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Artiodactyla Takımının Familya ve Türlerinin Karyotip Simetri/Asimetri İndeksi (S/A_I) ile Karşılaştırılması

The Comparison of the Families and Species of Order Artiodactyla with Karyotype Symmetry/Asymmetry Index (S/A_I)

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Özet. S/A_I formülü, hayvanlarda ve insanlarda karyotip asimetrisini belirlemek için kullanılan bir parametredir. Formül, 47 Artiodactyla türüne uygulanmıştır. Artiodactyla'da türler arası ve aileler arası ilişkileri gösteren dendrogramlar, 1.0000 ile 3.0000 arasında değişen S/A_I değerlerine göre çizilmiştir. Dişi karyotip tipleri; sekiz familya, 18 cins ve 36 türde simetrik ve asimetrik arası, beş familya, dokuz cins ve 10 türde simetrik ve sadece tek bir familya, cins ve türde ise tam simetriktir. Erkek karyotip tipleri; sekiz familya, 18 cins ve 34 türde simetrik ve asimetrik arası, beş familya, sekiz cins ve dokuz türde simetrik ve sadece tek bir familya, cins ve türde ise tam simetriktir.

Anahtar Kelimeler: Artiodactyla, karyotip, türlerarası ilişkiler.

Abstract. The S/AI formula is a parameter used to determine the karyotype asymmetry in animals and humans. The formula was performed to the 47 Artiodactyla species. According to the S/A_I values between 1.0000 and 3.0000, the dendrograms were drawn demonstrating the interspecies and interfamilies relationships in Artiodactyla. The female karyotype types are between symmetric and asymmetric in the eight families,

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18 genera and 36 species; symmetric in the five families, nine genera and 10 species; full symmetric in the only one family, genus and species. The male karyotype types are between symmetric and asymmetric in the 8 families, 18 genera and 34 species; symmetric in the five families, eight genera and nine species; full symmetric in the only one family, genus and species.

Key words: Artiodactyla, karyotype, interspecific relationships.

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1. Introduction

Artiodactyls are the most diverse, large, terrestrial mammals alive today with domestic and wild species. They include the predominantly herbivorous mammals known commonly as hoofed mammals. They consist of at least 240 species in 89 genera and 10 families. The number of Artiodactyla species has decreased because of human impacts [22–23]. According to the IUCN Red List, they are categorized as Endangered (37 species), Critically Endangered (11 species), Extinct in the Wild (two species) and Extinct (eight species) [23].

The chromosomal data are increasingly used in the cytotaxonomy. The basic number (x), diploid number ($2n$), and chromosome lengths are primary chromosomal data [10,30–31,35]. The chromosome numbers of Artiodactyla families are $2n = 58$ for Moschidae and Antilocapridae, $2n = 74$ for Camelidae, $2n = 30$ and 46 for Giraffidae, $2n = 32–38$ for Suidae, $2n = 20$, 26 and, 30 for Tayassuidae, $2n = 36$ for Hippopotamidae, $2n = 32$ for Tragulidae, between $2n = 30$ and $2n = 60$ for Bovidae and generally between $2n = 50$ and $2n = 70$ for Cervidae [1–9,11–21,24–29].

The primary chromosomal data are could be replaced numerically through aneuploidy and polyploidy, as well as through structural arrangements containing deletion, translocation, and inversion (which can change chromosome number by dysploidy mechanism). These chromosomal variations alter centromere position and chromosome morphology, and affect karyotype asymmetry. Therefore, the karyotype asymmetry is an important parameter supporting the morphological characters. [10,30–31,35]. The aim of this study is to determine the interspecific relationships among the species and families of Artiodactyla by karyological data and especially karyotype asymmetry (S/A_I).

2. Materials and Methods

2.1. The S/A_I Formula of Karyotype Asymmetry

The formula was reported by Eroğlu (2015) and given below [10].

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

The explanations of the abbreviations in the formula are given below in parentheses. M (metacentric chromosome number), SM (submetacentric chromosome number), A (acrocentric chromosome number), ST (subtelocentric chromosome number), T (telocentric chromosome number) and $2n$ (diploid chromosome number).

Eroğlu (2015) reported the new classification model with five types of karyotype symmetry/asymmetry. They are full symmetric, symmetric, between symmetric and asymmetric, asymmetric and, full asymmetric. A full symmetric karyotype is characterized by completely median chromosomes and the S/A_I value is 1.0000. On the contrary, a full asymmetric karyotype is characterized by telocentric chromosomes and the S/A_I value is 4.0000 [10].

