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1	The wing venation of a new fossil species, reconstructed using
2	geometric morphometrics, adds to the rare fossil record of Triassic
3	Gondwanian Odonata
4	
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16	Keywords : Wing venation – Molteno Formation – Stem-Odonata – Reconstruction
17	
18	Abstract
19	Probably, the most common rock imprint fossil insect remain is an incomplete, isolated
20	wing. This pitfall has been traditionally addressed by manually reconstructing missing parts,
21	which is not ideal to comprehend long-term evolutionary trends in the group, in particular
22	for morphological diversity (i.e., disparity) approaches. Herein we describe a new Triassic
23	relative of dragon- and damselflies (Odonata), Moltenophlebia lindae gen. et sp. nov., from

24 the Molteno Formation (Karoo Basin, South Africa), on the basis of three incomplete, 25 isolated wings. In order to provide a reconstruction of the complete wing venation of the 26 species, we formalized and applied a repeatable method aiming at inferring the missing parts 27 of a given specimen. It is based on homologous veins automatically identified thanks to a 28 standardized color-coding. The dedicated script can be applied broadly to the fossil record of 29 insect wings. The species occurs to be a member of the Zygophlebiida, within the 30 Triadophlebiomorpha. This discovery therefore represents the first ascertained occurrence of 31 the latter group in Gondwana, an area where the fossil record of Odonata is depauperate.

33 **1. Introduction**

32

Although the fossil record of Odonata (dragon- and damselflies, and their stem-relatives) is composed of about a thousand species (Paleobiology Database, 2019), many of the known fossils are represented by incomplete wings. Moreover, particular periods and geographical areas remain under-studied. This situation makes it difficult to comprehend long-term evolutionary trends in the group, using either taxonomic or morphological diversity (i.e., disparity) approaches.

Herein we describe a new species from the Molteno Formation (Triassic, South Africa). The species is represented by three incomplete, isolated wings. In order to provide a reconstruction of the entire wing venation of the species, we applied a standardized and repeatable method aiming at reconstructing missing parts. We used Thin Plate Splines (TPS), mathematical basis for deformation grids (Bookstein, 1989), to deform a reference shape onto a target shape using homologous landmarks and semi-landmarks subsampled along veins identified thanks to a standardized color-coding.

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al., 2017).

2. Terminology and materials

2.1. Nomenclature and abbreviations

55 We follow the serial insect wing venation ground pattern (Lameere, 1923, 1922). The 56 corresponding wing venation nomenclature is repeated for convenience: ScP, posterior Subcosta; 57 R, Radius; RA, anterior Radius; RP, posterior Radius; RP1+2, anterior branch of RP (to be further divided into RP1 and RP2); RP3+4, posterior branch of RP (to be further divided into 58 59 RP3 and RP4); MA, anterior Media; MP, posterior Media; Cu, Cubitus; CuA, anterior Cubitus; 60 CuP, posterior Cubitus; AA, anterior Analis. Based on this ground pattern we follow homology 61 conjectures for total-Odonata proposed by Riek and Kukalová-Peck (1984), Bechly (1996) and 62 Béthoux (2015; and see references therein). We follow Deregnaucourt et al. (2017) for the 63 terminology to apply to intercalary veins. In details, Irp₁-rp₂ is the intercalary vein occurring 64 between RP1 and RP2 (also termed 'IR1'), and $Irp_{1+2}-rp_{3+4}$ that occurring the RP1+2 and RP3+4 65 (also termed 'IR2'). In addition to this standard terminology, we propose to use additional terms, 66 as follows. For the strongly convex, oblique cross-vein located between MA and MP and aligned 67 with RP+MA/MA, we propose the term 'pons' ('bridge' in Latin; also termed 'MAb', e.g. by 68 Nel et al., 1996); for the strongly convex and aligned cross-veins located between MP and the

The new species adds to the fossil record of Odonata during the Triassic. Indeed it represents

the first well ascertained occurrence of Triadophlebiomorpha in the Southern Hemisphere, a

group previously known from Europe and Asia only (Nel et al., 2001; Pritykina, 1981; Zheng et

69 posterior wing margin, or CuA and the posterior wing margin, we propose the term 'pillar'.

Whether its portion located between CuP and the posterior wing margin AA (or one of its
branches) or a strengthened cross-vein is addressed in the Discussion.

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73	2.2.Docume	entation	of fossil	material
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The studied specimens are housed at the Evolutionary Studies Institute (PRE/F/; formerly
'Bernard Price Institute for Palaeontology'), University of the Witwatersrand, Johannesburg,
South Africa.

