al. 2001, Horcajada-Sánchez et al. 2019). Additionally, the core area receives regular interventions in habitat management, such as grassland management, weed eradication, and the creation and maintenance of artificial water holes to ensure forage and water availability for wild animals, especially during summer. Furthermore, previous studies in the same study area indicated that, during summer, chital and sambar frequently fed on fallen leaves of *Anogeissus pendula* (major vegetation covering 40% of the total area of STR) and shrubs such as *Grewia flavescens* and *Capparis sepiaria* that are rich in essential nutrients for the ungulates (Sankar 2007). Thus, adequate forage opportunities during the pinch period could sustain the overall good health of wild ungulates in STR, as indicated by other studies elsewhere (Dave 2008, Horcajada-Sánchez et al. 2019).

So far, few studies have been conducted on the body condition of wild ungulates in India. Previous studies indicated that the body condition of animals in any given area could be a strong indicator of a plethora of essential aspects ranging from individual health and reproductive potential of a population to the quality of resources available in the area (Flydal & Reimers 2001, Ezenwa et al. 2009, Courturier et al. 2009, Ramesh et al. 2011). All these aspects form the critical elements of any management strategy dedicated to the conservation of concerning species in a protected area (PA). Furthermore, the methodology used in this present study is a non-invasive and cost-effective technique that could be easily replicated elsewhere. In Sariska, chital and sambar are the two preferred wild prey species of the reintroduced tiger population, with sambar being the principal prey (Qureshi et al. 2017). Thus, a healthy wild prey population is imperative for the success and long-term conservation of the reintroduced tiger population in Sariska Tiger Reserve (Sankar et al. 2013a). In this context, our study would provide relevant information regarding the health of the preferred prey species and establish a foundation for further similar research on wild ungulates in India.

The present study was conducted in the core area, and we suggest the same be carried out periodically in the buffer area as well, as it represents a high human-wildlife interface due to the shared use of space between livestock and wild ungulates. Additionally, implementing such a rapid, cost-efficient survey should be extended beyond the boundaries of PAs, especially in human-dominated landscapes, to monitor the health of wild ungulates and devise management interventions accordingly.

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How many species of *Rangifer*?

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Abstract

Publications on genetics of reindeer and caribou were synthesized, together with data on morphology, ecology, and palaeontology, were synthesized to revise the genus *Rangifer*. Six species of *Rangifer* Smith, 1827, are recognized. This paper is a summary of the published revision.

Key words: caribou, reindeer, systematics

Resumen

Se sintetizaron publicaciones sobre genética de renos y caribúes, junto con datos sobre morfología, ecología y paleontología, para revisar el género *Rangifer*. Se reconocen seis especies de *Rangifer* Smith, 1827. Este documento es un resumen de la revisión publicada.

Introduction

Modern taxonomy of *Rangifer* derived mainly from (Banfield, 1961) that was widely regarded as seriously flawed (e.g., McTaggert Cowan, 1962). Banfield (1961) reduced the number of species from around 51—the number synonyms of *Rangifer tarandus* listed by the Mammal Diversity Database (Burgin et al., 2018)—to one. Especially since the DNA era, caribou and reindeer biologists and geneticists have remarked that current taxonomy does not reflect diversity in *Rangifer*. My recent revision of *Rangifer* (Harding, 2022a) was intended to correct this. The purpose of this article is to explain the resurrection of five previously-named species, making six species of *Rangifer*.

Species delineation

Delineation of species relies on morphology, ecology (including heritable behaviour), physiology, genetics (including genealogy) and phylogeny (Mayr, 2000, Baker & Bradley, 2006, de Queiroz, 2007, Zachos & Lovari, 2013). Regardless of what definition of species you prefer, reproductive isolation is *de rigueur*. The key is not whether they can produce offspring, but whether the offspring can survive and reproduce in the habitat of their parents. Barriers may be physiological (such as estrus out of sync), physical (parts don't fit), geographic or behavioural. Although it is not an immutable law, as some species do interbreed when brought together, and occasionally in the wild, isolation is the mother of evolution.

Methods

This summary is based on a revision of *Rangifer*, which was based on analysis of published data (Harding, 2022a). Genetic distances and other genetic measures of distinctiveness in *Rangifer* clades were reviewed in a supplementary file (Harding, 2022b). A synonymy was given in a supplementary file (Harding, 2022c).

Results

Rangifer evolution

Rangifer "evolved as a mountain deer, ...exploiting the subalpine and alpine meadows..." (Geist, 1998). *Rangifer* originated in the Late Pliocene and diversified in the Early Pleistocene (Croitor, 2018), a 2.5+ million-year period of multiple glacier advances and retreats. The oldest undoubted *Rangifer* fossil is from Omsk, Russia, dated to 2.1–1.8 Ma (Bondarev et al., 2017). Using ancient environmental DNA (eDNA), Kjær et al. (2022) found in North Greenland, dated to 2 million years ago, "ancient Capreolinae environmental mitochondrial genome … basal to the *Rangifer* genus". The oldest North American *Rangifer* fossils are from Alaskan and Yukon, 1.9–1.6 Ma (Guthrie & Matthews, 1971, Harington, 1989, Webb, 2000). In Eurasia, the oldest fossil is a skull fragment from Süßenborn, Germany, *R. arcticus stadelmanni* (Kahlke, 1963), with "rather thin and cylinder-shaped" antlers, dated to around 680,000 to 620,000 years ago (Croitor, 2010). This leaves about 0.4 million years of reindeer and caribou evolution unaccounted for in the fossil record of North America and 1.3 million years in Eurasia.

