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Karyotype Symmetry/Asymmetry Index (S/AI) in Bovidae Taxa

Halil Erhan EROĞLU

Yozgat Bozok University, Faculty of Science and Art, Department of Biology, Yozgat, Turkey

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* *Corresponding author e-mail: herhan.eroglu@bozok.edu.tr*

Abstract

The chromosomal data, particularly karyotype asymmetry, provide valuable information on karyotypic phylogeny and speciation. The karyotype asymmetry is a good expression of the general morphology of chromosomes. The S/AI is a formula used to calculate the karyotype asymmetry. The formula was applied to 79 species and five subspecies from 46 genera for female individuals and 72 species and five subspecies from 42 genera for male individuals in the Bovidae family. According to the S/AI values between 1.2903 and 3.0000, the dendrograms were drawn to demonstrate the interspecies relationships in the family. The karyotypes of females were symmetrical in 10 species and two subspecies from 6 genera and between symmetrical and asymmetrical in 69 species and three subspecies from 40 genera. Male karyotypes were symmetrical in 10 species and two subspecies from 6 genera and between symmetrical and asymmetrical in 62 species and three subspecies from 36 genera. The dendrograms will contribute to phylogenetic studies in mammals. Already, they showed results similar to those of molecular taxonomy.

Key Words: Karyotypic variations, Chromosome, Interspecific relationships

Bovidae Taksonlarında Karyotip Simetri/Asimetri İndeksi (S/AI)

Öz

Kromozomal veriler, bunlardan özellikle karyotip asimetrisi, karyotipik filogeni ve türleşme hakkında değerli bilgiler sağlamaktadır. Karyotip asimetrisi, kromozomların genel morfolojisini iyi bir şekilde ifade eder. S/AI, karyotip asimetrisini hesaplamak için kullanılan bir formüldür. Formül, Bovidae familyasında dişi bireyler için 46 cinsten 79 tür ve 5 alttüre, erkek bireyler için 42 cinsten 72 tür ve 5 alttüre uygulanmıştır. Familyadaki türler arası ilişkileri gösteren dendrogramlar, 1.2903 ile 3.0000 arasında değişen S/AI değerlerine göre çizilmiştir. Dişilerin karyotipleri 6 cinsin 10 tür ve 2 alttüründe simetrik, 40 cinsin 69 tür ve 3 alttüründe ise simetrik ve asimetrik arasındadır. Erkeklerin karyotipleri 6 cinsin 10 tür ve 2 alttüründe simetrik, 36 cinsin 62 tür ve 3 alttüründe ise simetrik ve asimetrik arasındadır. Dendrogramlar, memelilerdeki filogenetik çalışmalara katkıda bulunacaktır. Dendrogramlar ve moleküler taksonomi sonuçları benzer sonuçlar göstermişlerdir.

Anahtar Kelimeler: Karyotipik varyasyonlar, Kromozom, Türler arası ilişkiler

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1. INTRODUCTION

Bovidae (Gray, 1821) is placed in Artiodactyla (Owen, 1848). The family comprises 146 wild and domestic species in 51 genera (Lynx Nature Books 2023). The Bovidae are the most widespread family of extant Artiodactyla (Wolfe 2015; Itis 2023). The bovids include the ruminant mammals commonly known as gaur, bison, yak, sheep, duiker, and gazelle. Wild bovids can be found throughout Africa, much of Europe, Asia, and North America, and they characteristically inhabit grasslands. The number of Bovidae taxa decreases, especially with the human impact (Wolfe 2015). Humans have always hunted the bovids in America and Eurasia. According to the IUCN Red List of Threatened Species, 19 species are categorized as Endangered (EN), and six species are categorized as Critically Endangered (CR). *Hippotragus leucophaeus* (bluebuck), *Bos primigenius* (aurochs), *Gazella bilkis* (queen of Sheba's gazelle), and *Gazella saudiya* (Saudi gazelle) are categorized as Extinct (EX) (Iucnredlist 2023).

The family Bovidae is one of the most important members of the world's wildlife and natural life (ADW 2024).