77 Draft drawings were prepared with the aid of a Zeiss SteREO Discovery V8

78 Stereomicroscope equipped with a pair of W-PL 10x/23 eye pieces, a Plan Apo S 1.0x FWD

79 objective, and a drawing tube (Jena, Germany). Photographs were taken using a Canon EOS 5D

80 Mark III equipped with Canon 50 mm or MP-E 65 mm macro lenses. The light-mirror technique

81 was used to provide positive views of the specimens. Photographs were optimized [i.e. features

82 (e.g. contrast) uniformly adjusted to maximize information content] using Adobe Photoshop CS6

83 (Adobe Systems, San Jose, CA, USA). Vector line drawings were made using Adobe Illustrator

84 CS6 (Adobe Systems, San Jose, CA, USA) based on both scans of draft drawings and

85 photographs. The drawing of the wing base of the holotype of Zygophlebia tonchuanensis

86 Zheng, Nel, Wang, Jarzembowski, Chang and Zhang, 2017 was prepared based on published

87 data and photographs provided by D. Zheng.

88

3. Reconstruction of missing parts

90 *3.1.Methodology*

91 In the literature, reconstructing non-conserved part of a fossil, for example a wing, is usually

92 achieved following the author's appreciation, i.e., a non- repeatable, unstandardized method. The

material at hand, composed of several conspecific wings preserving different areas, was suitable
for exploring methodologies aiming at reconstructing missing parts.

95 Several standardized reconstruction methods have already been developed and tested in the 96 field of palaeoanthropology for 3D models of cranium (Gunz et al., 2009; Ogihara et al., 2015),

97 including bilateral symmetry, multivariate regression and/or thin-plate spline (TPS)

98 interpolation. Bilateral symmetry is not appropriate for our model (there is no inner symmetry in
99 an isolated wing). Multivariate regression requires a sample of complete specimens, which is not
100 available for our case. We therefore resorted to semi-landmarks and TPS deformation.

101 TPS deformation mimics the deformation of an infinitely thin metal plate (Bookstein, 1989). 102 Therefore, it minimizes the bending energy of the transformation from a reference shape (here 103 the wing used to infer the missing parts of the incomplete one) to a targeted shape (the wing to be reconstructed). As a consequence, the whole plan of the reference shape will be deformed. In 104 105 practice, the entire reference drawing will be affected by the deformation in such a way that the 106 placed points of reference (landmarks and semi-landmarks) fit perfectly the ones on the targeted 107 shape. Thus, the missing parts of the targeted shape will be inferred by those deformed from the 108 reference shape.

109 The two most complete specimens of *Moltenophlebia lindae*, PRE/F/20522 and

PRE/F/10626 (Fig. 2A, B), have largely overlapping parts. Therefore, each can be used as
reference shape to infer the missing parts of the other (Fig. 1A). Unfortunately, both specimens
lack the wing apex. Thus, a second TPS deformation was performed using data on *Zygophlebia ramosa* Pritykina, 1981, the closest relative known from a complete wing, to reconstruct the
missing apex (Fig. 1B).

For details, the missing parts of the specimen PRE/F/20522 (light lines in Fig. 2A) were inferred based on the specimen PRE/F/10626 (dark lines in Fig. 2B), and vice-versa. A drawing of the main veins and wing margin was first vectorized with Adobe Illustrator CS6. A specific color-code was applied to each vein. The vector files were then imported on R using grImport v.0.9-1 (Murrell, 2009).

120 Selection of sliding semi-landmarks was then performed (orange block in Fig. 1A). Fourteen 121 homologous vein portions present on both specimens were automatically selected thanks to their 122 color-coding. They were then sub-sampled to generate sets of landmarks with geomorph v.3.0.7 123 (Adams and Otárola-Castillo, 2013). For details, for each curve, the subsampling procedure 124 generates two landmarks (considered homologous) at its beginning and end, and 3 to 49 semi-125 landmarks between them (proportionally to the curve's length and complexity). Semi-landmarks 126 were allowed to slide using the minimum Bending Energy criterion. This method is more 127 suitable than minimizing Procrustes distances when there is large shape variation (Gunz and 128 Mitteroecker, 2013; Schlager, 2017), which is the case for the second step of the reconstruction 129 (see below; Fig. 1B). The actual disposition of landmarks and the rationale for placing them are provided as Supplemental Data 1 (Appendix A.). 130

A Procrustes superimposition (GPA) was then performed to correct for the effects of rotation, translation and size (Rohlf and Slice, 1990). Finally, a TPS deformation was applied to the specimen PRE/F/10626 (reference shape) so that its homologous points' coordinates fit those of the specimen PRE/F/20522 (targeted shape). The same deformation is applied to each pixel of the original drawing in order to obtain the image of PRE/F/20522 complemented by PRE/F/10626 original parts. The wing was almost completely reconstructed at that point, except for the apex.