Multiple waves of successively more advanced reindeer appeared in Europe from the middle Pleistocene onward and many authors assume that at least the later forms evolved in Beringia (e.g., Croitor, 2018). Beringia was non-glaciated land in eastern Siberia and western North America enclosed by continental glaciers at times of lower sea levels that temporarily connected Eurasia and North America (Bond, 2019). It was unglaciated because of scant precipitation; therefore, the lack of glaciers (and presence of a refugium) depended on global climates during each glacial period. Beringia did not exist outside of glacial periods and may not have existed as currently defined in glacial periods previous to the last glacial maximum (LGM).

Palaeontologists distinguish "modern" tundra reindeer (*Rangifer tarandus tarandus* L. 1758) and barren-ground caribou (*Rangifer arcticus arcticus* Richardson, 1829) from primitive forms—living and extinct—that did not have adaptations to extreme cold and to long-distance migration. These include a broad, high muzzle to increase the volume of the nasal cavity to warm and moisten the air before it enters the throat and lungs (Flerov, 1952), bez tines set close to the brow tines (as opposed to woodland caribou; see below), short legs and other adaptations for migrating long distances, and multiple behaviors suited to tundra, but not to forest, such as synchronized calving and aggregation during rutting, migration and post-calving (Croitor, 2018). Geist (1998) explains why aggregating during rut, individual-tending mating and synchronized calving were important adaptations to tundra that are absent in forest forms.

Extant Species

Greenland caribou

No one knows where Greenland caribou came from. A small, High Arctic-sized caribou (*R. t. eogroenlandicus* Degerbøl, 1957) lived in all parts of Greenland throughout the Holocene; in historic times it was a local, relict population in north-eastern Greenland that went extinct about 1900 (Meldgaard, 1986). A fossil 40,000 years old shows that it lived there in the last interstadial (Meldgaard & Bennike, 1989).

In the mid-Holocene, a larger, barren-ground-sized caribou appeared in south-western Greenland; it presumably immigrated from Baffin Island via Davis Strait (Meldgaard, 1986), and it is this that was first named Greenland reindeer *Cervus groenlandicus* Borowski, 1780. It is a "modern" caribou in the sense of increased air capacity of the rostrum mentioned above. However, it clusters genetically outside of both the North American (NAL, woodland) and Beringian-Eurasian (BEL, tundra) lineages and a reconstruction of glacial retreat and caribou advance shows colonization by NAL caribou more likely (Yannic et al., 2013). In any case, Baffin Island caribou are genetically distinct from barren-ground caribou (Jenkins et al., 2018), lack their long-distance migration and aggregating behaviours (Ferguson & Messier, 2000) and have NAL genetic legacy (Røed et al., 1991, Cronin et al., 2005). Greenland caribou are the most geographically isolated and genetically distant clade among all extant caribou (microsatellite loci, average fixation index 44%—Yannic et al., 2013). Cervid species within the same genus usually have F_{ST} around 3%–6% (reviewed in Harding, 2022b). Its morphological differences led Anderson (1946) to ally it with Eurasian *R. tarandus*, rather than Canadian barren-ground *R. arcticus*. It has a different mating system and different migration and aggregation behaviours from barren-ground caribou (Poole et al., 2013, Raundrup, 2018). I left it as *R. groenlandicus* (Borowski, 1780).

Woodland caribou

The woodland caribou, *Rangifer caribou* (Gmelin, 1788), lineage split from other caribou 300,000 (Yannic et al., 2013) to 357,000 (Horn et al., 2018) years ago. This was before modern tundra caribou had evolved.

Woodland caribou average 60%–65% larger than barren-ground caribou, based on live weight, and 12% larger by metatarsus length (data from Banfield, 1961). They have proportionately longer legs, different antler architecture and darker pelage. The antler architecture—short, straight, minimal palmation distally, beams flattened in cross-section and “bushy” (relative to barren-ground caribou)—results from their dispersed harem-defense mating system (versus individual-tending in large herds in barren-ground caribou), an adaptation of their social system to a forest environment (Butler, 1986). Because woodland caribou males have frequent and intense combat during rutting (Barrette & Vandal, 1990), their antlers are short and strong.

Besides genetic, morphological and behavioural distinctiveness, they may have descended from extinct forest caribou, such as *Torontoceros [Rangifer] hypogaeus* (Churcher and Peterson, 1982), which had short, robust pedicles and a high bez tine that relate it to forest caribou (Croitor, 2022). If so, lacking a direct common ancestor with barren-ground caribou, it cannot be conspecific.

This physiological and morphological disparity is why caribou geneticists have found very little introgression of barren-ground caribou genes into woodland caribou and almost none the other way (Klütsch et al., 2012, Horn et al., 2018, Taylor et al., 2020). Under any definition of species, woodland caribou warrant species status: *R. caribou* (Gmelin, 1788).