Therefore, many taxonomic and cytotaxonomic studies have been reported related bovids till now. The chromosome numbers of Bovidae were generally between $2n = 50$ and $2n = 60$. Many species have 56, 58, and 60 chromosomes (See Table 1 for References). On the other hand, there were also species with lower chromosome numbers, such as $2n = 30$, which were *Gazella dorcas*, *Gazella marica* (formerly *Gazella subgutturosa*), and *Raphicerus campestris* (Wallace and Fairall 1967; Wurster 1972; Tez et al. 2005; Saatoğlu et al. 2019). These karyotypic variations resulted from the centric fusions. The biarmed translocation formed the Robertsonian chromosomes (Gallagher and Womack 1992; Oh et al. 2011).

Karyotype asymmetry is a good expression of the general morphology of chromosomes. One of the most cheap, popular and most preferred methods in comparative cytotaxonomy is that concerning karyotype asymmetry. Scientists have developed various methods to assess karyotype asymmetry within a set of chromosomes to date. (Paszko, 2006; Eroğlu et al. 2013; Eroğlu 2015). All these quantitative methods depend on parameters such as total chromosome length and arm lengths. Unlike these, S/A_I is a useful parameter that calculates asymmetry according to chromosome type and centromere position (Eroğlu 2015). This study aims to determine interspecific relationships in the family Bovidae using the S/A_I parameter and to discuss the effects of karyotypic variations and centric fusions, which play an important role in speciation, on karyotype asymmetry in Bovidae.

2. MATERIAL AND METHOD

2.1. Karyotype Asymmetry Formula

Karyotype asymmetries were calculated with the formula given below.

$$S/A_I = (1 \times M) + (2 \times SM) + (3 \times A \text{ or } ST) + (4 \times T) / 2n$$

In formula, M, SM, A, ST, and T means the number of metacentric, submetacentric, acrocentric, subtelocentric, and telocentric chromosomes, respectively. S/A_I value varies between 1.0 and 4.0, and accordingly, karyotypes are full symmetric (1.0), symmetric ($1.0 < S/A_I \leq 2.0$), between symmetric and asymmetric ($2.0 < S/A_I \leq 3.0$), asymmetric ($3.0 < S/A_I < 4.0$) and, full asymmetric (4.0) (Eroğlu 2015).

2.2. The Chromosomal Data

An extensive literature review identified the chromosome numbers, karyotype formulae, karyotype asymmetries, and karyotype types of 79 species and 5 subspecies belonging to 46 genus. The scientific names were checked from the Integrated Taxonomic Information System (Itis 2023) and the IUCN Red List of Threatened Species (Iucnredlist 2023). The scientific names of some species can be reported differently in the literature. The water buffalo is an important example: *Bubalus bubalis* (Itis 2023) and *Bubalus arnee* (Iucnredlist 2023). Another example is mouflon and domestic sheep. The mouflon is the ancestor of domestic sheep, but sometimes the same scientific name is used for both (Itis 2023).

2.3. Drawing the Dendrograms

According to the chromosomal data, the dendrograms were drawn showing the interspecific relationships by Past 4.14 software. The first and second dendrograms consisted of karyotypes of 78 species and six subspecies for female individuals and 71 species and six subspecies for male individuals, respectively. There were not seven species in the male dendrogram for two reasons. (i) Only the female karyotype had been reported in *Philantomba maxwellii*, *Pelea capreolus*, and *Kobus ellipsiprymnus* (Hard 1969; Gallagher and Womack 1992; Robinson et al. 2014). (ii) In *Capra aegagrus*, *Ammotragus lervia*, *Budorcas taxicolor*, and *Boselaphus tragocamelus*, because the Y chromosome was too small, its chromosome type could not be determined (Chandra et al. 1967; Nadler et al. 1974; Pasitschniak-Arts et al. 1994).

3. RESULTS

Table 1 gives the diploid chromosome numbers, karyotype formulae, S/AI values, and karyotype types of the taxa. The diploid numbers and S/A_I values ranged from 30 to 60 and 1.2000 to 3.0000. While 14 species had the highest S/A_I value, the lowest value was only in *Gazella marica*.

Table 1. The karyotype formulae, index values and karyotype types of the taxa.