2.2. S/A_I Values of Species and Applications

The karyotype formula, S/A_I value, and karyotype type of 47 species belonging to 10 families have been identified by an extensive literature review. The scientific names were checked from IUCN Red List and Integrated Taxonomic Information System [22–23].

The dendrograms were drawn demonstrating the interspecies and interfamilies relationships. The dendrograms showing karyological relationships were drawn with chromosome numbers, karyotype types, and S/A_I values by Past 4.12 software. The dendrograms contain the karyotypes of 47 females and 44 males, respectively. Three species are missing from two reasons in the male dendrogram. (i) Only the female karyotype has been reported in *Capreolus pygargus*. (ii) In *Capra aegagrus* and *Hylochoerus meinertzhageni*, Y chromosome is very small and its type has not been reported.

3. Results

In Table 1, the diploid chromosome numbers are observed from 20 to 74. Although the chromosome number in Moschidae, Antilocapridae, Bovidae, Cervidae and Camelidae is greater than 50, there are 46 or fewer chromosomes in Giraffidae, Suidae, Tayassuidae, Hippopotamidae and Tragulidae (Figures 1 and 2). As an interesting note, the species of Giraffidae, Suidae, Tayassuidae, Hippopotamidae and Tragulidae excluding okapi, pygmy hog, wild boar and collared peccary have both the less chromosome number and symmetric and full symmetric karyotypes.

Table 1
The karyological information of the studied species. The data are diploid numbers, karyotype formulae, S/A_I values, and karyotype types.

Species **(Author) (Common name)**	***2n***	**References**	**Chromosomes**	**S/A_I-F** **S/A_I-M**	**Karyotype Type**
Moschus berezovskii (Flerov, 1929) (Forest musk deer)	58	[8]	56A X = A, Y = A	3.0000 3.0000	T3
Antilocapra americana (Ord, 1815) (Pronghorn antelope)	58	[40]	56A X = A, Y = A	3.0000 3.0000	T3
Aepyceros melampus (Lichtenstein, 1812) (Impala)	60	[41]	58A X = A, Y = M	3.0000 2.9667	T3
Hippotragus equinus (É. Geoffroy St-Hilaire, 1803) (Roan antelope)	60	[11]	58A X = A, Y = A	3.0000 3.0000	T3
Hippotragus niger (Harris, 1838) (Sable antelope)	60	[11]	58A X = A, Y = A	3.0000 3.0000	T3
Capra ibex (Linnaeus, 1758) (Alpine ibex)	60	[29]	58A X = A, Y = A	3.0000 3.0000	T3
Capra falconeri (Wagner, 1839) (Markhor)	60	[29]	58A X = A, Y = A	3.0000 3.0000	T3
Capra aegagrus (Erxleben, 1777) (Wild goat)	60	[33]	58A; X = A, Y minute*	3.0000	T3
Capra hircus (Linnaeus, 1758) (Domestic goat)	60	[24]	58A X = A, Y = M	3.0000 2.9667	T3
Bos frontalis (Lambert, 1804) (Domestic gaur)	58	[13]	2SM + 54A X = SM, Y = SM	2.9310 2.9310	T3
Bos gaurus (C.H. Smith, 1827) (Wild gaur)	58	[12]	2SM + 54A X = SM, Y = M	2.9310 2.9138	T3
Bos taurus (Linnaeus, 1758) (Cattle)	60	[29]	58A X = SM, Y = SM	2.9667 2.9667	T3
Bos javanicus (d'Alton, 1823) (Banteng)	60	[12]	58A X = SM, Y = M	2.9667 2.9500	T3
Bos grunniens (Linnaeus, 1766) (Domestic yak)	60	[36]	58A X = SM, Y = SM	2.9667 2.9667	T3
Bison bison (Linnaeus, 1758) (American bison)	60	[12]	58A X = SM, Y = A	2.9667 2.9833	T3
Bison bonasus (Linnaeus, 1758) (European bison)	60	[12]	58A X = SM, Y = A	2.9667 2.9833	T3
Axis porcinus (Zimmermann, 1780) (Hog deer)	68	[41]	2M + 64A X = A, Y = A	2.9412 2.9412	T3