138 To reconstruct this last area we applied the same procedure using data on Zygophlebia 139 ramosa which, among the Zygophlebiida, to which Moltenophlebia lindae belongs (see 140 Systematic Paleontology section), is the only species for which a complete wing is documented 141 (Fig. 1B). However this specimen, like others excavated in the corresponding locality, is 142 assumed to have been uniformly deformed by tectonics (Sharov, 1971, 1968; Voigt et al., 2006). 143 To take that bias into account, we added a 'retrodeformation' step (blue block in Fig. 1B): the 144 wing of Zygophlebia ramosa was submitted to 37 rotations (over 180°) and 11 elongations (from 145 100% to 200%) to create 407 retro-deformed wings (see examples in Supplemental Data 1, 146 Appendix A). The Procrustes superimposition was then performed. The retro-deformed drawing 147 selected for reconstruction was the one minimizing distances between landmarks coordinates and 148 those of the previously reconstructed wing (purple wing in Fig. 1). The TPS deformation was 149 then realized on this retro-deformed wing so that its homologous points' coordinates fit those of 150 the previously reconstructed wing (penultimate step in Fig. 1B). A fully reconstructed wing was 151 then obtained (main script, functions and functions description are available as Supplemental 152 Data 2, 3 and 4 respectively, Appendix A.).

153 The same procedure was used to reconstruct the wing of the specimen PRE/F/10626 (but 154 using the specimen PRE/F/20522 as reference shape for the first step).

155

156 3.2. Method limitations

Several sets of main veins were tested for reconstruction. Notably, the pertinence of using semi-landmarks on RP2, for the second part of the process (aiming at reconstructing the wing apex; Fig. 1B), was examined. Indeed, the area between RP3 and the anterior branch of RP2 is very dissimilar in the reference and targeted shapes: RP2 is branched more basally than RP3+4

in *Zygophlebia ramosa* whereas in *Moltenophlabia lindae* RP2 is forked close to the posterior
wing margin. Additionally, RP3+4 has many more branches in *Moltenophlabia lindae*. In a first
attempt, RP2 was not used because of this important variation between the two wing shapes.
However, the obtained reconstructed wing was not realistic: it was very elongated and the apex
had a marked posterior bending. This reconstructed wing could have hardly flown.

166 In a second attempt, semi-landmarks were placed on the portion of RP2 before its first split 167 on each wing shape, assuming that this variable area would be more constrained so as to better fit 168 the targeted shape. The obtained reconstruction, more realistic, is the one presented here (Fig. 169 2A). However, given the remarkable differences in this area between the two wings (viz. the 170 reconstructed Moltenophlabia lindae and the retro-deformed Zygophlebia ramosa), the TPS 171 deformation generated unrealistic distortions of some vein portions. These distortions were not 172 taken into account for the final reconstruction because they affected parts which were preserved 173 in the targeted shape. The proposed reconstruction (Fig. 2A) is therefore a smoothened version of 174 the R output to fit the fossil's preserved parts. R outputs are provided in Supplemental Data 1 175 (Appendix A.).

Unrealistic distortions were probably due to shape differences too important to be managed by the method. Indeed, semi-landmarks are allowed to slide along a curve, while only the first and last points are homologous landmarks (i.e., are not allowed to slide). Some semi-landmarks slid away from the original curve, not fitting anymore the original wing shape, probably because of the constraint induced by the use of RP2 curve for such a different area. The use of a more closely related species as reference shape might fix this issue. An additional improvement would be to consider more than one closely related species as reference shapes. Indeed, Gunz et al.

(2009) used several references to reconstruct their target and obtained different results. However,for now, there is no other complete wing appropriate for such a reconstruction.

