



## The monophyly of *Magelona* F. Müller, 1858 (Polychaeta, Magelonidae): Comments on Meißner *et al.*'s (2023) reinstatement of *Octomagelona* Aguirrezabalaga, Ceberio & Fiege, 2001

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### Abstract

The first published phylogenetic hypotheses involving members of the polychaete taxon Magelonidae Cunningham & Ramage, 1888, were reported by Mortimer *et al.* (2021), wherein results showed that for the two genera in the family, *Magelona* F. Müller, 1858, was paraphyletic relative to *Octomagelona* Aguirrezabalaga, Ceberio & Fiege, 2001. The only option to formally name at least some of the resultant phylogenetic hypotheses was to place *Octomagelona* into synonymy with *Magelona*, leaving the definition of Magelonidae redundant with that of a monophyletic *Magelona*. Meißner *et al.* (2023) subsequently described specimens as members of new species, *Octomagelona borowskii* Fiege, Knebelberger & Meißner, 2023, and *O. sp. cf. O. borowskii*, with the view that *Octomagelona* should be maintained as distinct from *Magelona*. We present reasons why reestablishing the paraphyly of *Magelona* is scientifically unwarranted.

**Key words:** Nomenclature, paraphyly, phylogenetic hypotheses, specific hypotheses, systematics

### Introduction

One of the consequences of Mortimer *et al.*'s (2021: fig. 17) phylogenetic inference involving members of Magelonidae Cunningham & Ramage, 1888, was to acknowledge that *Magelona* F. Müller, 1858, is paraphyletic relative to the monophyletic *Octomagelona* Aguirrezabalaga, Ceberio & Fiege, 2001 (Fig. 1). The only feasible nomenclatural solution was to synonymize *Octomagelona* with *Magelona* (cf. Rouse *et al.* 2022, Read & Fauchald 2024 *partim*), with the consequence that defining the name *Magelona* is redundant with the monotypic Magelonidae, insofar as both names refer to phylogenetic hypotheses causally accounting for the same set of characters. The formal definition of Magelonidae, and thus *Magelona*, is,

