



Contents lists available at ScienceDirect

International Journal for Parasitology

journal homepage: www.elsevier.com/locate/ijpara

Seeing the branches for the leaves: insight into parasite biodiversity from the discovery rates of genera rather than species

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ARTICLE INFO

Article history:

Received 16 June 2026

Received in revised form 5 August 2026

Accepted 8 August 2026

Available online xxxx

Keywords:

Accumulation curves

Helminths

Phylogenetic distinctness

Species richness

Taxonomy

ABSTRACT

The cumulative number of parasite species known to science keeps increasing steadily year after year, suggesting we are far from the end of our inventory of extant parasite biodiversity. However, what about higher taxa such as genera or families: are their known numbers also still rising? Finding new genera or families represents the discovery of clades with greater evolutionary uniqueness than the discovery of new species belonging to already known lineages. We surveyed the taxonomic literature between 2010 and 2025 to quantify patterns in the discovery of new helminth genera and families. Few new families were proposed during the study period, however 271 new genera were established, with 80% of them being 'true' new genera, i.e. previously unknown lineages based entirely on the discovery of new specimens. Whereas we might expect that the more genera one has already found, the harder it could be to find new ones, we instead found a positive relationship between the number of new genera found per higher taxon and the currently known species richness of that taxon. This supports a sampling hypothesis whereby species-rich taxa like Trematoda are also the ones likely to yield more new genera. Indeed, the cumulative number of new trematode genera found in the 2010–2025 period has increased linearly, suggesting many more genera await discovery in this taxon as well as in Nematoda, Monopisthocotylea and Polyopisthocotylea. In contrast, an asymptote has been reached in Acanthocephala and Cestoda, indicating the final list of genera is at hand in those taxa. Our findings suggest that the quest to document parasite biodiversity is far from complete as we still lack knowledge of many phylogenetically distinct helminths characterised by morphologies that do not fit within currently known genera.

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1. Introduction

Most discussions of parasite biodiversity and all empirical assessments of how close we are to discover it all have focused on the number of known species relative to the estimated total (both known and unknown) species diversity (Dobson et al., 2008; Poulin, 2014; Carlson et al., 2020). However, newly discovered parasite species do not all have the same weight in terms of their contribution to our growing knowledge of parasite biodiversity. Some new species belong to previously known and highly diverse genera, whereas others may represent evolutionary distinct clades that force us to re-think the phylogeny of the group. To use a real tree as an analogy, some newly discovered species add leaves to the tree, whereas others add new branches. The discovery of a new genus or family represents the discovery of a lineage with greater uniqueness (phylogenetically, morphologically,

ecologically) than the discovery of a new species belonging to an already known genus or family. Thus, the former contributes more to knowledge of phylogenetic diversity than the latter, because biodiversity is more than just the number of extant species.

A quick look at the last few years of research in parasite taxonomy reveals that new higher taxa (genera, families) are still regularly described, yet several questions remain. First, some new higher taxa are proposed based on taxonomic revisions of the classification of already described species. For instance, an existing genus may be split into two based on new molecular data, with some previously known species shifted to a newly-named genus. This does not truly represent the discovery of a new branch in the phylogenetic tree; it is instead the recognition of a known branch that was previously not distinguished as separate. A 'true' new branch involves the erection of a new genus or family based on the discovery of new specimens that cannot be assigned to an existing higher taxon, as their morphology and gene sequences do not fit in existing clades. How many parasite genera and

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<https://doi.org/10.1016/j.ijpara.2026.104944>

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families described in recent years represent truly new phylogenetic branches?

Second, the discovery of new genera or families may not be equally distributed among higher parasite groups. In an analysis across the entire tree of life including both free-living and parasitic organisms, Wiens et al. (2026) found that new genera, families, orders and even classes are more frequently found in taxa with small body sizes living in particular habitats. From a statistical perspective, discovering new genera may follow the collector's curve: the more one has already found, the harder it is to find new ones (Pimm and Gittleman, 2026). Alternatively, if the probability of finding new species from different groups is proportional to the currently known richness of these groups (Li et al., 2025) and if finding new genera is simply a function of sampling enough new species, then we might expect a positive relationship between the number of new genera discovered and currently known richness among major groups (Wiens et al., 2026). Does this sampling-driven hypothesis apply to parasites, i.e., do most newly discovered genera belong to groups that are already species-rich?