185 Other issues can also be mentioned. It was not always possible to delimit vein portions based 186 on well-defined points such as vein branching. We therefore resorted to a manual pre-alignment 187 of the two sub-complete wings, inducing some degree of subjectivity. As arose by Gunz et al. (2009) and Ogihara et al. (2015), other parameters are susceptible to lead to differing 188 189 reconstructions, such as the number of landmarks and semi-landmarks. In our case, a minimal 190 number of semi-landmarks is needed to faithfully quantify a vein curvature, but too many render 191 the sliding computation more complicated, time-consuming and prone to generate unrealistic 192 crossings of semi-landmarks (due to their proximity).

193 Also, we ignore whether the two specimens of *Moltenophlebia lindae* used in the first step 194 (Fig. 1A) belonged to homologous thoracic segments (i.e., were both forewings, or hind wings), 195 or to individuals of the same sex. Some of the observed differences could reflect fore- vs. hind 196 wing differentiation and/or sexual dimorphism, both variations occurring among extant Odonata. 197 Indeed, i.e., hind wings are commonly broader and shorter than forewings in these insects. This 198 differentiation is much less conspicuous in those possessing petiolated wings (Zygoptera and 199 Anisozygoptera; i.e., damselflies and Epiophlebia spp., respectively), as Moltenophlebia lindae 200 does. In Calopterygidae (i.e., broad-winged damselflies) females commonly have wings more 201 elongated than those of males. However, leaving apart purely shape-related aspects, the main 202 veins pattern remains essentially unchanged, especially in the distal two-thirds of the wing. This 203 general appreciation was confirmed by Blanke (2018) who, on the basis of a broad-scale 204 morphometric analysis of Anisoptera wing venation, demonstrated that fore- and hind wings 205 correlate with each other in their shape variation. It can then be expected that our reconstruction

method will satisfactorily account for fore- vs. hind wing differentiation and/or sex-related shape
differences. This is indeed exemplified by the fact that the obtained reconstruction of the
specimen PRE/F/20522 (Fig. 2A) is broader than the used reference shape, which likely
represents a genuine differentiation.

210 The obtained reconstructions are based on a standardized repeatable method which could be 211 used on any wing that needs to be reconstructed for comparative analysis, or any fossil 212 equivalent to a 2D model lacking bilateral symmetry. Gunz et al. (2009) tested several aspects of 213 the reconstruction approach (e.g. error induced by reconstruction against intra-specific variability 214 within an inter-specific framework) and highlight the relevance of the TPS deformation for cases 215 such as the one presented here. We proposed an adaption of this method to insect wings and 216 detailed it step by step to ensure a complete transparency. However, further testing could be 217 valuable focusing on our model, for the reconstruction and also the retro-deformation step. 218 A possible venue would be to simulate missing parts on extant species and comparing the 219 obtained reconstructions with the original wing shape. The number and distribution of missing 220 areas, as well as their extents, likely are critical elements. For example, the reconstruction of a 221 wing apex, as we endeavored herein, is likely to be less reliable than that of an inner part. Indeed, 222 we performed an extrapolation, i.e., constraints were only applied on one side of the 223 reconstructed part. That could explain why the firstly reconstructed wing apex was 224 unrealistically elongated. In contrast, the reconstruction of a part located in the middle of a wing 225 could be more accurate because it is an interpolation, i.e., with constraints on several sides. Also, 226 phylogenetic closeness between the reference and target shapes is likely another prevalent factor 227 to be tested. The number of landmarks and semi-landmarks also needs to be tested. Ultimately, 228 the error induced by the reconstruction could be tested against intra-specific variability, within an

229	inter-specific framework (Gunz et al., 2009). Considering additional constraints, for example in
230	relation with flight biomechanics (Wootton and Kukalová-Peck, 2000) and developmental
231	modelling (Hoffmann et al., 2018), could further help obtaining more reliable reconstruction.
232	
233	4. Systematic paleontology
234	
235	Order Odonata Fabricius, 1793
236	TAXON PANDISCOIDALIA NEL ET AL., 2001
237	TAXON DISCOIDALIA BECHLY, 1996
238	TAXON TRIADOPHLEBIOMORPHA PRITYKINA, 1981
239	TAXON ZYGOPHLEBIIDA NEL ET AL., 2001
240	
241	Emended diagnosis
242	RP2 and Irp ₁₊₂ -rp ₃₊₄ fused for some distance shortly after the origin of the former, and Irp ₁ -
243	rp ₂ and RP2 fused for some distance; CuA without posterior branches; and, occurrence of a pillar
244	(ranging either from CuA to the posterior wing margin, or from MP to the posterior wing
245	margin).
246	
247	Included families
248	Zygophlebiidae, Xamenophlebiidae, Permophlebiidae and Kargalotypidae.
249	
250	Remarks