Newfoundland caribou, *R. c. terraenovae*, and Labrador caribou, *R. c. caboti*, are well differentiated subspecies (Grubb, 2005, Wilson & Mittermeier, 2011). An unnamed clade in Gaspésie, Quebec, separated by the St. Lawrence Seaway, has the largest genetic distances from all other populations (F_{ST}=0.14–0.15) that Dedato (2021) observed and possibly merits subspecies status.

Arctic caribou

The unavailability of *groenlandicus* left barren-ground caribou without a name. Because its behaviours, genetics and morphology differ at the species level from *R. tarandus* (see below), it reverted to *R. arcticus* Richardson, 1829. This brought the four western montane clades, which have been shown to be of the "BEL" lineage (Horn et al., 2018) and quite distinct from each other ecologically and behaviourally (c.f. COSEWIC, 2011), back under Arctic caribou as Alaskan mountain or Stone's caribou *R. a. stonei* Allen, 1901*,* Northern Mountain or Osborn's caribou *R. a. osborni* Allen, 1902, Rocky Mountain caribou *R. a. fortidens* Hollister, 1912 and Selkirk Mountain *R. a. montanus* Seton-Thompson, 1899, as they were (Anderson, 1946) before Banfield (1961) synonymized them (Fig. 1).

As a hunter, I used to watch Osborn's caribou stream down off their alpine summer pastures in the fall and out onto the flat muskeg, where they wintered, a migration of some 200 km that woodland caribou, which I studied for two winters, could not have done.

Figure 1. Selkirk Mountain caribou, *R. arcticus montanus*. Photo by Lee E. Harding.

By contrast, Selkirk Mountain caribou migrate only altitudinally, but twice per year: in fall they come down before the advancing snow line but return to high elevation in mid-winter when the snow becomes dense enough to support them as they forage arboreal lichens; in spring they return to low elevation to avoid having to travel in freezing-thawing crusted snow, and to forage early-greening vegetation.

Allen (1902) described Grant's caribou from specimens from the west end of the Alaska Peninsula and nearby islands (where genetically unique caribou still live—Mager et al., 2014):

"Rangifer granti is a representative of the Barren Ground group of Caribou, which includes R. arcticus of the Arctic Coast ... It is not closely related to R. stonei of the Kenai Peninsula, from which it differs not only in its very much smaller size, but in important cranial characters and in coloration."

Murie (1935) and Anderson (1946) renamed it *R. a. granti*. Banfield (1961) erred in assigning all Alaskan mountain and barren-ground caribou to *granti*, which has a limited range as originally described. Barren-ground caribou remain *R. arcticus arcticus* (Fig. 2).

Figure 1. Barren-ground caribou of the Porcupine herd, Yukon, *R. arcticus arcticus*, in post-calving aggregation. Photo by Lee E. Harding.

Arctic caribou arose from a split between its ancestors and those of woodland caribou, *R. caribou* about 300,000 to 357,000 as noted above. The ancestors of the four western montane subspecies (each of which has a different mix of sublineages—Horn et al., 2018) split from those of barren-ground caribou, *R. a. arcticus*, about 120,000-130,000 years ago (Taylor et al., 2021), well before the LGM when Beringia did not exist. Barren-ground caribou may have specialized to extreme cold during the LGM within Beringia, but their migratory, aggregating and individual-tending rutting behaviours (c.f. Geist, 1998) must have evolved in early Holocene, after the Laurentide and Cordilleran ice sheets separated and gave them access to boreal forest winter range. They have short legs and other morphological and physiological adaptations to long-distance migration. Their antlers—beams are thin, round in cross-section, and semi-palmated distally—are more ornamental than functional (Markusson & Folstad, 1997), as their individual-tending mating system results in mild, infrequent combat. The low-set bez tines assist the brow tine in clearing snow to forage (Pruitt Jr., 1966).

Arctic caribou have many novel genes, such as those for vitamin D metabolism, fat metabolism, retinal development, circadian rhythm suppression and tolerance to cold temperatures, that are lacking or rudimentary in forest types (Cavedon et al., 2019, Prunier et al., 2021, Cavedon et al., 2022). For this reason, forest-adapted caribou could not easily survive in tundra or polar deserts, and vice-versa. Molecular analyses confirm mutually exclusive mtDNA haplotypes (Klütsch et al., 2012, Yannic et al., 2013). Nevertheless, introgression of Arctic caribou nuclear alleles into woodland caribou during re-colonization after the LGM gave the migratory behaviours to Labrador caribou, *R. c. caboti* (Boulet et al., 2007, McQuade Smith, 2009, Klütsch et al., 2016, Leclerc et al., 2021).

High Arctic or Peary's caribou, *R. a. pearyi* are not closely related to Svalbard reindeer and descend from Canadian (or Beringian) tundra caribou (Gravlund et al., 1998, Kvie et al., 2016a), but distantly. High Arctic and barren-ground caribou separated > 100,000 years ago and diversified within the High Arctic 185,000–96,000 years BP, well before the LGM (Klütsch et al., 2017).