Scientific name (common name)	*2n*	Chromosomes	References	S/A_I-F S/A_I-M	Karyotype type
Litocranius walleri (Gerenuk)	60	58A X = A, Y = A	Wurster and Benirschke1968	3.0000 3.0000	T2
Oreotragus oreotragus (Klipspringer)	60	58A X = A, Y = A	O'Brien et al. 2006	3.0000 3.0000	T2
Philantomba maxwellii (Maxwell's duiker)	60	58A X = A, Y = ?*	Hard 1969	3.0000	T2
Procapra gutturosa (Mongolian gazelle)	60	58A X = A, Y = A	Soma et al. 1980	3.0000 3.0000	T2
Pantholops hodgsonii (Chiru)	60	58A X = A, Y = A	Liu et al. 2012	3.0000 3.0000	T2
Hippotragus equinus (Roan antelope)	60	58A X = A, Y = A	Fordyce–Boyer et al. 1995	3.0000 3.0000	T2
Hippotragus niger	60	58A	Fordyce–Boyer	3.0000	T2

(Sable antelope)		X = A, Y = A	et al. 1995	3.0000	
Capra ibex (Alpine ibex)	60	58A X = A, Y = A	Lux et al. 2004	3.0000 3.0000	T2
Capra falconeri (Markhor)	60	58A X = A, Y = A	Lux et al. 2004	3.0000 3.0000	T2
Capra aegagrus (Wild goat)	60	58A X = A, Y minute**	Nadler et al. 1974	3.0000	T2
Capra hircus (Domestic goat)	60	58A X = A, Y = M	Iannuzzi et al. 1996	3.0000 2.9667	T2
Aepyceros melampus (Impala)	60	58A X = A, Y = M	Wurster and Benirschke 1967a	3.0000 2.9667	T2
Naemorhedus goral (Goral)	56	54A X = A, Y = A	Soma et al. 1980	3.0000 3.0000	T2
Naemorhedus baileyi (Red Goral)	56	54A X = A, Y = A	Liu et al. 1994	3.0000 3.0000	T2
Naemorhedus caudatus (Long–tailed goral)	56	54A X = SM, Y = A	Oh et al. 2011	2.9643 2.9821	T2
Naemorhedus griseus (Chinese goral)	54	2SM + 50A X = A, Y = A	Liu et al. 1994	2.9630 2.9630	T2
Tetracerus quadricornis (Four–horned antelope)	38	36A X = A, Y = M	Wurster and Benirschke 1967a	3.0000 2.9474	T2
Cephalophus niger (Black duiker)	60	58A X = SM, Y = A	Hard 1969	2.9667 2.9833	T2
Cephalophus silvicultor (Yellow–backed duiker)	60	58A X = SM, Y = A	Hard 1969	2.9667 2.9833	T2
Cephalophus zebra (Zebra duiker)	58	2SM + 54A X = M, Y = A	Hard 1969	2.8966 2.9310	T2
Bison bison (American bison)	60	58A X = SM, Y = A	Gallagher et al. 1999	2.9667 2.9833	T2
Bison bonasus (European bison)	60	58A X = SM, Y = A	Gallagher et al. 1999	2.9667 2.9833	T2
Bos frontalis (Domestic gaur)	58	2SM + 54A X = SM, Y = SM	Gallagher and Womack 1992	2.9310 2.9310	T2
Bos gaurus (Wild gaur)	58	2SM + 54A X = SM, Y = M	Gallagher et al. 1999	2.9310 2.9138	T2
Bos taurus (Cattle)	60	58A X = SM, Y = SM	Lux et al. 2004	2.9667 2.9667	T2
Bos javanicus (Banteng)	60	58A X = SM, Y = M	Gallagher et al. 1999	2.9667 2.9500	T2
Bos grunniens (Domestic yak)	60	58A X = SM, Y = SM	Popescu 1969	2.9667 2.9667	T2
Connochaetes taurinus (Common wildebeest)	58	2SM + 54A X = A, Y = A	Gerneke 1967	2.9655 2.9655	T2
Connochaetes gnou (Black wildebeest)	58	2SM + 54A X = A, Y = A	Wurster and Benirschke1968	2.9655 2.9655	T2
Addax nasomaculatus (Addax)	58	2SM + 54A X = A, Y = A	Claro et al. 1996	2.9655 2.9655	T2
Oryx dammah (Scimitar–horned oryx	58	2SM + 54A X = A, Y = A	Claro et al. 1994	2.9655 2.9655	T2
Oryx leucoryx (Arabian oryx)	58	2SM + 54A X = A, Y = A	Cribiu et al. 1990	2.9655 2.9655	T2
Oryx gazella (Gemsbok)	56	4SM + 50A X = A, Y = A	Hsu and Benirschke 1968	2.9286 2.9286	T2
Nilgiritragus hylocrius (Nilgiri tahr)	58	2SM + 54A X = A, Y = SM	Bernischke and Kumamoto1980	2.9655 2.9483	T2
Rupicapra rupicapra (Northern chamois)	58	2SM + 54A X = A, Y = SM	Gallagher and Womack 1992	2.9655 2.9483	T2
Tragelaphus angasii (Nyala)	56	2SM + 52A X = A, Y = A	Wurster and Benirschke1968	2.9643 2.9643	T2
Tragelaphus imberbis (Lesser kudu)	38	10M + 10SM + 16A X = A, Y = A	Benirschke et al. 1980	2.2105 2.2105	T2
Tragelaphus strepsiceros	32	8M + 18SM + 4A	Hsu and	1.9375	T1