251 Nel et al. (2001) listed six character states as diagnostic of the taxon Zygophlebiida. Two of 252 them relate to the particular organisation of Irp₁-rp₂, RP2, and Irp₁₊₂-rp₃₊₄. We provide a 253 tentative interpretation of the corresponding area (Fig. 2) consistent with statements made by 254 Bechly (1996) and Nel et al. (2001), positing that (1) in the basal part, RP2 briefly fuses with 255 Irp₁₊₂-rp₃₊₄, and, (2) in the distal part, Irp₁-rp₂, briefly fuses with RP2. These two states might 256 have been acquired concurrently as a consequence of the relocation of the bases of Irp₁-rp₂, RP2, 257 and $Irp_{1+2}-rp_{3+4}$ towards the wing base. Therefore we propose to treat them as a single character 258 state, which is obviously derived, as it is absent in the most remote stem-Odonata (Riek and 259 Kukalová-Peck, 1984). Note that, as indicated by Nel et al. (2001), this character state was 260 acquired convergently within Protomyrmeleontidae, belonging to the Stigmoptera 261 (Deregnaucourt et al., 2021, and references therein), a group therefore only remotely related to 262 the Zygophlebiida. 263 Other character states listed by Nel et al. (2001) are present in various other Pandiscoidalia, 264 such as the Triadotypomorpha (Nel et al. 2001; Deregnaucourt et al., 2017). In other words, these 265 states form a corpus relevant only if observed jointly. The most relevant is 'CuA simple', 266 allowing Zygophlebiida to be distinguished from other Triadophlebiomorpha. However, it might 267 represent the apomorphy of a larger group, including all extant forms. 268 Whether the posterior-most portion of the pillar is composed of AA (or one of its branches) 269 or a strengthened cross-vein, as favored herein, is addressed in the Discussion. Regardless of its 270 nature, the occurrence of the pillar itself is a putative diagnostic trait of Zygophlebiida, or of a 271 subset within this group, as pointed out by Nel et al. (2001). 272

273 FAMILY UNCERTAIN

274	GENUS MOLTENOPHLEBIA GEN. NOV.
275	
276	Type species
277	Moltenophlebia lindae gen. et sp. nov.
278	
279	Diagnosis
280	By monotypy, as for the type species
281	
282	Etymology
283	The name derives from that of the geological Formation and from 'phlebia', itself derived
284	from the Ancient Greek 'phlebos' (vein).
285	
286	Remarks
287	The genus Moltenophlebia can be confidently assigned to the Discoidalia owing to the
288	occurrence of the pons. It can be further assigned to the Zygophlebiida owing to the occurrence
289	of the diagnostic character states of this taxon (see above).
290	
291	Moltenophlebia lindae gen. et sp. nov.
292	(FIGS. 2–4)
293	
294	Type specimens
295	Holotype: PRE/F/20522 (negative imprint). Paratypes: PRE/F/10626 (negative and positive
296	imprints), PRE/F/10615 (negative and positive imprints).

298 Diagnosis

CuA-CuP fork located basal to the pillar (i.e., CuP not capturing the pillar; putative
plesiomorphy within Zygophlebiida; see section 5.1); RP4 branched (putative plesiomorphy
within Zygophlebiida; see *Remarks* section).

302

303 Occurrence

All the specimens are from Aasvoëlberg locality (locality code "Aas 411"; see Anderson and
Anderson, 1984), Karoo Basin, South Africa; Molteno Formation; Carnian, Triassic (Anderson
et al., 1998).

307

308 *General description*

309 Wing total length and maximum width unknown (about 98 mm, and 23 mm respectively when 310 considering the reconstructions); wing broad with numerous small cells, slightly petiolate, 311 narrowing from the second third of the wing to the apex; ScP fused with the anterior wing 312 margin at the first third of the wing; many antenodal cross-veins; RA parallel to the anterior wing 313 margin distal to the nodus, with a single row of cell between the two; RP+MA diverging 314 obliquely from RA basal to the second antenodal cross-vein; RP+MA divided in RP and MA 315 distal to the second antenodal cross-vein; RP divided into RP1+2 and RP3+4 basal to the nodus 316 (inferred from preserved parts of the holotype); Irp₁-rp₂, RP2 and Irp₁₊₂-rp₃₊₄ fused for some 317 distance, forming a 'rectilinear convex stem' parallel to RP1 and seemingly diverging from this 318 vein just distal to the nodus; Irp_1-rp_2 and RP2 diverging shortly after the wing mid-length; 319 Irp₁₊₂-rp₃₊₄ diverging obliquely from the 'rectilinear convex stem' at wing mid-length; RP2

