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## Which chromosomes are subtelocentric or acrocentric? A new karyotype symmetry/asymmetry index

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Karyotype asymmetry is well known in karyological studies of plants; however, there is no calculation of karyotype symmetry/asymmetry in other organisms. This study introduces a new formula ( $S/A_1$ ) for the measurement of the karyotype symmetry/asymmetry index. The main questions investigated are as follows. (i) Why is the new karyotype symmetry/asymmetry formula necessary? (ii) Which chromosomes are subtelocentric or acrocentric? (iii) What are the limits of symmetry/asymmetry according to the new formula? (iv) Is the human karyotype symmetrical or asymmetrical? In addition, the symmetry/asymmetry index is applied to the species and families of Cetacea as an example.

**Keywords:** Cetacea; new formula; phylogeny; symmetry/asymmetry index

### Introduction

Karyotype asymmetry is well known in karyological studies of plants. There are nine methods for the calculation of karyotype asymmetry in plants: Stebbins classification; karyotype asymmetry index (AsK%); total form percent (TF%); Syi and the Rec indices; intrachromosomal asymmetry (A1) and interchromosomal asymmetry (A2) indices; dispersion index (DI); degree of asymmetry of karyotype (A); asymmetry index (AI) and mean centromeric asymmetry ( $M_{CA}$ ) (Peruzzi and Eroğlu 2013). Despite the widespread use of these methods in plants, there is no calculation of karyotype symmetry/asymmetry in other organisms. Especially in higher animals and humans, it is important to know the values of the karyotype symmetry/asymmetry, so that species, genera, families and orders can be compared. Also the evolutionary relationships of higher organisms can be determined.

### Why is the new karyotype symmetry/asymmetry formula necessary?

(i) All the indexes mentioned above use parameters such as the total length of the chromosome and/or short and long arm length of chromosomes. The new formula uses chromosomal type, and consequently centromeric position. Increasing chromosomal asymmetry occurs because of the shift in centromere position from the median or submedian to the subterminal or terminal (Stebbins 1971). A symmetrical karyotype is characterized by mainly median and submedian chromosomes of approximately equal size. Changes to an asymmetric karyotype can occur by shifts in centromere position towards the telomere (Peruzzi et al. 2009). The new symmetry/asymmetry index will therefore be easier to implement with the human karyotype. (ii) In different karyotype

studies related to the same species, there may be small differences in chromosomal length and arm ratios (Denver Study Group 1960a) (Table 1). As these differences do not affect the chromosome type and centromeric position, the formula gives more reliable results.

### Which chromosomes are subtelocentric or acrocentric?

In mammalian karyotype studies it is particularly difficult to determine whether chromosomes are subtelocentric or acrocentric. The Denver Study Group (1960b) reported that human mitotic chromosomes were acrocentric. Also Levan et al. (1964) reported that human mitotic chromosomes were subtelocentric. There is ambiguity about certain chromosomes between the two reports: chromosomes 13, 14, 15, 21, 22 and Y were named acrocentric with nearly terminal centromeres in the Denver report, but were subtelocentric chromosomes in the Levan system. There are many other similar examples in the literature (Duffield et al. 1967; Kulu et al. 1971; Arnason 1974; Bonifácio et al. 2012). It remains unclear which statement should be used in karyotype studies. Both expressions are currently used; only one is preferred in some studies, while both are used together in others. For this reason, a new formula is required containing both of these terms.

### Material and methods

#### *The karyotype symmetry/asymmetry index formula ( $S/A_1$ )*

The formula includes chromosomal type and centromeric position. The chromosome types are determined according to nomenclature recommended by Levan et al. (1964). The general formula is described with the different use of chromosome types (Table 2):

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Table 1. The arm ratio of the human mitotic chromosomes.

		Chromosome																						Reference
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	Y	
1.1	1.6	1.2	2.9	3.2	1.7	1.3	1.5	1.9	2.4	2.8	3.1	8.0	7.3	10.5	1.8	2.8	3.8	1.4	1.3	3.7	3.3	1.9	$\infty$	Tio and Puck 1958
1.1	1.5	1.2	2.9	3.2	1.8	1.9	1.7	2.4	2.3	2.1	3.1	9.7	9.5	11.9	1.6	2.1	3.8	1.9	1.3	6.8	6.0	2.8	$\infty$	Chu and Giles 1959
1.1	1.6	1.2	2.7	2.6	1.7	1.9	1.6	1.8	2.0	2.2	1.7	5.0	4.0	4.7	1.4	2.4	2.6	1.3	1.3	2.5	2.3	1.6	2.9	Levan and Hsu 1959

Table 2. Chromosomal groups.

