# Set theory and types of groups in phylogenetics

**Running title:** Set theory and types of groups in phylogenetics

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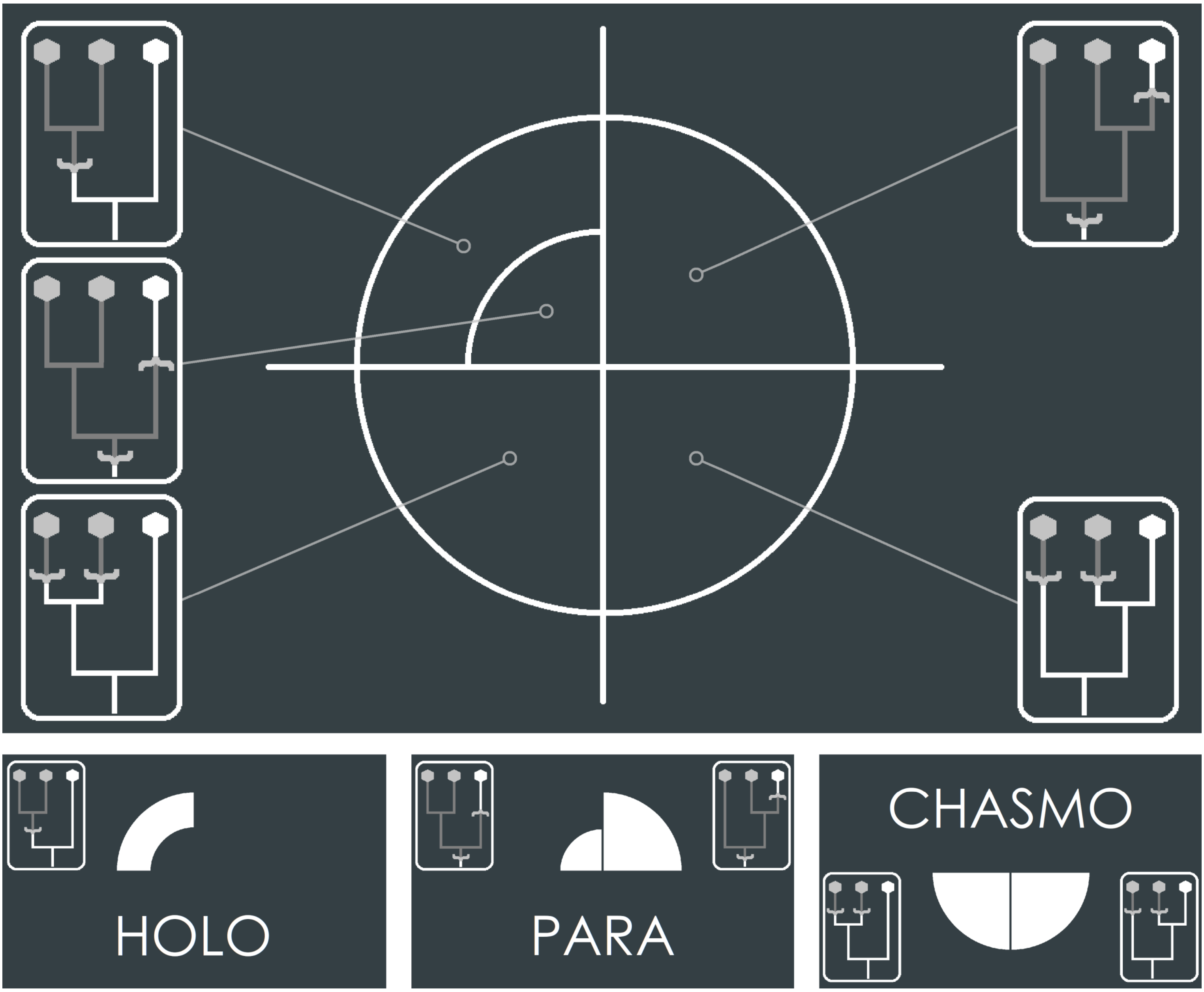

***Abstract.***—Mathematically, it is possible to be a subset (⊂) of a set and not to be its member (∈)—*e.g.* the empty set. Here, I highlight that a similar principle applies to undiscovered objects in sets of real objects. The current definitions of holophyly (monophyly *sensu stricto*) and paraphyly suggest a direct membership (∈) of ancestors in taxa. These ancestors are almost always unknown (undiscovered) in phylogenetics. Undiscovered entities are hard to be members of a taxonomical system in organismic biology. There are still several questions, which are problematic not to phylogeny but to the current conceptual framework. Are Pisces *sensu* Linnaeus, 1756 (including cetaceans and sirenians along with fishes) paraphyletic or they are polyphyletic? If a group is composed of all discovered members of some lineage but based on their homoplasy, is this group holophyletic or polyphyletic? Are choanomonads holophyletic, if some ancestor they share with animals was a collar-bearing (*choano*-) monad? Can something with a true nucleus be called an "*ancestor* of eukaryotes"? Accompanying the problematic membership of undiscovered ancestors in groups of discovered organisms, the list of the problems includes further facts. (1) Any organisms of now-known life have a common ancestor (deniable for Haeckel who started this conceptual framework). Therefore, the division principle by the inclusiveness of groups, which gives us the dichotomy "polyphyly"–(holophyly + paraphyly) requires clarification. (2) The definition "*the ancestor plus all its descendants*" does not allow any clade to be divided into subclades completely—at least the ancestor from the definition will remain. (3) The definitions "*the ancestor plus all its descendants*" and "*the ancestor plus not all its descendants*" left no place for the sole-member groups. At least two are needed (one ancestor and one its descendant) to be holophyletic or paraphyletic. I wish to propose and discuss a redesigned system of concepts to solve logical issues. Here, the direct membership/non-membership (∈/∉) of undiscovered ancestors was replaced with the ability/disability of the definition of the systematic group to contain them as members. At the same time, the inclusion (⊂) of the sets corresponding to undiscovered objects remains untouched. The proposed system of the types of systematic groups does not ignore ancestors and deals with their existence more carefully. Simultaneously, undiscovered ancestors do not require membership in systematic groups. Other logical problems also could be solved. To provide a concise definition of holophyly some concepts behind this were named and reduced to one word (phylon, startestor, intrendon, jugiphyly). Holophyly was finally defined using them near the end of the paper.

**Keywords:** *plerophyletic*; *merophyletic*; *jugiphyletic*; *chasmophyletic*; *drade*; *skade*.

## INTRODUCTION

Taxonomy was called the first human occupation by Joel Hedgpeth (1961). "[*The hu*]*man's oldest profession*" he has (sardonically?) stated. Any ethical load of the phrase is debatable (Mattson, 2015; Goldenberg *et al.*, 2021; Czechowski *et al.*, 2022). So is the identification of a single one among numerous activities as the oldest for humans. Nonetheless, this cognitive activity in its foundation is among the ones that predate humankind.

The mental aggregation of objects into groups—members (elements) into sets—and groups into more inclusive groups—sets into more inclusive sets—is a cognitive activity that appeared in animals millions of years before humans (Freedman & Assad, 2006, 2016; Antzoulatos & Miller, 2011; Hanson & Hanson, 2017; Castro & Wasserman, 2017; Reinert *et al.*, 2021). Subsequently, humans have formalised this activity, it stunningly developed and became known as set theory (Cantor, 1873; 1874; Zermelo, 1930; see Johnson, 1972; Kanamori, 2003; 2012; and Ferreirós, 2007 for review).

In introductory lectures to his students, one of the founders of descriptive set theory (Martin, 1977; Kanamori, 1995) N. N. Luzin suggested the following analogical representation of a set. Think of a transparent, impenetrable shell, something like a transparent and tightly closed bag. Suppose that all the contents of some set *A* (and no other objects) are inside the shell. This *shell and the objects* in it can serve as a representation of set *A*. The transparent shell represents the act of uniting the members that gives rise to set *A*. (Retold after Vilenkin 1995 p. 34 [orig. p. 43]). What about the shell? Let us say, "Voltaire" is both the person and the word-pointer to this person. Similarly, a set is both an instruction for the selection of objects and the objects selectable in accordance with this instruction. Luzin's very "transparent bag" is the instructional component of a set. This exists physically on any recording medium: human brains, discs, semiconductor-memory drives, paper, magnetic tapes, 2D electron gas (Moon *et al.*, 2009) *etc*. That which processes an instruction exists physically, as well. It is due to this instructional component, a set is not merely a number of its members (Kanamori, 2003).

Along with the instructions allowing the selection of some objects, there are instructions allowing the selection of a single object (*e.g.* "*the set composed of the Sun*", "*the set composed of Mount Fuji*")—the instructions of singleton sets. Also, there are instructions allowing the selection of only no objects (*e.g.* "*black holes reflecting light*" (Davies, 1978; Wald, 1984; Hawking & Ellis, 2023), "*cold non-rotating lone neutron stars with a mass of seven solar ones*" (Bombaci, 1996; Kalogera & Baym, 1996; Rezzolla *et al.*, 2018))—the instructions of the empty set.

Also, when we apply a set theory to real objects (as opposed to imaginary, fictional, or supposed ones), our non-omniscience comes into play. In reality, some object (or some feature of an object) can either exist or not exist. In the civilisational picture of reality, a third alternative is added. Along with proven existence or non-existence, it can be unknown. In reality at every point in time, there could be objects about which we know no true facts. There are objects, for which we can not in the given time prove their existence or completely exclude the probability of their non-existence. These are undiscovered objects. When (rarely) we have something about an entity before its discovery, all this is either our hypotheses about this entity or what we give in its definition. Frequently, this creates a sketchy image of an undiscovered object in our head and sometimes—an illusion of any facts about it.

Due to the shortage of knowledge about undiscovered objects, they could not be treated in the same way as discovered ones. Nevertheless, unobserved objects fall under our definitions of numerous sets. The open question is: should unobserved objects be treated as *members* of sets of real objects or as something else inside them?