Axis axis (Erxleben, 1777) (Chital)	66	[34]	2M + 2SM + 60A X = A, Y = A	2.9091 2.9091	T3
Cervus elaphus (Linnaeus, 1758) (Red deer)	68	[19]	2M + 64A X = A, Y = M	2.9412 2.9118	T3
Cervus canadensis (Erxleben, 1777) (Wapiti)	68	[28]	2M + 64A X = A, Y = A	2.9412 2.9412	T3
Cervus nippon (Temminck, 1838) (Sika deer)	67	[18]	3M + 62A X = A, Y = SM	2.9104 2.8955	T3
Cervus albirostris (Przewalski, 1883) (White-lipped deer)	66	[39]	2M + 2SM + 60A; X = A, Y = SM	2.9091 2.8939	T3
Capreolus capreolus (Linnaeus, 1758) (European roe deer)	70	[41]	68A X = SM, Y = ST	2.9714 2.9857	T3
Capreolus pygargus (Pallas, 1771) (Siberian roe deer)	70	[38]	68A; X = SM, Y ?**	2.9714	T3
Odocoileus virginianus (Zimmermann, 1780) (White-tailed deer)	70	[40]	2SM + 66A X = SM, Y = M	2.9429 2.9286	T3
Odocoileus hemionus (Rafinesque, 1817) (Mule deer)	70	[40]	2SM + 66A X = SM, Y = M	2.9429 2.9286	T3
Lama guanicoe (P.L.S. Müller, 1776) (Guanaco)	74	[7]	6SM + 66A X = SM, Y = A	2.8919 2.9054	T3
Lama glama (Linnaeus, 1758) (Llama)	74	[7]	6SM + 66A X = SM, Y = A	2.8919 2.9054	T3
Camelus dromedarius (Linnaeus, 1758) (Arabian camel)	74	[37]	8M + 2SM + 62A X = M, Y = M	2.7027 2.7027	T3
Camelus bactrianus (Linnaeus, 1758) (Bactrian camel)	74	[27]	8M + 2SM + 62A X = M, Y = M	2.7027 2.7027	T3
Vicugna pacos (Linnaeus, 1758) (Alpaca)	74	[9]	14M + 18SM + 20ST + 20T; X = M, Y = M	2.5946 2.5946	T3
Vicugna vicugna (Molina, 1782) (Vicugna)	74	[21]	14M + 58A; X = SM, Y = SM	2.5946 2.5946	T3
Okapia johnstoni (P.L. Sclater, 1901) (Okapi)	46	[20]	4M + 8SM + 32A X = M, Y = A	2.5652 2.6087	T3
Giraffa camelopardalis (Linnaeus, 1758) (Giraffe)	30	[20]	10M + 16SM + 2A X = M, Y = A	1.6667 1.7333	T2
Porcula salvania (Hodgson, 1847) (Pygmy hog)	38	[6]	10M + 10SM + 16ST X = M, Y = M	2.1053 2.1053	T3
Sus scrofa (Linnaeus, 1758) (Wild boar)	38	[2]	10M + 14SM + 12A X = SM, Y = M	2.0526 2.0263	T3
Babyrousa babyrussa (Linnaeus, 1758) (Hairy babirusa)	38	[5]	14M + 12SM + 10ST X = M, Y = ST	1.8421 1.8947	T2
Potamochoerus porcus (Linnaeus, 1758) (Red river hog)	36	[32]	20M + 6SM +8A X = M, Y = M	1.6111 1.6111	T2
Phacochoerus aethiopicus (Pallas, 1766) (Warthog)	36	[32]	18M + 12SM + 4A X = M, Y = M	1.5556 1.5556	T2
Hylochoerus meinertzhageni (Thomas, 1904) (Forest hog)	32	[32]	18M + 14SM X***, Y***	1.4375	T2
Pecari tajacu (Linnaeus, 1758) (Collared Peccary)	30	[1]	2M + 18SM + 8A X = SM, Y = SM	2.2000 2.2000	T3
Tayassu pecari (Link, 1795) (White-lipped peccary)	26	[15]	16M + 6SM + 2A X = A, Y = A	1.5385 1.5385	T2
Catagonus wagneri (Rusconi, 1930) (Chacoan peccary)	20	[4]	18M X = M, Y = M	1.0000 1.0000	T1
Hippopotamus amphibious (Linnaeus, 1758) (Nil hippopotamus)	36	[14]	20M + 14SM; X = SM, Y = A	1.4444 1.4722	T2

Choeropsis liberiensis (Morton, 1849) (Pygmy hippopotamus)	36	[14]	20M + 14SM X = SM, Y = A	1.4444 1.4722	T2
Tragulus javanicus (Osbeck, 1765) (Javan chevrotain)	32	[26]	30M X = SM, Y = SM	1.0625 1.0625	T2
Tragulus napu (F. Cuvier, 1822) (Greater oriental chevrotain)	32	[26]	30M X = SM, Y = SM	1.0625 1.0625	T2

Abbreviations: metacentric (M); submetacentric (SM); subtelocentric (ST); telocentric (T); acrocentric (A); male (M); female (F); full symmetric (T1); symmetric (T2); between symmetric and asymmetric (T3). * Could not determine the type of chromosome, ** There is no male, *** Not identified.