Third, as more and more parasite species are discovered and described over time, we might expect that new genera have become more difficult to find. Some authors have argued that most of Earth's biodiversity has already been discovered (Costello et al., 2013). Certainly, the temporal accumulation of newly-described families and orders appears to have reached an asymptote across all domains of life (Mora et al., 2011). However, the same pattern is not so clear for new genera; the cumulative curve of known genera as a function of time shows no clear inflexion point even if an asymptote can be statistically extrapolated from existing data (Mora et al., 2011). These temporal patterns have only been explored across the entire tree of life or at domain level, not on a finer taxonomic scale such as among high groups of parasites. Assessments of whether or not we are approaching the end of our inventory of extant parasite species differ among authors (Poulin, 2014; Costello, 2016; Carlson et al., 2020), however there has been no investigation of the discovery rates of new parasite genera over time. Is there any evidence that these rates are slowing down, i.e., that fewer new genera are found now than a few years ago? Cribb and Bray (2011) thought this might be the case for trematodes, however this has not been confirmed in the years that followed their observation.

Here, we address the three questions above for helminth parasites based on a comprehensive survey of the taxonomic literature between 2010 and 2025. Our analyses focus on 6 distinct higher helminth groups: the phyla Acanthocephala and Nematoda, as well as four classes of the phylum Platyhelminthes: Trematoda, Cestoda, Monopisthocotylea and Polyopisthocotylea (the latter two formerly lumped as 'Monogenea'; see Brabec et al., 2023). Specifically, for each of these 6 groups, (i) we quantify what proportion of newly described genera represent 'true' new genera actually based on the discoveries of new specimens; (ii) we test the sampling hypothesis, i.e., whether the number of new genera discovered is proportional to the currently known species richness of each group; and (iii) we reveal the temporal patterns in the discovery of new genera in each group. Our findings provide a new perspective on where we currently stand in our quest to fully inventory parasite biodiversity on Earth.

2. Methods

We assembled a dataset on the new genera and new families proposed between 2010 and 2025 inclusively, by manually searching the list of articles published in all volumes of the following 11 journals: *Acta Parasitologica*; *Comparative Parasitology*; *Folia Parasitologica*; *International Journal for Parasitology*; *International Journal*

for Parasitology–Parasites and Wildlife; *Journal of Helminthology*; *Journal of Parasitology*; *Parasitology*; *Parasitology International*; *Parasitology Research*; and *Systematic Parasitology*. All articles with "n. gen.", "new genus", "n. g.", "new family" or "n. fam." in their title were retained. Advanced searches in each journal were also conducted using the same key words to ensure no relevant article had been missed. A couple of instances where a genus was given a nom. nov. because of homonymy with a previous genus were excluded as they were just changes of names, not taxonomic actions. Although not including all new helminth genera and families established in the 2010–2025 period, the above journals should nonetheless capture most of them.

Each new genus or family was classified as either a 'true' new taxon based on the discovery of new specimens that could not be placed in existing taxa, or a taxon erected as part of the reclassification of previously known species. We also considered as 'true' new taxa those (i) erected for existing species but only identified and described (at least in part) from newly collected material; (ii) erected for newly collected trematode adults of a previously known larva of "genus" *Cercaria*; and (iii) erected following the collection of new material even if some previously known species were then moved to the new taxon as new combinations. For each 'true' new genus or family, we also recorded the following information: which of the 6 higher taxa considered (Acanthocephala, Nematoda, Trematoda, Cestoda, Monopisthocotylea or Polyopisthocotylea) it belonged to, the order and family to which it belonged (only the order in the case of new families), the year in which it was proposed, the journal in which it was published, and its authors. We recorded the family and/or order to which the new taxon belonged as given in the original article, but then updated it where necessary following the taxonomy of the World Register of Marine Species (WoRMS; <https://www.marinespecies.org/>); we only departed from WoRMS by recognising the distinction of classes Monopisthocotylea and Polyopisthocotylea, following Brabec et al. (2023).

First, we determined how many new genera and families were truly new, i.e., based on the discovery of new specimens that could not be assigned to existing taxa. This was done separately for each of the 6 higher taxa considered. The statistical analyses below include only these 'true' new genera.

Second, to test the sampling hypothesis, we obtained the currently known species richness of each of the 6 higher taxa considered from the Catalogue of Life (<https://www.catalogueoflife.org/>), accessed on 21st May 2026. For nematodes, because not all species are parasitic and the Catalogue of Life provides an estimated species richness including both free-living and parasitic species, we multiplied the phylum's current species richness by 0.45, based on the estimate that 45% of living nematodes are parasitic in animals (Hugot et al., 2001; Schratzberger et al., 2019). Because relatively few new families were established in the 2010–2025 study period, we only performed a qualitative contrast between the species richness of the 6 higher taxa and the number of new families per higher taxon. For genera, the relationship between the number of new genera proposed in the 2010–2025 period and the higher taxon's species richness was tested using a linear model. We also tested the sampling hypothesis at a lower taxonomic level, by testing the relationship between the number of new genera and the species richness of the family to which they belonged. For this, we again used the Catalogue of Life to obtain the species richness of all families involved. Since in this case the data did not pass a Shapiro-Wilk normality test, they were also analysed using a generalised linear model with negative binomial distribution, and with a Spearman's correlation, to validate the robustness of the relationship. These analyses were conducted in R version 4.4.2 (R Core Team, 2024) and implemented using the packages stats, lmerTest (version 0.9.40, Zeileis and Hothorn, 2002) and MASS (version

7.3.61, Venables and Ripley, 2002). Data visualization was performed using the ggplot2 package (version 4.0.3, Wickham, 2016).