The founder of set theory (Kanamori, 2003; 2012; Ewald, 2007; Ferreirós, 2007), Georg Cantor (1895 p. 481) defined members of "any set *M*" (*jede Zusammenfassung M*) as "certain well-distinguished objects *m* of our observations or our thoughts" (*bestimmten wohlunterschiedenen Objecten m unsrer Anschauung oder unseres Denkens*; see Carus, 1892; Thompson, 1895; Payne, 1969; Breazeale, 1979; and Merriam-Webster, 2023 for the word *Anschauung*). In this way, if we classify not any thought abstract objects, then objects must be observed and discovered to be members. Also, we should be able to surely uniquely identify these objects and draw sure borders between them. Nonetheless, we can create instructions for the selection of some objects regardless even of their existence (instructions for the selection of a single object included).

There are two ways to fill a set with members (Russell, 1919 p. 12): extensional and intensional.

With the extensional way, the objects to be added in a certain set as its *members* are simply demonstrated (indicated). This way results in an instruction in the form of a simple list of individual objects or a reference—"*objects indicated by someone (something), sometime, and somewhere*". Only a discovered object can be demonstrated.

With an intensional definition, certain criteria are formulated and objects that satisfy them are considered to be the contents of the set. In order to become a *member* of such a set, an object from reality must be checked with them. To be checked with criteria an object must be discovered.

The intensional type of definition has a specific subkind—the ostensive definition. When a set is defined ostensively, the definition is not initially formulated, but a certain type object is demonstrated. The audience is invited to identify some of its features that are essential for the selection of other similar objects in the set. Thus, as a result, the audience creates an intensional definition(s) of the set—the criteria that objects must meet. You can demonstrate only a discovered object. In order to add members to such a set in addition to the type one(s), it is required to check something from reality with the criteria, which are based on the type member(s). To be checked with these criteria an object must be discovered, too.

If a member of a set is an object attributed to the set, then undiscovered objects could not be *members* when we compose sets of real objects. This way left no opportunity for an undiscovered entity to become a *member* of a set of real objects. Nevertheless, there obviously could be instructions able to embrace undiscovered objects together with members (*e.g.* "*the set of all stars in space*") and instructions that embrace only undiscovered objects (*e.g.* "*the set of undiscovered stars*")—*sets* of undiscovered.

Although it is impossible to make undiscovered objects the members of sets of real objects, it is possible to single out subsets of undiscovered objects in sets with discovered objects. This is exactly what Peter Higgs and Dmitri Mendeleev did, for example.

In 1964, Peter Higgs (the equation (2b) in Higgs, 1964*b*; see also Higgs, 1964*a*; 1966) explicitly postulated a type of physical particle (the scalar boson), subsequently named after him (Lee, 1972; Ellis *et al.*, 1976). Higgs did not discover it. This was done almost half a century later (O'Luanaigh, 2013; The ATLAS and CMS collaborations, 2013). Higgs, in the sixties, created a single-seater set of undiscovered. The definition of this set quite accurately corresponded to reality and subsequently, it actually received its member. Higgs predicted the discovery of the Higgs boson and directed it.

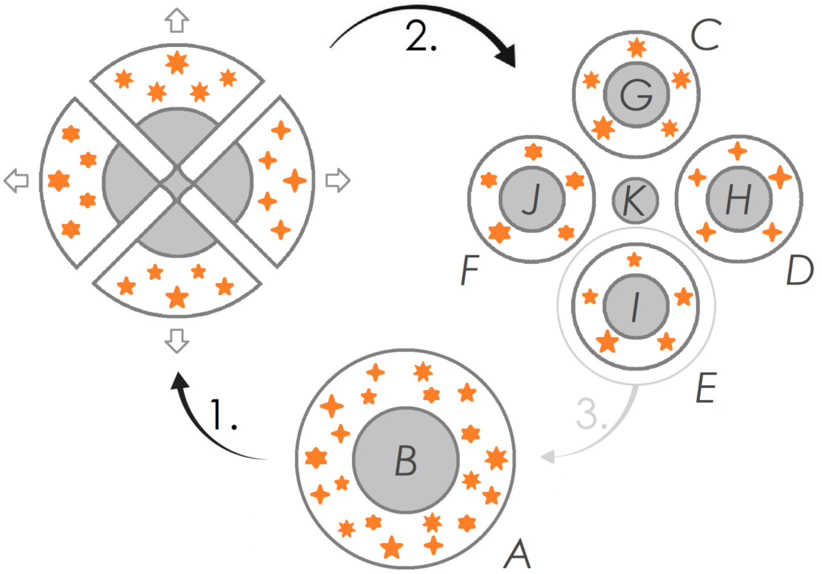

**Figure 1.** *Steps 1 and 2*. A partition of a set of real objects that underlies any classification of them. *A* — the symbolic set of all stars. *B* — the subset of all undiscovered stars. *C*–*F* — element-containing ("regular") subsets of the partitioned set *A*. *G*–*J* — subsets of undiscovered stars of the kinds *C*–*F*, respectively. *K* — the subset of undiscovered stars of non-*C*–*F* kinds. For instance, *K* may cover numerous eight-pointed stars (✴) if they exist. Alternatively, this may become the empty set. Subsets of the type like *K* are omitted in classifications. *Step 3*. The transition to *steps 1* and *2* on set *E* instead of set *A*.

When Dmitri Mendeleev first published the periodic table of chemical elements, there were unfilled table cells in it (Mendeleev, 1869). A year and a half later, Mendeleev named three of these unfilled cells: "eka-boron", "eka-aluminum", and "eka-silicon" (Mendeleev in von Richter, 1870; Mendeleev, 1871). In this way, he created three single-seater sets of undiscovered. Their definitions, as it subsequently turned out, quite accurately fitted the reality. Later, these chemical elements were discovered. Each of these unfilled table cells got its member. Mendeleev's single-seater sets of the undiscovered became singletons. As singletons, these three sets became known as scandium (Sc; Nilson, 1879*a*,*b*), gallium (Ga; Lecoq de Boisbaudran, 1875), and germanium (Ge; Winkler, 1887*a*,*b*), respectively. Not all chemical elements predicted by Mendeleev have proven their existence (*e.g.* his "element *x*" with the name "Newtonium" tentatively proposed by him as well; Mendeleev, 1903). In other words, some his single-seater sets of undiscovered have become singletons and others have been proven to be identical to the empty set. An unfilled cell of Mendeleev's initial tables is a good example of a set of undiscovered objects.

It turns out that the filling of sets of real objects is not only members. (At least if the readers are non-omniscient.) The number of members in some set (accessed cardinality of this set; $\mathrm{card}_c$) may differ from the number of all objects (discovered and undiscovered) that satisfy the definition of this set (actual cardinality of this set; $\mathrm{card}_t$). In other words, in each set of real objects, there is at least one subset of undiscovered objects that satisfies the definition of this set.

$$\boldsymbol{\forall A\ \exists\ B \mid B \subseteq A \wedge \mathrm{card}_c B = 0 \wedge \mathrm{card}_t B \in \mathbb{N}} \tag{1.1}$$

*For any set of real objects, there exists a subset of undiscovered objects in this set*. Such an axiom complements a set theory when applied to real objects. The corollaries of this include the following:

*1)* $$\boldsymbol{\forall A \mid \mathrm{card}_c A > 0\ \exists\ B \mid B \subsetneq A \wedge \mathrm{card}_c B = 0 \wedge \wedge\ \mathrm{card}_t B \in \mathbb{N}} \tag{2.1}$$

*For any* element-containing *set of real objects, there exists a subset of undiscovered objects in this set.*

*2)* $$\forall A \mid \mathrm{card}_c A = 0 \wedge \mathrm{card}_t A \in \mathbb{N} \wedge A \subseteq \varnothing\ (A \equiv \varnothing) \tag{2.2}$$

*A subset of undiscovered objects in the empty set is identical to the empty set.*

*3)* $$\forall A\ \exists!\ B \mid B \subseteq A \wedge \mathrm{card}_c B = 0 \wedge \mathrm{card}_t B = \mathrm{card}_t A - - \mathrm{card}_c A \tag{2.3}$$

*For any set of real objects, there exists (only one) subset of* all *undiscovered objects in this set.*

*a)* $$\boldsymbol{\forall A \mid \mathrm{card}_c A > 0\ \exists!\ B \mid B \subsetneq A \wedge \mathrm{card}_c B = 0 \wedge \mathrm{card}_t B = = \mathrm{card}_t A - \mathrm{card}_c A} \tag{2.3.1}$$

*For any element-containing set of real objects, there exists a subset of all undiscovered objects in this set.*

*b)* $$\begin{aligned} &\mathrm{card}_t B \mid [B \subseteq A \wedge (\mathrm{card}_t B = \mathrm{card}_t A - \mathrm{card}_c A) \wedge \\ &\wedge (\mathrm{card}_c A = 0 \wedge \mathrm{card}_t A \in \mathbb{N})] = \mathrm{card}_t A - \mathrm{card}_c A \\ &\mathrm{card}_t B = \mathrm{card}_t A - 0 \\ &\mathrm{card}_t B = \mathrm{card}_t A \\ &B \subseteq A \wedge \mathrm{card}_t B = \mathrm{card}_t A \Rightarrow B \equiv A \end{aligned} \tag{2.3.2}$$

*The subset of all undiscovered objects in a set of undiscovered objects is identical to this set of undiscovered objects.*

*c)* $$\begin{aligned} &\mathrm{card}_t B \mid [B \subseteq \varnothing \wedge (\mathrm{card}_t B = \mathrm{card}_t \varnothing - \mathrm{card}_c \varnothing)] = \\ &= \mathrm{card}_t \varnothing - \mathrm{card}_c \varnothing \\ &\mathrm{card}_t B = 0 - 0 \Rightarrow B \equiv \varnothing \end{aligned} \tag{2.3.3}$$

*The subset of all undiscovered objects in the empty set is identical to the empty set.*

Sets of real objects have a sharper difference between equivalence ($=$ or $=^-$) and identity ($\equiv$ or $=^+$) (see Gilmore, 1974; Hollander, 2012; Antonutti Marfori & Quinon, 2021). Two sets of real objects with non-synonymous definitions can be equivalent (have the same members and the same $\mathrm{card}_c$) but not identical, since their definitions cover different undiscovered objects and different numbers of them (these sets have different $\mathrm{card}_t$).

