



## “Morphological compatibility” or subjective expectation? A response to Cadena-Castañeda (2026) and Braun (2026)

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In a recent paper, Cadena-Castañeda (2026) presented a morphology-based revision of short-winged Phaneropterinae worldwide, with particular emphasis on the delimitation and reorganization of tribes traditionally associated with Odonturini and Barbitistini. As part of this broader classificatory proposal, he incorporated and reinterpreted results from Fianco & Melo (2025), a molecular phylogenetic study designed to test relationships between species of *Angara* and selected Neotropical short- and long-winged phaneropterines using multiple genetic markers.

His treatment of Fianco & Melo (2025), however, is internally inconsistent and methodologically problematic. On one hand, he explicitly refers to that study as “valuable”, “informative”, and based on an extensive and “robust dataset”. On the other hand, he dismisses one of the central results of Fianco & Melo’s study, namely the placement of the type species of *Angara* within *Xenicola*, that resulted in the synonymy of *Xenicola* under *Angara*. Cadena Castañeda invokes “sample misidentification” to justify why he would not follow Fianco & Melo (2025). His double standards are difficult to reconcile. A dataset cannot reasonably be described as robust and informative while its principal result is selectively rejected as a labeling error in the absence of direct evidence.

The allegation of sampling mistake is the main issue here. It is not based on examination of vouchers, sequencing anomalies, traceable laboratory problems, or demonstrable inconsistencies in the dataset. Instead, it is inferred from the fact that the recovered topology does not conform to prior taxonomic expectations. In other words, the hypothesis of error is advanced not because error was shown, but because the result was considered morphologically unexpected.

Cadena-Castañeda’s (2026) argument relies on a supposed “morphological compatibility”, a concept invoked by him without any theoretical justification. In his own words: “Specifically, the synonymy of *Xenicola* under *Angara* is not supported by morphological compatibility.” (Cadena-Castañeda 2026: 64). This expression is revealing. It does not refer to an explicit analytical criterion, a tested framework, or a reproducible method. Rather, it appeals to a subjective expectation of morphological coherence, as though phylogenetic results should be accepted only when they confirm a pre-existing classificatory scheme. That is not a scientific standard. It is an interpretive preference elevated to the status of evidence.

Such reasoning is especially troubling because incongruence between morphological and molecular evidence is neither rare nor, by itself, indicative of error. For example, morphological convergence and character lability are well-known sources of conflict between phylogenies inferred from morphological and molecular datasets (e.g., Keating *et al.* 2023). The apparent contradiction between the phylogenetic evidence and the morphology-based classification proposed by Cadena-Castañeda (2026) does not place both lines of evidence on equal epistemological terms but rather highlights a contrast between results derived from explicit, testable analytical frameworks and those founded on subjective assessments of morphological coherence derived from Cadena-Castañeda’s own work. To move directly from topological incongruence to an accusation of sample misidentification is therefore not a cautious inference. It is a speculative leap. It bypasses alternative biological explanations and treats disagreement with expectation as evidence of methodological failure.

After that, Braun (2026) mentioned Fianco & Melo’s paper as a cautionary case against what he calls molecular-based taxonomy, arguing that the synonymizing of *Xenicola* under *Angara* would render a genus-level diagnosis impossible and suggesting that our conclusions resulted from confusion of molecular samples. His interpretation must be seen as plainly inaccurate. Fianco & Melo (2025) did not rely exclusively on molecular evidence. Our study has explicitly integrated morphology and provides a diagnosis for the genus as circumscribed there, and discusses character evolution in detail.

The claim that diagnosis would no longer be possible is, therefore, unsupported by the content of the study itself. It reflects, once again, an a priori refusal to accept that morphologically divergent taxa may nevertheless form a clade.

Braun (2026) also discusses Fianco & Melo (2025) in the context of the debate on taxonomic vandalism in Orthoptera raised by Çıplak *et al.* (2026), but his interpretation reflects a fundamental misunderstanding of both the study and the conceptual basis of scientific taxonomy. Braun reframes the discussion as a dichotomy between molecular and morphological-based taxonomy. In so doing, he suggests that Fianco & Melo (2025) exemplifies a problematic, “molecular-only” approach leading to taxonomic instability, particularly by rendering genus-level diagnoses difficult or impracticable. This interpretation is not supported by the actual content or methodology of the study. The synonymy proposed by Fianco & Melo (2025) is not an arbitrary consequence of relying on molecular data, but the result of an explicit, testable phylogenetic hypothesis based on empirical evidence. As emphasized by Çıplak *et al.* (2026), taxonomy is a scientific enterprise precisely because it operates through such hypotheses, which must be evaluated against data rather than constrained by the convenience of diagnosability or traditional expectations of morphological distinctiveness.