For two winters, watching through a night-vision telescope, I never saw High Arctic caribou stand still (Harding, 1975). They foraged at a brisk walk on bare, windswept ridges, where they do not have to dig craters in the snow, and kept moving at a remarkable rate while foraging. They did not stop foraging when a pack of wolves came by; the wolves seemed to ignore them, too, knowing that High Arctic caribou can outrun them. Their energy expenditure/locomotion strategy is opposite that of Svalbard reindeer. I left them as a subspecies of Arctic caribou, *R. a. pearyi*.

Eurasian tundra reindeer

Geist (1998) classified Eurasian tundra reindeer and American barren-ground reindeer as separate subspecies, based on behaviour and morphology (pelage and antler architecture). Molecular analyses (e.g., Yannic et al., 2013) gave haplotype and allele variations and genetic distances typical of species within a genus (c.f. Harding, 2022b). Davydov [Давыдов] et al. (2009), based on mtDNA, also concluded that "… there are no significant genetic exchanges" between eastern Eurasian reindeer and western North American caribou, which have been isolated since the end of the Pleistocene. They remain *R. tarandus* with alpine (*R. t. tarandus*) and tundra (*R. t. sibiricus*) subspecies.

Svalbard reindeer

Svalbard reindeer, *R. platyrhynchus* Vrolik 1829, are the smallest Palaearctic form (skull median length 318 mm, about 85% the length of Siberian reindeer, median 373 mm—Flerov, 1933) with a wide, high rostrum and other cranial and dental differences, very short legs, and light pelage.

Svalbard reindeer—along with Franz Joseph Land and Novaya Zemlya reindeer, which cluster together (Weldenegodguad et al., 2020)—split from the Eurasian mainland reindeer in the early Holocene (Kvie et al., 2016b). During the LGM, most of the Eurasian northern continental shelf was dry and presumably inhabited by reindeer. Since the Barents Sea is seasonally covered with ice, reindeer could have dispersed across the ice at least episodically throughout the Holocene. Nevertheless, they show no introgression either way, have unique alleles (Røed, 1985) and have four unique mtDNA haplotypes (Weldenegodguad et al., 2020). Although founder effects, genetic drift, and bottlenecks may explain some of their genetic uniqueness, they have doubtless experienced intense selection pressures.

Despite their close ancestry, Svalbard reindeer are very different from mainland tundra reindeer. They remain in small seasonal home ranges and do not migrate. They do not aggregate and they have a dispersed, harem-tending mating system with smaller harem sizes (1–5) than other harem-tending forms (Heatta, 2009). Since there are no wolves on Svalbard, they are slow runners (a deficit occasionally exploited by polar bears—Derocher et al., 2000). They have adaptations specific to their cold, polar desert environment: they spend more time lying or standing than other reindeer, have much lower metabolic rates whether standing or lying, and are less energetic in terms of locomotion (Cuyler & Øritsland, 1993); they accumulate unusual amounts of fat (Pond et al., 1993) and their fat metabolism lets them tolerate "lower critical temperatures" of -50° C, compared to just -30° C in wild Norwegian reindeer; and they have genetic adaptations to 24 hours/day darkness in winter and daylight in summer, such as lack of circadian rhythms and melatonin production, that are lacking or reduced in Norwegian reindeer (*R. t. tarandus*), which enjoy periods of daylight in midwinter and night all summer (Nilssen et al., 1984, van Oort et al., 2005). The unique haplotypes, plus the physiological and morphological differences that would doubtless prevent reproductive success if given a chance to mate with mainland tundra reindeer, and vice versa, were factors in the Svalbard reindeer's return to species status, *R. platyrhynchus* (Vrolik, 1829), as Flerov (1933, 1952) and Sokolov (1937, 1963) insisted.

Eurasian forest reindeer

Eurasian forest reindeer, *R. fennicus* Lönnberg, 1909, has a "…longer and slenderer skull … compared to the tundra type … large bodied and long-legged, hence well adapted to movement through deep snow and wooded and marshy habitats. Their antlers are big but narrower and V-shaped, which ease movement in dense forest. Their body [fat] reserves in fall are small and not comparable to the High Arctic [Svalbard] form" (Holand et al., 2022 and references therein). Its metatarsus averages 21% longer than that of Eurasian tundra reindeer (measurements of Willemsen, 1983 for the former and Banfield 1961 for the latter) and males are about 48% heavier (data from Jacobi, 1931, Nieminen & Helle, 1980). Its mating system is harem-tending; most migrate altitudinally between summer pastures and their winter forest range, but some do not migrate from their summer pastures (Kojola, 1986, Panchenko et al., 2021).

Banfield (1961) and others, based on significant cranial differences from tundra reindeer, particularly their arched nasal bones (vs. flattened in tundra reindeer), and the lack of such differences among the forest types he studied, synonymised *phylarchus, buskensis (= valentinae), angustirostris* and several other forest types with *R. t. fennicus*.

Flagstad and Røed (2003), using mtDNA, found "three major haplogroups … representing three separate populations during the last glacial", the third (after NAL and BEL) being the Finnish forest reindeer, *R. f. fennicus*; this was confirmed by Yannic et al. (2013). Genetic reviews have shown some introgression from domestic tundra reindeer, but the latter generally do not survive in the forest reindeer's deep-snow forest habitat (Nieminen & Helle, 1980). Morphological, physiological, ecological differences, and genetic distance, were the reasons for re-elevating *R. fennicus* (Harding, 2022a).

