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INGRID COSTA MARÇAL

**EGLÍDEOS (CRUSTACEA, ANOMURA) DA BACIA DO RIO
TIBAGI:
RIQUEZA, DISTRIBUIÇÃO E TAXONOMIA INTEGRATIVA**

Londrina
2021

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Tese apresentada ao Programa de Pós-graduação em Ciências Biológicas da Universidade Estadual de Londrina - UEL, como requisito parcial para a obtenção do título de Doutor.

Orientador: Prof. Dr. Gustavo Monteiro Teixeira
Coorientadora: Dra. Lenice Souza-Shibatta

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RESUMO

Os crustáceos dulcícolas do gênero *Aegla* são endêmicos do sul da América do Sul. A grande maioria das espécies está restrita a cursos d'água de baixa ordem, sendo altamente suscetíveis às alterações ambientais. No sul do Brasil, o estado do Paraná é a região menos estudada, mas demonstra grande potencial para abrigar uma elevada diversidade de *Aegla*. Na bacia do rio Tibagi, por exemplo, quatro espécies foram registradas até agora (*Aegla castro*, *A. schmitti*, *A. lata* e *A. jacutinga*). A necessidade de inventários e estudos taxonômicos sobre este gênero, como uma medida de conservação da biodiversidade, é evidente. No entanto, a morfologia do grupo é conservadora e caracterizações moleculares têm sido utilizadas para a realização de interpretações seguras da diversidade, incluindo a detecção de espécies crípticas. Diante disso, o presente trabalho foi desenvolvido com o objetivo de contribuir com o conhecimento da riqueza, distribuição geográfica e taxonomia do gênero *Aegla*. Os resultados deste trabalho foram organizados em três capítulos. No primeiro discorremos sobre a diversidade críptica de *Aegla* no estado do Paraná, apresentando as descrições de três novas espécies coletadas na bacia do rio Tibagi. De acordo com os critérios da IUCN, uma das novas espécies pode ser classificada como “Em perigo” e as outras duas como “Vulneráveis”. O segundo capítulo é dedicado a atualizar a distribuição geográfica dos eglídeos da bacia do rio Tibagi. Foram analisados espécimes depositados na Coleção de Crustáceos do Museu de Zoologia da Universidade Estadual de Londrina. Novos registros de ocorrência foram obtidos para *A. castro* (10), *A. lata* (5) e *A. jacutinga* (10). Análises morfológicas e moleculares permitiram identificar duas novas espécies para a região do Médio Tibagi. As novas espécies têm distribuição limitada e são categorizadas como “Em perigo” de acordo com os critérios da IUCN. Além disso, uma chave de identificação para as espécies de *Aegla* da bacia do rio Tibagi é fornecida. No terceiro capítulo avaliamos a eficácia da região barcode do gene COI na discriminação de espécies de *Aegla*, baseado na diferença dos valores de divergência intra e interespecíficas. Das 74 espécies analisadas, 68 (92%) foram corretamente identificadas por suas sequências, confirmando a eficácia da região barcode do COI na identificação de espécies de *Aegla*. Além disso, a aplicação do limiar de distância genética de 2% revelou possíveis táxons crípticos e linhagens geneticamente divergentes em 22 espécies investigadas. Espera-se que os dados fornecidos por nossa pesquisa contribuam para revelar a real diversidade e padrões de distribuição dos eglídeos. Em suma, nossos resultados enfatizam a importância da bacia do rio Tibagi para a conservação dos eglídeos e reforçam o alto potencial de descoberta de espécies novas no estado do Paraná.

Palavras-chave: aeglidae; COI; conservação; diversidade críptica; identificação de espécies.

MARÇAL, Ingrid Costa. **Aeglids (Crustacea, Anomura) from the Tibagi River basin: richness, distribution and integrative taxonomy.** 2021. 172 p. Thesis (Doctorate degree in Biological Sciences) – Universidade Estadual de Londrina, Londrina, 2021.

ABSTRACT

Freshwater crustaceans of the genus *Aegla* are endemic to southern South America. Most species are restricted to low-order watercourses, being highly susceptible to environmental changes. In south Brazil, the Paraná state is the least studied region but shows great potential for harboring a high diversity of *Aegla*. For example, in the Tibagi River basin, four species have been recorded so far (*Aegla castro*, *A. schmitti*, *A. lata*, and *A. jacutinga*). The need for inventories and taxonomic studies on this genus as a measure of biodiversity conservation is evident. However, the morphology of the group is conservative and molecular characterizations have been used to make safe interpretations of diversity, including the detection of cryptic species. Thus, the present work aimed to contribute to the knowledge of the richness, geographic distribution, and taxonomy of the genus *Aegla*. The results of this work were organized into three chapters. In the first, we discuss the cryptic diversity of *Aegla* in the state of Paraná, presenting the descriptions of three new species collected in the Tibagi River basin. According to IUCN criteria, one of the new species can be classified as “Endangered” and the other two as “Vulnerable”. The second chapter is dedicated to updating the geographic distribution of the aeglids from the Tibagi River basin. Specimens deposited at the Crustacean Collection of the Museu de Zoologia of Universidade Estadual de Londrina were analyzed. New records of occurrence were obtained for *A. castro* (10), *A. lata* (5), and *A. jacutinga* (10). Morphological and molecular analyzes allowed to identify two new species for the Middle Tibagi region. New species have limited distribution and are categorized as “Endangered” according to IUCN criteria. In addition, a diagnostic key for *Aegla* species from the Tibagi River basin is provided. In the third chapter, we evaluated the effectiveness of the COI gene barcode in discriminating *Aegla* species based on the difference in intra and interspecific divergence values. Of the 74 species analyzed, 68 (92%) were correctly identified by their sequences, confirming the effectiveness of the COI barcode in identifying *Aegla* species. In addition, the 2% genetic distance threshold application revealed possible cryptic taxa and genetically divergent lineages in 22 investigated species. We hope that the data provided by our research will contribute to the real diversity and distribution patterns of aeglids. In summary, our results emphasize the importance of the Tibagi River basin for the conservation of aeglids and reinforce the high potential of finding new species in the Paraná state.

Key words: aeglidae; COI; conservation; cryptic diversity; species identification.