320 diverging obliquely from the 'rectilinear convex stem' further distally; areas between RP1 and 321 Irp₁-rp₂, and between RP2 and Irp₁₊₂-rp₃₊₄ with a single row of cells; RP2 with at least two 322 branches (some of the concave veins located between Irp1-rp2 and RP2, visible in PRE/F/10626, 323 might actually be branches of RP2, as in Zygophlebiidae); RP3+4 divided in RP3 and RP4 at the 324 two-third of the wing length, each with at least two branches; area between RP4 and MA with a 325 single row of cells; MA with a strong angle when dividing from RP; presence of a convex pons 326 aligned with the RP+MA and the basal portion of MA; MA and MP close and parallel to each 327 other basal to the nodus, diverging distal to it, and converging close to their endings; area 328 between MA and MP ranging from one row of cells up to four; a cross-vein occurring in the area 329 between R+MA and MP, basal to the first antenodal cross-vein; MP with no evident fork, but 330 delimiting a large area filled with several concave branches (intercalaries?) and convex 331 intercalaries, subparallel; Cu close to the posterior wing margin at the end of the petiole; Cu 332 divided into CuA and CuP at the level of the point of divergence of RA and RP+MA; CuA and 333 CuP parallel with one row of cells between them, occasionally divided into two cells in a same 334 wing; CuP with no evident fork, but delimiting an area filled with several concave branches 335 (intercalaries?) and convex intercalaries, subparallel.

336

337 Specimen description

Holotype specimen PRE/F/20522 (Figs. 2A and 3A): Left wing, almost complete, apex and
posterior wing margin missing; preserved length 79.6 mm, maximum width 19.6 mm; CuA and
CuP more bent than in the specimen PRE/F/10626.

341	Paratype specimen PRE/F/10626 (Figs. 2B, 3B): Two-third of a right wing, antero-basal
342	third and apex missing; preserved length 74.7 mm, maximum width 20.6 mm; posterior wing
343	margin and distal portions of RP2, RP3 and RP4 branches preserved.
344	Paratype specimen PRE/F/10615 (Figs. 2C, 3C): Two broken segments of a left wing, the
345	base and a part of the third quarter; preserved length 19.2 mm, maximum width 34 mm.
346	
347	Etymology
348	The name is dedicated to Linda Terblanche, who allowed access to the site where the fossils
349	were discovered.
350	
351	Remarks
352	There is virtually no doubt that the specimens PRE/F/20522 (holotype) and PRE/F/10626
353	(paratype) are conspecific. Our reconstruction suggests that the former is slightly broader, but
354	this could represent differences between a hind wing and a forewing, and/or sexual dimorphism.
355	The specimen PRE/F/10615 can be attributed to the same species thanks to the presence of a
356	convex pons aligned with the RP+MA and the basal portion of MA, and also the CuA-CuP split
357	located basally (at the level of the point of divergence of RA and RP+MA). It is also very similar
358	in size with the two other specimens.
359	The occurrence of a cross-vein in the area between R+MA and MP near the wing base,
360	observed in the holotype specimen is unusual for the group. It is not unlikely that it represents a
361	rare, uncommon feature for the species (it could then be an atavism).
362	In the Zygophlebiida and more generally in Triadophlebiomorpha MP is distinct from Cu at
363	the wing base (the two veins then remaining fused for some distance). This character state is

364 plesiomorphic, being observed in the earliest odonates (Riek and Kukalová-Peck, 1984). In our 365 reconstruction we therefore assumed that Moltenophlebia lindae displayed this state. 366 Within the Zygophlebiida, the new species can neither be attributed to the 367 Xamenophlebiidae nor to the Permophlebiidae, as it lacks the diagnostic characters of these 368 families as delimited by Nel et al. (2001). The family Zygophlebiidae currently lacks a diagnosis 369 (Bechly, 1996; Nel et al., 2001). The family currently contains four genera, from which 370 Moltenophlebia lindae differs in many aspects, including a RP2 branched close to the posterior 371 wing margin (whereas RP2 is widely developed in known Zygophlebiidae genera). Also, in the 372 new species both RP3 and RP4 are branched (as in Triadotypomorpha, suggesting that this state 373 is a plesiomorphy; see Pritykina, 1981; Nel et al., 2001). The resulting wide area (between RP3 374 and RP4) is also present in *Mixophlebia mixta* Pritykina, 1981, but RP4 is simple in this species. 375 The observed differences justify the erection of a new genus. However, given uncertainties on 376 the occurrence of several character states in various genera of Zygophlebiidae, and on the 377 polarity of several character states, we refrained from erecting a new family to accommodate 378 Moltenophlebia.