(Greater kudu)		X = A, Y = A	Benirschke 1971	1.9375	
Tragelaphus spekii (Sitatunga)	30	6M + 20SM + 2A X = A, Y = A	Wurster et al. 1968	1.9333 1.9333	T1
Ammotragus lervia (Aoudad)	58	2M + 54A X = A, Y minute**	Nadler et al. 1974	2.9310	T2
Eudorcas rufifrons (Red–fronted gazelle)	58	2SM + 2ST + 52A X = SM, Y = M	Vassart et al. 1995	2.9310 2.9138	T2
Eudorcas thomsonii (Thomson's gazelle)	58	2SM + 2ST + 52A X = SM, Y = M	Nelson-Rees et al. 1967a	2.9310 2.9138	T2
Antidorcas marsupialis (Springbok)	56	4SM + 50A X = A, Y = M	Wurster and Benirschke1967b	2.9286 2.8929	T2
Pelea capreolus (Grey rhebok)	56	4SM + 50A X = A, Y = ?*	Robinson et al. 2014	2.9286	T2
Madoqua kirkii (Kirk's dik–dik)	48	4SM + 42A X = A, Y = A	Kumamoto et al. 1994	2.9167 2.9167	T2
Redunca fulvorufula (Mountain reedbuck)	56	2M + 2SM + 50A X = A, Y = A	Rubes et al. 2007	2.8929 2.8929	T2
Nesotragus moschatus zuluensis (Suni)	56	2M + 2SM + 50A X = A, Y = A	Kingswood et al. 1998	2.8929 2.8929	T2
Nesotragus moschatus moschatus (Suni)	54	4M + 2SM + 46A X = A, Y = A	Kingswood et al. 1998	2.8148 2.8148	T2
Nesotragus moschatus akeleyi (Suni)	52	2M + 6SM + 42A X = A, Y = A	Kingswood et al. 1998	2.8077 2.8077	T2
Pseudois nayaur (Bharal)	54	6SM + 46A X = A, Y = A	Bunch et al. 2000	2.8889 2.8889	T2
Ovis ammon (Argali)	56	4M + 50A X = A, Y = M	Bagirov et al. 2012	2.8571 2.8214	T2
Ovis orientalis (Mouflon)	54	6M + 46A X = A, Y = M	Bagirov et al. 2012	2.7778 2.7407	T2
Ovis aries (Domestic sheep)	54	6M + 46A X = A, Y = M	Bagirov et al. 2012	2.7778 2.7407	T2
Ovis canadensis (Bighorn sheep)	54	6M + 46A X = A, Y = M	Bagirov et al. 2012	2.7778 2.7407	T2
Ovis dalli (Thinhorn sheep)	54	6M + 46A X = A, Y = M	Bagirov et al. 2012	2.7778 2.7407	T2
Ovis nivicola (Snow sheep)	52	8M + 42A X = A, Y = M	Bagirov et al. 2012	2.6923 2.6538	T2
Budorcas taxicolor (Takin)	52	8SM + 42A X = A, Y minute**	Pasitschniak-Arts et al. 1994	2.8462	T2
Syncerus caffer (African buffalo)	52	8SM + 42A X = A, Y = A	Gallagher et al. 1999	2.8462 2.8462	T2
Bubalus bubalis (Water buffalo)	50	10SM + 38A X = A, Y = A	Gallagher et al. 1999	2.8000 2.8000	T2
Bubalus depressicornis (Lowland anoa)	48	12SM + 34A X = A, Y = A	Low and Benirschke 1973	2.7500 2.7500	T2
Neotragus pygmaeus (Royal antelope)	36	6SM + 28A X = SM, Y = A	Placentation 2007	2.7778 2.8056	T2
Kobus kob (Kob)	50	2M + 8SM + 38A X = A, Y = A	Kingswood et al. 2000	2.7600 2.7600	T2
Kobus ellipsiprymnus (Waterbuck)	50	10SM + 38A X = SM, Y = ?*	Gallagher and Womack 1992	2.7600	T2
Kobus leche (Southern lechwe)	48	12SM + 34A X = A, Y = A	Wurster and Benirschke1968	2.7500 2.7500	T2
Hemitragus jemlahicus (Himalayan tahr)	48	12SM + 34A X = A, Y = SM	Nelson–Rees et al. 1967b	2.7500 2.7292	T2
Capricornis crispus (Japanese serow)	50	4M + 6SM + 38A X = A, Y = A	Benirschke et al. 1972	2.7200 2.7200	T2
Capricornis swinhoei (Formosan serow)	50	4M + 6SM + 38A X = A, Y = A	Soma et al. 1981	2.7200 2.7200	T2
Capricornis sumatraensis (Sumatran serow)	48	2M + 10SM + 34A X = A, Y = A	Soma et al. 1982	2.7083 2.7083	T2
Ovibos moschatus	48	4M + 8SM + 34A	Pasitschniak–Arts	2.6667	T2