Third, we investigated a possible slowing down in the rate of discovery of new genera as a function of time by plotting the cumulative number of new genera as a function of year for each of the 6 higher taxa separately. To test whether the cumulative number of new genera discovered over time is reaching an asymptote, we fitted a nlsLM model to the data, separately for each of the 6 higher taxa, implemented with the nlsLM function in the package minpack.lm (Elzhov et al., 2023). The nlsLM model uses the Levenberg-Marquardt method to fit an asymptotic model to the data and estimate the upper bound (asymptote value) at which the curve reaches a plateau. The model is: number of genera = $A * (1 - e^{-kt})$, where A is the asymptote, k is the rate of approach, and t is time in years. We compared the asymptotic model to a simple linear model using ΔAIC (Linear – Asymptotic), with values >2 indicating that the asymptotic model provides a better fit than the linear model.

3. Results

Our data compilation included a total of 271 new genera and 16 new families proposed in the 11 journals surveyed between 2010 and 2025. Most new genera were established for trematodes, followed by cestodes. Similarly, most newly proposed families were for trematodes. Our dataset is available as [Supplementary material \(Tables S1–S3\)](#).

Of the 271 new genera, 218 (80.4%) were ‘true’ new genera, representing previously unknown lineages established after the discovery of new specimens. The percentages vary among the 6 higher taxa, however ‘true’ new genera always outnumber those based on taxonomic reclassification of previously known material (Fig. 1). Only one of 16 families was classified as truly new, i.e. based on the discovery of new specimens: the acanthocephalan family Gymnorhadinorhynchidae.

There was an apparent match between the current species richness of the 6 higher taxa and how many ‘true’ new genera have been established within those taxa in the past 15 years (Fig. 2). For instance, the highest number of new genera were

proposed for trematodes, which have the highest known species richness, whereas the fewest new genera were proposed for acanthocephalans and polyopisthocotyleans, which have the lowest known species richness. Similarly, most new families were established for the species-rich trematodes, although these include families not truly new as they were based on previously known species.

Across the 6 higher helminth taxa, there was a significant positive relationship between the number of new genera and the higher taxon’s species richness ($F_{1,4} = 8.264$, adjusted $R^2 = 0.592$, $P = 0.0453$): the higher the current known species richness of a taxon, the more new genera have been proposed for it in recent years (Fig. 3A). We repeated this analysis at a lower taxonomic level, by testing the relationship between the number of new genera and the species richness of the 97 families to which they belonged, and again found a significant positive relationship ($F_{1,95} = 9.991$, adjusted $R^2 = 0.086$, $P = 0.0021$). Among the 97 families, known species richness ranges from fewer than 10 species to over 1,000 in the most speciose families (Dactylogyridae and Ancyrocephalidae). However, for many families, regardless of their species richness, only 1 new genus has been established in the years covered by our survey (Fig. 3B), resulting in a non-normal data distribution. To confirm the validity of the family-level positive relationship between known species richness and the number of new genera established, we validated it with a GLM with negative binomial distribution (estimate = 0.0011, SE = 0.0002, Z-value = 3.852, $P = 0.0001$) and with a Spearman’s correlation ($r_s = 0.402$, $N = 97$, $P < 0.0001$).

The numbers of new genera proposed in each of the 6 higher helminth taxa have been increasing steadily from 2010 to 2025 (Fig. 4). A curve with an asymptote provided the best fit to the data for two higher taxa, Acanthocephala and Cestoda (Table 1), indicating that the rate at which new genera are found is slowing down and that the total number has almost reached a stable plateau in those taxa. For the other 4 higher taxa, however, the linear model provided the best fit, with the rate at which new genera are found showing no evidence of slowing down to an asymptote (Table 1). In fact, for Trematoda and Polyopisthocotylea, the nlsLM asymptotic model failed to converge, with the algorithm unable to find a valid