The Altai forest reindeer, *R. f. valentinae*, shares three mtDNA haplotypes with Finnish forest reindeer, and has two unique haplotypes, indicating a unique lineage; there was no introgression from domestic reindeer (Vasilchenko et al., 2020). It and the Karelian forest reindeer cluster together with the Finnish forest reindeer, but the Kamchatka forest reindeer, *R. f. phylarchus*, clustered as a sister clade to all forest and tundra reindeer except for the alpine tundra reindeer, *R. t. tarandus*, with clustered outside of all of the above (Rozhkov [Рожков] et al., 2020). The narrow-nosed reindeer, *R. f. angustirostris*, has not been sampled for genetic analysis. The uncertain phylogenetic position of these two eastern Siberian reindeer is reflected in Fig. 3.

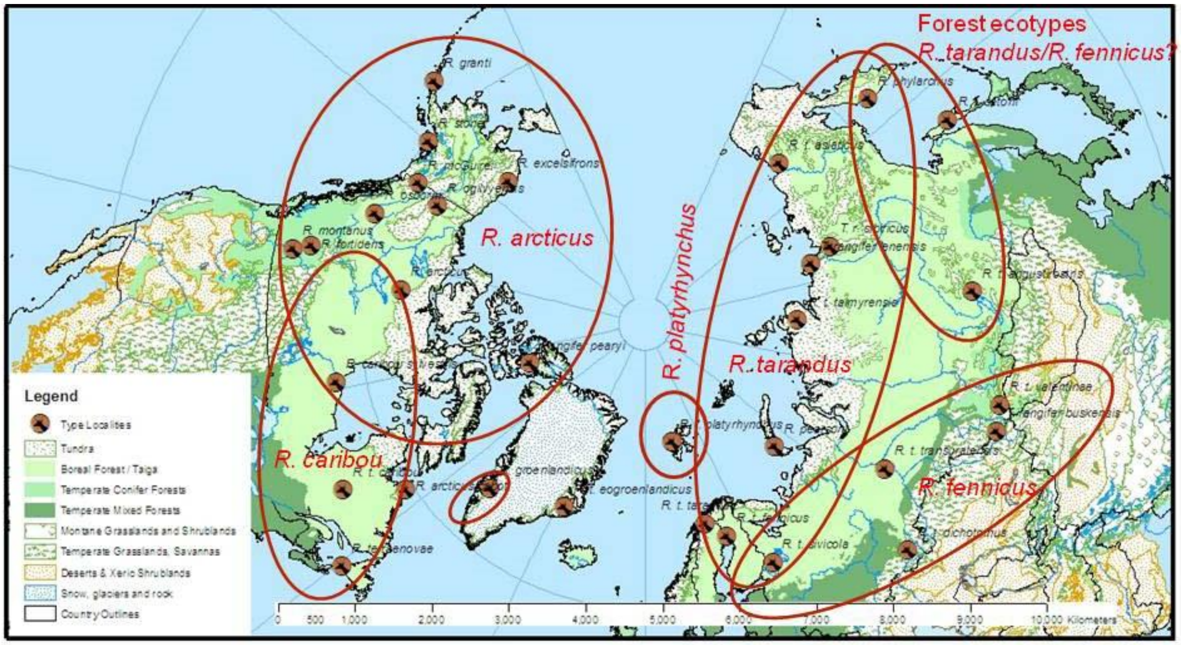

Figure 2. Approximate caribou and reindeer species distribution overlaid on Fig. 1 from Harding, 2022. Most type localities of named species and subspecies are shown. The ellipse in the upper right is labeled "*R. tarandus/R. fennicus*" to indicate uncertainty (see text). Biomes are from World Wildlife Fund Terrestrial Ecozones.

Besides their genetic and morphological distinctiveness, Eurasian forest reindeer may have different ancestry. They probably descended from a primitive ancestor, *Cervus [R.] guettardi* Desmarest, 1822, that was isolated in a western Europe refugium (Croitor, 2018). *C. guettardi* was replaced elsewhere (except in the western refugium) by a more evolved grassland-adapted reindeer, *R. constantini* Flerov, 1934, in the late Pleistocene; *R. constantini* was later replaced by modern tundra reindeer, *R. tarandus* (Croitor, 2018). Lacking a direct common ancestor, Eurasian forest reindeer cannot be conspecific with *R. tarandus*. It is *R. fennicus* Lönnberg, 1909 (Miller Jr., 1912).

Discussion

In revising *Rangife*r, I concurred with earlier authors (e.g., Anderson, 1946, Ellerman & Morrison-Scott, 1951, Banfield, 1961) who found that most species (*R. excelsifrons, R. mcquirei, R. ogilviensis, R. sylvestris*) and subspecies (*R. t. sivicola, R. t. transuralensis, R. t. dichotomus, R. t. taimyrensis, T. r. lenensis, R. t. setoni*, *T. r. ogilviensis* and *T. r. keewatinensis*) described from 1890 to 1937 were either invalid or were junior synonyms of a smaller number of valid species (type localities are mapped in Fig. 1 in Harding, 2022a).