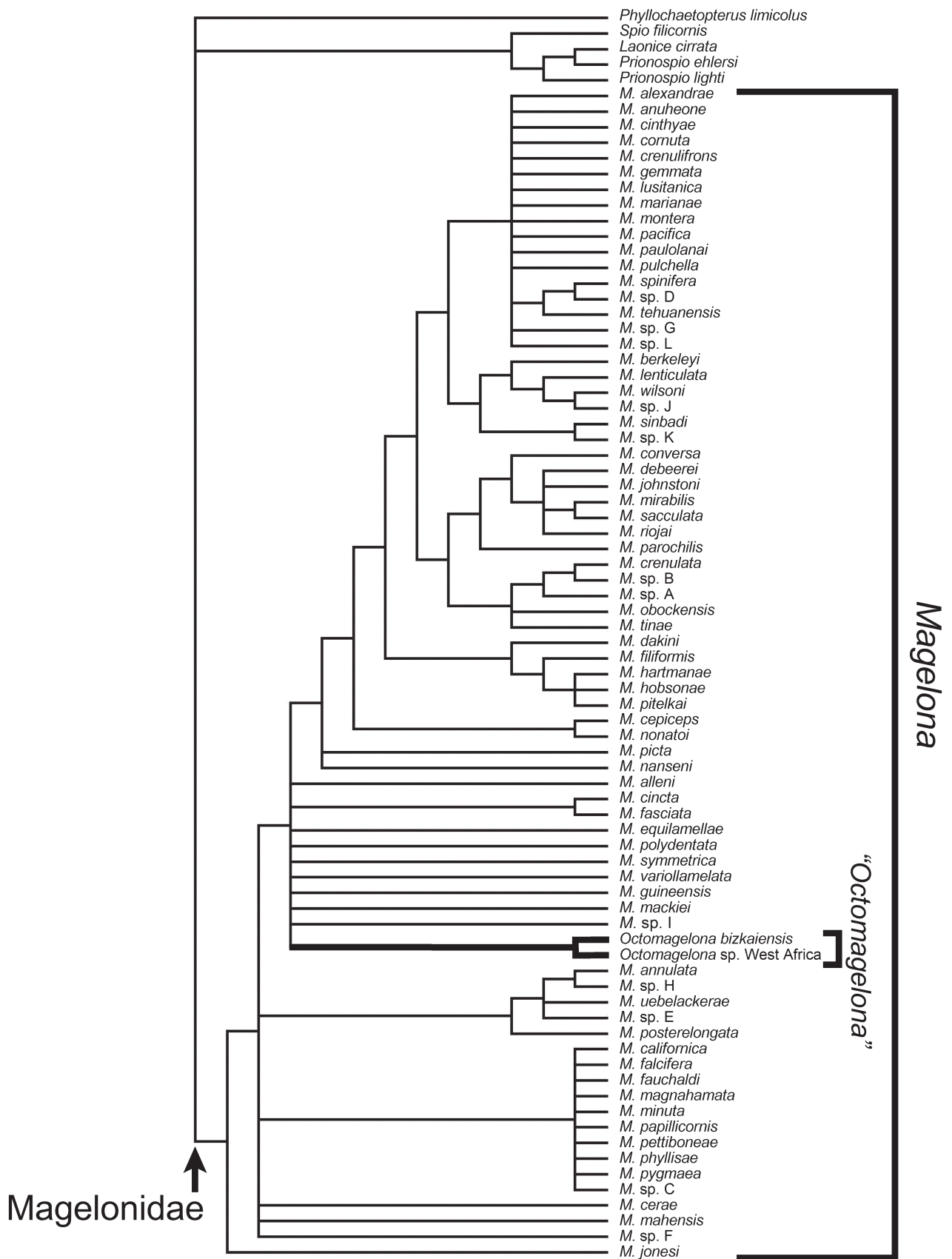
Magelonidae Cunningham & Ramage, 1888

Type genus. *Magelona* F. Müller, 1858, by monotypy.

*Definition.* A composite phylogenetic hypothesis (Fig. 1), causally accounting for (a) presence of a shovel-shaped prostomium, (b) absence of nuchal organs, (c) presence of prostomial ridges, (d) ventral palps with (e) papillate surfaces, (f) presence of a burrowing organ, and (g) magelonid-like body regionation.

Contrary to Mortimer *et al.*'s (2021) definition of Magelonidae/*Magelona*, Meißner *et al.* (2023) reinstate *Octomagelona* as part of their descriptions of specimens from the Southeast Pacific, for which specific hypothesis *O. borowskii* Fiege, Knebelberger & Meißner, 2023, is introduced, as well as *O. sp. cf. O. borowskii* from the Southeast Atlantic. Justification for this decision is presented in the authors' remarks regarding *Octomagelona* (Meißner *et al.* 2023: 21–22),

“Mortimer *et al.* (2021), considered *Octomagelona* a junior synonym of *Magelona* following their phylogenetic analysis based on morphological characters. We agree with these authors that the ‘magelonid-like body regionation’



**FIGURE 1.** Strict consensus tree, modified from Mortimer *et al.* (2021: fig. 17), indicating a paraphyletic *Magelona* relative to *Octomagelona* (bold). The only viable solution to remove paraphyly was to make *Octomagelona* a junior synonym of *Magelona*; i.e., provide a formal definition of *Magelonidae/Magelona* as a phylogenetic hypothesis, wherein all less inclusive phylogenetic hypotheses are unnamed.

is an important synapomorphy for Magelonidae (Mortimer *et al.* 2021: 67 and abstract) but we regard the two different character states for the thoracic body region, i.e. the presence of eight versus nine thoracic chaetigers, as an easy to observe and taxonomically sufficient character to distinguish between the two genera. Therefore, we prefer to maintain *Octomagelona* as a valid genus for the time being and hope that studies of genetic markers will add significant information to characterize the two genera.”<sup>1</sup>