Arm ratio (r)*	Group 1	Group 2
1.0–1.7	Metacentric (M)	Metacentric (M)
1.7–3.0	Submetacentric (SM)	Submetacentric (SM)
3.0–7.0	Subtelocentric (ST)	Acrocentric (A)
7–∞	Telocentric (T)	Telocentric (T)
Reference	Levan et al. 1964	Denver Study Group 1960b

$$S/A_I = (1 \times M) + (2 \times SM) + (3 \times ST) + (4 \times T) / 2n \quad (1)$$

according to Group 1 in Table 2; and:

$$S/A_I = (1 \times M) + (2 \times SM) + (3 \times A) + (4 \times T) / 2n \quad (2)$$

according to Group 2 in Table 2. In these equations) M = metacentric chromosome number; SM = submetacentric chromosome number; ST = subtelocentric chromosome number; A = acrocentric chromosome number; T = telocentric chromosome number and 2n = diploid chromosome number.

**Results**

*The limits of symmetry/asymmetry according to the formula*

A perfectly symmetrical karyotype is characterized by completely metacentric chromosomes. In contrast, an asymmetric karyotype consists of a complete set of telocentric chromosomes. For example, thinking that all human chromosomes are uniform, karyotype symmetry/asymmetry index is calculated as follows.

2n = 46 (metacentric chromosome number = 46)

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

$$S/A_I = (1 \times 46) + (2 \times 0) + (3 \times 0) + (4 \times 0) / 46$$

$$S/A_I = 1.0$$

2n = 46 (submetacentric chromosome number = 46)

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

$$S/A_I = (1 \times 0) + (2 \times 46) + (3 \times 0) + (4 \times 0) / 46$$

$$S/A_I = 2.0 \quad (4)$$

2n = 46 (acrocentric or subtelocentric chromosome number = 46)

$$S/A_I = (1 \times M) + (2 \times SM) + (3 \times A \text{ or } ST) + (4 \times T) / 2n \quad (5)$$

$$S/A_I = (1 \times 0) + (2 \times 0) + (3 \times 46) + (4 \times 0) / 46$$

$$S/A_I = 3.0$$

2n = 46 (telocentric chromosome number = 46)

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

$$S/A_I = (1 \times 0) + (2 \times 0) + (3 \times 0) + (4 \times 46) / 46$$

$$S/A_I = 4.0 \quad (6)$$

According to the results, while the most symmetrical karyotype value is 1.0, the most asymmetric karyotype value is 4.0. Other karyotypes vary between these values (Table 3).

*Is the human karyotype symmetrical or asymmetrical?*

The human karyotype consists of 44 autosomal chromosomes and two sex chromosomes. While autosomal chromosomes are metacentric (1, 2, 3, 16, 19, 20), submetacentric (4, 5, 6, 7, 8, 9, 10, 11, 12, 17, 18) and acrocentric (13, 14, 15, 21, 22), sex chromosomes are submetacentric (X) and acrocentric (Y) (Tio and Puck 1958; Denver Study Group 1960b; Levan et al. 1964). The karyotype formulae of the male and female chromosomes are different.

Female karyotype formula = 12M + 24SM + 10A

$$S/A_I = (1 \times M) + (2 \times SM) + (3 \times A) + (4 \times T) / 2n$$

$$S/A_I = (1 \times 12) + (2 \times 24) + (3 \times 10) + (4 \times 0) / 46$$

$$S/A_I = 1.9565 \quad (7)$$

Table 3. The new classification model for karyotype symmetry/asymmetry.