(Muskox)		X = A, Y = M	et al. 1994	2.6250	
Nanger dama (Dama gazelle)	38	18SM + 18A X = A, Y = A	Wurster and Benirschke1968	2.5263 2.5263	T2
Nanger granti (Grant's gazelle)	30 (F) 31 (M)	10M + 18SM X = SM, Y1,Y2 = A	Hsu and Benirschke 1975	1.6667 1.7419	T1
Beatragus hunteri (Hirola)	44	8M + 8SM + 26A X = A, Y = A	Kumamoto et al. 1996	2.4545 2.4545	T2
Boselaphus tragocamelus (Nilgai)	46	4M + 26SM + 16A X***, Y***	Chandra et al. 1967	2.2609	T2
Oreamnos americanus (Mountain goat)	42	18M + 22A X = A, Y = M	Wurster and Benirschke1968	2.1429 2.0952	T2
Alcelaphus buselaphus (Hartebeest)	40	20M + 18A X = A, Y = A	Wurster and Benirschke 1967a	2.0000 2.0000	T1
Damaliscus pygargus pygargus (Blesbok)	38	16M + 6SM + 14A X = A, Y = A	Kumamoto et al. 1996	2.0000 2.0000	T1
Damaliscus pygargus phillipsi (Blesbok)	38	16M + 6SM + 14A X = A, Y = A	Kumamoto et al. 1996	2.0000 2.0000	T1
Damaliscus lunatus (Topi)	36	12M + 12SM +10A X = A, Y = A	Kumamoto et al. 1996	2.0000 2.0000	T1
Gazella spekei (Speke's gazelle)	32 (F) 33 (M)	14M + 12SM + 4A X = SM, Y1,Y2 = A	Hsu and Benirschke 1974	1.6875 1.7576	T1
Gazella dorcas (Dorcas gazelle)	30 (F) 31 (M)	18M + 10SM X = A, Y1,Y2 = SM	Wurster 1972	1.4667 1.4839	T1
Gazella marica (Arabian sand gazelle)	30 (F) 31 (M)	24M +4SM X = SM, Y1,Y2 = A	Tez et al. 2005	1.2000 1.2903	T1
Raphicerus campestris (Steenbok)	30	20M + 8SM X = A, Y = M	Wallace and Fairall 1967	1.4000 1.3333	T1

Abbreviations: M-metacentric, SM- submetacentric, A-acrocentric, ST-subtelocentric, T-telocentric, F-female, M-male, T1-symmetric, T2-between symmetric and asymmetric. * There is no male in the karyotype study, ** Could not determine the type of chromosome, *** Not identified.