The goal of the present paper is to provide reasons why formal recognition of the name *Octomagelona* is neither scientifically valid nor systematically useful.<sup>2</sup>

## The Objective of Systematics Means Negating Paraphyly

The most apparent problem is that recognizing *Octomagelona* results in *Magelona* once again being paraphyletic; an issue not acknowledged by Meißner *et al.* (2023). We will not argue the traditional defences that monophyly is preferred because it defines supraspecific taxa by way of synapomorphies, refers to all descendants derived from a common ancestor, or favours natural groups (e.g., Oosterbroek 1987, Schmidt-Lebuhn 2012, Zachos 2014). Rather, Mortimer *et al.* (2021) emphasize the importance of recognizing formal names of phylogenetic hypotheses as referring to explanatory accounts of specified characters of organisms, as mentioned in the previous section, which by default necessitates monophyly (Fitzhugh 2005, Fitzhugh 2006a, Fitzhugh 2006b, Fitzhugh 2008, Fitzhugh 2009, Fitzhugh 2012, Fitzhugh 2013, Fitzhugh 2014, Fitzhugh 2016a, Fitzhugh 2016b, Fitzhugh 2016c, Fitzhugh 2021). Too often discussions of mono- and paraphyly lay emphasis on *groups* of organisms rather than phylogenetic *hypotheses qua* past causal conditions of character origin/fixation and subsequent population splitting events.

Compounding the problem is that systematists are obliged to follow nomenclatural rules set forth by the International Codes of Nomenclature (e.g., International Commission on Zoological Nomenclature 1999) that impose ranks on formal names of specific and phylogenetic hypotheses, as well as requiring specific hypotheses to be recognized using binomial names, wherein a specific hypothesis must be conjoined to a phylogenetic hypothesis at the rank of genus, even though the two classes of hypotheses involve separate inferential actions (Fitzhugh 2009, 2013; Mortimer *et al.* 2021). Ideally, formal names of phylogenetic hypotheses should be in accordance with scientific principles, i.e., defined as explanatory accounts for specified characters (e.g., Fitzhugh 2008, Fitzhugh *et al.* 2015, Nogueira *et al.* 2010, Nogueira *et al.* 2013, Nogueira *et al.* 2017, Mortimer *et al.* 2021), thus ensuring monophyly, notwithstanding that the International Codes of Nomenclature are silent on the topic of paraphyly.

Forcing *Magelona* to be paraphyletic in order to recognize *Octomagelona* is a consequence of arbitrarily elevating a phylogenetic hypothesis to the rank of genus that is in fact subsumed under *Magelona*, as indicated in Fig. 1. This erroneously implies that phylogenetic hypotheses named *Magelona* and *Octomagelona* are epistemically equivalent, yet arbitrarily ignores all other unnamed phylogenetic hypotheses under either of those names (cf. Mortimer *et al.* 2021: fig. 17). *Octomagelona* is an artefact of a nomenclatural system that enables personal biases over scientific objectives. What is important to realize is that the *status* of the phylogenetic hypothesis originally named *Octomagelona* is not compromised by Mortimer *et al.*'s (2021) actions. The hypothesis still stands; it is simply no longer given a formal name, just as the multitude of other phylogenetic hypotheses under *Magelona* are not formally named.