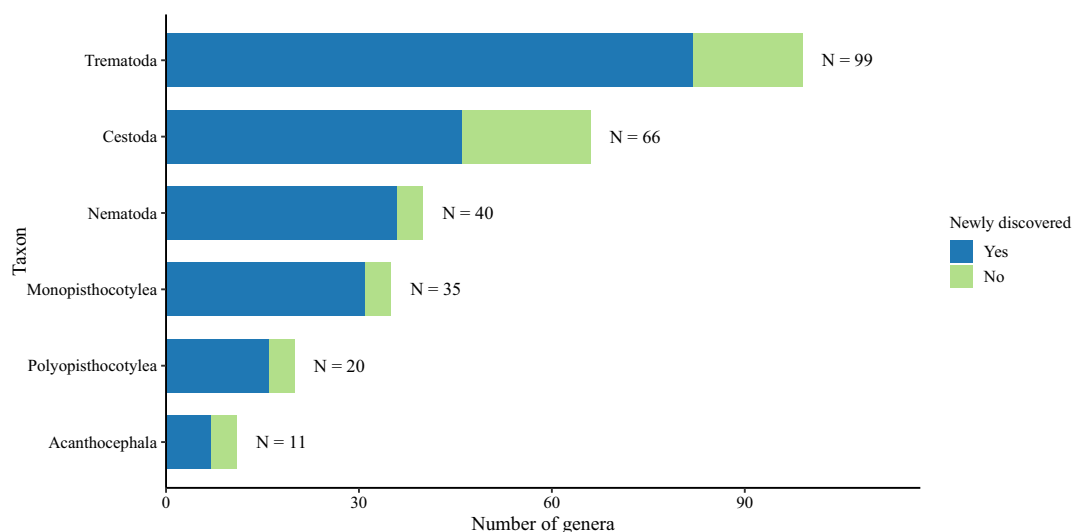


Fig. 1. Relative numbers of new genera proposed in the literature between 2010 and 2025 that are either ‘true’ new genera based on newly discovered specimens, or genera not based on new specimens but erected following reclassification of previously known species. Data are shown separately for 6 higher helminth taxa (N = total number).

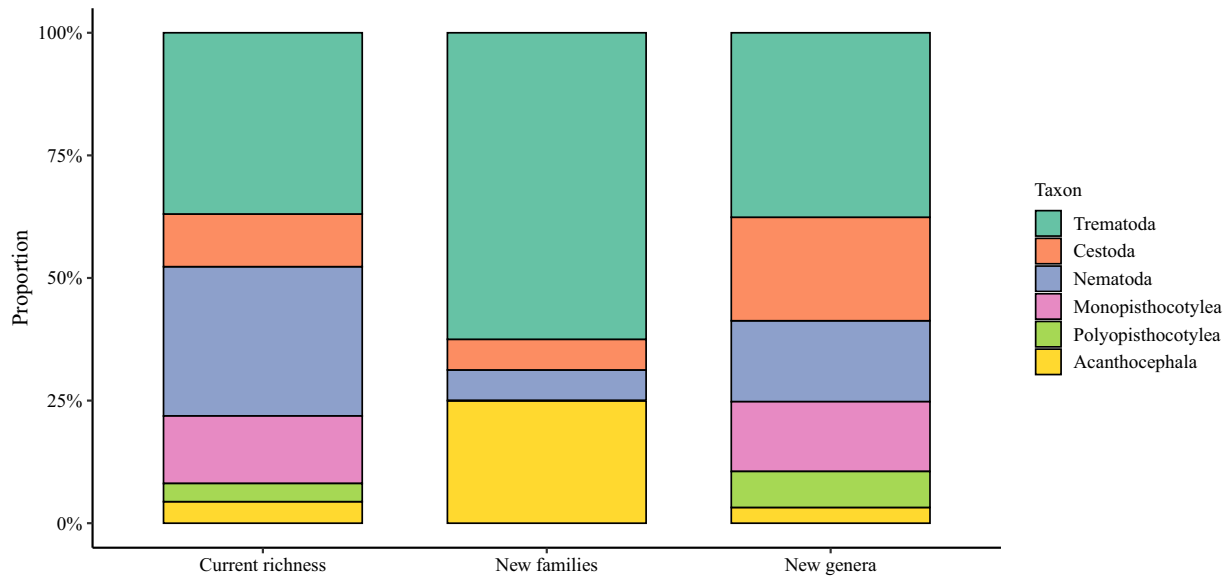


Fig. 2. Proportional distribution of current known species richness, and new families and new genera established between 2010 and 2025, among 6 higher helminth taxa. Note: data on new families include all families established during the study period, whereas data on new genera include only 'true' new genera based on the discovery of new specimens.