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AAD	Marcação areolar anterior
AH	Altura da aréola
APM	Margem posterior da aréola
bp	Pares de bases
CAPES	Coordenação de Aperfeiçoamento de Pessoal de Nível Superior
CL	Comprimento da carapaça incluindo o rostro
CLE	Comprimento da carapaça sem o rostro
CNPq	Conselho Nacional de Desenvolvimento Científico e Tecnológico
COI	Citocromo c Oxidase subunidade I
CW	Largura da carapaça
DNA	Deoxyribonucleic acid
EN	Em perigo
GMYC	Generalized Mixed Yule-coalescent
HWT	Metade da largura máxima do telson
IUCN	International Union for Conservation of Nature
K2P	Modelo Kimura-2-Parâmetros
LabIAS	Laboratório de Invertebrados Aquáticos e Simbiontes
LMR	Margem lateral do rostro
LT	Baixo Tibagi
MGSP	Parque Estadual Mata dos Godoy
MHNCI	Museu de História Natural Capão da Imbuia
MN/UFRJ	Museu Nacional da Universidade Federal do Rio de Janeiro
m.s.n.m.	Metros sobre o nível do mar
MT	Médio Tibagi
MZUEL	Museu de Zoologia da Universidade Estadual de Londrina
MZUSP	Museu de Zoologia da Universidade de São Paulo
NJ	Neighbor-joining tree
NMNH	National Museum of Natural History of the Smithsonian Institution
PCR	Polymerase Chain Reaction
PCW	Largura pré-cervical
PMC	Região mesial da margem posterior do cefalotórax
RBW	Largura da base do rostro

TDL	Comprimento da linha dorsal transversal
UFRGS	Universidade Federal do Rio Grande do Sul
UT	Alto Tibagi
VU	Vulnerável
WU	Largura máxima do endopodito

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1 1. INTRODUÇÃO GERAL

2 Com base em extensa pesquisa na literatura, De Grave et al. (2009) estimaram que a
3 ordem Decapoda consiste em 233 famílias, 2.725 gêneros e 17.635 espécies, sendo 14.756
4 espécies existentes e 2.979 espécies fósseis. A infraordem Anomura representa em torno de
5 15% desta diversidade, tendo 2.470 espécies existentes e 230 espécies fósseis (De Grave et
6 al., 2009). Apesar das relações filogenéticas entre os anomuros serem debatidas há muitos
7 anos, estudos recentes baseados tanto em dados morfológicos como moleculares têm
8 contribuído para decifrar essas relações (De Grave et al., 2009). McLaughlin et al. (2007), por
9 exemplo, revisaram amplamente os caracteres morfológicos externos dos representantes da
10 infraordem Anomura e propuseram que a mesma fosse dividida em sete superfamílias
11 (Paguroidea, Kiwaoidea, Lomisoidea, Galatheaidea, Aegloidea, Lithodoidea e Hippoidea).
12 Desta forma, a família Aeglidae foi elevada à classificação de superfamília (McLaughlin et
13 al., 2007).

14 Aeglidae é a única família que constitui a superfamília Aegloidea (McLaughlin et al.,
15 2010). Das 92 espécies que compõe a família Aeglidae, 90 são espécies e subespécies do
16 gênero *Aegla* Leach, 1820 (Moraes et al., 2017; Jara et al., 2018; Páez et al., 2018; Trombetta
17 et al., 2019; Marçal et al., 2020, 2021) e duas são fósseis. *Haumuriaegla glaessneri*
18 Feldmann, 1984 foi descoberta em rochas marinhas na Nova Zelândia (Feldmann, 1984) e
19 *Protaegla minuscula* Feldmann, Veja, Applegate & Bishop, 1998 foi encontrada em rochas
20 marinhas no México (Feldmann et al., 1998). Diferentemente destas espécies fósseis, os
21 representantes do gênero *Aegla* são exclusivamente de águas continentais do sul da América
22 do Sul, ocorrendo nas bacias hidrográficas do Brasil, Chile, Argentina, Uruguai, Paraguai e
23 Bolívia (Bond-Buckup & Buckup, 1994; Bond-Buckup & Buckup, 1999; Bond-Buckup,
24 2003).

25 Os registros fósseis (Feldmann, 1984; Feldmann et al., 1998) sugerem que a origem de

1 Aeglidae ocorreu em um ambiente marinho e posteriormente houve uma dispersão em direção
2 ao ambiente dulcícola. Diferentes trabalhos debatem sobre qual teria sido a direção da
3 dispersão desses crustáceos nos habitats de água doce do sul da América do Sul. Alguns
4 pesquisadores postularam que essa dispersão ocorreu a partir do oceano Atlântico (Schmitt,
5 1942; Ringuelet, 1948; Morrone & Loppretto, 1994). Entretanto, estudos sobre os padrões de
6 distribuição (Ortmann, 1902), evidências fósseis (Feldmann, 1984; Feldmann et al., 1998),
7 biogeografia e sistemática molecular de *Aegla* (Pérez-Losada et al., 2004) dão maior suporte a
8 hipótese de que essa dispersão ocorreu a partir do oceano Pacífico.

9 Os padrões de distribuição geográfica atuais de *Aegla* têm sido associados à fatores
10 históricos, como transgressões marinhas e elevações tectônicas (Pérez-Losada et al., 2004),
11 glaciação e a formação de refúgios glaciais (Xu et al., 2009; Oyanedel et al., 2011). Trevisan
12 et al. (2009) associaram a distribuição de *Aegla platensis* Schmitt, 1942 e *Aegla singularis*
13 Ringuelet, 1948 ao longo da bacia do rio Jacutinga, no estado do Rio Grande do Sul (Brasil),
14 ao uso e ocupação do solo. Estes autores sugeriram que a predominância de *A. platensis* em
15 nascentes de rios e pastagens e de *A. singularis* em áreas urbanas e agrícolas podem estar
16 relacionadas à cobertura de mata ciliar, grau de erosão das margens, disponibilidade de
17 alimento, diversidade de habitats, competição interespecífica, entre outros. Tumini et al.
18 (2016) atestaram que as distribuições de decápodes de água doce no sul da América do Sul
19 (Argentina) são fortemente influenciadas por variáveis ambientais locais, como altitude,
20 estabilidade do corpo d'água, faixa anual de temperatura, pH e condutividade. Além disso,
21 Gonçalves et al. (2018) usaram a modelagem de distribuição de espécies de *Aegla* para
22 identificar e propor áreas prioritárias para conservação em quatro ecorregiões de água doce na
23 América do Sul, mais especificamente no extremo sul do Brasil e em áreas adjacentes na
24 Argentina e no Uruguai.

25 De acordo com a literatura, a área de distribuição de *Aegla* é limitada ao norte pelo

1 registro de *Aegla franca* Schmitt, 1942 no município de Claraval, estado de Minas Gerais,
2 Brasil (20°18'47"S; 47°16'37"O) e ao sul pelo relato de *Aegla alacalufi* Jara & López, 1981
3 na ilha de Duque de York, Chile (50°33'31"S; 75°19'17"O) (Bueno et al., 2007; Oyanedel et
4 al., 2011). Embora algumas espécies tenham registro de ocorrência em mais de uma bacia
5 hidrográfica (Schmitt, 1942; Bond-Buckup & Buckup, 1994; Jara & Palacios, 1999; Oyanedel
6 et al., 2011), a maioria é conhecida por ocorrer em afluentes de um mesmo rio ou somente em
7 sua localidade tipo (Buckup & Rossi, 1977; Jara, 1982; Rocha & Bueno, 2011; Santos et al.,
8 2009, 2010, 2012, 2013, 2014, 2015; Moraes et al., 2016, 2017; Bueno et al., 2017; Jara et al.,
9 2018; Páez et al., 2018; Trombetta et al., 2019; Marçal et al., 2020, 2021).