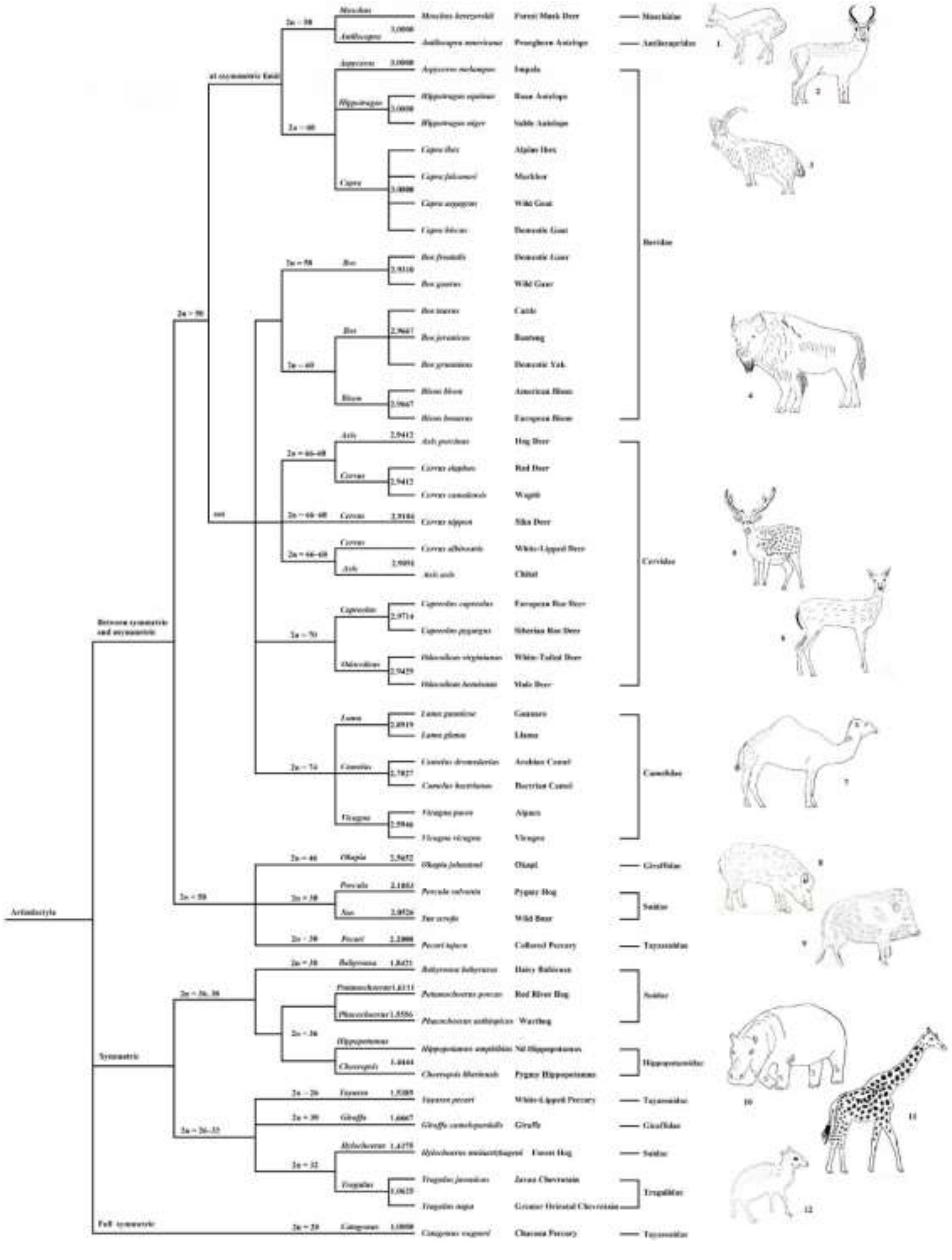

Figure 1. The dendrogram demonstrating the interspecies and interfamilies relationships in female. (1) *Moschus berezovskii*; (2) *Antilocapra americana*; (3) *Capra ibex*; (4) *Bison bison*; (5) *Axis axis*; (6) *Odocoileus virginianus*; (7) *Camelus dromedaries*; (8) *Sus scrofa*; (9) *Pecari tajacu*; (10) *Hippopotamus amphibious*; (11) *Giraffa camelopardalis*; (12) *Tragulus javanicus*.