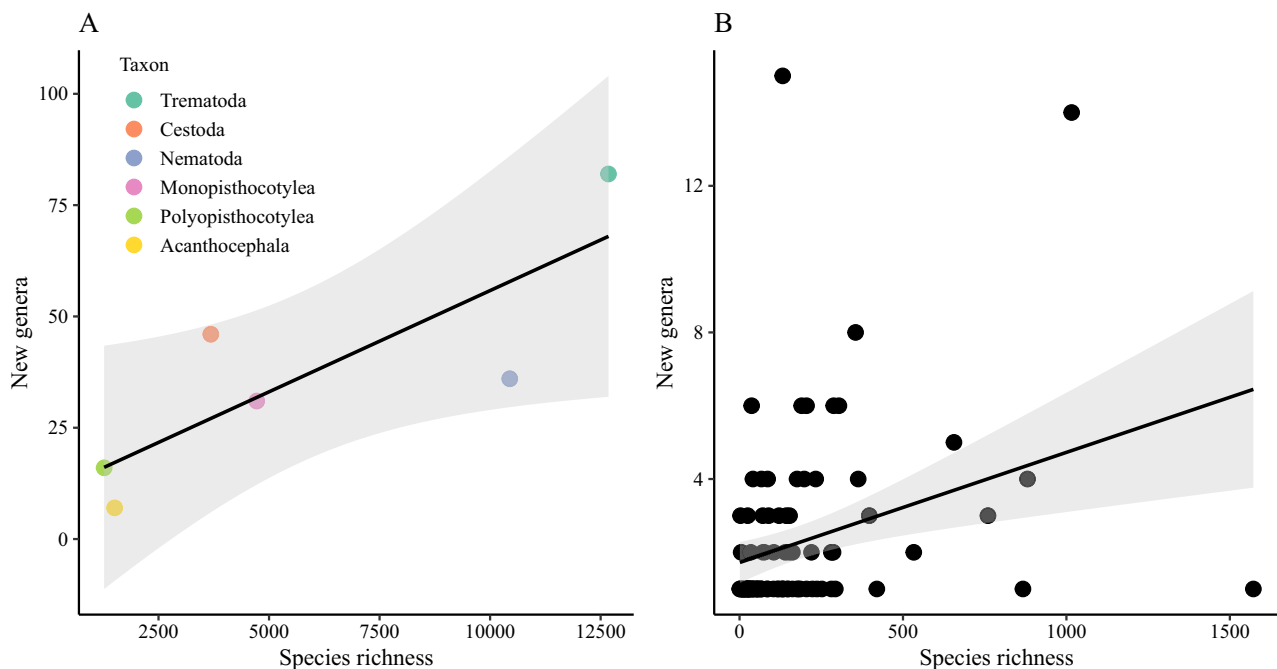


Fig. 3. Relationship between the number of new genera established between 2010 and 2025 and current known species richness among 6 higher helminth taxa (A) and among 97 helminth families (B). The best-fit lines (and 95% confidence intervals; shaded area) are from linear models.

solution and providing an unrealistically high asymptote, suggesting there are many more genera to be found.

4. Discussion

The number of new parasite species described and named each year has been growing steadily in recent decades (Poulin, 2014; Carlson et al., 2020), and a look at what has already been published this year indicates that this trend continues as strong as ever. New species correspond to leaves on the tree of life. What about branches on that tree? Are we still also discovering new clades and not only new species? Our study reveals that (i) most new hel-

minth genera proposed in recent years are based on newly discovered specimens as opposed to arising from reclassification of previously known species; (ii) new genera are more likely to be found in higher taxa that already have a high known species richness; and (iii) while for some higher taxa the end may be in sight, for others the discovery of new genera shows no sign of slowing down. Below we discuss these findings and their interpretation for parasite biodiversity.

Taxonomic restructuring often involves erecting new higher taxa without the discovery of new lower taxa. For instance, new cestode orders have been established for previously known families or genera based on new phylogenetic analyses (Caira et al.,