In Figure 1, while the karyotype type was between symmetric and asymmetric in the 40 genus, 69 species, and three subspecies, it was symmetric in the six genera, ten species, and two subspecies. The S/A_I values of females ranged from 1.2000 to 3.0000. In Figure 2, while the karyotype type was between symmetric and asymmetric in the 36 genus, 62 species, and three subspecies, it was symmetric in the six genera, ten species, and two subspecies. The S/A_I values of male ranged from 1.2903 to 3.0000. The genera *Tragelaphus* and *Nanger* had karyotype types both symmetric and between symmetric and asymmetric. All other genera showed only a single karyotype type.

4. DISCUSSION AND CONCLUSION

The ancestral bovid karyotype was $2n = 60$ (Wurster and Benirschke1968). Central fusions or Robertsonian translocations had been reported to caused interspecific karyotype variations in the family Bovidae (Gallagher and Womack). Although the chromosome number in genera *Alcelaphus*, *Damaliscus*, *Gazella*, *Tragelaphus*, *Nanger*, and *Raphicerus* was 40 or less, in other genera were greater than 40 (Figures 1 and 2). Interestingly, all species with fewer than forty chromosome numbers had symmetrical karyotypes, excluding lesser kudu, dama gazelle, royal antelope, and four-horned antelope. In the *Nanger* genus, karyotypic variation between dama and Grant's gazelle was due to differences in X and autosomal chromosomes. While Grant's gazelle had a symmetric karyotype with submetacentric X and metacentric, submetacentric autosomes; Dama's gazelle had more asymmetric karyotype with acrocentric X and submetacentric, acrocentric autosomes (Wurster and Benirschke1968; Hsu and Benirschke 1975). In the *Tragelaphus* genus, karyotypic variations were due to differences in autosomal chromosomes. While greater kudu and sitatunga had symmetric karyotype with few acrocentric chromosomes; nyala and lesser kudu had more asymmetric karyotype with more acrocentric chromosomes (Wurster and Benirschke1968; Wurster et al. 1968; Hsu and Benirschke 1971; Benirschke et al. 1980).

The karyotypes of domestic goat (*Capra hircus*) and four-horned antelope were located at the asymmetric limit in Figure 1, but this was not the case in Figure 2. The main reason was a heteromorphism between metacentric Y and acrocentric X (Table 1). In other *Capra* species, all chromosomes were acrocentric (Lux et al. 2004). The metacentric chromosome of the domestic goat probably originated from centric fusion. It was reported that the bovids biarmed chromosomes resulted from Robertsonian translocation (Oh et al. 2011).