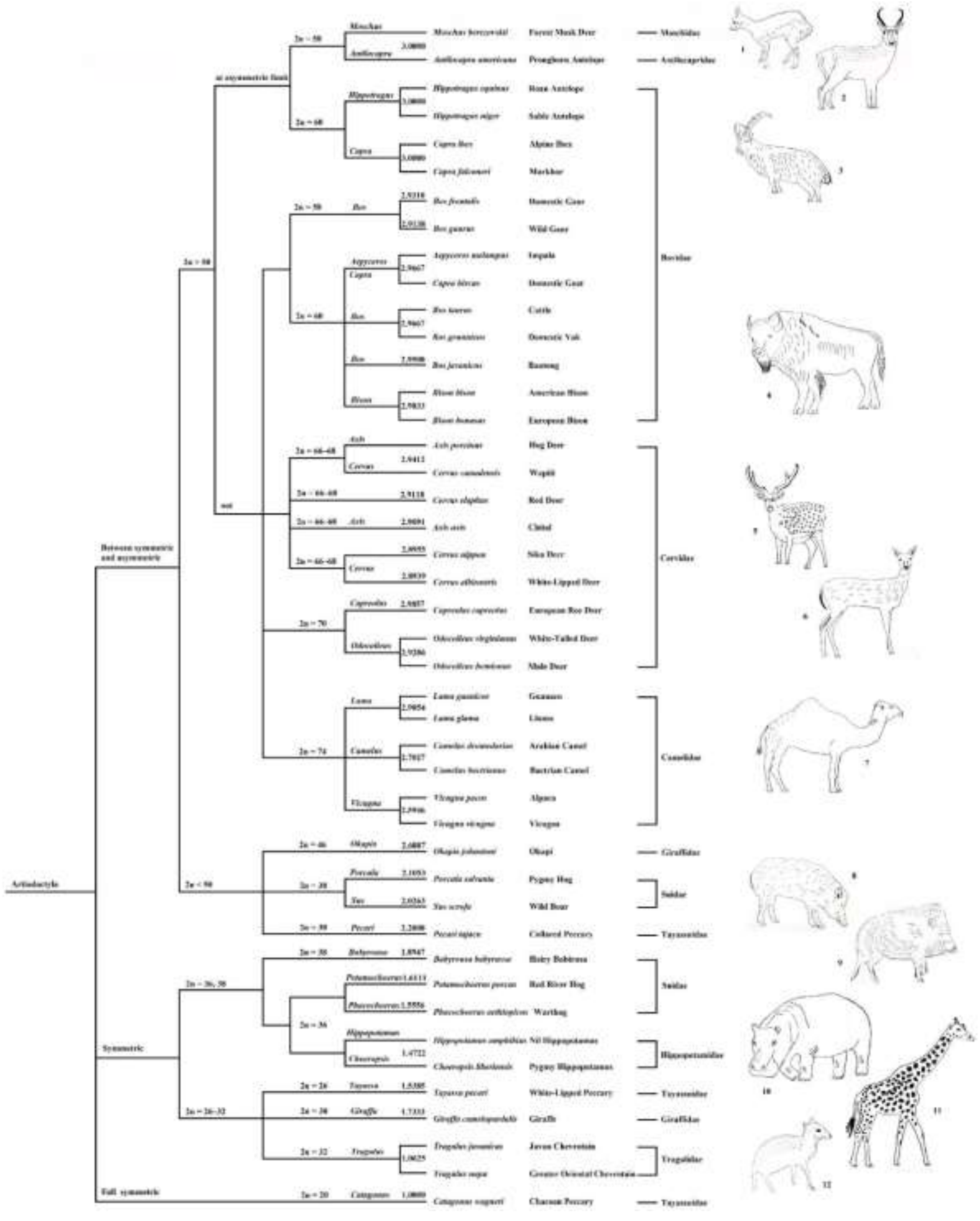

Figure 2. The dendrogram demonstrating the interspecies and interfamilies relationships in male. (1) *Moschus berezovskii*; (2) *Antilocapra americana*; (3) *Capra ibex* ; (4) *Bison bison*; (5) *Axis axis;* (6) *Odocoileus virginianus*; (7) *Camelus dromedarius*; (8) *Sus scrofa*; (9) *Pecari tajacu*; (10) *Hippopotamus amphibious*; (11) *Giraffa camelopardalis*; (12) *Tragulus javanicus*.

In Figure 1, the karyotype types are between symmetric and asymmetric in the eight families, 18 genera and 36 species; symmetric in the five families, nine genera and 10 species; full symmetric in the only one family, genus and species.