Geist (2007) said that Banfield's (1961) principal error in synonymizing most of the subspecies was using only skeletal (mainly cranial) metrics that, although seemingly objective, vary by age, gender and condition of the specimens; he advocated using highly conserved "nuptial" characteristics such as pelage colour patterns and antler shape, which are sexually selected and vary with mating systems, to diagnose subspecies:

> *…segregate populations by their nuptial or rutting dress, or "uniform". These characteristics vary with the age of the males, are minimally affected by environment and are best expressed in old males at breeding time… selection for nuptial characteristics is done through female sexual selection (Geist, 2007).*

The visual stimuli that differ by caribou/reindeer subspecies are the "mate recognition system," a central component of the biological species definition (Patterson, 1980). Geist (1998) illustrated the pelage patterns and antler types of mature males of most recognized subspecies: woodland, Newfoundland, High Arctic, barren-ground, Osborn's and Labrador caribou and European alpine and Siberian tundra and Svalbard reindeer; and he described diagnostic nuptial pelage and antler shapes of those that he recognized but did not illustrate: European forest, Novaya Zemlya, Altai and Kamchatka reindeer. All of these, and a few others, have genetic distances from each other, and other markers such as shared versus unique haplotypes, to separate them as at least subspecies (Harding, 2022a, Harding, 2022b). Not surprisingly, they line up well with subspecies formerly described by quantitative morphometrics.

The phylogenetic species concept —"the smallest diagnosable cluster of individual organisms within which there is a parental pattern of ancestry and descent" (Cracraft, 1983) is controversial when applied to species (e.g., Zachos & Lovari, 2013). Applied to subspecies, however, it works: a population of the same lineage, with characters that are consistently diagnosable and is monophyletic. This is consistent with de Queiroz (2007), "a separately evolving metapopulation lineage" with "secondary properties (intrinsic reproductive isolation, diagnosability, monophyly) as operational criteria relevant to assessing lineage separation". These principles and molecular data (Table 1) have guided me in resurrecting five species (six total: Fig. 3) and four subspecies of *Rangifer* (Table 2) that had been previously named, but not internationally recognized by Grubb (2005) and Mattioli (2011).

Ethics: No live animals were used in preparation of this article. However, as a hunter, or as a researcher sharing meals with Dene or Inuit colleagues, I have tasted caribou venison from all of the ecotypes from western and Arctic Canada mentioned herein, and one from Europe.

Table 1. Summary of pairwise comparisons of genetic distance between species of *Rangifer* from Harding (2022a, 2022b).

Pairwise species (subspecies or population)	F_{ST} or other as specified	Notes	Source
Greenland caribou (*R. groenlandicus*)–all other clades	Σ = 0.44	Microsatellite loci	(Yannic et al., 2013)
Greenland caribou (*R. groenlandicus*)–all other clades	0.69–2.21	Nei: Microsatellite loci	Røed (2005)
Svalbard (*R. platyrhynchus*)–all other clades	Σ = 0.41	Microsatellite loci	(Yannic et al., 2013)
Greenland caribou (*R. groenlandicus*–Svalbard (*R. platyrhynchus*)	0.69	Microsatellite loci	(Yannic et al., 2013)
“Russian and Scandinavian reindeer” (*R. tarandus*)–Canadian barren-ground (*R. arcticus*)	0.306–0.333	Microsatellite loci	Cronin et al. (2006)
Scandinavian tundra (*R. tarandus*)–Alaskan barren-ground (*R. arcticus*)	0.332	mtDNA	Cronin et al. (2006)
Russian tundra (*R. tarandus*)–Alaskan barren-ground (*R. arcticus*)	0.053	Microsatellite loci	Cronin et al. (2006)
Alaskan Barren-ground (*R. arcticus arcticus*) – woodland (Slave Lake boreal, *R. caribou caribou)*	0.124–0.146	mtDNA	(Weckworth et al. 2012)
Alaskan Barren-ground (*R. arcticus arcticus*) – woodland (Slave Lake boreal, *R. caribou caribou)*	0.281–0.355	mtDNA	(Cronin et al. 2005)
Canadian barren-ground (*R arcticus arcticus*)–woodland (*R. caribou*)	0.412–0.518	mtDNA	(Cronin et al. 2005)

Woodland, 12 herds (*R. caribou*)–Arctic caribou, Rocky Mountain, 10 herds (*R. a. fortidens*)	0.06–0.92	mtDNA, Φ_{ST}	(Weckworth et al. 2012)
Woodland, 12 herds (*R. caribou*)–Arctic caribou, Rocky Mountain, 10 herds (*R. a. fortidens*)	0.033 to 0.32	Microsatellite loci	(Weckworth et al. 2012)
High Arctic (*R. a. pearyi*)–southern mountain (*R. a. montanus*)	0.22	Microsatellite loci	(Serrouya et al. 2012)
Graham herd (*R. a. osborni*–Qamanirjuaq barren-groud *R. a. arcticus*	0.04	Microsatellite loci	(Serrouya et al. 2012)
Eurasian tundra (*R. tarandus*)—Eurasian taiga/forest (*R. fennicus*)	0.038–0.094	SNP	(Kharzinova et al., 2018)

Table 2. Summary of revised and original names of caribou and reindeer species and subspecies from Harding (2022a, 2022c) [1] .