Most particular axiomatic set theories are developed for only extensionally defined sets (see Kanamori, 2003 for review). Applied to sets of real objects, they—as well as any precise calculations—work only with member-content of real objects sets. Under their control are the differences of sets with their subsets of all undiscovered in them—“unknownless” sets—the relative complement of the subset of all undiscovered objects of the set $A$ in this set $A$ (the set minus its subset of all undiscovered objects):

$$A' \equiv A \setminus B \mid B \subseteq A \wedge \mathrm{card}_c B = 0 \wedge \mathrm{card}_t B = \mathrm{card}_t A - \mathrm{card}_c A$$

Also, along with extensional set theories, there are a number of intensional set theories, embracing intensionally defined sets together with extensionally defined ones as well as extensional set theories *in toto* (Gilmore, 1974; Myhill, 1985; Hinnion, 2006; 2007; Hollander, 2012).

The exact cardinality of the subset of undiscovered objects is usually unknown. In the most general case, it can be defined as belonging to the set of non-negative integers ($\mathbb{N}$; *i.e.* 0, 1, 2, 3 ...). Inside this, approximate and probabilistic estimates of the actual cardinality of some particular set are possible (*e.g.* Erwin, 1982; 1983; 1991; Ødegaard, 2000; Stork, 2018 for Arthropoda). Along with this, our definition of some particular sets of undiscovered objects could robustly establish a more narrow diapason of possible values of the actual cardinality inside $\mathbb{N}$ rather than the whole $\mathbb{N}$. The examples are the single-seater set of the axion particle type ($\mathrm{card}_c = 0$; $\mathrm{card}_t \in \{0; 1\}$) (Wilczek, 1978; Weinberg, 1978) and the three-seater set of the particles of the axion–axino–saxino trio ($\mathrm{card}_c = 0$; $\mathrm{card}_t \in \{0; 1; 2; 3\}$) (Abe *et al.*, 2002). Finally, there are sets where this diapason is reduced to a single number by the definition of a set. The examples are the sets defined as “*the first two asteroids* [Rubin & Grossman, 2010] *that impacted the Earth’s continental crust*” ($\mathrm{card}_c = 0$; $\mathrm{card}_t = 2$); “*the first living* [Trifonov, 2011] *object on Earth*” ($\mathrm{card}_c = 0$; $\mathrm{card}_t = 1$); and “*the last organism ancestral to all known living things*” ($\mathrm{card}_c = 0$; $\mathrm{card}_t = 1$).

Thus, let us say, a discovered hexapod is Hexapoda. An undiscovered hexapod is Hexapoda as well. The former sentence means that a discovered hexapod is the member ($\in$) of the set Hexapoda. The latter sentence means that an undiscovered hexapod is a single-seater subset ($\subset$) of the undiscovered in the set Hexapoda. Along with this, undiscovered objects are scarcely mentioned one by one. Usually, we can see sentences like “*There are millions of undiscovered Hexapoda*” (Stork, 2018) where the subset of all undiscovered objects (.  ) in the set Hexapoda is taken.

Classifications of real objects are (and should be) made up only of element-containing sets. In classifications, the empty set (the subset of all sets) is omitted as well as sets consisting only of undiscovered objects (like *K* in Fig. 1; see also Tab. 1). The principles of classification, such as comprehensiveness of coverage and non-intersection of classes, apply only to discovered objects. Along with this, in phylogenetics, discovered objects are linked through undiscovered ones—by kinship (“consanguinity”; the lack of any blood in many living objects is disregarded).

Anyone who considers any phylogenetic reconstruction to be a reflection of the real phylogeny *de facto* uses a kind of model-dependent realism (Hawking & Mlodinow, 2010*a*,*b*; Koonin, 2011; partly similar to the constructive empiricism of Van Fraassen, 1980). Here, objective reality and absolute truth exist and we have accessible signals from the former. The robustness of these signals varies depending on the object of study. Along with it, for many aspects of nature at each particular time we have only a rating of models, but not the single absolute truth. This rating is built based on four values of models: their empirical adequacy; self-consistency; explanatory power; and parsimony.

| **Sets** | **Their cardinality** | |
|---|---|---|
| | **Accessed cardinality** (*i.e.* the cardinality of the discovered; number of elements) **card$_c$** | **Actual cardinality** (number of elements and undiscovered objects covered by the set definition) **card$_t$** |
| ◉<br>**“regular” sets (sets containing discovered objects)** | $a \mid a \in \mathbb{N}^*$ | *<br>$b \mid b \in \{c \mid c \geqslant a \wedge c \in \mathbb{N}^*\}$ |
| ?⃝<br>**sets of undiscovered objects** | 0 | $d \mid d \in \mathbb{N}$ |
| ∅<br>**the empty set** | 0 | 0 |
| | | |
| ⚲$_X$<br>**the subset of *all* undiscovered objects in a set *X*;**<br>**the particular case of ?⃝.** | 0 | $e = \mathrm{card}_t X - \mathrm{card}_c X$ |

**Table 1.** Cardinalities of the general types of sets that could be applied to real objects. ℕ is the set of natural numbers (non-negative integers; *i.e.* 0, 1, 2, 3 …) and ℕ* is ℕ with zero excluded (the set of positive integers; *i.e.* 1, 2, 3 …) according to the ISO 80000-2:2019 (ISO, 2021); *a*, *b*, *c*, *d*, and *e* are variables that have a value equal to some number in the corresponding set (ℕ* or ℕ). ***** Please, note that while *a* here is the variable only (known for any particular element-containing set of real objects), *b*–*e* are in most cases also the unknowns with exact value remaining unknown for most specific sets. Nevertheless, for some particular sets of undiscovered objects, we could establish a more narrow diapason of possible values of the actual cardinality inside ℕ rather than the whole ℕ. The examples are the single-seater set of the axion particle type (card$_c$ = 0; card$_t \in \{0; 1\}$) (Wilczek, 1978; Weinberg, 1978) and the three-seater set of the particles of the axion–axino–saxino trio (card$_c$ = 0; card$_t \in \{0; 1; 2; 3\}$) (Abe *et al.*, 2002). Finally, there are sets where this diapason is reduced to a single number by the definition of a set. The examples are the sets defined as “*the first two asteroids* [Rubin & Grossman, 2010] *that impacted the Earth's continental crust*” (card$_c$ = 0; card$_t$ = 2); “*the first living* [Trifonov, 2011] *object on Earth*” (card$_c$ = 0; card$_t$ = 1); and “*the last organism ancestral to all known living things*” (card$_c$ = 0; card$_t$ = 1). *Note 1.* The membership of *a*–*e* minimally defined up to ℕ implies the infinity of spacetime. If for any reason this infinity is not true, then cardinalities of sets of real objects can not be infinite. Then, cardinalities could be minimally defined not up to the entire ℕ but up to its part (although limited by an extremely big number *k*; $\mathbb{N}_k$). *Note 2.* In the case of the application of fuzzy mathematics (Zadeh, 1965 and the references in Kerre & Mordeson, 2005), the set of all non-negative rational numbers ($\mathbb{Q}_{\geqslant 0}$) replaces the set of non-negative integers (ℕ) in everything mentioned and the set of all positive rational numbers ($\mathbb{Q}_{>0}$) replaces the set of positive integers (ℕ*).

Concerning the phylogeny of life, this approach manifests itself in the following chain: 1) characters of discovered organisms serve as the base for the construction of a modelled phylogenetic tree; 2) this reconstructed phylogenetic tree is regarded as a reflection of the real phylogeny in each particular case; 3) this reflection serves as the base for conclusions on a type of a group[1] and on features of some ancestors of discovered organisms. Examples are the last common ancestor of discovered eukaryotes (Koonin, 2010; Desmond *et al.*, 2011; O’Malley *et al.*, 2019) or the last common ancestor of discovered eukaryotes plus discovered archaea (Forterre, 2013; Doolittle, 2020). In this way, undiscovered organisms appear in scientific discussions.

Notwithstanding, there are certain difficulties with the

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[1] In the mathematical sense, throughout the manuscript, the term “group” is used synonymously with “element-containing set”. No relation to the group theory.

handling of undiscovered entities. In natural sciences, the key criterion for proving the existence of an object (like an astronomical object of a previously undiscovered kind, an atom of a previously undiscovered element or an organism of a previously undiscovered species) is an observation of this object and/or observation of traces of its existence (radiation, remains of vital activity *etc.*).

Undiscovered organisms sister to discovered ones can be almost completely compared with undiscovered objects in any other science. Along with them, there is one special kind of undiscovered organisms and species. It is the undiscovered ancestors of discovered organisms.

Their remarkable feature is that discovered descendants inevitably imply the existence of their ancestors, even if these ancestors are unobserved. Just like in police practice any proven crime implies that there are criminals. Murder implies the existence of a killer. Theft implies a thief. However, this data alone is not enough to put any person into prison with other criminals. The police need to specify the identities of the criminals and find them. Similarly, the implication of the existence and the role is not enough to "specify the identity" for each of the undiscovered ancestors and put them as members into any taxon with similar species.

There is no natural or government law, which prohibits putting undiscovered (or even purely hypothetical) entities into groups and systems. As there is no such law, which prohibits the creation of systems of life composed exclusively of form-taxa. But is it better to do it one way or another in phylogenetics and systematics?

If we consider the undiscovered organisms to be direct members of groups, then, for instance, we must write right now that life is polyphyletic if somewhere in the endless universe there is (or was) a life besides our lineage. Also, in this case, we must write right now that intelligent life is polyphyletic if there is (or was) intelligent life besides us. I guess this is premature before the discovery of these if it ever happens. With the membership of the undiscovered in taxa, any group with classical morphological definition can not be called holophyletic, as there always is a possibility of the existence of an undiscovered "member" of the same lineage, but which does not fit the definition and is outside the group. It seems excessive before its discovery. Also, if we consider undiscovered organisms the same way as discovered ones, then no clade can be divided into subclades evenly (Fig. 2A; Cavalier-Smith, 1993 p. 955; 1998 p. 211). In this case, we must introduce at least one paraphyletic group per holophyletic one (Cavalier-Smith, 1993; 1998).