S/A <sub>I</sub> value	Karyotype symmetry/asymmetry
1.0	Full symmetric
1.0 < S/A <sub>I</sub> ≤ 2.0	Symmetric
2.0 < S/A <sub>I</sub> ≤ 3.0	Between symmetric and asymmetric
3.0 < S/A <sub>I</sub> < 4.0	Asymmetric
4.0	Full asymmetric

Male karyotype formula = 12M + 23SM + 11A

$$S/A_I = (1 \times M) + (2 \times SM) + (3 \times A) + (4 \times T) / 2n$$

$$S/A_I = (1 \times 12) + (2 \times 23) + (3 \times 11) + (4 \times 0) / 46$$

$$S/A_I = 1.9782 \quad (8)$$

$$\begin{aligned} \text{Mean } S/A_I &= (\text{Female } S/A_I + \text{Male } S/A_I) / 2 \\ &= 1.9565 + 1.9782 / 2 = 1.9673 \quad (9) \end{aligned}$$

### Sample application of symmetry/asymmetry on families and species

The karyotypes of cetacean taxa were used for the example application. The Cetacea (infraorder) includes the marine mammals commonly known as whales, dolphins and porpoises. According to World Register of Marine Species (WoRMS, <http://www.marinespecies.org>), Cetacea comprises two superfamilies, 13 families and 40 genera. After a comprehensive literature search, karyotype formulae, index values and karyotype types of 26 species belonging to two superfamilies and 11 families have been identified (Table 4). According to the index values in Table 4, a phylogenetic tree was drawn showing relationships among the families and species of cetaceans (Figure 1).

The predominant diploid number of chromosomes in Cetacea is  $2n = 44$ . Another common chromosome number is  $2n = 42$ . Although there are 44 chromosomes in many families and species, there are 42 chromosomes in only three (Physeteridae, Ziphiidae and Balaenidae) of the 11 families in the Table 4. As an interesting note, these families have the different chromosome numbers ( $2n = 42$ ) and the smallest index values. The karyotypes of these families are symmetric types together with Pontoporiidae. The karyotype type is between symmetric and asymmetric in the other seven families and 19 species. The karyotype symmetry/asymmetry values of 11 families are 2.0455–2.3409.

In Figure 1 the female karyotype index values of 26 species are located to the left, and the values of 16 males are located to the right. Ten species are missing from the male tree for two reasons. (i) There is no male in the karyotype studies of *Globicephala macrorhynchus*, *Lagenorhynchus albirostris*, *Orcinus orca*, *Delphinapterus leucas*, *Mesoplodon carlhubbsi*, *Mesoplodon europaeus*, *Balaenoptera musculus* and *Eschrichtius robustus*; only the female karyotype has been reported (Arnason 1974, 1980, 1981a, 1981b; Arnason et al. 1977, 1985; Jarrell and Arnason 1981). (ii) There are males and Y chromosomes in the karyotype studies of *Inia geoffrensis* and *Balaena*

*mysticetus*, but the Y chromosome is very small. The type of chromosome was not reported (Jarrell 1979; Bonifácio et al. 2012).

There are similarities in the positive direction between the female tree consisting of 26 species and the male tree consisting of 16 species in Figure 1. The results of Balaenopteridae, Balaenidae and Eschrichtiidae families belonging to the Mysticeti superfamily are quite close.

The karyotype of Balaenidae is symmetric, together with Pontoporiidae, Ziphiidae and Physeteridae. The karyotypes of Balaenopteridae and Eschrichtiidae are between symmetric and asymmetric types, together with Lipotidae, Monodontidae, Delphinidae, Phocoenidae and Iniidae. Eschrichtiidae is located in a boundary between Balaenopteridae and Balaenidae. Ziphiidae and Physeteridae have the smallest index values. They are located in the most extreme together with some members of the Mysticeti superfamily. In this regard, the phylogeny was very similar to the phylogenetic tree of mitochondrial rRNA 12S and 16S sequences proposed by Milinkovitch et al. (1993). Also it is compatible with the phylogenetic trees of mitochondrial cytochrome b (Arnason and Gullberg 1996), morphological data (Heyning 1997; Messenger and McGuire 1998) and SINE insertions and flanking sequences (Nikaido et al. 2001). Both in the present study and in other studies (Heyning 1997; Messenger and McGuire 1998; Nikaido et al. 2001) it has been reported that Delphinidae and Lipotidae are close families. The species belonging to the family of Delphinidae are located close to the species belonging to the families of Lipotidae, Monodontidae and Phocoenidae. Nikaido et al. (2001) reported generally similar results.