Moreover, Braun’s suggestion that the resulting difficulty in establishing diagnoses undermines the validity of the taxonomic act conflates practical challenges with epistemological standards. The inability to produce an easily diagnosable set of morphological characters does not invalidate a clade supported by robust phylogenetic evidence, but rather reflects the complex nature of evolutionary history. Likewise, speculative concerns regarding potential sample confusion do not constitute evidence against the hypothesis and therefore falls outside the empirical framework required for scientific critique.

Then, what is being rejected is not merely a topology based on molecular evidence, but the possibility that morphology, as traditionally interpreted, may have failed to capture phylogenetic history in this case. That possibility is entirely legitimate and, indeed, commonplace in modern systematics. Yet instead of confronting it analytically, both Cadena-Castañeda (2026) and Braun (2026) resort to speculative claims of sample confusion. This is not a neutral interpretive move. It is a serious, formal allegation. And formal allegations require rigorous evidence.

They also require caution. When concerns arise regarding possible methodological error, such as sample misidentification, the responsible course is to investigate them carefully and substantiate them directly. In taxonomy, this includes reexamining material, checking voucher identity, consulting the relevant collections, and, where appropriate, contacting the original authors before publicly raising suspicion as the main mode of explanation. None of this has occurred here. Cadena-Castañeda’s interpretation of the species belonging to *Angara* was based on photographs, without direct examination of any physical specimens. No contact was made with the Coleção Entomológica Pe. Jesus Santiago Moure (DZUP, Curitiba, Brazil), in which our voucher specimens have been deposited (RJP Machado, curator of Orthoptera, *pers. comm.*). Nor was there any attempt to consult the first author, M. Fianco, who personally examined the type material in European collections, including *A. albofasciata*, *A. superba*, and *A. dohrni*, collected all specimens of *Angara* used in our studies, and carried the molecular laboratory procedures in Fianco & Melo (2025). Even so, suspicion was elevated to explanation.

This is precisely where the argument ceases to be merely weak and becomes irresponsible. Scientific criticism is not exempt from standards. One may disagree with a phylogenetic result. One may reject a taxonomic decision. One may argue that a molecular hypothesis is unconvincing. But one cannot, or at least should not, attribute error without evidence and then treat that unsupported attribution as a legitimate foundation for further classificatory action. To do so is to replace critical evaluation with conjecture and to substitute rhetorical confidence for demonstration. Guidelines from the Committee on Publication Ethics (COPE) emphasize that concerns about research integrity should be addressed through careful assessment and dialogue with the authors, rather than unsupported allegations, while the principle of organized skepticism requires that criticism remain impersonal and evidence based. Thus, although critical engagement is essential, prematurely attributing errors without prior verification undermines both the fairness and reliability of scientific evaluation.

The broader implications are not trivial. If molecular results are to be dismissed whenever they conflict with a preferred morphological framework, then evidence is no longer being weighed critically; it is being filtered for compatibility with prior belief. Under that logic, morphology would not function as one source of evidence among many others, but as an unquestionable arbiter to which all other data must submit. This is antithetical to integrative taxonomy and incompatible with the logic of phylogenetic inference. Evidence should be tested against alternative hypotheses, not rejected because it produces uncomfortable results.

The placement of the type species of *Angara* in Fianco & Melo (2025) may certainly be debated. What cannot be justified is the claim that such a placement reflects sample misidentification in the absence of direct supporting evidence.

Topological incongruence alone is not proof of procedural error. At most, it is a reason to investigate further. Converting that incongruence into an accusation of sample confusion without examination, verification, or prior communication is not scientifically defensible.

For this reason, the appeal to “morphological compatibility” in Cadena-Castañeda (2026) must be rejected as an insufficient basis for dismissing the results of Fianco & Melo (2025). It is not an analytical criterion, not an evidentiary demonstration, and not a substitute for direct verification. It is an expectation. And expectations, however strongly held, do not overturn data. Accordingly, there is no demonstrated basis for rejecting the synonymy of *Xenicola* under *Angara*, and therefore we reinstate here all taxonomic decisions proposed by Fianco & Melo (2025).

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