379

380 5. Discussion

381

382 5.1. Nature of the pillar

In Zygophlebiidae, the portion of the pillar located between CuP and the posterior wing margin has been interpreted as a branch of AA by Pritykina (1981) and Bechly (1996), and AA by Nel et al. (2001) and Zheng et al. (2017) (Fig. 4A). It implies that CuP and AA (or one of its branches) form a composite stem from the CuA-CuP split. However, the condition displayed by

387 Moltenophlebia lindae, previously undocumented for Zygophlebiida, provides a new perspective 388 on this particular aspect of wing venation homology conjectures. Instead of possessing a single, 389 convex stem in the area delimited by MP, the pillar and the posterior wing margin, 390 *Moltenophlebia lindae* displays a convex stem but also another, conspicuously concave one 391 (green arrow in Fig. 4B; and see Fig. 3C), the latter likely being CuP free from any other vein (a 392 configuration similar to that of Archizygoptera; Nel et al., 2012). It strongly suggests that the 393 pillar, in Moltenophlebia lindae, is exclusively composed of strengthened cross-veins (as 394 represented in Fig. 4D). 395

In turn, an alternative interpretation of the wing venation homology of other Zygophlebiidae, 396 consistent with this observation, can be proposed. In the petiole of Zygophlebia tongchuanensis, 397 a short vein-like element occurs in the area between the posterior wing margin and the vein 398 immediately anterior to it, between the point of fusion of MP with Cu+AA and the point of 399 divergence of MP. It was interpreted as a cross-vein by Zheng et al. (2017; Fig. 4A) but another 400 plausible interpretation is that it is AA (Fig. 4C), which would then end earlier than previously 401 assumed. It must be emphasized here that such early ending of AA has been conjectured for 402 many other members of Discoidalia, including members of the triassolestid assemblage, regarded 403 as closely related to the crown-group of Odonata (Nel et al., 2002; Tierney et al., 2020). In other 404 words, this conjecture is very plausible. Then, the pillar is composed of (i) a very oblique portion 405 of CuP and (ii) a strengthened cross-vein. With respect to the configuration in Moltenophlebia 406 lindae (Fig. 4D), it can then be hypothesized that the CuA-CuP split is located more distally in 407 Zygophlebia tongchuanensis (Fig. 4E) and in other Zygophlebiidae, to the point where CuP fuses 408 with the portion of the pillar previously located between it and CuA (i.e., CuP captures the first 409 cross-vein forming the pillar). Cross-veins forming the pillar being overall convex (Fig. 4B), this

410	elevation was likely imposed to CuP. This interpretation likely applies to the entire
411	Zygophlebiida. The state 'CuA-CuP split located basally' is present in stem-Odonata more
412	ancient than Zygophlebiida, including the Meganisoptera (see (Nel et al., 2009)) and the
413	'geropteromorphs' (see Riek and Kukalová-Peck, 1984).
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417	5.2. Triassic Gondwanian Odonata
418	Within early-diverging stem-Odonata (and, more specifically, within the Discoidalia), the
419	Triadophlebiomorpha were greatly diversified and widely distributed across Europe and Asia
420	during the Triassic (Nel et al., 2001; Pritykina, 1981; Zheng et al., 2017). The new species,
421	Moltenophlebia lindae, can be confidently assigned to one of the main lineages of this taxon,
422	namely the Zygophlebiida. It therefore represents the first ascertained occurrence of the
423	Triadophlebiomorpha in the Gondwana. This discovery concurs with previous accounts
424	suggesting that major groups of Triassic Odonata had a worldwide distribution. The Triassic,
425	Australian Iverya averyi Béthoux and Beattie, 2010, initially regarded as a Triadotypomorpha
426	(see original description) but which actually occupies an uncertain position within the
427	Discoidalia (Deregnaucourt et al., 2017), already indicated similarities between Laurasian and
428	Gondwanian faunas of stem-Odonata. Moreover, a representative of another group of stem-
429	Odonata, the Triadotymorpha, well-documented from Europe and Asia (Bechly, 1997; Béthoux
430	et al., 2009; Laurentiaux-Vieira et al., 1952; Pritykina, 1981; Reis, 1909) also occurred at