10 Esses anomuros ocorrem geralmente em riachos de cabeceira, com águas correntes e
11 bem oxigenadas e são considerados bons bioindicadores da qualidade do habitat (Bond-
12 Buckup & Buckup, 1994; Buckup & Bond-Buckup, 1999; Bortoluzzi et al., 2007; Correa-
13 Araneda et al., 2010; Santos et al., 2017). Algumas espécies, no entanto, são habitantes
14 obrigatórias de cavernas no sudeste do Brasil (Bueno et al., 2017). Em seu habitat natural, os
15 eglídeos¹ podem ser encontrados embaixo de rochas, pedaços de tronco e folhas, ou seja, são
16 animais de hábitos bentônicos (Bond-Buckup, 2003). Esses crustáceos são considerados elos
17 importantes nas cadeias alimentares dos ecossistemas aquáticos, pois servem de alimento para
18 diversos vertebrados (Arenas, 1976; Medina, 1998; Cassini et al., 2009) e, por serem
19 onívoros, generalistas e oportunistas, desempenham um papel importante na ciclagem de
20 nutrientes (Bueno & Bond-Buckup, 2004; Castro-Souza & Bueno, 2004; Santos et al., 2008;
21 Williner, 2010; Cogo et al., 2018; Collins, 2020; Almeida et al., 2021).

22 Das 90 espécies e subespécies de *Aegla* descritas, 58 ocorrem no Brasil, 23 no Chile,
23 14 na Argentina, 4 no Uruguai, 1 no Paraguai e 1 na Bolívia (Bueno et al., 2017; Santos et al.,
24 2017; Moraes et al., 2017; Jara et al., 2018; Páez et al., 2018; Trombetta et al., 2019; Marçal

¹ O termo “eglídeos” será aqui utilizado para se referir exclusivamente às espécies e subespécies do gênero *Aegla*.

1 et al., 2020, 2021). Apesar da alta diversidade, os eglídeos provavelmente são os crustáceos
2 decápodes de água doce mais ameaçados na América do Sul (Bueno et al., 2016). Entre as 58
3 espécies que ocorrem no Brasil, 39 são enquadradas em algum grau de ameaça, sendo 13
4 vulneráveis, 12 em perigo e 14 criticamente em perigo de acordo com critérios da IUCN
5 (Santos et al., 2017). A distribuição restrita de muitas populações, o alto grau de endemismo e
6 o fato de serem suscetíveis a impactos antrópicos são fatores que contribuem para esse quadro
7 (Bond-Buckup & Buckup, 1994; Bueno et al., 2016; Santos et al., 2017). Desta forma, os
8 eglídeos fazem parte de um contexto preocupante, em que a biodiversidade global nos
9 ambientes de água doce tem declinado em taxas mais elevadas que em outros ambientes (Sala
10 et al., 2000; Dudgeon et al., 2006; WWF, 2012).

11 Este cenário é agravado no frágil mosaico de fragmentos florestais do estado do
12 Paraná. De acordo com um recente mapeamento de uso e cobertura do solo, apenas 29,12%
13 dos 19.987.990,3 hectares deste estado contêm floresta nativa, a maioria cercada por
14 pastagens ou plantações agrícolas (IAT, 2020). Além disso, esta região é a menos investigada
15 e com menos estudos taxonômicos sobre *Aegla* no Brasil. Mesmo assim, há grande potencial
16 para descoberta de espécies novas e ampliação da distribuição de espécies já conhecidas
17 (Santos et al., 2015). Recentemente, *Aegla okora* Páez & Teixeira, 2018 foi descrita para a
18 porção média do rio Iguaçu (Páez et al., 2018) e *Aegla nebeccana* Trombetta, Páez, Santos &
19 Teixeira, 2019 para a bacia do rio Ivaí (Trombetta et al., 2019). Estudos investigando outras
20 populações de *Aegla*, morfologicamente semelhantes, revelaram a existência de três espécies
21 novas para as bacias do rio Tibagi (*Aegla jacutinga* Marçal & Teixeira, 2020, Marçal et al.,
22 2020), rio das Cinzas (*Aegla buenoi* Marçal & Teixeira, 2021, Marçal et al., 2021) e rio
23 Pirapó (Marçal et al., em preparação).

24 A bacia do rio Tibagi é uma das maiores bacias da drenagem do Alto Paraná no estado
25 do Paraná, cobrindo aproximadamente 25.000 km² (SEMA-PR, 2010). O rio Tibagi tem uma

1 extensão de 550 quilômetros com 65 tributários diretos e centenas de subafluentes (Maack,
2 2002). Os principais afluentes na margem direita são os rios Iapó, São Jerônimo e Congonhas,
3 já na margem esquerda os rios Taquara, ribeirão dos Apertados e ribeirão Três Bocas são os
4 maiores contribuintes (SEMA-PR, 2010). Além de possuir mais de 90 saltos e cachoeiras, o
5 rio Tibagi apresenta características geomorfológicas distintas ao longo do seu curso (Parolin
6 et al., 2010). A altitude, por exemplo, tem uma queda total de 792 metros, desde 1.100 metros
7 sobre o nível do mar (m.s.n.m.) em sua nascente na Serra das Almas (Arroio da Invernada),
8 no município de Ponta Grossa, até 298 m.s.n.m. quando deságua no reservatório da Usina
9 Hidrelétrica de Capivara no rio Paranapanema (Maack, 2002; Parolin et al., 2010). A
10 existência dessa diferença de altitude em seu percurso atribui à bacia um grande potencial
11 hidroenergético (Medri et al., 2002). Na bacia do rio Tibagi existem cinco usinas hidrelétricas,
12 Presidente Vargas e Mauá no rio Tibagi, Apucarantina no rio Apucarantina, Pitangui e São
13 Jorge no rio Pitangui (Parolin et al., 2010).

14 Em função das variações do clima, da altitude e do tipo de solo e vegetação, a bacia do
15 rio Tibagi pode ser dividida em três sub-regiões: alto, médio e baixo Tibagi (Anjos et al.,
16 1997). O alto Tibagi é a região localizada mais ao sul da bacia (> 800 m.s.n.m.), onde há
17 predomínio da vegetação do tipo estepe gramíneo-lenhosa (os Campos Gerais) e a
18 temperatura média anual é mais baixa (Anjos et al., 1997; Torezan, 2002). No médio Tibagi, a
19 região intermediária (800–600 m.s.n.m.), é possível encontrar a floresta ombrófila mista (ou
20 floresta de araucária) (Torezan, 2002). Já o baixo Tibagi, a região mais ao norte (600–300
21 m.s.n.m.), é caracterizado pela floresta estacional semidecidual com temperatura média anual
22 mais alta comparada à região sul da bacia (Anjos et al., 1997; Torezan, 2002).