Thus in numerous aspects, it seems premature to directly place the undiscovered as members into taxa (or create separate taxa for it) before its discovery. With no membership of the undiscovered, we can call life holophyletic until any independently occurring life is discovered (if it ever happens). Likewise, groups with classical morphological definitions can be called holophyletic until any member of the same lineage unmatching the definition is discovered. Also, clades become fully divisible into subclades (Fig. 2B).

Official codes of the nomenclature of life seem to support this position. According to them, only discovered entities are taxonomically nameable: Articles 1.3.1, 72.3, 72.5 of the *International Code of Zoological*

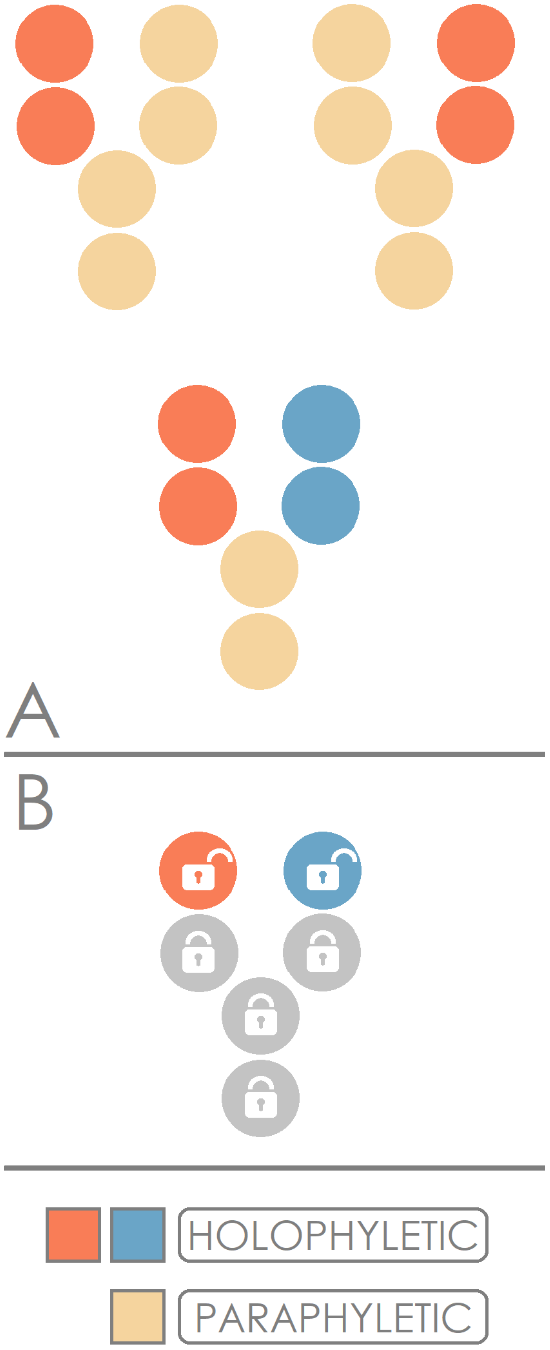

**Figure 2.** The trees of ancestor–descendant relationships. A. The indivisibility of a clade into subclades completely, if the clade is defined as "an ancestor and all its descendants". B. Divisibility of a clade if undiscovered ancestors are not direct members of this clade. Circles with open locks represent discovered basic units of organismal systematics—biological species (for segments of genealogy where the combination of genetic material from different organisms is necessary during existing sexual reproduction) or organisms (for segments of genealogy where reproduction occurs exclusively asexually, automictically, or via unfertilised gametes). Circles with closed locks represent undiscovered units. *Note:* There are two of everything in A (two members of each subbranch and two ancestors of subbranches) because the definitions like "the ancestor plus all its descendants" (holophyly) and "the ancestor plus not all its descendants" (paraphyly) left no place to the sole-member groups. At least two are needed (one ancestor and one its descendant) to be holophyletic or paraphyletic by these definitions.

*Nomenclature* (ICZN; International Commission on Zoological Nomenclature, 1999); Principle II and Articles 7.1 and 8.1 of the *International Code of Nomenclature for algae, fungi, and plants* (ICN[afp]; Turland *et al.*, 2018); Principle 5 and Rule 15 of the *International Code of Nomenclature of Prokaryotes* (ICNP; Parker *et al.*, 2019); and Articles 11.1, 11.4 of the *PhyloCode* (de Queiroz & Cantino, 2020); see also Principle III and Article 9.1 [10.1] of the *Draft BioCode* (Greuter *et al.*, 1996; 1998; 2011a,b). New species are described as new (*species novae*, sp. n.), rather than already existing in the group (although they exist in nature for millennia before discovery), because "new" here is about the *human knowledge* of biodiversity and not about their emergence in nature. Undiscovered organisms and species within the definitional boundary of a taxon can be naturally regarded as its subsets but only its potential *members*. If so, they become actual members only with their discovery by humanity. Any mention of an undiscovered object is a single-seater set (a set with actual cardinality of no more than one) having zero accessed cardinality. It is like Vaticanian *Sede Vacante* but not any person as the Pope.

Because of all the said, the present work is dedicated only to the approach where the undiscovered has no direct membership in groups of a classification.

Unfortunately, the non-membership of the undiscovered creates nonsense in the current system of phylogenetic concepts. It is not adapted to the separation of discovered and undiscovered organisms (as well as populations, species, etc.). The difference of holo- and paraphyletic groups from polyphyletic groups is whether the last common ancestor of discovered organisms in the group is a member of this group (*Encyclopedia of Life Science*—Cullen, 2009, p. 91; *PhyloCode*—de Queiroz and Cantino, 2020, Article 2.1; *Campbell biology* —Urry *et al.*, 2021 p. 560; Hawksworth, 2010; and others). Almost always the last common ancestor can not become a real member of a taxon because this ancestor is undiscovered. This makes almost all groups "polyphyletic" if take these definitions literally. Therefore, the membership of ancestors in taxa can not be only direct as under current definitions of holophyly and paraphyly.

Surprisingly, there seems no clear distinction between discovered and undiscovered objects in the history of types of groups in phylogenetics. This system stemmed from Haeckel (1866). He introduced the German terms *monophilie* and *polyphylie* but was ambiguous in the precise meaning and usage of both terms. It is unclear whether his monophyly was only holophyly (monophyly *sensu stricto*) or covered also paraphyly (Dayrat, 2003; Rieppel, 2010). He did not reject the possibility of multiple origins of known life (Haeckel, 1866 p. 198; 1868 p. 347; 1873 p. 371; 1894 p. 89) and true polyphyly has the practical sense under these views. Also, he made no distinction between discovered and undiscovered organisms and tended to give names to ancestors of hypothetical appearance (Haeckel, 1866; 1874). The concepts were rethought a hundred years later by Hennig (1950; 1965; 1966). He was implicitly close to the membership of only discovered species in taxa. At the same time, he considered the probability of finding an ancestor of any group so low that he did not stipulate the inclusion or membership of ancestors in any way in his definitions of phyletic terms. Ancestors *de facto* were excluded from the groups.

This theoretical inaccuracy led to the rapid making the last common ancestor a member of taxa by corrected definitions of holophyly and paraphyly by other authors (*e.g.* Ashlock, 1971). Its membership was unconditional. Like in the works of Hennig, Ashlock and others, the condition of being discovered for members is not stipulated by the "connected–disconnected" (Kwok, 2010) / "continuous–discontinuous" (Aubert, 2015) divide.

Different concepts are mixed, situationally used in different senses under the same name, and some are frequently used against their meaning (see below). All this makes it difficult to discuss the evolution of life productively. One example is the lack of an articulated awareness that plerophyly and holophyly are different concepts, the latter is narrower than the former. Plerophyly is a hypernym of holophyly and holophyly is a hyponym of plerophyly (see below). The system of group types would be nice to be redesigned for the precise distinction of discovered and undiscovered entities.

The lack of explicit differentiation between discovered and undiscovered organisms has led to confusion among taxonomists (see Podani, 2010 for review). Probably, both of the main types of the vision of phylogenetic trees shown, among others, by Podani (2009, Fig. 2) are not completely correct. The consensus seems possible and necessary. There are undiscovered ancestors of discovered organisms (unlike Podani, 2009 Fig. 2B,D), but they are better not to be treated in the same way as discovered species or organisms (unlike Podani, 2009 Fig. 2A,C; compare aforementioned figures of Podani and Figs. 2B, 3, 6, here). Regardless of the likelihood of discovering each specific ancestor, a theoretically consistent system of concepts should be designed for the case when ancestors are found. The likelihood of this is high near the terminals of the Tree of Life. However, the membership of undiscovered organisms (including undiscovered ancestors) can not be direct and immediate.

Thus, to be consistent we should either make undiscovered ancestors full members of taxa somehow, describe species for them and introduce at least one paraphyletic subtaxon per taxon, or not to make them members directly and amend the system of concepts. The differentiation between discovered and undiscovered organisms makes it possible to accurately and unambiguously define several phylogenetic terms, to avoid the problem of description of undiscovered organisms, and to make the cladistic systematics possible (*i.e.* a full division of one clade into two subclades).

The revised and supplemented system of concepts with definitions and comments is proposed below. It starts with the basic concepts (phylon, startestor, intrendon), which were used to define plerophyly and merophyly, together with holophyly, paraphyly, and chasmophyly, which follow after them.

From the actual content of a group coupled with a phylogenetic reconstruction, one can only conclude whether the group is plerophyletic or merophyletic (see below). To get more than two variants when any two organisms have a common ancestor and to determine whether a group is holo-, para-, or chasmophyletic, we are forced to conclude about a certain part of ancestors of discovered members of a group (intrendon, see below): 1) is the definition of this group capable of ensuring the membership of the intrendon completely, in the theoretical case if all them become discovered; 2) whether the intrendon gave rise to any discovered organisms outside the particular group.