Meißner *et al.* (2023) offer no scientifically credible argument for maintaining the formal name *Octomagelona*. Their reasoning appears to stem from the perspective that semaphoront distinctness is an important criterion. This is, however, at odds with the goal of scientific inquiry being the pursuit of causal understanding (Hanson 1958, Hempel 1965, Rescher 1970, Popper 1983, Popper 1992, Salmon 1984, Van Fraassen 1990, Strahler 1992, Mahner & Bunge 1997, Thagard 2004, Nola & Sankey 2007, Regt, Leonelli & Eigner 2009, Hoyningen-Huene 2013, Potochnik 2017, Potochnik 2020, Anjum & Mumford 2018, Currie 2018), which is echoed by Mortimer *et al.* (2021: **Methodological**

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1 Following the phylogenetic hypothesis of Mortimer *et al.* (2021; Fig. 1), the World Register of Marine Species (WoRMS) recognizes *Octomagelona* as a junior subjective synonym of *Magelona*, inclusive of type species *O. bizkaiensis* Aguirrezabalaga, Ceberio & Fiege, 2001 (Read & Fauchald 2024: <https://www.marinespecies.org/aphia.php?p=taxdetails&id=914> on 2024-07-22). Contrary to that, however, WoRMS recognizes *O. borowskii* but does not acknowledge it as a member of *Magelona*.

2 An updated Magelonidae phylogenetic analysis (Mortimer, Fitzhugh & Brasil, in prep.) will again provide an empirical basis for *Octomagelona* as a synonym of *Magelona*, inclusive of *O. borowskii* and *O. sp. cf. O. borowskii*.

**considerations: The goal of scientific inquiry).** To “distinguish between” *Magelona* and *Octomagelona* according to particular characters presumes genera are either concrete entities or mere class constructs. Both connotations are erroneous given that taxa are explanatory hypotheses (Mortimer *et al.* 2021 and references therein). Genera, like all supraspecific ranks, are largely arbitrarily applied to particular phylogenetic hypotheses in lieu of any number of unnamed phylogenetic hypotheses.

Meißner *et al.* (2023) state that the distinction between eight (*Octomagelona*) and nine thoracic chaetigers (paraphyletic *Magelona*) is “an easy to observe and taxonomically sufficient [*sic*] character to distinguish between the two genera.” This is not a scientifically credible argument favouring a paraphyletic *Magelona*. To correctly say two genera are “distinguished” from one another is to articulate differences between respective phylogenetic hypotheses. Taxa cannot be distinguished on the basis of characters of organisms; eight versus nine chaetigers only distinguish semaphoronts (*sensu* Hennig 1966), not phylogenetic hypotheses. Emphasizing eight versus nine chaetigers as justification for *Octomagelona* is an a priori decision—a matter of personal inclination—not scientific necessity.

Meißner *et al.*'s (2023) statement that they “hope that studies of genetic markers will add significant [*sic*] information to characterize the two genera” will not resolve the problem they suggest exists. Emphasizing sequence data over other classes of characters is part of the reductionist attitude that has consumed much of systematics, incorrectly assuming that sequence data offer better opportunities to elucidate “true relationships” or offer “stronger support.” The view that one should default to sequence data is based on the false premise that those data offer solutions to perceived problems that cannot be addressed with characters at higher levels of organization, typically morphological. This perspective overlooks the actual goal of systematics and evolutionary biology as a matter of scientific inquiry; that goal being to causally account for properties of organisms (Fitzhugh 2012, 2016b; Uller & Laland 2019), as opposed to attempting to “characterize” genera or other taxa. Systematics research is not accomplished through the reductionist agenda associated with sequence data. As aptly noted by Dupré & Nicholson (2018: 26–27),

“...it has become increasingly clear to many biologists, as well as philosophers, that reductionism is at best a severely limited approach to understanding living systems.... In a world of processes, reductionism makes little sense.... When we accept that the living world is a process world, we are able to understand why reductionism in biology, despite its countless limited successes in local and fixed contexts, can never fully succeed as a global explanatory enterprise, even in principle.”