23 Grande parte da bacia é ocupada por áreas de agricultura intensiva, com cultivo de
24 soja, milho, trigo e café (SEMA-PR, 2010). O alto volume de agrotóxicos comercializados, a
25 presença de indústrias com alto potencial contaminante e o déficit na infraestrutura urbana

1 quanto aos sistemas de drenagem e esgoto, representam elevado risco de contaminação aos
2 cursos de água da bacia, afetando diretamente o meio ambiente e as populações humanas
3 (SEMA-PR, 2010). Além disso, com o intenso processo de desmatamento no estado do
4 Paraná, a cobertura florestal nativa da bacia do rio Tibagi apresenta-se bastante fragmentada
5 (Torezan, 2002). Atualmente, restam somente alguns remanescentes de floresta estacional
6 semidecidual (p. ex. Parque Estadual Mata dos Godoy), de floresta ombrófila mista (p. ex.
7 Parque Ecológico da Klabin) e de vegetação rasteira dos Campos Gerais (p. ex. Parque
8 Estadual de Vila Velha) (Parolin et al., 2010).

9 Para muitas espécies de decápodes de água doce o risco de extinção é alto, devido
10 tanto à carência de planos de conservação direcionados ao grupo, quanto ao estágio avançado
11 de degradação dos ecossistemas límnicos (Cumberlidge et al., 2009). A necessidade de
12 inventários e estudos taxonômicos sobre *Aegla* como uma medida de conservação da
13 biodiversidade é evidente. Até agora, quatro espécies de eglídeos foram registradas na bacia
14 do rio Tibagi, *Aegla castro* Schmitt, 1942 (Schmitt, 1942), *Aegla schmitti* Hobbs, 1979
15 (Bond-Buckup & Buckup, 1994), *Aegla lata* Bond-Buckup & Buckup, 1994 (Bond-Buckup &
16 Buckup, 1994) e *A. jacutinga* (Marçal et al., 2020). O aumento dos esforços de pesquisa tem
17 elevado potencial para a ampliação do número de espécies conhecidas, bem como das áreas
18 de distribuição das espécies já descritas. Além disso, informações sobre distribuições
19 geográficas são cruciais para avaliar o risco de extinção das espécies (Boos et al., 2012). No
20 entanto, um fato complicador é a morfologia altamente conservadora dentro do gênero
21 (Schmitt, 1942; Ringuelet, 1948; Martin & Abele, 1988).

22 Vários taxonomistas têm usado técnicas moleculares juntamente com dados
23 morfológicos, em um panorama taxonômico integrativo, para discriminação mais precisa das
24 espécies (Jara et al., 2003; Bond-Buckup et al., 2010; Santos et al., 2009, 2010, 2012, 2013,
25 2015; Moraes et al., 2016; Jara et al., 2018; Páez et al., 2018; Trombetta et al., 2019; Marçal

1 et al., 2020, 2021). Segundo Hillis (1987), as técnicas moleculares podem revelar níveis de
2 diferenciação genética escondidos em populações morfologicamente semelhantes. *Aegla*
3 *paulensis* Schmitt, 1942, por exemplo, foi reportada como um complexo com sete espécies
4 crípticas (Santos et al., 2015; Moraes et al., 2016). A população da bacia do Ribeira de Iguape
5 foi descrita como *Aegla lancinhas* Bond-Buckup & Buckup, 2015 em Santos et al., 2015, e
6 quatro populações da bacia do Tietê foram descritas como novas espécies (Moraes et al.,
7 2016).

8 Existem vários outros exemplos de espécies crípticas dentro dos eglídeos. Moraes et
9 al. (2017) descreveram *Aegla quilombola* Moraes, Tavares & Bueno, 2017 a partir de uma das
10 populações anteriormente conhecida como *Aegla marginata* Bond-Buckup & Buckup, 1994.
11 Crivellaro et al. (2017) analisaram 17 populações atribuídas a *Aegla longirostri* Bond-Buckup
12 & Buckup, 1994, usando dois métodos de delimitação de espécies, e identificaram pelo menos
13 14 potenciais espécies. Jara et al. (2018) descreveram *Aegla chilota* Jara, Pérez-Losada &
14 Crandall, 2018 a partir de uma população designada preliminarmente como *Aegla*
15 *araucaniensis* Jara, 1980. Espécies crípticas também foram relatadas entre as populações de
16 *A. platensis* e *A. uruguayana* Schmitt, 1942 (Zimmermann et al., 2018, 2021). Além disso, *A.*
17 *jacutinga* foi descrita a partir de populações morfologicamente semelhantes a *A. lata* (Marçal
18 et al., 2020).

19 Uma técnica molecular comumente utilizada na identificação de espécies é o DNA
20 barcode, em que cada táxon seria identificado por ter uma sequência única de DNA (Hebert et
21 al., 2003). A região barcode do gene Citocromo c Oxidase subunidade I (COI) têm sido usada
22 eficazmente na discriminação de lepidópteros (Hebert et al., 2003; Janzen et al., 2005),
23 pássaros (Hebert et al., 2004), aranhas (Barrett & Hebert, 2005), formigas (Smith et al., 2005)
24 al., 2005), peixes (Ward et al., 2005; Pereira et al., 2011, 2013; Souza-Shibatta et al., 2018),
25 crustáceos (Lefébure et al., 2006; Costa et al., 2007; Havermans et al., 2011; Matzen da Silva

1 et al., 2011) e outros.

2 O método clássico de distância de pares baseado no modelo Kimura-2-Parâmetros
3 (K2P) é a abordagem predominante usada para analisar os padrões de diversidade com a
4 região barcode do COI (Matzen da Silva et al., 2011). Este método pressupõe que a distância
5 genética entre indivíduos da mesma espécie (divergência intraespecífica) é menor do que a
6 variação entre espécies diferentes (divergência interespecífica) (Hebert et al., 2004; Ribolli et
7 al., 2017). Assumindo um limiar intraespecífico de no máximo 2%, Matzen da Silva et al.
8 (2011) tiveram em torno de 98% de sucesso no reconhecimento de decápodes marinhos.
9 Lefébure et al. (2006) analisaram sequências COI de Aeglidae com outras 17 famílias
10 diferentes de Crustacea e propuseram um limiar molecular para ajudar na delimitação de
11 espécies. No entanto, esse limiar foi calculado excluindo as sequências do gênero *Aegla* da
12 análise. Desta forma, nenhum estudo analisou distâncias genéticas e avaliou a eficácia da
13 região barcode do COI para delimitar eglídeos.