Cladistic systematics is the drive to constantly reduce non-holophyletic groups to only undiscovered organisms. However, the definition of the clade disallowing it is widespread and adopted, for example, by the *PhyloCode* (de Queiroz and Cantino, 2020, Article 2.1). Regardless of how acceptable we think paraphyletic groups are, cladistics is possible only with no membership of the undiscovered. Well, let us go in search of "natural" groups' nature in this picture.

## SYSTEM OF CONCEPTS

### *THE CORE CONCEPT*

All our phyletic terms end on "-phyly" and are built to characterize the relation of a set of organisms/species to something with this etymological root. It seems useful to begin with a formulation of what this something is. This concept (*phylon*) has a definition similar to one currently widely used for a holophyletic group (monophyletic group *sensu stricto*; clade) but allowing a singleton to be a phylon.

**PHYLON**[1] (/ˈfaɪlɒn/; from Ancient Greek *φῦλον* [*phylon*] - tribe) — an organism[2] or a biological species[3] plus (if any) all its descendants.

Nevertheless, phylon and its definition is only a theoretical substratum, on which we superimpose the groups of discovered organisms like a stencil. The phylon is just the starting point having a direct practical application only in a case when the ancestor and all its descendants together are discovered (such a group can be named Zander's (2009) term euphyletic). Therefore, the phylon helps to distinguish group types of taxa but is not a type itself in phylogenetics of large taxa. On the base of the phylon it is possible to distinguish the organismal groups' types, which reflect the branching pattern of the groups' actual content. These types depend on whether or not a particular group comprises all discovered members of at least one phylon.

### *GROUP TYPES DEPENDING ON THE BRANCHING PATTERN OF DISCOVERED MEMBERS IN THE GROUP*

If we base our conclusions on the type of a group only on the group's discovered content, its branching pattern and no more (widespread path of analysis in current phylogenetics), there is only dichotomy (Figs. 3, 4). Whether or not there is at least one phylon, of which our group comprises all discovered members.

**PLEROPHYLETIC** group (/pliɹə(ʊ)fʌɪˈlɛtɪk/; from Late Koine Greek *πλήρης* [*plḗrēs*] - full, complete) — an element-containing set, all discovered members of which constitute the entire discovered part of at least one phylon.

**MEROPHYLETIC** group (/mɛɹə(ʊ)fʌɪˈlɛtɪk/; from Ancient Greek *μέρος* [*méros*] - part, portion) — an element-containing set (of organisms of common descent if more than one), all discovered members of which constitute the entire discovered part of no phylon.

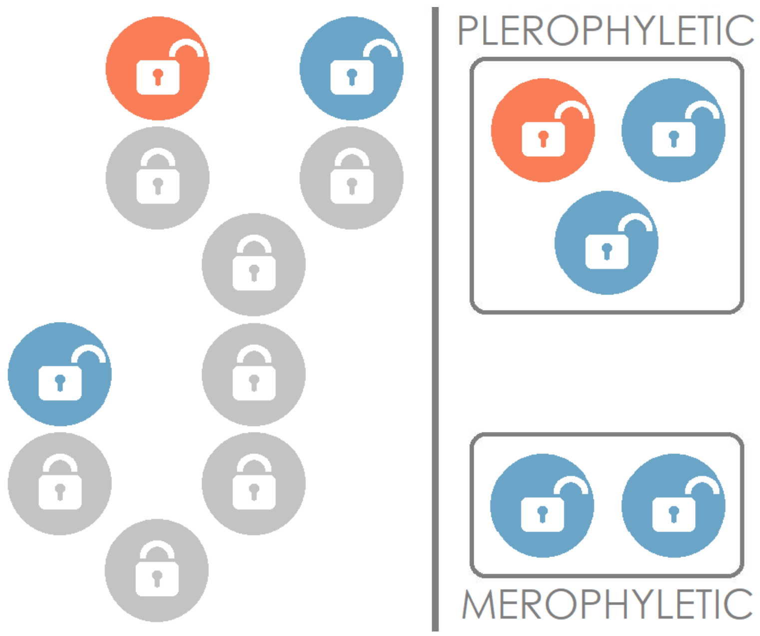

**Figure 3.** The tree of ancestor–descendant relationships. Circles with open locks represent discovered basic units of classification. Circles with closed locks represent undiscovered units.

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[1] The form "*phylon*"—the direct transliteration from Ancient Greek—is chosen here to avoid confusion with the phylum—the taxonomic rank.

[2] For segments of the genealogy of life where a reproduction occurred exclusively asexually, automictically, or via unfertilised gametes.

[3] For segments of the genealogy of life where the combination of genetic material from different organisms is necessary during existing sexual reproduction.

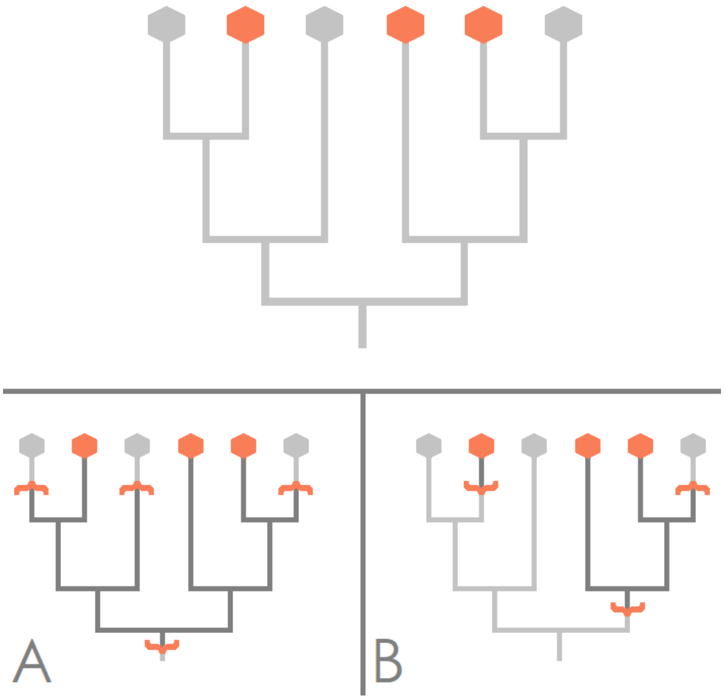

**Figure 4.** The inability to conclude whether the merophyletic group is paraphyletic (A) or "polyphyletic" (B) based only on the topology and content of the group without an analysis of the definition of the group. *See the three left trees of Fig. 7 (1, 2, 3) for the inability to conclude whether a plerophyletic group is holophyletic, paraphyletic or "polyphyletic".*

Nevertheless, the "plero–mero" divide is not enough for characterising a set as "natural" or not. A group of the former type must meet the additional criteria (be at least jugiphyletic; cf. connected/continuous). To achieve more than the two variants above, we have to deal with the undiscovered ancestors of discovered organisms and the definitional potential of groups to contain them as members. To do this, first, it is necessary to discuss the very concept of an ancestor.

## *ANCESTOR IS A CONCEPT WITH A NEGLECTED AND FREQUENT MISUSE*

Every evolutionary discussion uses the concept of an ancestor. The following text uses this, too. Notwithstanding, there is a neglected problem with the application of this in an evolutionary context. You can not simultaneously be an ancestor of some group and be (or can be) a part of this group. The phrase "*My mom is the ancestor of my mom, my sister and me*" is not correct. Ancestors end where the boundaries of the group begin. Anything inside cannot be any ancestor of the group. For more scientific instance, if eukaryotes are the first cell with (the thing possessing all characters of) the true nucleus inside together with all that cell's descendants, then anything called an ancestor of eukaryotes is an ancestor of this first cell with a nucleus. It means any ancestor of eukaryotes had no true nucleus. At the same time, the thing usually called "the last common *ancestor*" of eukaryotes obviously had a nucleus. An inconsistency and Francis Bacon's *idolum fori* (Franciscq de Verulamio, 1620; see also Bacon, 1605 p. 57) that leads us astray?

The root of the problem is quite old and fundamental. It seems, that here we deal with the definist fallacy (Frankena, 1939; Bunnin & Yu, 2004)—the definition of a concept solely by the properties of another term that is established and non-synonymous. The concept of an ancestor was initially created not to phylogenetics. The very word ancestor is derived from the Latin *antecessor* (*ante-* [before]*; -cessor* [going]) meaning "one who goes before" (but does not enter). This everyday concept of an ancestor serves consistently and well for domestic purposes and relationships of individuals in human and animal families. But it is far from good for evolutionary discussions in numerous cases. It is incorrect to call something an ancestor of some group and imply that it is (or can be) a member of this group. The wording "*ancestor* of eukaryotes" ("last common" or another) is incorrect for anything with a true nucleus. All the said about the concept of an ancestor is also true for the concept of a progenitor.

In contrast, our things should be able to become members of taxa and are their subsets. Thus, there are only two ways: either to redefine and complicate the everyday word "ancestor" or to use here the alternative concepts.

Following the latter way, the first proposition is the *rendestor*. It is the thing erroneously defined as "the last common ancestor" countless times. The new word was used as the existing words "*concestor*" and "*cenancestor*" are the different names of the same concept as the last common ancestor.

Also, there is the sometimes used wording "the first common ancestor" (*e.g.* Koumandou *et al.*, 2013; Dacks *et al.*, 2016; Eme *et al.*, 2017). It has a more obvious logical problem. Literally, the first common ancestor of any known group is the first living thing. Thus, "the first common ancestor" is certainly misused wording in the sense it is applied in the aforementioned works. Nevertheless, any other wording or word (*pridestor*) is currently absent, too.

The third is the previously undefined (but key) concept of *startestor*—the thing in a group, from which all (other) members are descended—the earliest (potential) member of a group covered by the definition of this group. Probably, sometimes something like this is erroneously called a progenitor (see above and Fig. 5). In discussions about the origin of a group (for example, about eukaryogenesis), we are talking primarily about the startestor of this group. A startestor is the immediate descendant of the literal progenitor and literal last common ancestor (Fig. 5). Also, I would note that the wording "universal ancestor" is nonsense as the ancestor can not be universal because it can not be an ancestor of itself.