The scope of causality that is the purview of evolutionary biology and systematics precludes reducing all or most explanatory interest to the level of nucleotides or amino acids, or thinking sequence data offer any kind of enhancement to the objective of inquiry. Also typically neglected in systematics is that explaining shared nucleotides or amino acids is not so simple a matter as implementing computer algorithms with those characters (cf. Fitzhugh 2016b, 2021, regarding downward causation; discussed by Mortimer *et al.* 2021). Such algorithms imply that all sequence data are explained via genetic drift or neutrality, whereas the spectre of downward causation accounting for sequence data in relation to natural selection due to emergent properties at higher organizational levels is unrealistically ignored (Fitzhugh 2016b, Mortimer *et al.* 2021). Implying that sequence data are somehow more worthy of attention than other classes of characters typically derive from thinking the objective of systematics is to obtain phylogenetic trees (e.g., “the tree of life”), “the” phylogeny, and/or that the larger number of characters provided by sequence data is more favourable under the guise of improving “statistical consistency” (Felsenstein 1978, Felsenstein 2004, Swofford *et al.* 1996, Heath, Hedtke & Hillis 2008, Assis 2014, Brower 2018; e.g., Goto 2016, Tilic *et al.* 2020). The popularity of “tree thinking” in systematics (e.g., O’Hara 1988, O’Hara 1994, O’Hara 1997, Meisel 2010, Baum & Smith 2012, Jenner 2024) has also encouraged the view that sequence data are the preferred means to infer phylogenetic trees *sensu* topologies, yet too often ignores acknowledging the multitude of explanatory hypotheses implied by those trees. Statistical consistency is a notion only relevant to the continual (inductive) testing of hypotheses “in the long run,” not the abductive inferences of those hypotheses (Peirce 1902, Peirce 1932: 2.774–777, Rescher 1978, Fitzhugh 2012, Fitzhugh 2016b, Mortimer *et al.* 2021). More sequence data does not equate with improved systematics results.

## Morphological Considerations

One of the further justifications that Meißner *et al.* (2023) make for recognizing *Octomagelona* is description of the thoracic chaetae among members of *Magelona bizkaiensis* in the analysis by Mortimer *et al.* (2021: table S1, coding matrix character 31). Meißner *et al.* (2023) suggest that these chaetae were incorrectly described as bilimbate by Mortimer *et al.* (2021), rather than unilimbate “as stated in the original description,” i.e., Aguirrezabalaga *et al.* (2001). There are several problems with this assertion. First, in the original description of members of *M. bizkaiensis*, it states that all thoracic chaetae are “long and limbate capillaries,” similar in size and form, but gives no further information. However, the illustration (albeit reproduced at low resolution) of a thoracic chaeta by Aguirrezabalaga *et al.* (2001: fig 2C) appears bilimbate, particularly in the basal half, so it is unclear from the original description the nature of the chaetae. Furthermore, it has long been recognized (Jones 1963, 1971, 1977, 1978; Mortimer & Clarke 2024) that there is intraspecific variation in limbate chaetae among magelonids. For instance, members of the following species have been recorded to possess both uni- and bilimbate chaetae: *M. papillicornis* F. Müller, 1858; *M. longicornis* Johnson, 1901; *M. pitelkai* Hartman, 1944; *M. riojai* Jones, 1963; *M. hartmanae* Jones, 1978; *M. debeerei* Clarke, Paterson, Florence & Gibbons, 2010, and *M. ekapa* Mortimer & Clarke, 2024. Although further observations of variation within magelonid thoracic chaetae are much needed, and many authors have undervalued the importance of fully describing chaetae (Brasil 2003, Mortimer *et al.* 2021), variation is nevertheless present. Observations by the current authors (KM, ACB) suggest that when both uni- and bilimbate chaetae are present, variation may occur along the thorax, shifting from unilimbate in the anterior thorax to bilimbate in the posterior (e.g., members of *M. debeerei*), whilst in other cases bilimbate chaetae may predominate but with more slender unilimbate chaetae at the outer margin of a fascicle, as is noted among members of *M. ekapa* (Mortimer & Clarke, 2024: figs 5p, r). In their phylogenetic analysis, Mortimer *et al.* (2021: 44) state that “For some individuals, both unilimbate and bilimbate chaetae have been recorded, however, the predominant form in each case was coded...” Therefore, the presence of unilimbate chaetae in *M. bizkaiensis* as noted by Meißner *et al.* (2023) does not indicate that the coding was incorrect. The SEM image in Meißner *et al.* (2023: fig. 12L) is from chaetiger 1, where, as noted above, chaetae are often more slender and unilimbate chaetae may occur. This is something which should be verified towards the posterior thorax, as well as within an individual fascicle.