14 Este trabalho de tese foi desenvolvido com o objetivo de contribuir com o
15 conhecimento da riqueza, distribuição geográfica e taxonomia dos crustáceos de água doce do
16 gênero *Aegla*. Dentre as perguntas desta tese estão:

- 17 1. As diversas populações morfológicamente semelhantes à *Aegla lata*, coletadas
18 dentro de sua ampla área de distribuição, constituem espécies crípticas? (Capítulo
19 1)
- 20 2. Qual a riqueza de *Aegla* na bacia do rio Tibagi e qual a distribuição e grau de
21 endemismo destas espécies? (Capítulo 2)
- 22 3. A análise morfológica permite a distinção segura entre espécies morfológicamente
23 semelhantes? (Capítulo 2)
- 24 4. A região barcode do COI permite discriminar com eficácia as espécies de *Aegla*?
25 (Capítulo 3)

1 5. O limiar de distância genética de 2% pode ser aplicado para a delimitação de
2 espécies de *Aegla*? (Capítulo 3)

3 Os resultados deste trabalho foram divididos em três capítulos em formato de artigo. O
4 primeiro intitulado “Cryptic diversity among populations of *Aegla* Leach, 1820 (Decapoda:
5 Anomura: Aeglidae) from Tibagi River basin, Paraná state, Brazil, with descriptions of three
6 new species” foi submetido à revista *Journal of Natural History*. O segundo capítulo
7 intitulado “Diversity and geographical distribution of aeglids crabs (Crustacea, Anomura,
8 Aeglidae) from Tibagi River basin, Paraná state, Brazil” encontra-se nas normas da revista
9 *Zoological Journal of the Linnean Society*. O terceiro intitulado “The effectiveness of DNA
10 barcoding as a tool in *Aegla* diversity (Crustacea, Aeglidae)” foi submetido à revista
11 *Zoologica Scripta*. A fim de facilitar a compreensão e permitir uma leitura contínua, dispomos
12 as figuras e tabelas próximas ao local em que foram citadas pela primeira vez no texto,
13 diferindo das normas de submissão.

14

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1 **2. CAPÍTULO 1**

2 **CRYPTIC DIVERSITY AMONG POPULATIONS OF *AEGLA* LEACH, 1820**
3 **(DECAPODA: ANOMURA: AEGLIDAE) FROM TIBAGI RIVER BASIN, PARANÁ**
4 **STATE, BRAZIL, WITH DESCRIPTIONS OF THREE NEW SPECIES**

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1 ABSTRACT

2 Freshwater crustaceans of the genus *Aegla* are endemic to southern South America. In Brazil,
3 the greatest diversity of species of the aeglid species occurs in river basins in the Rio Grande
4 do Sul state. Nevertheless, recent studies have shown that the potential for discovering new
5 species of *Aegla* in the Paraná state is huge. In recent years, for example, seven new species
6 have been described for the state of Paraná. Furthermore, there is a need to solve problems
7 related to cryptic species and refine taxonomic information about the group. Here we expand
8 our current knowledge of the freshwater biodiversity of *Aegla* in the region by describing
9 three new species. *Aegla* sp. n. 1, *Aegla* sp. n. 2, and *Aegla* sp. n. 3 were discriminated based
10 on morphological and molecular evidence. Particular morphological characters of the
11 carapace, chelipeds, epimeron and uropods distinguished the new taxa. Molecular results also
12 support the separation of the new species from the closely related species *A. jacutinga*, *A.*
13 *castro* and *A. lata*. The new species have limited distribution and are categorized as
14 endangered (*Aegla* sp. n. 1) and vulnerable (*Aegla* sp. n. 2 and *Aegla* sp. n. 3) according to
15 International Union for Conservation of Nature Red List Categories and Criteria.

16 **Keywords:** COI gene; morphology; species delimitation; taxonomy; threatened species

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1 INTRODUCTION

2 Freshwater crustaceans of the genus *Aegla* Leach, 1820 are endemic to southern South
3 America (Schmitt 1942). These anomuran crabs usually occur in headwater streams with
4 running and well-oxygenated waters, being quite susceptible to environmental disturbances
5 and therefore considered good bioindicators of water quality (Bond-Buckup and Buckup
6 1994; Bortoluzzi *et al.* 2007; Correa-Araneda *et al.* 2010; Santos *et al.* 2017). Of the 90
7 described species, approximately 70% are under some level of threat of extinction (Moraes *et*
8 *al.* 2017; Santos *et al.* 2017; Jara *et al.* 2018). The conservation of this fauna, therefore, must
9 be considered of extremely high priority.

10 This scenario is potentially aggravated in the fragile mosaic of forest fragments in the
11 Paraná state, southern Brazil. According to a recent mapping of land use and coverage, only
12 29.12% of the 19,987,990.3 hectares of this state contains native forest, most of which is
13 surrounded by pastures or agricultural plantations (IAT 2020). Moreover, this region is the
14 least explored and has been subject to the fewest taxonomic studies on *Aegla* in Brazil. Even
15 so, recent work suggests that the potential to discover new species of *Aegla* in Paraná state is
16 huge (Santos *et al.* 2015). Notably, seven new species were described in the last 6 years:
17 *Aegla meloi* Bond-Buckup and Santos, 2015 (Santos *et al.* 2015), *Aegla loyolai* Bond-Buckup
18 and Santos, 2015 (Santos *et al.* 2015), *Aegla lancinhas* Bond-Buckup and Buckup, 2015
19 (Santos *et al.* 2015), *Aegla okora* Páez and Teixeira, 2018 (Páez *et al.* 2018), *Aegla*
20 *nebeccana* Trombetta, Páez, Santos and Teixeira (Trombetta *et al.* 2019), *Aegla jacutinga*
21 Marçal and Teixeira, 2020 (Marçal *et al.* 2020) and *Aegla buenoi* Marçal and Teixeira, 2021
22 (Marçal *et al.* 2021) – the penultimate species described for the Tibagi River basin.

23 The Tibagi River basin is one of the largest basins of the Upper Paraná drainage in the
24 Paraná state, covering approximately 25,000 km² (SEMA-PR 2010). Its main river starts in
25 the Serra das Almas, Ponta Grossa city, and flows into the Paranapanema River (Maack 2002;
26 Parolin *et al.* 2010). According to Pérez-Losada *et al.* (2009), the rivers located in the
27 Paranapanema River basin, in the Upper Paraná region, support high biodiversity of aeglids
28 compared with other rivers from the same ecoregion. In the Tibagi River basin, for example,
29 four species of aeglids were recorded until now, namely *Aegla castro* Schmitt, 1942 (see
30 Schmitt 1942), *Aegla schmitti* Hobbs, 1979 (see Bond-Buckup and Buckup 1994), *Aegla lata*
31 Bond-Buckup and Buckup, 1994 (see Bond-Buckup and Buckup 1994) and *A. jacutinga* (see
32 Marçal *et al.* 2020).