In Figure 2, the karyotype types are between symmetric and asymmetric in the eight families, 18 genera and 34 species; symmetric in the five families, eight genera and nine species; full symmetric in the only one family, genus and species.

4. Discussion

In Figures 1 and 2, there are similarities in the positive direction between female dendrogram consisting of 47 species and male dendrogram consisting of 44 species.

Although closely related species, there are chromosomal differences in the family Tayassuidae. For this reason, the karyotype types are between symmetric and asymmetric in collared peccary, symmetric in white–lipped peccary and full symmetric in chacoan peccary (Figures 1 and 2).

The Bovidae and Cervidae have a lot of genera and species. Further studies will be needed to draw distinct dendrograms for these families. The karyotypes of Bovidae species are between symmetric and asymmetric. While the karyotypes of genera *Hippotragus* and *Capra* are located in the asymmetric limit together with Moschidae and Antilocapridae, the genera *Bos* and *Bison* are not. This difference is a result of polymorphism between X and Y chromosomes. This variation is also seen in chromosome types. Although the chromosomes of roan antelope, sable antelope, alpine ibex, and markhor are acrocentric, they are metacentric, submetacentric and acrocentric in *Bos* and *Bison* species (Table 1). In addition, the karyotypes of impala and domestic goat are located in the asymmetric limit in Figure 1, but this is not the case in Figure 2. The main reason is a heteromorphism between acrocentric X and metacentric Y (Table 1). Robertsonian translocations or centric fusions are thought to have caused the interspecies karyotype differences in Bovidae and Cervidae [13].

The karyotypes of all Cervidae species are between symmetric and asymmetric. *Capreolus* and *Odocoileus* with $2n = 70$ and submetacentric X chromosome are different from *Cervus* and *Axis* with $2n = 66–68$ and a large acrocentric X chromosome (Table 1).

Because of the karyotype homology and other similarities, the genera *Cervus* and *Axis* can interbreed and produce fertile generations [3].

The karyotypes of all Camelidae species are between symmetric and asymmetric. The index values of Arabian camel–bactrian camel, guanaco–llama and alpaca–vicugna are same. Arabian camels and bactrian camels can produce viable hybrids (*Camelus dromedarius hybridus*), but hybrid males are thought to be sterile [17]. It is reported that the guanaco is one of four subspecies (*Lama guanicoe guanicoe*) [16]. More recently, molecular evidence has shown that there is no variation among the proposed subspecies and that the guanaco is a monophyletic group and the ancestor of the domestic llama, whereas the vicunas are ancestors of the domestic alpacas [25]. Although the index values of alpaca and vicugna are same, the chromosome types are quite different.

The karyotypes of Giraffidae are symmetric type (giraffe) and between symmetric and asymmetric (okapi). The chromosome number and index values of giraffe and okapi are quite different. Two species are quite different both karyologically and morphologically.

The karyotypes of Suidae are symmetric type and between symmetric and asymmetric type. Robertsonian translocations, which occur as centric fusion of acrocentric chromosomes, are thought to have caused the interspecies karyotype differences in Suidae [32]. In Figure 1 and 2, the chromosome numbers of genera are $2n$ = 32, 36 and 38. In family Suidae not only interspecies, but there are also intraspecific karyotype differences. The wild boar has intraspecific polymorphism cause by Robertsonian translocation. The Suidae, Tayassuidae and Hippopotamidae are close families in terms of morphological characters. In Figure 1 and 2, the index values and karyotypes of Suidae, Tayassuidae and Hippopotamidae families are close.

The karyotype types of two Hippopotamidae species are symmetric. The karyotypes of the Nile hippopotamus and pygmy hippopotamus are same. Hybrids are unknown.

The Tragulidae are small ruminants similar to Cervidae. The karyotype types of all Tragulidae species are symmetric. The karyotypes of the javan chevrotain and greater–oriental chevrotain consist of 15 pairs of metacentric autosomes and one pair of sex chromosomes. This complement comprises of all metacentric chromosomes in Tragulidae is different from those of most species in Bovidae and Cervidae comprise of acrocentric chromosomes (Table 1). It is reported that the chromosomal evolution in the Tragulidae occurred by centric fusions from pecoran ancestor (the ancestor of artiodactyls, $2n = 58$) [26].

In conclusion, this study presents new data into the karyological characteristics of Artiodactyla that may be useful for understand or interpret relationships among the species. The variations of karyotype asymmetry may probably play an important role in speciation. In this respect, the results will be contributed to the Artiodactyla cytotaxonomy. S/A_I formula together with the other parameters may use in phylogenetic trees of mammals.