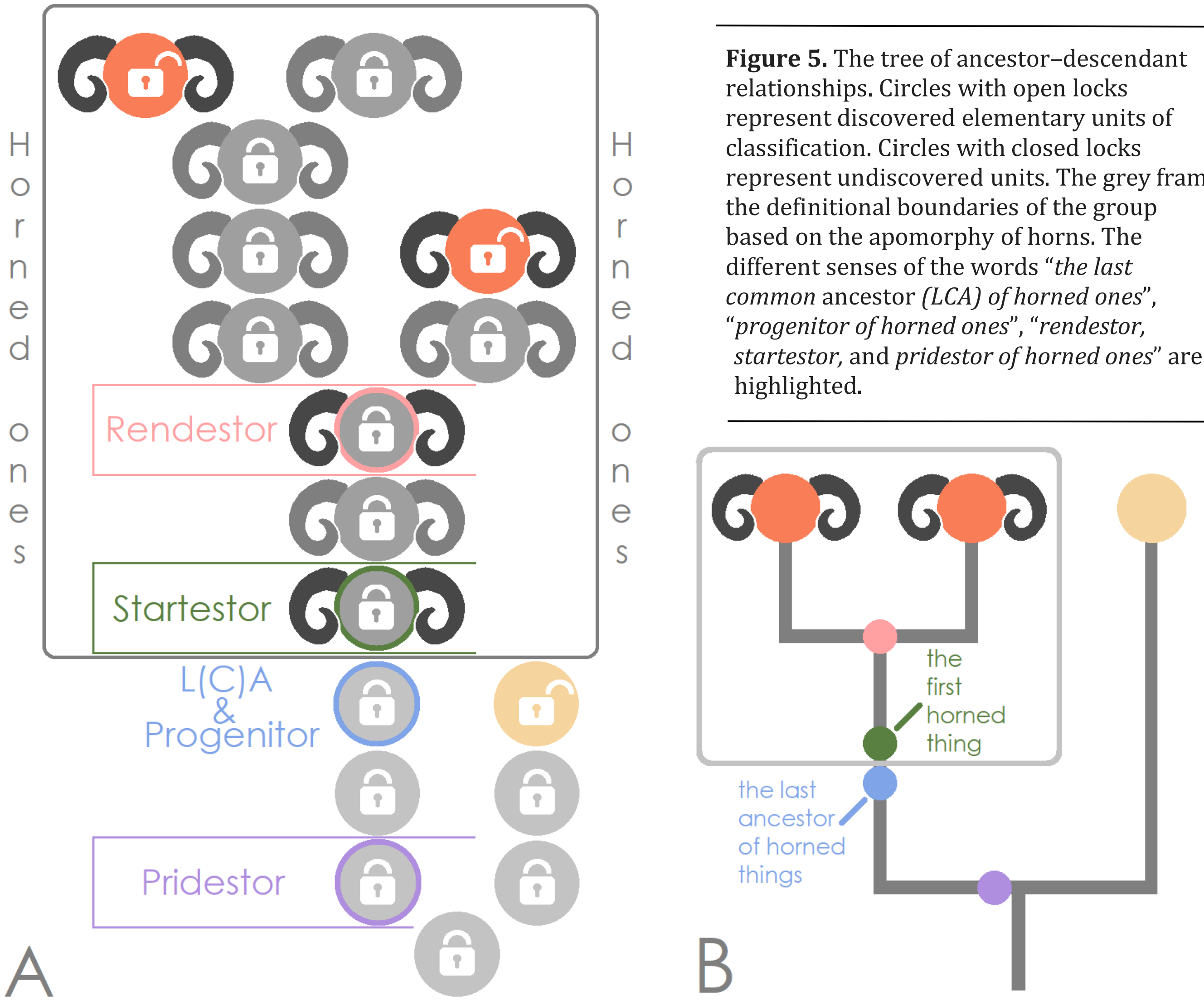

**Figure 5.** The tree of ancestor–descendant relationships. Circles with open locks represent discovered elementary units of classification. Circles with closed locks represent undiscovered units. The grey frame is the definitional boundaries of the group based on the apomorphy of horns. The different senses of the words "*the last common* ancestor *(LCA) of horned ones*", "*progenitor of horned ones*", "*rendestor, startestor,* and *pridestor of horned ones*" are highlighted.

**Rendestor** of a group (/'rɒndɛstə/; from French ***rendez**vous* - a meeting at an agreed time and place, and the ending -***estor***, like in the word *ancestor*) — the last in natural history common ancestor of all (two or more) discovered members of the group except this ancestor itself (if this ancestor is discovered and is a member of the group).

**Pridestor** of a group (/'prɪdɛstə/; from Ancient Greek πρώτα [***pró**ta*] - first; Ancient Greek ἴδῖος [***íd**ios*] - pertaining to self, one's own, private (as opposed to public); and the ending ***-estor***, like in the word ancestor) — the first in natural history ancestor of all discovered members of the group except this ancestor itself (if this ancestor is discovered and is a member of the group) and no discovered organisms outside the group.

**Startestor** of a group (/'stɑːtɛstə/; from English ***start*** - the beginning, the beginning point, and the ending -***estor***, like in the word *ancestor*) — the first in natural history organism[1] or biological species[2], which satisfies the definition of the group and is ancestral to all (if any) discovered members of the group except this organism/species itself (if this organism/species is discovered).

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[1] For segments of the genealogy of life where reproduction occurs exclusively asexually, automictically, or via unfertilised gametes.

[2] For segments of the genealogy of life where the combination of genetic material from different organisms is necessary during existing sexual reproduction.

## *AN ANCESTRAL LINK*

Along with the important single points (rendestor, startestor, pridestor) at a sequence of ancestors of discovered organisms, the branching sequence of ancestors connecting discovered organisms is also important itself. Among numerous possible kinds of such sequences, one is key for systematic purposes—the sequence starting with the startestor. It is the “tendon” of a group connecting the progenitor of this group with all its discovered members (Fig. 5). The part of this sequence, that a group can include is precisely what distinguishes holophyly and paraphyly from “polyphyly” (chasmophyly)—*i.e.* all our group types other than plero- and merophyly. Nevertheless, the concept of this thing has yet been formulated.

**INTRENDON** (/ɪnˈtrɛndən/; contraction from *intra-* and *tendon*) of a group — the startestor of the given group plus (if any) all the startestor’s descendants, which also are ancestors of discovered members of the given group.

Intrendon can contain discovered organisms, undiscovered organisms or a mixture of both. Also, it can be the only ancestor (if all discovered members of the group are its direct descendants). Using the concept of intrendon, it is possible to define the following basic duet of group types (Fig. 7).

## *GROUP TYPES DEPENDING ON THE ABILITY TO CONTAIN THE WHOLE INTRENDON AS MEMBERS*

Typically, the line between polyphyly and (holophyly + paraphyly) was drawn by whether or not the rendestor (called “last common ancestor”) is a member of a group (Cullen, 2009; Hawksworth, 2010; Urry *et al.*, 2021). Nevertheless, this is a utilitarian frequent sign of this dichotomy, but not its logical essence. A “natural” group must not be interrupted within all of its definitional boundaries and not only in the rendestor point. An “unnatural” group is interrupted.

The sign with a rendestor-interruption does work in most practical cases, but not in all. Any non-singleton group, which is unable to contain the rendestor is “unnatural”. But not every “unnatural” group is unable to contain the rendestor. The group may be able to contain the rendestor, but be interrupted somewhere before or after it. For example, the group Pisces *sensu* Linnæus, 1735; 1740; 1744; 1756 is able to contain the rendestor, but is interrupted in the segment between fishes (in the current sense) and cetaceans and sirenians. The Protista group in the sense including Myxozoa is able to contain the rendestor, but is interrupted in the segment between choanomonads and myxozoans. Therefore, in the concepts here, the key role is given not to the rendestor, but to the startestor and the whole intrendon of groups (the part of which the rendestor is).

**JUGIPHYLETIC** group (/i̯uːɡɪfʌɪˈlɛtɪk/; from Latin *jūgis* - continuous, incessant, unceasing, uninterrupted) — an element-containing set of organisms, which is able to contain its entire intrendon[1,2].

**CHASMOPHYLETIC** (frequently misleadingly called “**POLYPHYLETIC**”) group (/kæzmə(ʊ)fʌɪˈlɛtɪk/; from Ancient Greek *χάσμα* [*khásma*] - gap, cleft) — an element-containing set of organisms (of common descent), which is unable to contain its entire intrendon[1,3,4].

A jugiphyletic group has the potential to contain undiscovered units as members of its intrendon but does not have them as members before they are discovered.

The jugiphyly is enough to conclude that a group is “natural” only for ones who accept paraphyly in systems. For others, to be “natural”, a group should not forbid itself to be a phylon by definition. For this, a plero- and jugiphyletic group should have no excluded organisms descended from it (*i.e.* from ts startestor). The group should be holophyletic.

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[1] By the definition of the systematic group.

[2] ...and no undiscovered ancestors of discovered organisms outside the group unless these ancestors are part of the intrendon or the continuous sequence of immediate descendants of the intrendon.

[3] ... or able to contain undiscovered ancestors of discovered organisms outside the group if these ancestors are not the members of the intrendon and not the continuous sequence of immediate descendants of the intrendon.

[4] The inability due to the lack of the intrendon included (lack of the single common starting organism/species covered by the set—the startestor).

## *GROUP TYPES DEPENDING ON WHETHER THE GROUP'S STARTESTOR GAVE RISE TO DISCOVERED ORGANISMS OUTSIDE THE GROUP*

Having the two basic dichotomies (plero–mero and jugi–chasmo) it is finally possible to define the duet of group types emerging at the intersection of jugiphyly with plero- and merophyly (Fig. 7). It is holophyly and paraphyly.

**HOLOPHYLETIC** (**MONOPHYLETIC** *sensu stricto*) group (/hɒlə(ʊ)fʌɪˈlɛtɪk/; from Ancient Greek *ὅλος* [*hólos*] whole) — a jugiphyletic group from the startestor of which no discovered organism outside the group is descended.