33 Since 1991 the Museu de Zoologia of the Universidade Estadual de Londrina
34 (MZUEL) has made a relevant collection of freshwater decapod crabs of Paraná state,

1 primarily Aeglidae crabs. Some of this material has already been studied by Galves *et al.*
2 (2007), Silva *et al.* (2017), Marçal *et al.* (2018), Páez *et al.* (2018), Chaves *et al.* (2019),
3 Trombetta *et al.* (2019), Marçal *et al.* (2020), Almeida *et al.* (2021) and Silva *et al.* (2021).
4 Galves *et al.* (2007) recorded the occurrence of *A. lata* in two streams in the city of Londrina,
5 in the northern region of Paraná state. As a result, the distribution area of the species, which
6 was previously known only for the type locality in the city of Ponta Grossa, was expanded.
7 Within this wide area of distribution, there are diverse populations morphologically similar to
8 *A. lata*. However, some of these specimens probably constitute cryptic species. *Aegla*
9 *jacutinga*, for example, was described from two populations collected in sub-tributaries that
10 flow into the left bank of the Tibagi River, confirming this assumption (Marçal *et al.* 2020).
11 Surprisingly, *A. lata* is considered ‘critically endangered’ (Santos *et al.* 2017), and is highly
12 likely to be extinct in its type locality (Pérez-Losada *et al.* 2009). Thus, the discovery of
13 cryptic species in the *A. lata* distribution area, as well as the confident identification of other
14 populations of *A. lata*, plays a critical role in the conservation assignment and maintenance of
15 aeglid diversity. Here, we present the description of three new species of *Aegla* from the
16 Tibagi River basin, Paraná state, Brazil. Both morphological and molecular approaches were
17 used to compare and delimit species. We also evaluate the conservation status of the new
18 species according to the criteria established by the International Union for Conservation of
19 Nature (IUCN 2019).

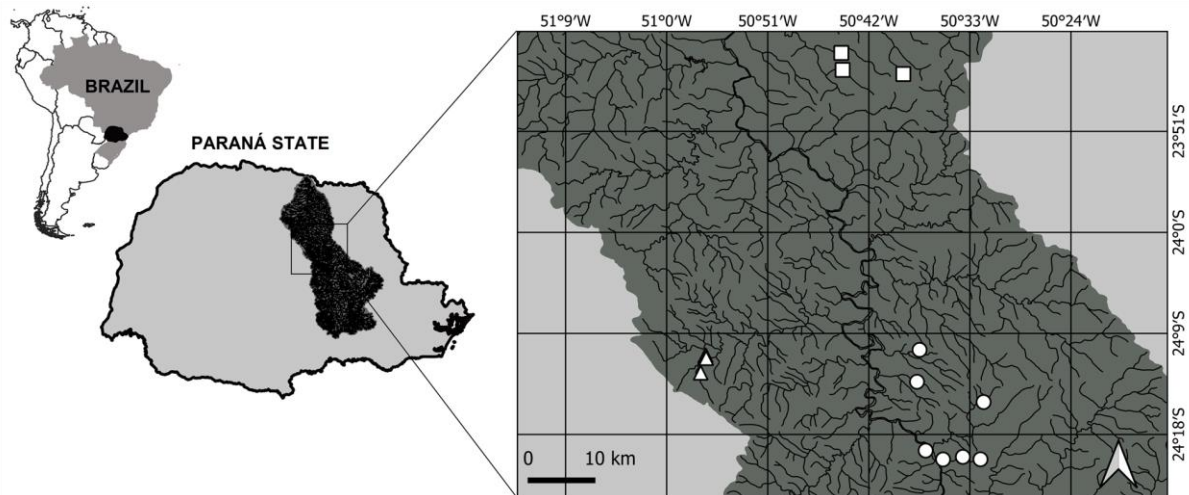
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21 MATERIAL AND METHODS

22 Sampling

23 Specimens of the new species were collected in watercourses of the Tibagi River basin
24 (Figure 1) during 16 sampling campaigns. To obtain fresh material for molecular analysis,
25 additional collections were carried out at the type localities. Submerged pebbles and small
26 rocks were manually removed to dislodge aeglids from their hidings and to subsequently be
27 captured by a hand net (90 cm diameter, 4 mm mesh size) immediately positioned and against
28 the water flow. Ten sampled specimens per locality were placed on crushed ice to be
29 anaesthetised. Then, abdominal muscle tissue was removed and fixed in absolute alcohol for
30 DNA extraction. The remaining specimens were preserved in 70% alcohol for morphological
31 analysis. All sampled specimens are deposited in the Crustacean Collection of MZUEL.

32



1
2 **Figure 1.** Map showing the distribution of *Aegla* sp. n. 1 (squares), *Aegla* sp. n. 2 (triangles)
3 and *Aegla* sp. n. 3 (circles) in the Paraná state, Brazil. The dark gray area indicates the Tibagi
4 River basin.

5
6 **Morphological Analysis**

7 The descriptions are based on morphological characters of the holotypes. The variations are
8 based on examination of the paratypes. The morphological terms used in the descriptions
9 follow Martin and Abele (1988), Bond-Buckup and Buckup (1994), and Moraes *et al.* (2016).
10 We adopted the methods of Bond-Buckup and Buckup (1994) and Moraes *et al.* (2016) to
11 take the measurements with a calliper (0.01 mm precision). The following abbreviations are
12 employed in the text: AAD, areolar anterior demarcation; AH, areolar height; APM, areolar
13 posterior margin; CL, carapace length including rostrum; CLE, carapace length excluding
14 rostrum; CW, carapace width; HWT, half the maximum width of telson; LMR, lateral margin
15 of rostrum; PCW, pre-cervical width; PMC, mesial region of the posterior margin of the
16 cephalothorax; RBW, rostral base width; TDL, transversal dorsal linea length; WU, width of
17 uropod. The shape of the rostrum, areola, cardiac area, and uropods was determined through
18 morphometric relationships, according to Moraes *et al.* (2016). The eyestalks were positioned
19 in parallel alignment with the rostrum to determine the extent of the apex of the anterolateral
20 spine relative to the basal margin of the cornea (Moraes *et al.* 2016). We used a
21 stereomicroscope equipped with a program for stacking images and a digital camera with a 4
22 megapixel frame to take photographs.