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References

[1] Adega F., Chaves R., Kofler A., Krausman PR., Masabanda J., Wienberg J., Guedes-Pinto H., High-resolution comparative chromosome painting in the Arizona collared peccary (*Pecari tajacu*, Tayassuidae): a comparison with the karyotype of pig and sheep, Chromosome Res., 14, 243-251, (2006).

[2] Arslan A., Albayrak İ., C–banded karyotype and nucleolar organizer regions of wild boar, *Sus scrofa* (Artiodactyla: Suidae) from Anatolia, Turk. J. Biol., 33, 29-33, (2009).

[3] Asher GW., Gallagher DS., Tate ML., Tedford C., Hybridization between sika deer (*Cervus nippon*) and axis deer (*Axis axis*), J. Hered., 90, 236-240, (1999).

[4] Benirschke K., Kumamoto AT., Meritt DA., Chromosomes of the chacoan peccary, *Catagonus wagneri* (Rusconi), J. Hered., 76, 95-98, (1985).

[5] Bosma AA., de Haan NA., The karyotype of *Babyrousa babyrussa* (Suidae, Mammalia), Acta Zool. Pathol. Antwer., 76, 17-27, (1981).

[6] Bosma AA., Oliver WLR., Macdonald AA., The karyotype, including G– and C–banding patterns, of the pigmy hog *Sus* (*Porcula*) *salvanius* (Suidae, Mammalia), Genetica, 61, 99-106, (1983).

[7] Bunch TD., Foote WC., Maciulis A., Chromosome banding pattern homologies and NORs for the bactrian camel, guanaco, and llama, J. Hered., 76, 115-118, (1985).

[8] Chi J., Fu B., Nie W., Wang J., Graphodatsky AS., Yang F., New insights into the karyotypic relationships of Chinese muntjac (*Muntiacus reevesi*), forest musk deer (*Moschus berezovskii*) and gayal (*Bos frontalis*), Cytogenet. Genome Res., 108, 310-316, (2005).

[9] Di Berardino D., Nicodemo D., Coppola G., King AW., Ramunno L., Cosenza G.F., Iannuzzi L., Di Meo G.P., Balmus G., Rubes J., Cytogenetic characterization of alpaca (*Lama pacos,* fam. Camelidae) prometaphase chromosomes, Cytogenet. Genome Res., 115, 138-144, (2006).

[10] Eroğlu HE., Which chromosomes are subtelocentric or acrocentric? A new karyotype symmetry/asymmetry index, Caryologia, 68, 239-245, (2015).

[11] Fordyce-Boyer R., Sanger T., Loskutoff N., Kumamoto A.T., Johnston L., Armstrong D., Comparative cytogenetic study of the roan and sable antelope, *Hippotragus equinus* and *Hippotragus niger*, Appl. Cytogen., 21, 189-191, (1995).

[12] Gallagher Jr DS., Davis SK., De Donato M., Burzlaff JD., Womack JE., Taylor JF., Kumamoto AT., A molecular cytogenetic analysis of the tribe Bovini (Artiodactyla: Bovidae: Bovinae) with an emphasis on sex chromosome morphology and NOR distribution, Chromosome Res., 7, 481-492, (1999).

[13] Gallagher Jr DS., Womack JE., Chromosome conservation in the Bovidae, J. Hered., 83, 287-298, (1992).

[14] Gerneke WH., The chromosomes and neutrophils nuclear appendages of *Hippopotamus amphibius* Linnaeus 1758, Onderstepoort J. Vet., 32, 181-186, (1965).

[15] Giannoni MA., Ferrari I., Estudo biometrico do cariotipo da especie *Tayassu albirostris* Illinger 1815, Ciencia e Cultura Sao Paulo, 28, 432-435, (1976).

[16] González BA., Palma RE., Zapata B., Marín JC., Taxonomic and biogeographical status of guanaco *Lama guanacoe* (Artiodactyla, Camelidae), Mammal. Rev., 36, 157-178, (2006).

[17] Gray AN., Mammalian hybrids: A check-list with bibliography, 10. Wallingford, UK, Commonwealth Agricultural Bureaux, pp. 60-120, (1972).

[18] Gustavsson I., Sundt C., Karyotypes in five species of deer (*Alces alces* L., *Capreolus capreolus* L., *Cervus elaphus*, *Cervus nippon nippon* Temm and *Dama dama* L.), Hereditas, 60, 233-248, (1968).

[19] Herzog S., The karyotype of the red deer (*Cervus elaphus* L.), Caryologia, 40, 299-305, (1987).