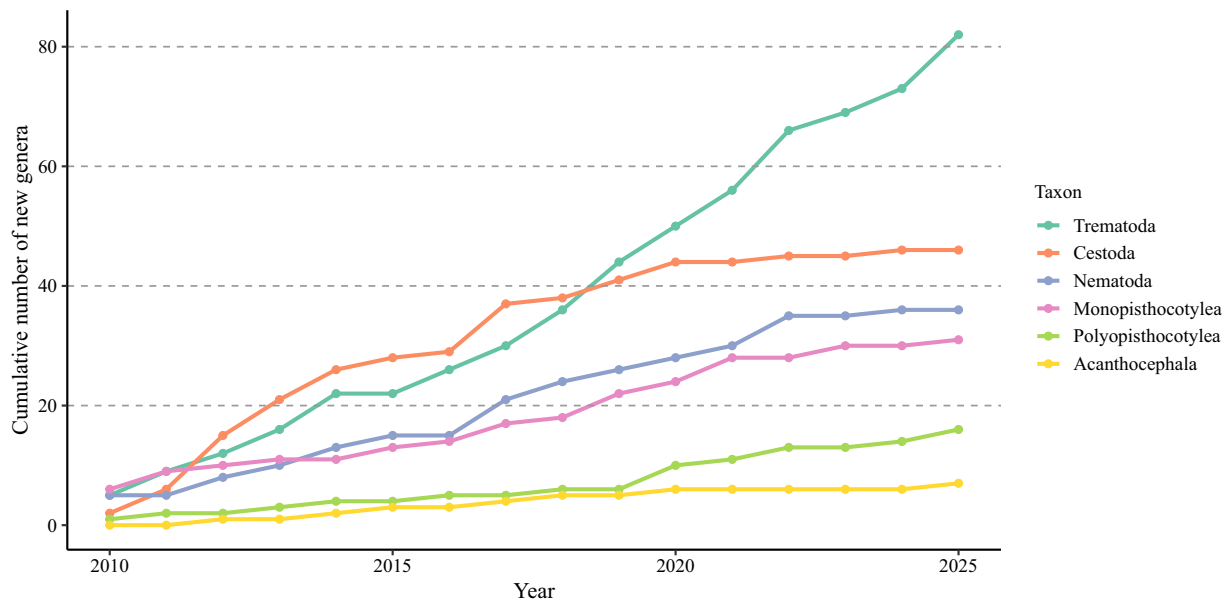


Fig. 4. Cumulative number of new genera established from 2010 to 2025 shown separately for 6 higher helminth taxa.

Table 1

Comparison of linear versus asymptotic models fitted to the cumulative number of new genera proposed over time, for 6 higher helminth taxa.

Taxon	ΔAIC (Linear – Asymptotic)	Estimated asymptote	Best model
Acanthocephala	6.17	13.53	Asymptotic
Nematoda	–6.30	75.78	Linear
Trematoda	–0.19	10474.68*	Linear
Cestoda	37.40	51.54	Asymptotic
Monopisthocotylea	–20.22	51.30	Linear
Polyopisthocotylea	–0.29	3002.84*	Linear

* Invalid estimate: model failed to converge.

2013), such that these families and genera are older than the order to which they now belong. In our study, about one-fifth of the new genera established between 2010 and 2025 did not arise from the discovery of new specimens that could not be placed in existing genera. For example, the genus *Spinulacorpus* was erected for *Rhadinorhynchus bififormis* Smales, 2014 (Acanthocephala) because, in phylogenetic analyses based on genetic data, it fell outside of the Rhadiochynchidae clade, rendering the family paraphyletic. Recognising it as forming a distinct lineage, the authors placed the species in the new genus *Spinulacorpus* and the new family Spinulacorpidae, a decision supported by close examination of additional specimens that revealed morphological characters to support the hypothesis (Huston and Smales, 2020). In this and many other cases, the species forming a distinct genus were already known, just not yet recognized as such. The other 80% of new helminth genera established in recent years are truly new: they are based on newly discovered parasites that revealed previously unknown genus-level clades. In the near totality of cases, the proposal of a new genus was based on combined morphological and molecular data, but was usually prompted by phylogenetic analyses indicating that the new specimens fell outside previously known clades. In the last six full years we surveyed (2020–2025), the number of truly new helminth genera proposed in the literature has averaged a dozen per year. This indicates that our knowledge of the structure of helminth phylogenetic trees is incomplete and always changing. Our findings have implications for the extinction crisis, where the loss of entire clades is seen as greater threat to extant phylogenetic diversity than the loss of species.

Some analyses have documented the accelerated rate of genus-level extinctions driven by human activities (e.g., Ceballos and Ehrlich, 2023). Our results suggest that these extinctions, which are nonetheless tragic, may not impact helminth phylogenetic diversity as much as previously thought, since many more genus-level clades remain to be discovered.

Interestingly, there were far fewer new helminth families proposed in the 2010–2025 period, suggesting that at this higher taxonomic level, the structure of helminth phylogenetic trees is less likely to be changed by the discovery of new branches. Most of the new families were in Trematoda, the most species-rich of the higher taxa we considered. Although we did not include them in our analyses, we note that many new subfamilies were also proposed for the Trematoda in the period we surveyed.

The positive relationship we observed between the number of new genera discovered and the currently known species richness of the higher taxa to which they belong supports the sampling hypothesis, in line with the results obtained by Wiens et al. (2026) at a much coarser taxonomic level. Thus, there are probably more new clades waiting to be found in the super-diverse Trematoda than in the relatively species-poor Acanthocephala or Polyopisthocotylea. Although this seems logical, the opposite pattern of saturation would also have been plausible from a statistical perspective, as the more species and genera one has already found, the harder it could be to find new ones (the collector's curve, *sensu* Pimm and Gittleman, 2026). Our results re-emphasise how poorly we know parasite biodiversity.