23
24 **Molecular Analysis**

25 Genomic DNA was extracted from preserved tissues following the method described by

1 Shiozawa *et al.* (1992), with some modifications. Approximately 100 mg of tissue was
2 minced with scissors into a micro-centrifuge tube containing 200 μ l of TE9 buffer (100 μ l
3 Tris [pH 8.0], 71.6 μ l H₂O, 8 μ l 0.5 M EDTA, 0.4 μ l 5 M NaCl, 20 μ l SDS). Soon after, 5 μ l
4 of proteinase K (Invitrogen) was added to each sample and they were incubated for 4 hours at
5 63 °C. Following incubation, the DNA was purified by successive washes with equal volumes
6 of phenol, chlorophane (1 phenol: 1 chlorophyll), and chlorophyll (24 chloroform: 1 isoamyl
7 alcohol). The DNA was precipitated with 10% of 3 M NaCl and 2 ½ of the volume of
8 absolute ethanol and stored at -20 °C for 12 hours. After that, the DNA was washed with 70%
9 ethanol and resuspended in 200 μ l of Tris-EDTA buffer. The region of the mitochondrial
10 cytochrome c oxidase subunit I (COI, \pm 600 bp) gene was amplified using primers COI-f and
11 COI-r (van Syoc 1995), following the PCR conditions proposed by Pérez-Losada *et al.*
12 (2002). PCR products were visualized on a 0.8% agarose gel, stained with SYBR® Safe DNA
13 Gel Stain (Life Technologies), following the manufacturer's protocol, and purified using
14 ExoSAP IT® (Prodimol Biotecnologia). The samples were then sequenced bidirectionally in
15 independent reactions and the product of the sequencing reactions was analyzed in an ABI
16 3500 XL automatic sequencer (Applied Biosystems Inc., CA, USA) using ABI Big Dye
17 Terminator v 3.1. The quality of the sequences was verified using the Eletropherogram
18 Quality Analysis software (Togawa and Brigido 2003), also used to produce consensus
19 sequences between forward and reverse. The sequences generated in this study were deposited
20 in Bold Systems under access numbers AEGLA003-21, AEGLA004-21, AEGLA005-21,
21 AEGLA006-21, AEGLA009-21 and AEGLA010-21. These sequences were aligned and
22 edited in the MEGA v. 6 software (Tamura *et al.* 2013), together with other sequences of the
23 *Aegla* species that are morphologically similar and that occur in the Tibagi River basin. The
24 sequences included in the analyses were retrieved from GenBank or the Bold database (*Aegla*
25 *odebrechtii* Müller, 1876: AY595571, AY595572; *A. castro*: AY595561, AY595586; *A.*
26 *strinatii* Türkay, 1972: AY595560, AY595640; *A. perobae* Hebling and Rodrigues, 1977:
27 AY595587, AY595588; *A. schmitti*: AY595563, AY595583; *A. lata*: AEGPR001-18,
28 AEGPR002-18; *A. jarai* Bond-Buckup and Buckup, 1994: AY595581, AY595595; *A.*
29 *jacutinga*: AEGPR006-18, AEGPR021-19). Intraspecific and interspecific genetic distances
30 were calculated based on the Kimura-two-parameter model (Kimura 1980). To test the
31 hypothesis of new species, an *a posteriori* species delimitation strategy, based on the topology
32 of phylogenetic trees, was used. The Generalized Mixed Yule Coalescent (GMYC) method
33 was performed in the Splits package (Pons *et al.* 2006; Fujisawa and Barraclough 2013) with
34 the R 3.5.1 program, from an ultrametric tree. Using this method it is possible to calculate the

1 number of clusters, classifying the bifurcation rates of a phylogram as resulting from the
2 processes of interspecific or intraspecific ramifications of the lineages (Pons *et al.* 2006;
3 Fujisawa and Barraclough 2013). The ultrametric tree was obtained via Bayesian inference in
4 the BEAST v. 2.6.2 program (Bouckaert *et al.* 2019) with a strict molecular clock and a birth-
5 death model (Heled and Drummond 2010). The data were analyzed as a single partition and
6 the evolutionary model used was HKY+I+G (proportion of invariant sites = 0.620; gamma
7 shape = 0.629), previously specified by the jModelTest2 (Darriba *et al.* 2012). The analyses
8 were carried out for 10 million generations, sampling a tree every 1000 generations. The
9 TRACER v. 1.5 (BEAST package) was used to verify the subsequent probability of sufficient
10 minimum effective size (ESS > 200) and a significant estimate of the parameters and the
11 average age of the nodes, considering a burn-in of 25 million generations. The trees were
12 summarized and visualized using the programs TREEANNOTATOR 1.5.3 and FIGTREE
13 1.3.1, respectively (Drummond and Rambaut 2007; Rambaut 2009).

14

15 RESULTS

16

Family Aeglidae Dana, 1852

17

Aegla sp. n. 1 Marçal and Teixeira

18

(Figures 2–5)

19

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20 ***Holotype***

21 Male [CLE 19.9 mm], Brazil, Paraná, São Jerônimo da Serra, Paranapanema River basin,
22 Tibagi River sub-basin, Tigre River, 23°44'00.50"S, 50°44'26.74"W, altitude 836 m, F.C.
23 Jerep, E. Santana and A. de Souza coll., 9 January 2019 (MZUEL 513).

24 ***Paratypes***

25 5 females [CLE 14.9–16.5 mm], same data as holotype (MZUEL 487). 3 males [CLE 14.5–
26 25.6 mm] and 6 females [CLE 14.2–16.8 mm], Brazil, Paraná, São Jerônimo da Serra,
27 Paranapanema River basin, Tibagi River sub-basin, Tigre River, 23°45'53.90"S,
28 50°38'55.49"W, altitude 1034 m, G.M. Teixeira and I.C. Marçal coll., 17 March 2020
29 (MZUEL 502).

30 ***Additional material examined***

31 2 males [size not recorded] and 7 females [size not recorded], Brazil, Paraná, São Jerônimo da

1 Serra, Paranapanema River basin, Tibagi River sub-basin, Tigre River, 23°45'53.90"S,
 2 50°38'55.49"W, altitude 1034 m, G.M. Teixeira and I.C. Marçal coll., 17 March 2020
 3 (MZUEL 507, genetic vouchers: Bold Systems access AEGLA009-21, AEGLA010-21). 4
 4 males [CLE 12.8–16.3 mm] and 2 females [CLE 14.1–14.9 mm], Brazil, Paraná, São
 5 Jerônimo da Serra, Paranapanema River basin, Tibagi River sub-basin, Pilões stream,
 6 23°45'31.25"S, 50°44'19.70"W, altitude 912 m, F.C. Jerep, E. Santana and A. de Souza coll.,
 7 1 August 2018 (MZUEL 465).