[20] Hösli P., Lang EM., A preliminary note on the chromosomes of the Giraffidae: *Giraffa camelopardalis* and *Okapia johnstoni*, Mamm. Chrom. News., 11, 109-110, (1970).

[21] Hsu TC., Benirschke K., *Vicugna vicugna* (Vicuna), An Atlas of Mammalian Chromosomes, 1, 157-159, (1967).

[22] https://www.itis.gov/ (Erişim tarihi: 14.02.2023).

[23] http://www.iucnredlist.org/ (Erişim tarihi: 14.02.2023).

[24] Iannuzzi L., Di Meo GP., Perucatti A., G- and R-banded prometaphase karyotypes in goat (*Capra hircus* L.), Caryologia, 49, 267-277, (1996).

[25] Kadwell M., Fernandez M., Stanley H., Baldi R., Wheeler JC., Rosadio R., Bruford M., Genetic analysis reveals the wild ancestors of the llama and alpaca, P. Roy. Soc. Lond. B. Bio., 268, 2575-2584, (2001).

[26] Kim KS., Tanaka K., Ismail DB., Maruyama S., Matsubayashi H., Endo H., Fukuta K., Kimura J., Cytogenetic comparison of the lesser mouse deer (*Tragulus javanicus*) and the greater mouse deer (*T. napu*), Caryologia, 57, 229-243, (2004).

[27] Koulischer L., Tijskens J., Montelmans J., Mammalian cytogenetics IV. The chromosomes of two male Camelidae: *Camelus bacterianus* and *Lama vicugna*, Acta Zool. Pathol. Antverp., 52, 89-92, (1971).

[28] Koulischer L., Tyskens J., Mortelmans J., Mammalian cytogenetics. VII. The chromosomes of *Cervus canadensis, Elaphurus davidianus*, *Cervus nippon* (Temminck) and *Pudu pudu*, Acta Zool. Path. Antver., 56, 25-30, (1972).

[29] Lux E., Perez M., Volobouev VT., G– and C–banded karyotype of the markhor *Capra falconeri heptneri,* and comparison of its banding patterns with the Alpine ibex *Capra ibex* and cattle *Bos taurus,* Acta Theriol., 49, 131-137, (2004).

[30] Martin E., Celep F., Eroğlu HE., Comparative chromosomal features and new karyological data in *Salvia*: B‑ chromosomes, polyploidy, dysploidy and symmetric karyotypes, Braz. J. Bot., 45, 625-634, (2022).

[31] Martin E., Kahraman A., Dirmenci T., Bozkurt H., Eroğlu HE., New chromosomal data and karyological relationships in *Geranium*: basic number alterations, dysploidy, polyploidy, and karyotype asymmetry, Braz. Arch. Biol. Technol., 65, e22210354, (2022).

[32] Melander Y., Melander EH., Chromosome studies in African wild pigs (Suidae, Mammalia), Hereditas, 92, 283-289, (1980).

[33] Nadler CF., Hoffmann RS., Woolf A., G–band patterns, chromosomal homologies, and evolutionary relationships among wild sheep, goats, and aoudads (mammalia, artiodactyla), Experientia, 30, 744-746, (1974).

[34] Naik SN., Bhatia HM., Baxi AJ., Naik PV., Hematological study of Indian spotted deer (*Axis deer*), J. Exp. Zool., 155, 231-235, (1964).

[35] Peruzzi L., Eroğlu HE., Karyotype asymmetry: again, how to measure and what to measure? Comp. Cytogen., 7, 1-9, (2013).

[36] Popescu CP., Idiograms of yak (*Bos grunniens*), cattle (*Bos taurus*) and their hybrids, Ann. Génét. Sél. Anim., 1, 207-217, (1969).

[37] Samman MA., Al-Saleh AA., Sheth KV., Detailed description and nomenclature of G–banded Arabian camel (*C. dromedarius*) chromosomes, Caryologia, 45, 359-365, (1992).

[38] Sokolov VE., Orlov VN., Chudinovskaya GA., Danilkin AA., Chromosomal differences between two roe subspecies (*Capreolus capreolus* L. and *Capreolus capreolus pygargus* Pall.), Zool. Zh., 57, 1109-1112, (1978).

[39] Wang Z., Du DR., Karyotypes of Cervidae and their evolution, Acta Zool. Sinica, 29, 214-222, (1983).

[40] Wurster DH., Benirschke K., Chromosome studies on some deer, the springbok, and the pronghorn with notes on placentation in deer, Cytologia, 32, 273-285, (1967a).

[41] Wurster DH., Benirschke K., The chromosomes of twenty-three species of Cervoidea and Bovoidea, Mamm. Chrom. News., 8, 226-229, (1967b).