The positive relationship between the number of new genera discovered and known species richness was also apparent across families, though it was much weaker. Indeed, only one or two new genera have been found for most families (71 out of 97 families), yet their species richness ranges from fewer than 10 to over 1,000 species. The partial disconnect between species richness and the number of new genera found at the family level may result from variation in body sizes among helminth families. Indeed, the body size of new taxa correlates negatively with their year of description, i.e., small-bodied helminth taxa take longer to be discovered (Poulin, 2002; Poulin and Morand, 2004; Randhawa and Poulin, 2020). Alternatively, or additionally, the weak relationship between the species richness of families and the number of new genera discovered may arise from the well-documented taxonomic

biases in study effort across helminth taxa (Poulin and Jorge, 2019; Poulin et al., 2019). More taxonomists are working on certain groups than others, with the allocation of effort not always reflecting the species richness of those parasite taxa. For example, a few taxonomists have proposed a disproportionate number of new trematode genera compared to others, with the families they work on therefore benefiting from accelerated taxonomic advances (Cribb and Bray, 2011). As a consequence, a disproportionate effort into species discovery and genetic characterization is devoted to some helminth clades, based on geographic distribution, economic or conservation importance, or simply due to idiosyncratic preferences of individual researchers, with other clades receiving less attention.

We also found no evidence that the number of newly found genera is reaching an asymptote in 4 of the 6 higher taxa we investigated. While the data suggest few if any new genera are yet to be found in Acanthocephala and Cestoda, for the other groups, most obviously for Trematoda, the linear relationship as a function of time predicts many more truly new genera, based on yet to be discovered specimens, will be found in coming years. Our findings contrast with the observation made by Cribb and Bray (2011) several years ago. They noted that the number of recognised trematode genera rose steadily, almost linearly, since the early 1900s, but they thought the rate at which new trematode genera were proposed had started to decrease since the year 2000. Our results contradict that. The trends we observed match those reported by Wiens et al. (2026), who found a similar steady accumulation of new tetrapod genera over time in the period 2011–2020.

The dataset on which our results are based has some limitations. In particular, we included all new helminth genera and families proposed in published papers as valid and universally accepted. There is an element of subjectivity in taxonomic decisions: what one expert considers to be a valid taxon may be dismissed by another expert (see Poulin et al., 2026). These disagreements often lead to a new taxon being invalidated in the years after it was first proposed (Poulin and Presswell, 2024). Here, we accepted all new genera proposed in articles published in the journals we surveyed as valid, and assumed that taxonomic practices have not shifted significantly in recent years toward the “splitting” end of the “lumping versus splitting” continuum (Endersby, 2009). However, even if a few newly proposed genera later see their status become questionable, it is unlikely that the general trends we identified would no longer apply. Another important limitation is that, because of access restrictions, we included only publications in 11 major English-language journals. Given how much of the world’s biodiversity is concentrated in tropical areas, including Latin America, it is possible that some papers describing new helminth genera or families appeared in journals in Spanish, Portuguese, or some other language. We expect that including these might change the magnitude, but not the general direction, of the trends we report here.

Overall, our findings indicate that not only are there still a huge number of parasite species left to be discovered and described, as documented in earlier studies, but also many genera. Perhaps counterintuitively, this is particularly true in higher taxa that already have a high known species richness; in those groups, the fact that many species are known does not mean that all higher-level clades have been found. The Trematoda are one such group, where the rate at which new genera are found is not slowing down and a final number of genera cannot even be estimated with any degree of confidence. The ongoing quest to document parasite biodiversity (see Dobson et al., 2008; Poulin, 2014; Carlson et al., 2020) is therefore more than just completing an inventory of extant species, it also requires the discovery of distinct phylogenetic clades of parasites characterised by morphologies that do not fit within currently known genera.

CRediT authorship contribution statement

Robert Poulin: Writing – original draft, Project administration, Methodology, Conceptualization. **Bronwen Presswell:** Writing – review & editing, Methodology, Investigation, Data curation, Conceptualization. **Chen-Hua Li:** Writing – review & editing, Visualization, Methodology, Formal analysis, Conceptualization.

Declaration of generative AI use in the writing process

We made no use of generative AI or AI-assisted technologies in the preparation of this article.

Funding sources

No particular funding support is associated with this study.

Data availability

All data used in this article are available in the [Supplementary material](#).

Acknowledgements

We acknowledge the large community of parasite taxonomists whose immense efforts over many decades have generated the vast knowledge on which our study is based.

Appendix A. Supplementary material

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.ijpara.2026.104944>.