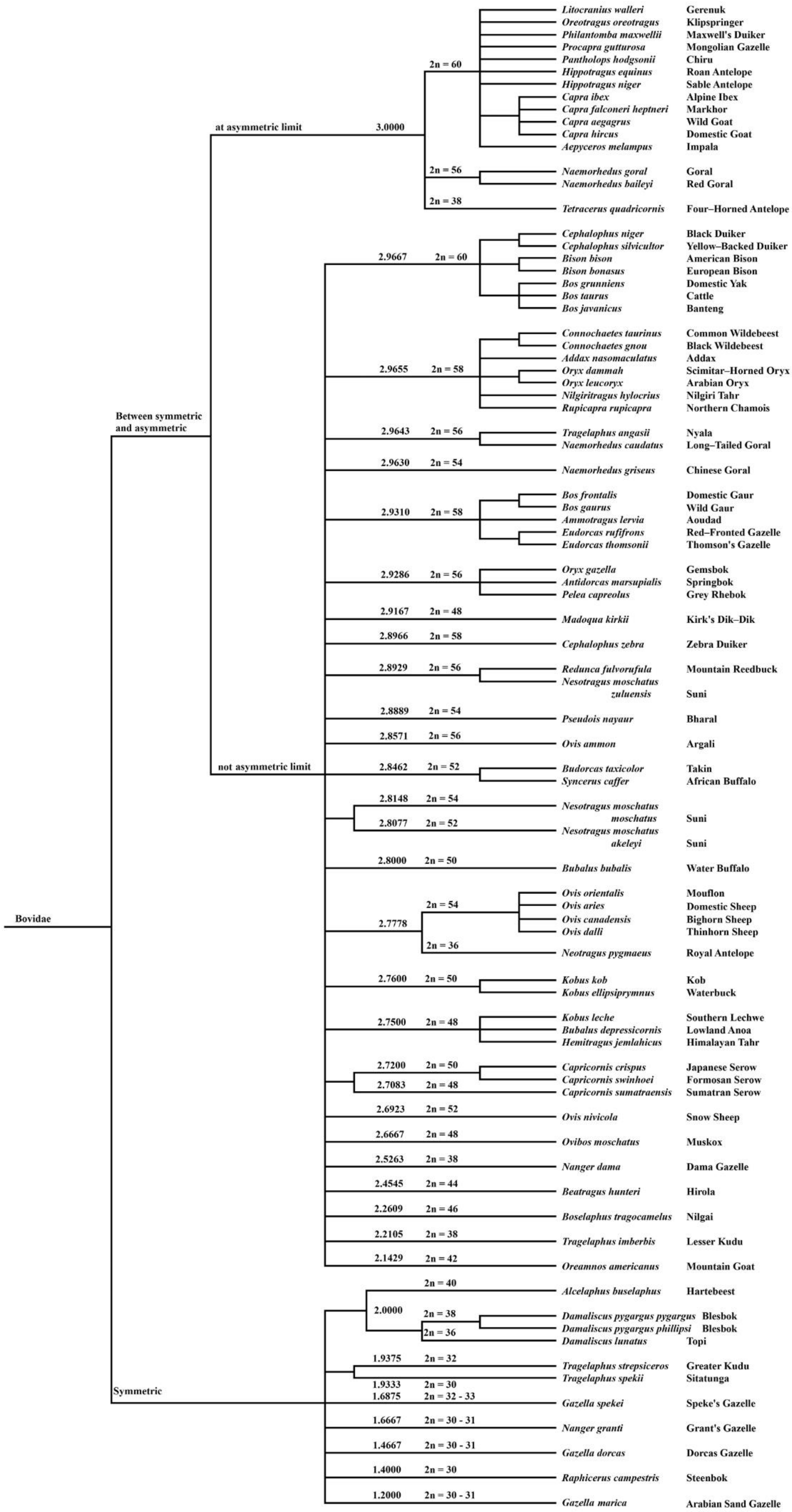

Figure 1. The female dendrogram demonstrating the interspecific relationships in family Bovidae