Both heterogeneous distribution of the species of Balaenopteridae and the settling in the most extreme of Iniidae are different data. These differences may be due to a number of reasons. Different authors may report different results, due to chromosomal polymorphism or changes in chromosome structure. For example, the karyotype formula of *Inia geoffrensis* (Bonifácio et al. 2012) used in the present study is different from that described by Kulu et al. (1971). The index values from Kulu et al. (1971) are 2.1818 (female) and 2.2045 (male). When using these values, Iniidae is placed very close to Delphinidae. However, the karyotype formula of Bonifácio et al. (2012) is used here instead because this study is a more recent study and contains molecular cytogenetic techniques. Another example is the karyotype formula of *Balaenoptera acutorostrata* (Arnason 1974; Arnason et al. 1977) which used in the present study and is different from that described by Arnason (1981a). The index values from Arnason (1981a) are 2.0455 (female) and 2.0682 (male). When using these values, it is not too much change at position of *Balaenoptera acutorostrata*.

Table 4. Karyotype formulae, index values and karyotype type of families and species.

No	Family/superfamily Species/scientific name and common name	Autosomes and sex $2n$ chromosomes	Reference	S/A <sub>I</sub>	Karyotype Type
<b>Delphinidae / Odontoceti</b>					
1	<i>Delphinus delphis</i> (Linnaeus, 1758) (Short-beaked common dolphin)	44 12M + 10SM + 20A X = SM, Y = A	Kulu et al. 1971	2.1818 (F) 2.2045 (M)	Between symmetric and asymmetric
2	<i>Globicephala macrorhynchus</i> (Gray, 1846) (Short-finned pilot whale)	44 12M + 16SM + 6ST + 8T X = SM, Y ?*	Arnason 1974	2.2273 (F)	Between symmetric and asymmetric
3	<i>Lagenorhynchus albirostris</i> (Gray, 1846) (Whitebeak dolphin)	44 12M + 18SM + 4ST + 8T X = M, Y ?*	Arnason 1980; 1981a	2.1364 (F)	Between symmetric and asymmetric
4	<i>Lagenorhynchus obliquidens</i> (Gill, 1865) (Pacific white-sided dolphin)	44 12M + 10SM + 20A X = SM, Y = A	Duffield et al. 1967	2.1818 (F) 2.2045 (M)	Between symmetric and asymmetric
5	<i>Orcinus orca</i> (Linnaeus, 1758) (Killer whale)	44 12M + 18SM + 4ST + 8T X = SM, Y ?*	Arnason 1981a	2.1818 (F)	Between symmetric and asymmetric
6	<i>Stenella clymene</i> (Gray, 1850) (Clymene dolphin)	44 12M + 18SM + 4ST + 8T X = M, Y = T	Arnason 1980	2.1364 (F) 2.2045 (M)	Between symmetric and asymmetric
7	<i>Stenella dubia</i> (G. Cuvier, 1812) (Spotted dolphin)	44 12M + 18SM + 4ST + 8T X = M, Y = T	Arnason 1974	2.1364 (F) 2.2045 (M)	Between symmetric and asymmetric
8	<i>Tursiops truncatus</i> (Montagu, 1821) (Bottlenose dolphin)	44 12M + 10SM + 20A X = SM, Y = A	Duffield et al. 1967	2.1818 (F) 2.2045 (M)	Between symmetric and asymmetric
<b>Iniidae / Odontoceti</b>					
9	<i>Inia geoffrensis</i> (de Blainville, 1817) (Amazon river dolphin)	44 12M + 14SM + 6ST + 10T X = M, Y minute**	Bonifácio et al. 2012	2.2727 (F)	Between symmetric and asymmetric
<b>Lipotidae / Odontoceti</b>					
10	<i>Lipotes vexillifer</i> (Miller, 1918) (Baiji dolphin)	44 12M + 18SM + 4ST + 8T X = M, Y = T	Minrong et al. 1996	2.1364 (F) 2.2045 (M)	Between symmetric and asymmetric
<b>Monodontidae / Odontoceti</b>					
11	<i>Delphinapterus leucas</i> (Pallas, 1776) (Beluga whale or white whale)	44 12M + 18SM + 4ST + 8T X = M, Y ?*	Jarrell and Arnason 1981	2.1364 (F)	Between symmetric and asymmetric
<b>Phocoenidae / Odontoceti</b>					
12	<i>Neophocaena phocaenoides</i> (Cuvier, 1829) (Finless porpoise)	44 10M + 18SM + 4A + 10T X = M, Y = T	Peng and Chen 1985	2.2727 (F) 2.3409 (M)	Between symmetric and asymmetric
13	<i>Phocoena phocoena</i> (Linnaeus, 1758) (Harbor porpoise)	44 12M + 14SM + 8ST + 8T X = M, Y = T	Arnason 1974	2.2273 (F) 2.2955 (M)	Between symmetric and asymmetric
14	<i>Phocoenoides dalli</i> (True, 1885) (Dall's porpoise)	44 12M + 10SM + 20A X = SM, Y = A	Kulu et al. 1971	2.1818 (F) 2.2045 (M)	Between symmetric and asymmetric
<b>Physeteridae / Odontoceti</b>					
15	<i>Kogia breviceps</i> (de Blainville, 1838) (Pygmy sperm whale)	42 18M + 16SM + 6ST X = M, Y = M	Arnason 1974	1.6667 (F) 1.6667 (M)	Symmetric
16	<i>Physeter macrocephalus</i> (Linnaeus, 1758) (Kaskelot or sperm whale)	42 20M + 18SM + 2ST X = M, Y = ST	Atwood and Razavi 1965; Arnason 1974, 1981a, 1981b	1.5238 (F) 1.5714 (M)	Symmetric
<b>Pontoporiidae / Odontoceti</b>					
17	<i>Pontoporia blainvillei</i> (Gervais & d'Orbigny, 1844) (Franciscana dolphin)	44 14M + 18SM + 10A X = M, Y = M	Heinzelmann et al. 2008	1.8636 (F) 1.8636 (M)	Symmetric
<b>Ziphiidae / Odontoceti</b>					
18	<i>Mesoplodon carlhubbsi</i> (Moore, 1963) (Hubbs' beaked whale)	42 28M + 6SM + 6ST X = ST, Y ?*	Arnason et al. 1977	1.5238 (F)	Symmetric
19	<i>Mesoplodon europaeus</i> (Gervais, 1855) (Gervais'/Antillian beaked whale)	42 28M + 6SM + 6ST X = ST, Y ?*	Arnason et al. 1977	1.5238 (F)	Symmetric