Revised Name	**Original accepted name**
Greenland caribou, *R. groenlandicus* (Borowski, 1780	*Cervus grönlandicus* (Borowski, 1780: 72)
Svalbard reindeer, R. *platyrhynchus* (Vrolik, 1829)	*Cervus (Tarandus) platyrhynchus* (Vrolik, 1829: 160)
Arctic caribou, *Rangifer arcticus (*Richardson, 1829) • Barren-ground caribou, *R. a. arcticus (*Richardson, 1829) • Selkirk Mountain caribou, *R. a. montanu*s Seton-Thompson, 1899 • Rocky Mountain, caribou, *R. a. fortidens* Hollister, 1912 • Osborn's or Northern Mountain caribou, *R. a. osborni* Allen, 1902 • Stone's or Alaska Mountain caribou, *R. a. stonei* Allen, 1901 • Grant's or Alaska Peninsula caribou, *R. a. granti* Allen, 1902 • High Arctic or Peary's caribou, *R. a. pearyi*	*Cervus tarandus* var. α *arctica* (Richardson, 1829: 341)
Woodland caribou, *R. caribou* (Gmelin, 1788) • Boreal woodland caribou, *R. c. caribou* (Gmelin, 1788) • *R. c. caboti* Allen, 1914 • *R. c. terrænovæ* Allen, 1896	[*Cervus tarandus*] γ *caribou* (Gmelin, 1788: 177)
Eurasian tundra reindeer, *R. tarandus* (L., 1758) • Alpine reindeer, *R. t. tarandus* (L., 1758) • Tundra reindeer, *R. t. sibiricus (*von Schreber, 1784)	*Cervus tarandus* (Linnaeus, 1758: 67)
Eurasian forest reindeer, *Rangifer fennicus* Lönnberg, 1909	*Rangifer tarandus fennicus* Lönnberg, 1909: 10

- Finnish forest reindeer, *R. f. fennicus*

  Lönnberg, 1909
- Altai forest reindeer, *R. f. valentinae*

  Flerov, 1933
- Narrow-nosed reindeer, *R. f. angustirostris*

  Flerov, 1932
- Kamchatka forest reindeer, *R. f. phylarchus*

  Hollister, 1912

[1] Authorities who named a species in a different genus are in parentheses, as per the ICZN rules of nomenclature.

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The outlier: new data on a free-ranging marsh deer push the upper limit of the species' body size

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The marsh deer (*Blastocerus dichotomus*) occurs in wetlands and marshy habitats from southern Amazonia to Argentina (Pinder & Grosse 1991). It is the largest deer in South America, with reported adult head and body lengths of 153-191 cm and body weight of 80-150 kg (Pinder & Grosse 1991, Piovezan et al. 2010, Galindo et al. in press). Most of the information available on body measurements of the marsh deer has been obtained in Brazil, where field research and captive programs provided opportunities to collect such data (e.g., Duarte 2008, Galindo et al. in press).

The southernmost population of the marsh deer inhabits the Paraná River Delta, Argentina (Varela 2003) and differs genetically from other populations (Márquez et al. 2006, Wolfenson 2021). Furthermore, the Paraná River Delta population has been recently categorized as Endangered because of poaching, habitat loss, and dog predation (Pereira et al. 2019). Since 2015, as a part of an initiative aimed at studying and conserving this population ("Pantano Project", www.proyectopantano.org, see Pereira et al. 2018), marsh deer individuals have been captured and fitted with satellite collars to evaluate habitat use and movement patterns. On August 19, 2022, an adult male was captured and anesthetized (Fig. 1) on a property of the forestry company Arauco Argentina S.A. (33°59´S and 58°54´W) in the province of Buenos Aires, Argentina. Head plus body length (excluding tail) of this individual was 209 cm, whereas body weight was 154.8 kg. These figures were larger than those recorded for another 13 males previously captured in this population (range head and body length = 146-194 cm; range body weight = 87-126 kg). The male presented light tooth wear and robust antlers in the hard stage, with 5- and 4-points on the right and left sides, respectively.

Figure 1. Adult male marsh deer (*Blastocerus dichotomus*) captured on August 19, 2022, in the Paraná River Delta. Photo credits: Juan F. Tellarini.

Although tooth wear patterns suggested that the individual was a young adult, tooth wear rates can vary based on diet, habitat, and tooth characteristics (e.g., Hewison et al. 1999), preventing us from accurately estimating its age. To the best of our knowledge, body measurements documented for this male represent World records for the species, exceeding the upper limits of head and body length and body weight previously reported in the literature. Since very-large marsh deer individuals are often observed in the Paraná River Delta (Fig. 2), future data collection on this population might push even further the upper limits of body measurements of this species.

Figure 2. Two large marsh deer (Blastocerus dichotomus) individuals observed in the Paraná River Delta. Photo credits: Javier A. Pereira (left) and Silvia Usatorre (right).

These data, in turn, would help to clarify patterns of intra-specific body size variation (e.g., Bergmann´s rule; Mayr 1956) in the largest deer of South America.