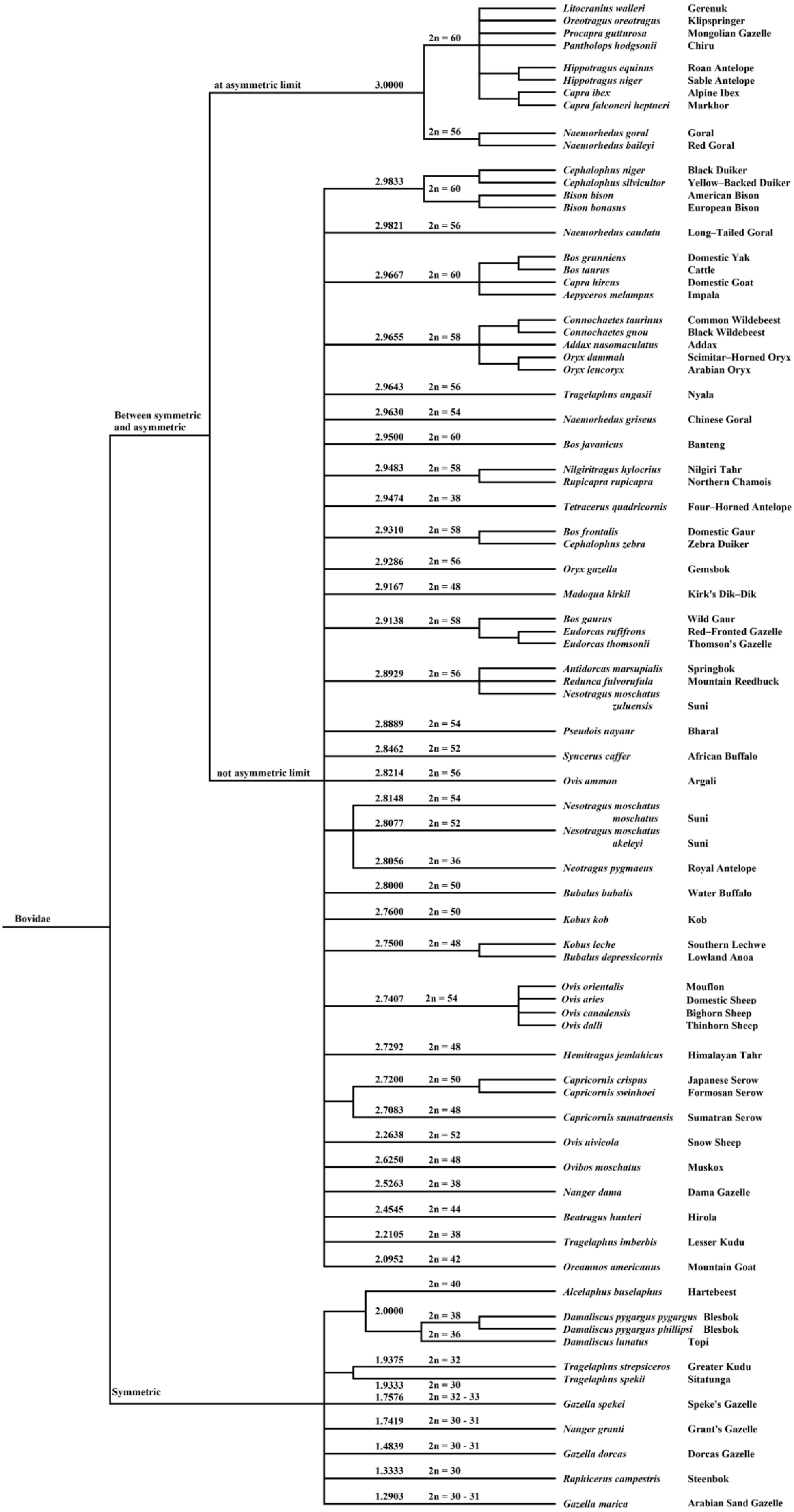

Figure 2. The male dendrogram demonstrating the interspecific relationships in family Bovidae

The karyotypes of the large genus *Bos*, *Bison*, and *Ovis* were between symmetric and asymmetric, but not at the asymmetric limit. The Bison genus had no karyotypic variation (Gallagher et al. 1999). In genus Bos, the variations were from the centric fusion between chromosome 2 and chromosome 28 of the ancestral karyotype (cattle). The centric fusion gave rise to the gaur karyotype consisting of one pair of submetacentric chromosomes (Gallagher and Womack 1992).

In genus *Ovis*, there was marked karyotypic variation. The karyotypic variation gradually occurred through centric fusions forming four classes. Class I was the ancestral karyotype and included one pair of metacentric chromosomes. Class II included two pairs of metacentric chromosomes; the argali was used in this class. Class III included three pairs of metacentric chromosomes and the mouflon, domestic sheep, bighorn sheep, and thinhorn sheep were in this class. Class IV included four pairs of metacentric chromosomes, and the snow sheep were included in this class (Bagirov et al. 2012). The karyotype asymmetry decreased with increasing metacentric chromosome pairs from Class I to IV.

In conclusion, the karyotypic variations that gradually arise through the centric fusions described above apply to the entire family. The variations in karyotype asymmetry result from the centric fusions that play an important role in the speciation of family Bovidae. The results present new data regarding the karyological characteristics of the family Bovidae that may be useful to understand interspecific relationships. The karyotype asymmetry and S/A_I parameter may be used together with the other parameters in phylogenetic studies of mammals. Already the dendrograms showed similar results with molecular taxonomy results (Bibi 2013; Bibi and Tyler 2022). For example, Bibi (2013) determined 16 fossil calibration points of relevance to the phylogeny of Ruminantia and Bovidae and constructed a dated molecular phylogeny with a reanalysis of the full mitochondrial genome of over 100 taxa. There are many similarities between his phylogenetic tree and the dendrograms in terms of species placement, especially *Bos*, *Ovis*, *Raphicerus*, *Nanger*, and *Gazella* species.

CONFLICT OF INTEREST

There is no conflict of interest.

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