References

- Brabec, J., Salomaki, E.D., Kolísko, M., Scholz, T., Kuchta, R., 2023. The evolution of endoparasitism and complex life cycles in parasitic platyhelminths. *Curr. Biol.* 33, 4269–4275.
- Caira, J.N., Jensen, K., Waeschenbach, A., Olson, P.D., Littlewood, D.T.J., 2013. Orders out of chaos: molecular phylogenetics reveals the complexity of shark and stingray tapeworm relationships. *Int. J. Parasitol.* 44, 55–73.
- Carlson, C.J., Dallas, T.A., Alexander, L.W., Phelan, A.L., Phillips, A.J., 2020. What would it take to describe the global diversity of parasites? *Proc. R. Soc. B* 287, 20201841.
- Ceballos, G., Ehrlich, P.R., 2023. Mutilation of the tree of life via mass extinction of animal genera. *Proc. Nat. Acad. Sci. U.S.A.* 120, e2306987120.
- Costello, M.J., 2016. Parasite rates of discovery, global species richness and host specificity. *Integr. Comp. Biol.* 56, 588–599.
- Costello, M.J., Wilson, S., Houlding, B., 2013. More taxonomists describing significantly fewer species per unit effort may indicate that most species have been discovered. *Syst. Biol.* 62, 616–624.
- Cribb, T.H., Bray, R.A., 2011. Trematode families and genera: have we found them all? *Trends Parasitol.* 27, 149–154.
- Dobson, A., Lafferty, K.D., Kuris, A.M., 2008. Homage to Linnaeus: how many parasites? How many hosts? *Proc. Nat. Acad. Sci. U.S.A.* 105, 11482–11489.
- Elzhov, T.V., Mullen, K.M., Spiess, A., Bolker, B., 2023. minpack.lm: R interface to the Levenberg-Marquardt nonlinear least-squares algorithm found in MINPACK, plus support for bounds. R package version 1.2-4, <https://CRAN.R-project.org/package=minpack.lm>.
- Endersby, J., 2009. Lumpers and splitters: Darwin, Hooker, and the search for order. *Science* 326, 1496–1499.
- Hugot, J.-P., Baujard, P., Morand, S., 2001. Biodiversity in helminths and nematodes as a field of study: an overview. *Nematology* 3, 199–208.
- Huston, D.C., Smale, L.R., 2020. Proposal of *Spinulacarpus biforme* (Smales, 2014) n. g., n. comb. and the Spinulacarpidae n. fam. to resolve paraphyly of the acanthocephalan family Rhadinorhynchidae Lühe, 1912. *Syst. Parasitol.* 97, 477–490.
- Li, X., Yang, D., Wang, L., Wiens, J.J., 2025. The past and future of known biodiversity: rates, patterns, and projections of new species over time. *Sci. Adv.* 11, ead3071.
- Mora, C., Tittensor, D.P., Adl, S., Simpson, A.G.B., Worm, B., 2011. How many species are there on Earth and in the ocean? *PLoS Biol.* 9, e1001127.
- Pimm, S.L., Gittleman, J.L., 2026. Earth’s biodiversity: how much is there? *Proc. Nat. Acad. Sci. U.S.A.* 123, e2604886123.

- Poulin, R., 2002. The evolution of monogenean diversity. *Int. J. Parasitol.* 32, 245–254.
- Poulin, R., 2014. Parasite biodiversity revisited: frontiers and constraints. *Int. J. Parasitol.* 44, 581–589.
- Poulin, R., Jorge, F., 2019. The geography of parasite discovery across taxa and over time. *Parasitology* 146, 168–175.
- Poulin, R., Morand, S., 2004. *Parasite Biodiversity*. Smithsonian Books, Washington, DC.
- Poulin, R., Presswell, B., 2024. Nomenclatural stability and the longevity of helminth species names. *Syst. Parasitol.* 101, 34.
- Poulin, R., Bennett, J., Presswell, B., 2026. Variability among taxonomists in helminth species discrimination decision: a noise audit. *Int. J. Parasitol.* 56, 104702.
- Poulin, R., Hay, E., Jorge, F., 2019. Taxonomic and geographic bias in the study of helminth parasites. *Int. J. Parasitol.* 49, 429–435.
- R Core Team, 2024. R: a language and environment for statistical computing. Version 4.4.2. R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>.
- Randhawa, H.S., Poulin, R., 2020. Tapeworm discovery in elasmobranch fishes: quantifying patterns and identifying their correlates. *Mar. Freshwat. Res.* 71, 78–88.
- Schratzberger, M., Holterman, M., Van Oevelen, D., Helder, J., 2019. A worm's world: ecological flexibility pays off for free-living nematodes in sediments and soils. *Bioscience* 69, 867–876.
- Venables, W.N., Ripley, B.D., 2002. *Modern Applied Statistics with S*. Springer, New York.
- Wickham, H., 2016. *ggplot2: Elegant Graphics for Data Analysis* (Version 3.5.1). Springer-Verlag, New York.
- Wiens, J.J., Blomenkamp, E.G., Corliss, M., Li, X., 2026. Global biodiversity and the expanding tree of life. *Proc. Nat. Acad. Sci. U.S.A.* 123, e2530656123.
- Zeileis, A., Hothorn, T., 2002. Diagnostic checking in regression relationships. *R News* 2 (3), 7–10 <https://CRAN.R-project.org/doc/Rnews/>.