(Continued)

Table 4. (Continued).

Family/superfamily No	Species/scientific name and common name	Autosomes and sex 2n chromosomes	Reference	S/A <sub>I</sub>	Karyotype Type
<b>Balaenidae / Mysticeti</b>					
20	<i>Balaena mysticetus</i> (Linnaeus, 1758) (Bowhead Greenland rightwhale)	42 18M + 10SM + 6ST + 6T X = M, Y minute**	Jarrell 1979	1.9524 (F)	Symmetric
21	<i>Eubalaena glacialis</i> (Müller, 1776) (North Atlantic right whale)	42 12M + 22SM + 6ST X = M, Y = ST	Pause et al. 2006	1.8095 (F) 1.8571 (M)	Symmetric
<b>Balaenopteridae / Mysticeti</b>					
22	<i>Balaenoptera acutorostrata</i> (Lacépède, 1804) (Minke whale)	44 16M + 12SM + 6ST + 8T X = M, Y = SM	Arnason 1974, 1981a; Arnason et al. 1977	2.0909 (F) 2.1136 (M)	Between symmetric and asymmetric
23	<i>Balaenoptera borealis</i> (Lesson, 1828) (Sei whale)	44 14M + 14SM + 6ST + 8T X = M, Y = M	Arnason 1970, 1974	2.1364 (F) 2.1364 (M)	Between symmetric and asymmetric
24	<i>Balaenoptera musculus</i> (Linnaeus, 1758) (Blue whale or Blåval)	44 14M + 14SM + 6ST + 8T X = M, Y ?*	Arnason et al. 1985	2.1364 (F)	Between symmetric and asymmetric
25	<i>Balaenoptera physalus</i> (Linnaeus, 1758) (Fin whale)	44 16M + 12SM + 6ST + 8T X = ST, Y = M	Arnason 1969, 1974, 1981a	2.1818 (F) 2.1364 (M)	Between symmetric and asymmetric
<b>Eschrichtiidae / Mysticeti</b>					
26	<i>Eschrichtius robustus</i> (Lilljeborg, 1861) (Gray whale)	44 18M + 10SM + 6ST + 8T X = M, Y ?*	Arnason 1974, 1981a, 1981b	2.0455 (F)	Between symmetric and asymmetric

Abbreviations: M, metacentric; SM, submetacentric; A, acrocentric; ST, subtelocentric; T, telocentric; F, female; M, male.

\*There is no male in the karyotype study.

\*\*Could not determine the type of chromosome.