Meißner *et al.* (2023) describe members of *Octomagelona borowskii* as having thoracic capillaries that are partly bilimbate, with irregularly bilimbate chaetae also present. They (Meißner *et al.* 2023: 22) argue that it “remains to be evaluated whether irregularly indented limbation represents a natural character state or an artefact due to the effect of fixative or mechanical treatment during sampling.” Whilst we are in agreement that this is a character that needs further investigation, it is something that has been noted before, e.g., Hartman (1944), Jones (1978), Bolívar & Lana (1986) and Brasil (2003). The character appears consistently among members of a species, whilst is absent among others, suggesting its validity.

The phylogenetic analysis of Mortimer *et al.* (2021) highlights several characters of importance in the recognition of magelonid species: (1) presence/absence of prostomial horns (in addition to their form, i.e., distinct or rudimentary); (2) relative dimensions of the prostomium; (3) morphology of anterior lamellae, including presence/absence of superior dorsal lobes; (4) development of the anterior lamellae; (5) presence/absence of specialised chaetae on chaetiger 9; and (6) presence of lateral abdominal pouches. The notable morphological characters among individuals to which the phylogenetic hypothesis formerly named *Octomagelona* refer include (1') wider than long prostomia with rudimentary horns carrying one pair of prostomial ridges; (2') a large achaetous region; (3') filiform anterior lamellae in subchaetal position, without superior dorsal lobes; (4') rounded/bulbous anterior chaetigers; (5') anterior region which tapers from the achaetous region to “thoracic/abdominal” junction. These characters are, however, shared with members of some other magelonid species which possess nine anterior chaetigers. Not surprisingly, the phylogenetic analyses of Brasil (2003) and Mortimer *et al.* (2021) found *Magelona* paraphyletic relative to *Octomagelona*, and members of the latter genus closely related to members of species such as *M. variolamellata* Bolívar & Lana (1986), *M. equilamellae* Harmelin, 1964, *Magelona* sp. I of Uebelacker & Jones (1984), and *M. polydentata* Jones, 1963, on the basis of many shared morphological characters.

Unfortunately, the specimens of *Magelona borowskii* and *M. sp. cf. M. borowskii* were illustrated by Meißner *et al.* (2023: fig. 12) using SEM (the paratype SEMs being the main source to illustrate members of the species; no illustrations of the holotype are provided) and appear to have shrivelled during critical point drying, such that the overall conditions of the material make it very difficult to relate to members of other magelonid species. There are

specimens from Mexico, Australia and West Africa that are members of several undescribed magelonid species with eight anterior chaetigers awaiting description (Brasil, 2003; Mortimer *et al.*, 2021, Parapar *et al.*, 2021). These will undoubtedly be informative in future analyses.

## Conclusion

There are no scientific justifications for reinstating the formal name *Octomagelona* and force *Magelona* to again be paraphyletic. Nomenclatural decisions are secondary to the goal of scientific inquiry as applied to biological systematics, not *vice versa*. It is critical to again emphasize Mortimer *et al.*'s (2021) discussion that since taxa are explanatory hypotheses, they are products of non-deductive reasoning known as abduction (Fitzhugh 2006a, 2012, 2016c, 2021; Mortimer *et al.* 2021), and as a consequence those hypotheses must take into account the requirement of total evidence (Fitzhugh 2006b, 2014). Consideration of all relevant characters is imperative, not just one or several characters deemed “distinctive” (limitations imposed by downward causation in relation to sequence data notwithstanding, cf. Fitzhugh 2016b, Mortimer *et al.* 2021). Just as important, specimens with “distinctive” characters cannot warrant formal names that result in paraphyly.

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