**PARAPHYLETIC** group (/pɛɹə(ʊ)fʌɪˈlɛtɪk/; from Ancient Greek *παρά* [*pará*] - beside, near, alongside) — a jugiphyletic group from the startestor of which at least one discovered organism outside the group is descended.

## *HOLOPHYLY OR MONOPHYLY?*

The term *holophyletic* was preferred here because of the number of meanings of the term *monophyletic*, both definitional and etymological. As already noted, a monophyletic group defined as "the ancestor plus all its descendants" has very limited application if we take the definition literally—only the sets having more than one member where both the ancestor and all its descendants are discovered (monophyletic group *sensu strictissimo*/euphyletic group). Actually, phylogenetic taxonomists use it in the more loose sense (monophyly *sensu stricto*), probably the same as *holophyletic* group as it was defined here. Evolutionary taxonomists use it probably in the same sense as *jugiphyly* (monophyly *sensu lato*). As there was no differentiation between discovered and undiscovered organisms relatively to types of groups before, additional confusion arose. This confusion allows the term *monophyly* to be treated as a synonym of *plerophyly* or *jugi-plerophyly* or to cover both *plero-* and *merophyly*. It is quite attractive to treat *monophyly* in the last sense ("descendants of *one* ancestor"/"belonging to a *single* phylon"; *sensu latissimo*) opposite to *polyphyly*, although it extremely reduces the term's usefulness (now only sci-fi texts or futurological hypotheses). Haeckel, who introduced the concepts *monophyly* and *polyphyly* (Haeckel 1866), also used them as antonyms and, notably, did not reject the possibility of multiple origins of known life (*e.g.* Haeckel 1866 p. 198; 1868 p. 347; 1873 p. 371; 1894 p. 89; see Dayrat, 2003 and Rieppel, 2010 for review). In such views, the terms *polyphyly* (as a set in which discovered organisms have no common ancestor) and *monophyly* (as its antonym) were applicable.

Despite all this and the vulnerability to etymological fallacies, it is still possible to treat monophyly as the synonym of holophyly and the definition of holophyletic group used here can also be treated definition of monophyly (*sensu stricto*). Although, the term, then, became misleading and the etymology is violated. It can not be deduced from Ancient Greek *μόνος* [mónos] ("one", "alone", "only", "sole", "single") like in the cases of monophyletic group *sensu strictissimo* (it is exactly one phylon) or *sensu latissimo* (members of the group belong to one phylon) as the meaning of the concept is exactly "whole", "entier" (Ancient Greek *ὅλος* [hólos]) concerning both discovered organisms and undiscovered objects of the intrendon.

## *THE "-ADE" TERMS*

The diversity of possible group types and their logical intersections have been overviewed above (see also Fig. 7). This diversity reiterates the question to which theoretical category the term *clade* should be ascribed. Merophyletic groups now are not generally considered clades. Nevertheless, there are still three candidates for the name *clade*: 1) a plerophyletic group (Fig. 7: 1, 2, 3), 2) a jugi-plerophyletic group (Fig. 7: 1, 2) or 3) a holophyletic group (Fig. 7: 1). The lack of differentiation between these three is the Achilles' heel of existing systems of phylogenetic concepts. At the same time, the choice of any single option of three leads to some issues overviewed below.

In current literature, the term clade is now used generally in a sense similar to plerophyletic groups. If authors have made the phylogenetic reconstruction and their organisms grouped together, they say that this is the clade. Nevertheless, the etymology of the term *clade* (from Greek *κλάδος* [*kládos*] — shoot, branch) minds no gaps or omissions in the branch (*i.e.* dictates the ability to contain the whole intrendon). Therefore, the use of

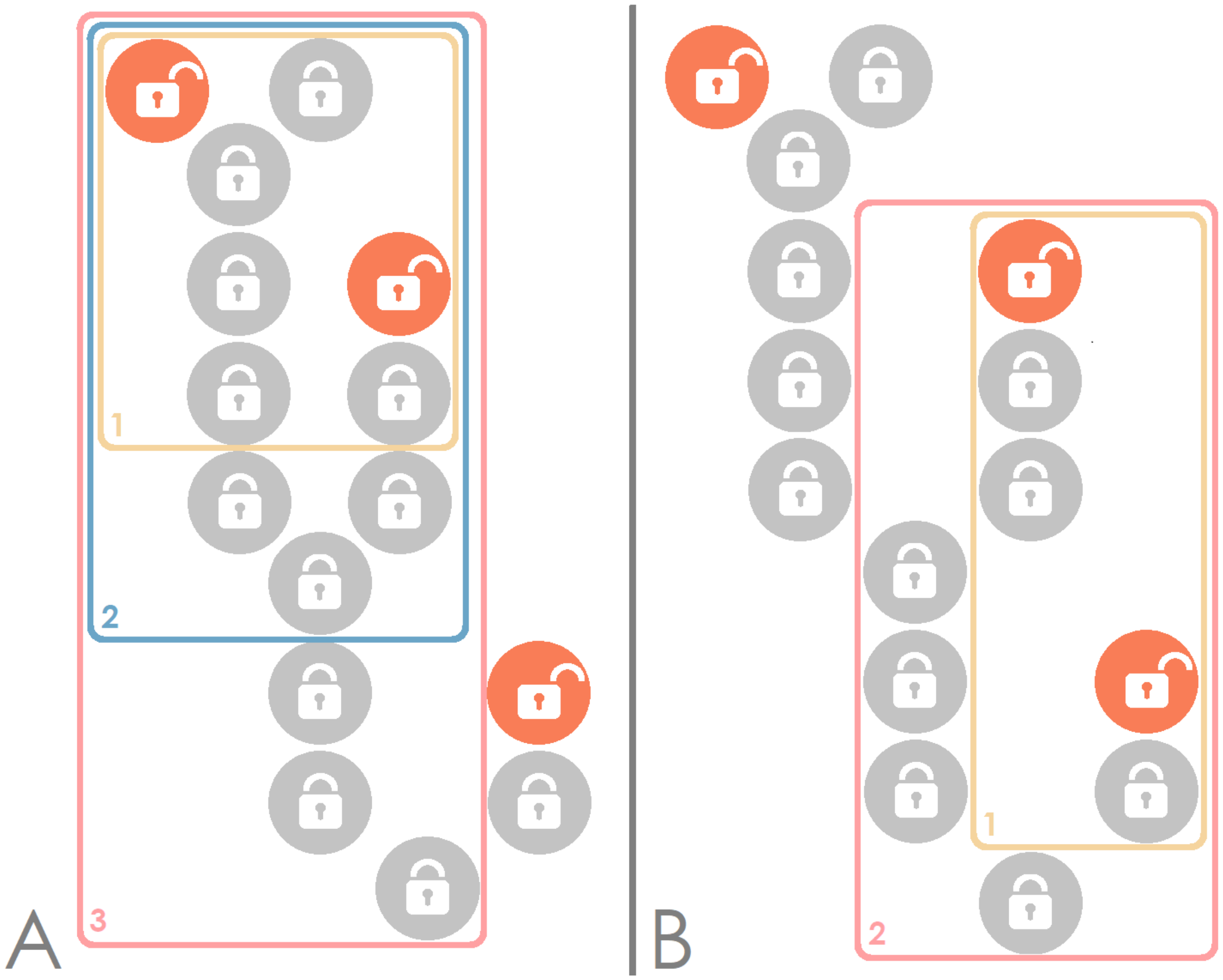

**Figure 6.** Possible definitional boundaries for the equivalent sets of two discovered species (extant *and/or* extinct): plerophyletic (A) and merophyletic (B). The groups A1 and B1 (yellow) are chasmophyletic. A2 (blue) is holophyletic. A3 and B2 (pink) are paraphyletic.

the term clade for any plerophyletic group is an etymological overgeneralisation. At the same time, any other use requires the additional analytic step—not only the branching pattern and the content but also an evaluation of the group's definition. The application of the term clade to only jugi-plerophyletic groups (Fig. 7: 1, 2) is better in the exclusion of the disconnected (chasmophyletic) groups. Along with it, the paraphyletic groups are still partly included (para-plerophyly; Fig. 7: 2). Obviously, the latter groups do not correspond to "the whole branch". So, this possible application of the term clade is anti-etymological, too.

The use of the term clade to holophyletic groups only seems to be etymologically correct. At the same time, there are two issues: 1) a need for more cautious use and consideration of groups' definitions; 2) the consequential lack of a short word for plerophyletic groups—the sense in which the term clade seems currently frequently applied.

The first issue concerns para-plerophyletic groups like choanomonads. Also, it concerns the chasmo-plerophyletic groups. Among the latter are the extensionally defined groups—formed by a simple listing of their members or subgroups. They are technically disconnected (unable to contain their intrendon wholly). For example, the group TSAR was defined as "Telonemia + Sar grouping" (Strassert *et al.*, 2019, p. 761), wherein, Telonemia were defined based on the complex of morphological traits (Shalchian-Tabrizi *et al.*, 2006, p. 1840) and Sar were defined with the minimal-clade definition (Adl *et al.*, 2012, p. 431). Therefore, this group is chasmophyletic by definition although plerophyletic (chasmo-plerophyletic; see Fig. 7: 3 and Fig. 8). If we will use the word "clade" in a narrow sense, the following wordings will not be correct: "Sar+Telonemia clade" or "Telonemia formed the clade with Sar" or "TSAR clade" (see Strassert *et al.*, 2019 for the phylogeny).

The second issue is that if we use the word clade for holophyletic groups only, then any short word for plerophyletic groups is absent. Then, this (*drade*) seems useful for the groups like TSAR or choanomonads as well as for holophyletic groups.