Molteno (Deregnaucourt et al., 2017). Even the gracile, damselfly-like Protomyrmeleontoidea

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432 Handlirsch, 1906, which dispersal capabilities might have been more limited than those of larger,

contemporaneous stem-Odonata, have been documented from Triassic outcrops in Australia
(Henrotay et al., 1997; Tillyard, 1922) and also from Molteno (Deregnaucourt et al., 2021). In
summary, this South African outcrop testifies to a great diversity of Triassic Odonata in the
Gondwana, and to a widespread distribution of the main lineages of Odonata during this period.

438 Authors contributions

Isabelle Deregnaucourt: Conceptualization, Data curation, Formal analysis, Investigation,
Methodology, Visualization, Writing — original draft. Jérémie Bardin: Conceptualization,
Formal analysis, Investigation, Methodology, Supervision, Writing — review & editing. John
M. Anderson: Resources, Writing — review & editing. Olivier Béthoux: Conceptualization,
Investigation, Funding acquisition, Supervision, Visualization, Writing — review & editing.

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560 Figures and Figure Captions

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502 Fig. 1 Filow chart explaining the standardized method asea to reconstruct the wing of spec	the wing of specificity
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563 PRE/F/20522. A, first step, reconstruction of specimen PRE/F/20522 with specimen

564 PRE/F/10626. **B**, second step, reconstruction of the firstly reconstructed wing of specimen

565 PRE/F/20522 with the holotype of *Zygophlebia ramosa* PIN 2785/20. GPA = generalised

566 Procrustes analysis; TPS = thin plate splines; squares correspond to process and circles to data.
567

- 568 Fig. 2. Moltenophlebia lindae gen. et sp. nov., from Carnian (Triassic) of Aasvoëlberg locality,
- 569 Molteno Formation, Karoo Basin, South Africa, line drawings. A, specimen PRE/F/20522 (left

570 wing; holotype). **B**, specimen PRE/F/10626 (right wing; paratype). **C**, specimen PRE/F/10615

- 571 (left wing). RA = anterior Radius; RP = posterior Radius; RP1+2 = anterior branch of RP (to be
- 572 further divided into RP1 and RP2); RP3+4 = posterior branch of RP (to be further divided into
- 573 RP3 and RP4); $Irp_1-rp_2 = intercalary vein between RP1 and RP2; Irp_{1+2}-rp_{3+4} = intercalary vein$
- between RP1+2 and RP3+4; MA = anterior Media; MP = posterior Media; CuA = anterior
- 575 Cubitus; CuP = posterior Cubitus. Light lines were reconstructed.
- 576

Fig. 3. *Moltenophlebia lindae* gen. etsp. nov., from Carnian (Triassic) of Aasvoëlberg locality,
Molteno Formation, Karoo Basin, South Africa, photographs. A, specimen PRE/F/20522, left
wing (light-mirrored; holotype). B, specimen PRE/F/10626a, right wing (light-mirrored, flipped
horizontally; paratype). C, specimen PRE/F/10615a left wing (flipped horizontally). White frame

refers to Fig. 4B.

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583 Fig. 4. Detail of the area of the pillar. A, Zygophlebia tonchuanensis Zheng, Nel, Wang, 584 Jarzembowski, Chang and Zhang, 2017, detail of holotype, homology conjectures by Zheng et al. (2017). **B**, *Moltenophlebia lindae* gen. et sp. nov., detail of specimen PRE/F/20522, left wing 585 586 base (light-mirrored; holotype). C, as in A, except for the course of AA, following the homology 587 conjecture we favoured herein. **D–E**, simplified schemes of the respective positions of CuP and 588 of the pillar as in **B** and **D**, as favored herein. RA = anterior Radius; RP = posterior Radius; MA 589 = anterior Media; MP = posterior Media; CuA = anterior Cubitus; CuP = posterior Cubitus; AA 590 = anterior Analis; small white arrows (bordered in green -gray in grayscale version) indicate the 591 CuA-CuP split; in A-C, large black arrow indicates the pons, white arrows indicate the pillar; in

- **B**, very large green arrow (grey in grayscale version) indicates the portion of CuP basal to the
- 593 pillar (and see Fig. 3A).