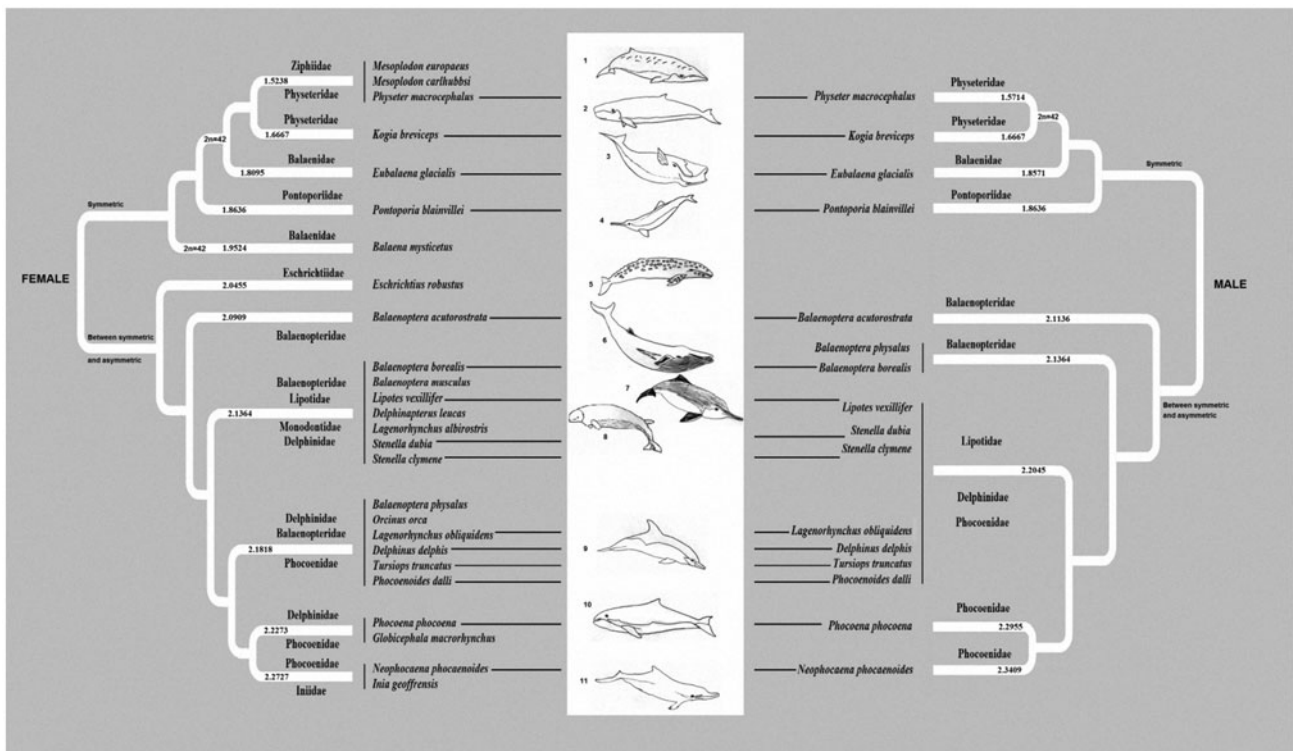


Figure 1. Phylogenetic tree showing relationships of the index values among the families and species of cetaceans. (1) Ziphiidae; (2) Physeteridae; (3) Balaenidae; (4) Pontoporiidae; (5) Eschrichtiidae; (6) Balaenopteridae; (7); Lipotidae (8) Monodontidae; (9) Delphinidae; (10) Phocoenidae; (11) Iniidae. Sixteen male specimens are equally settled with females according to the black lines.

## Discussion

The new formula was given with three samples in the results.

- (1) The limits of symmetry/asymmetry according to the formula. Although exemplified in the human karyotype, these limits of symmetry/asymmetry are identical in all organisms. The classification can be reported from metacentric and submetacentric to acrocentric/subtelocentric and telocentric. The new classification model explains the situation of symmetry/asymmetry of the karyotype (Table 3).
- (2) Is the human karyotype symmetrical or asymmetrical? The results show that both female and male human karyotypes are symmetrical, but all values are close to the category between symmetric and asymmetric.
- (3) The sample application of symmetry/asymmetry on families and species. The karyotypes of cetacean taxa were used. As shown in Figure 1, S/A<sub>I</sub> values together with the other parameters will contribute to phylogenetic trees of mammals.

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## Disclosure statement

No potential conflict of interest was reported by the author.

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