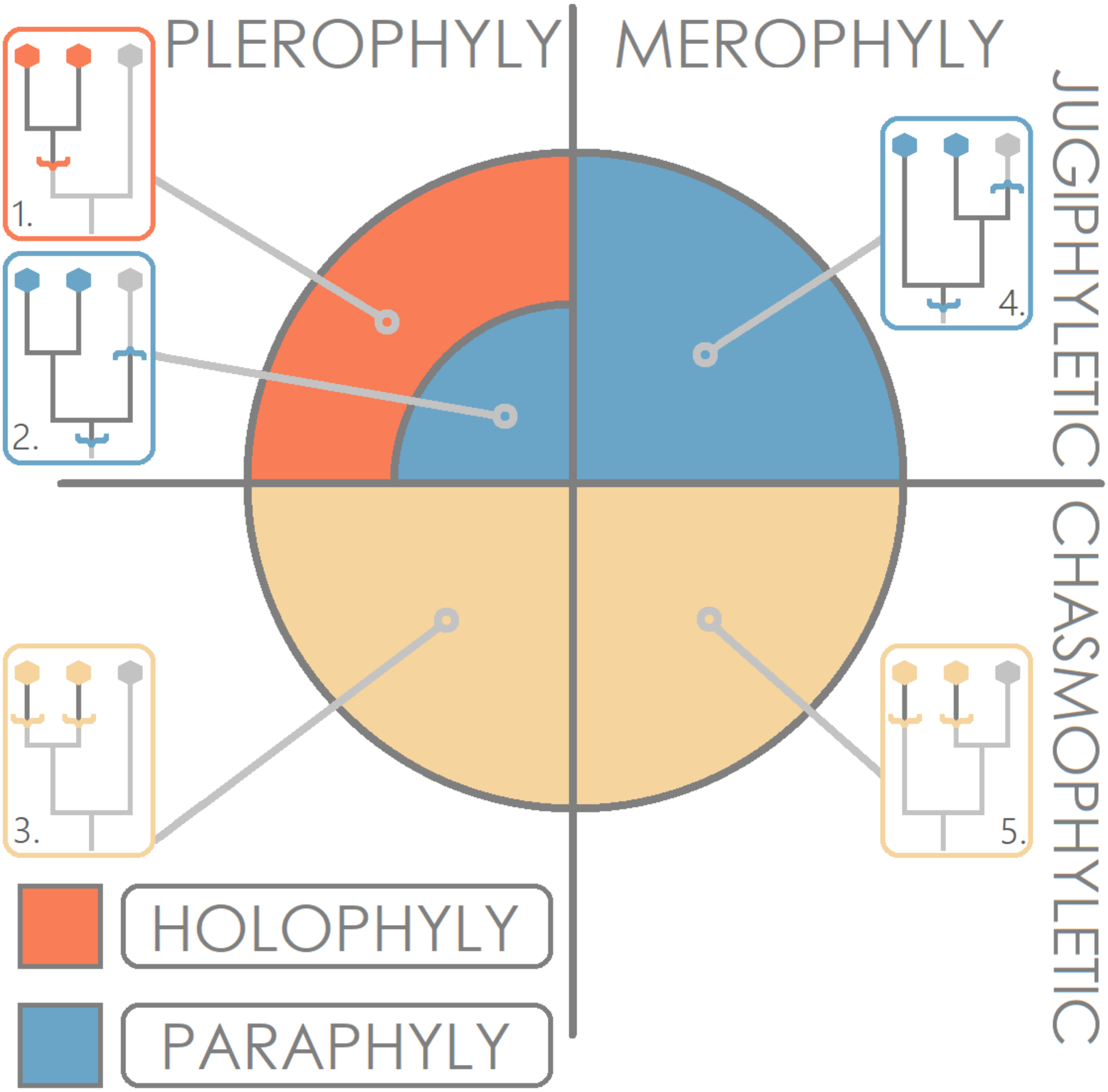

**Figure 7.** The diagram of the interrelationships of group types in phylogenetics. Coloured hexagons represent discovered group members. Grey hexagons represent the discovered organisms outside the group. The groups: on all three trees on the left are plerophyletic; on all two trees on the right are merophyletic; on all three trees above are jugiphyletic; on all two trees below are chasmophyletic. The colour of the hexagons and boundaries around each tree matches the colour of the segment of the vertical half of the diagram. Examples of five types of groups shown: **1. HOLOPHYLETIC**—mammals (Mammalia), birds (Aves); **2. PARA-PLEROPHYLETIC**—choanomonads (Choanomonada; as the rendestor of choanomonads and metazoans had a collar and was a monad, *i.e.* is inside the definitional boundaries of choanomonads), see Cavalier-Smith, 2013; **3. CHASMO-PLEROPHYLETIC**—TSAR grouping (see below), probably (see Fowke and Pickett-Heaps, 1969; Sawitzky and Grolig, 1995) charophytes with phragmoplasts (Phragmoplastophyta), “photokaryotes” of Cavalier-Smith, 1999 in the case if his (Cavalier-Smith, 2018) hypothesis on the single origin of plastids in Chromista is true (as then there is no startestor of photokaryotes and are two their independent origin points: plastid acquisition at the base of Archaeplastida and of Chromista; cf. chasmo-plerophyletic “photokaryotes” and holophyletic Diaphoretickes); **4. PARA-MEROPHYLETIC**—reptiles (Reptilia); **5. CHASMO-MEROPHYLETIC**—warm-blooded animals (Homotherma); Pisces *sensu* Linnæus, 1735; 1740; 1744; 1756 (containing cetaceans and sirenians along with fishes); Protista *sensu ante* Smothers *et al.*, 1994 (containing Myxozoa); also, eukaryotes were initially introduced erroneously as a chasmo-merophyletic taxon (Shɨshkin, 2022).

**DRADE** (/dɹeɪd/; from the two first letters of the semantic core in L. *poly***dr***upa*—the type of fruit to which raspberries belong, bramble fruit, the type of aggregate fruit easily separable from the receptacle—and the ending *-ade*, like in the terms *grade* and *clade*) — a plerophyletic group.

**CLADE** (/kleɪd/; from Greek *κλάδος* [*kládos*] - shoot, branch) — a holophyletic group.

**SKADE**[1] (/skeɪd/; from Greek *σκαλών* [*skalón*] - flight of stairs) — a paraphyletic group.

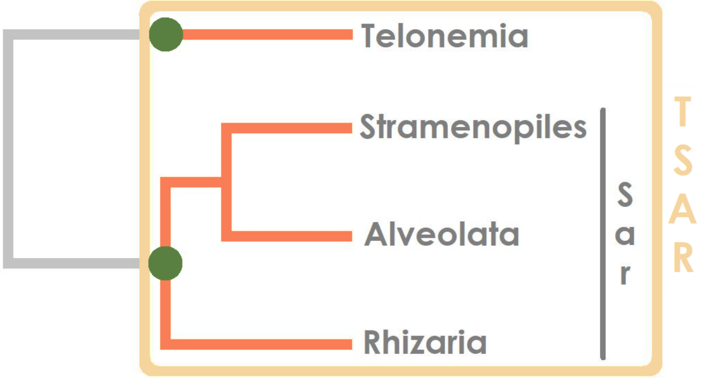

**Figure 8.** Schematic phylogenetic tree of Telonemia, Stramenopiles, Alveolata, and Rhizaria illustrating chasmophyly of the union of Telonemia with Sar (TSAR drade). Definitional boundaries of TSAR are shown in yellow. The ancestral part, which TSAR do not include is shown in grey. Startestors of Telonemia and of Sar are shown with green circles. As Sar are the minimal-clade, the startestor, in this case, has the same identity as the rendestor.

## ORIGINS OF THE USED OR MENTIONED TERMS

The number of terms used here was introduced by other authors with different definitions and/or applications. The terms *monophyly*/*monophyletic* and *polyphyly*/*polyphyletic* originated from Haeckel (1866). The terms *paraphyly*/*paraphyletic* originated from Hennig (1962). The terms *holophyly*/*holophyletic* were introduced by Ashlock (1971). The terms *merophyly*/*merophyletic* originated from Ghiselin (1981; probably having a priority: "Winter", the first *Paleobiology* issue of the year) or Bernardi (1981; probably later: the fourth *Revista Brasileira de Entomologia* issue of the year). The terms *euphyly*/*euphyletic* originated from Zander (2009). The term *clade* originated from Cuénot (1940).

Although the aforementioned authors clearly applied their terms to the types of groups of organisms, some of the terms seem to have a prehistory of different applications. The wording "*holophyletische Wirkung*" appearedin Boas, 1949 (p. 79). Kühn (1935 p. 131) used "*paraphyletische Variation*" and the wording "*paraphyletic process*" appeared in *The Madras Agricultural Journal* (Editor[s] of this journal, 1949 p. 283). I have not been able to figure out the exact meaning of these uses.

The term *concestor* was coined by Nicky Warren and popularised by Dawkins (2004; see p. 7). The term *cenancestor* was coined by Fitch and Upper (1987).

Also, the term *monophylie* (the same spelling is used for "monophyly" in French and German—the native language of Haeckel and Hennig) appears in some digitalised versions of some French dictionaries of the early 19th century (Bosc in Sonnini *et al.*, 1803 p. 541; Poiret in Lamarck and Poiret, 1804 p. 168; Lunier, 1805 p. 94; Loiseleur Deslongchamps in Lacroix *et al.*, 1821 p. 47; Richard in Audouin *et al.*, 1825 p. 538). Nevertheless, all of these sources contain the imprecisely digitalised/printed word "*monophylle*" (confer the different links under each aforementioned source in the References section)—the adjective used for the type of construction of a flower calyx (or what was taken for it).

The terms *plerophyly*/*plerophyletic*, *jugiphyly*/*jugiphyletic*, *chasmophyly*/*chasmophyletic*, *drade*, *skade*, *pridestor*, *startestor*, *rendestor*, and *intrendon* are believed by the author to be new. Please note that Dawkins (2004) also used the analogy with rendezvous, although he did not create a term or a concept similar to the rendestor on this base. Instead, he used the standart concept of the last common ancestor, which was termed concestor (to reduce the wording "last common ancestor").

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[1] The term [evolutionary] *grade* does not mean "a paraphyletic group". Grades can also be *holophyletic* and *chasmophyletic* (see Huxley, 1957; 1958; 1959). At the same time, the etymological "flight of stairs" better corresponds to the concept by the exclusion of the top floor.

## CONFLICT OF INTEREST

None declared.

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## LICENSE

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