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Latest edition of International studbook (ISB) for Visayan Spotted Deer (*Rusa alfredi*) published

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Recently, the International studbook (ISB) for Visayan Spotted Deer (*Rusa alfredi*) was published. The studbook has been kept at Landau Zoo, Germany, since 2004, and in 2019 an European Ex-Situ Programme (EEP) for the species was established by the European Association of Zoos and Aquaria (EAZA). On 31.12.2021 a total of 48,45 [93] Visayan spotted deer were held at 28 institutions in Europe. Another 19,24,3 [46] deer were kept in 2 institutions in the Philippines, so the official total population under human care (comprised in the studbook) adds up to 67,69,3 [139] animals. *Rusa alfredi* is listed as "Endangered" under the IUCN red list. Habitat conversion and intensive hunting are the main threats to the species. The back-up population under proper human management is also important for environmental education, and the European Zoological Gardens support the on-site conservation measures of the Talarak Foundation in the Philippines, which runs rescue and breeding stations and works to protect the remaining forests. In 2020, Visayan Spotted Deer were released into the wild for the first time in the Danapa Nature Reserve in the Philippines. This 300 ha forested reserve is being used as a reintroduction site for the deer bred ex-situ and is now home to 29 specimen (18 males 11 females), introduced between June and September 2020, along with a group of 17 reintroduced Visayan Warty Pigs (*Sus cebifrons*), which are also closely monitored.

10th International Deer Biology Congress
Osijek, Croatia, 4th - 9th September 2022.

10th International Deer Biology Congress

Miljenko Bujanić, Nikolina Škvorc, Jo Anne Smith-Flueck, Dean Konjević

The Faculty of Veterinary Medicine University of Zagreb, in cooperation with the Faculty of Agrobiotechnical Sciences Osijek University Josip Juraj Strossmayer, organized the 10th International Deer Biology Congress (IDBC) in Osijek from September 4th to 9th, 2022. Dean Konjević was the president of the Organizing Committee, and Jo Anne Smith-Flueck was the president of the Scientific Steering Committee. The Congress was held under the High Patronage of the President of the Republic of Croatia.

Figure 1. President of Organizing Committee Dean Konjević (Faculty of Veterinary Medicine University of Zagreb) with professor Tihomir Florijančić from Faculty of Agrobiotechnical Sciences Osijek University Josip Juraj Strossmayer

The first International Deer Biology Congress (IDBC) was organized in Dunedin (New Zealand) in 1983. The main purpose of the IDBC is to gather professionals from Europe, North and South America, Asia, Australia and New Zealand, who are experts in deer biology, diseases, conservation, and management in both wild and captive conditions. The Congress provides opportunities for discussion, exchange of knowledge and experiences, reviving old ones and creating new acquaintances and collaborations.

The participants of the 10th IDBC came from 22 countries and presented their research within four thematic units: *Deer Antlers and Conservation* (17 presented topics), *Deer Habitat and Management* (17 presented topics), *Deer Health and Diseases* (16 presented topics) and *Deer Physiology and Nutrition* (16 topics presented). In addition, 19 papers were presented in the poster section. In total, 130 scientists presented 85 studies.

Figure 2. Participants of 10th International Deer Biology Congress

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A special value to this Congress was given by seven invited speakers. Uwe Kierdorf presented a plenary lecture "*Antlers as bioindicators of environmental pollution: principles, achievements, and future research directions*"; Tomás Landete-Castillejos: "*From a general anti-cancer treatment to deer osteoporosis: the consequences of antler as the fastest growing tissue*"; Christian Nellemann: "*Global threats to Deer conservation in a changing world*"; Marco Apollonio: "*Deer and climate change impacts and perspectives*"; Emily Latch: "*Genetics informs meaningful intraspecific taxonomy: the black-tailed and mule deer complex*"; Francisco Ceacero Herrador: "*Combined effects of supplementation of amino acids and immunocastration in first antler growth of farmed fallow deer (Dama dama)*" and Dean Konjević: "*Fascioloides magna – the development of host-parasite interactions in Europe*". Unfortunately, due to the COVID-19 situation, Colin Mackintosh was not able to attend as a guest plenary speaker. Moreover, the pandemic restricted several Chinese deer biologists and scientists from attending. The eminent list of invited lecturers, supervision by the International Deer Biology Society, the tradition of the Deer Conferences, and the beauty of the Baranja region guaranteed a successful Congress on a wide international level.

An international three-member committee presented the George A. Bubenik Memorial award, in honor of one of the leading world deer researchers – for the best lecture presented by a young scientist. This award went to Savannah Grace. Another three-member international committee presented the Award for the best poster to Christian Ehrmantraut.

The last IDBC in Europe was held in 2006 in the Czech Republic. We are very proud that after so many years the congress venue came back to Europe and this time we managed to organize this congress in beautiful Croatia, with the opportunity to present autochthonous products, nature, customs and cultural events of the region. The satisfied participants and their supportive comments at the end of the Congress are confirmation that they returned back to their homes with a handful of positive impressions.

Finally, a team of scientists from New Zealand proposed the organization of the 11th IDBC in Dunedin, which completes the cycle by returning the Congress to the first place of its organization.

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