8 *Diagnosis*

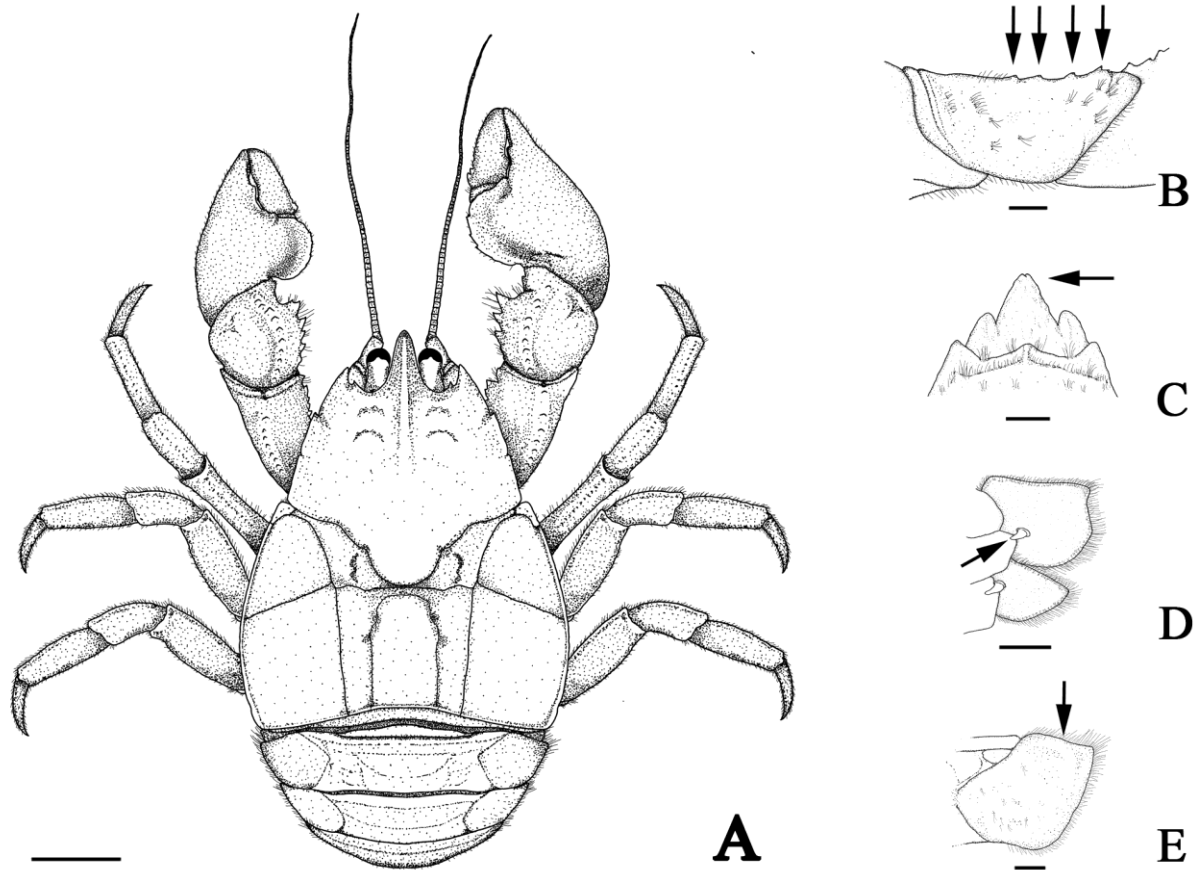
9 Rostrum triangular, narrow base, extending beyond distal apex of compound eyes, carinate
 10 along entire length. Subrostral process well developed, occupying proximal third of subrostral
 11 margin, anterior and posterior margins forming obtuse angle. Orbital and extra-orbital sinuses
 12 deep. Anterolateral spines not reaching basal margin of cornea. Protogastric lobes
 13 pronounced. Cervical groove U-shaped. Areola trapezoidal. Cardiac area trapezoidal.
 14 Epibranchial area strongly elongated. Palmar crest disciform, outer surface excavated, margin
 15 poorly serrated. Subterminal lobe of carpus well defined, pointed. Carpal ridge high on outer
 16 surface of carpus. Ventromesial border of cheliped ischium with 4 or 5 tubercles.
 17 Anteromesial region of third thoracic sternite tapered. Rudimentary pleopods in adult male
 18 specimens. Anterolateral angle of second abdominal epimeron unarmed. Anterior margin of
 19 second abdominal epimeron almost straight. Uropods wide.

20 *Description of holotype*

21 Carapace moderately convex, gastric region convex, dorsal surface scabrous, covered with
 22 punctations, anterior and posterior branchial areas expanded laterally (CW/CLE = 1.01)
 23 (Figure 2A). Rostrum triangular, narrow base (RBW/LMR = 0.91), extending beyond distal
 24 apex of compound eyes, carinate along entire length, small corneous scales on lateral margins
 25 and tip; ventral portion of rostrum much higher than dorsal in profile. Rostral carina
 26 beginning at level of protogastric lobes, with one row of corneous scales extending next to
 27 apex. Subrostral process well developed, occupying proximal third of subrostral margin, tip
 28 rounded, anterior and posterior margins forming obtuse angle (131°) (Figure 3A).

29 Eyestalk and cornea well developed. Orbital and extra-orbital sinuses deep. Orbital
 30 sinus U-shaped. Orbital spines well developed, with small terminal corneous scale.
 31 Anterolateral spines acuminate apically with small corneous scales terminally, not reaching
 32 basal margin of cornea.

33

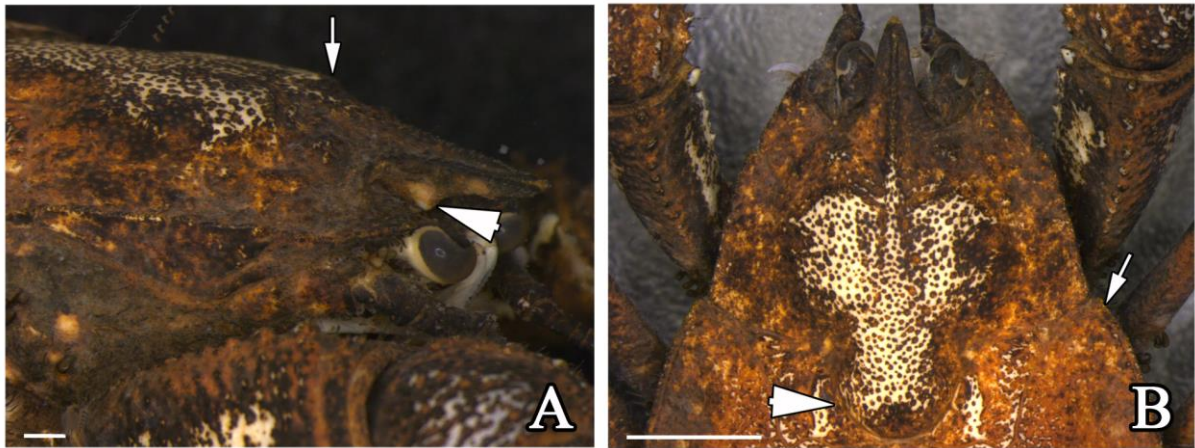


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2 **Figure 2.** *Aegla* sp. n. 1, male holotype, CLE 19.9 mm, Tigre River, São Jerônimo da Serra,
 3 Paraná, Brazil (MZUEL 513). (a) dorsal view of the cephalothorax and anterior portion of the
 4 abdomen. (b) ventral view of ischium of minor cheliped (left) showing four tubercles
 5 (arrows). (c) third thoracic sternite tapered (arrow). (d) ventral view of pleon showing
 6 rudimentary pleopods (arrow). (e) dorsal view of second abdominal epimeron (right side)
 7 showing anterior margin almost straight (arrow). Scale bars: a = 5.0 mm; b–e = 1.0 mm.

8

9



1
2 **Figure 3.** *Aegla* sp. n. 1, male holotype, CLE 19.9 mm (MZUEL 513). (a) external surface
3 view of the anterior portion of the cephalothorax showing pronounced protogastric lobes (thin
4 arrow) and well-developed subrostral process (thick arrow). (b) dorsal view of the anterior
5 region of the cephalothorax showing U-shaped cervical groove (thick arrow) and strongly
6 elongated epibranchial area (thin arrow). Scale bars: a = 1.0 mm; b = 5.0 mm.

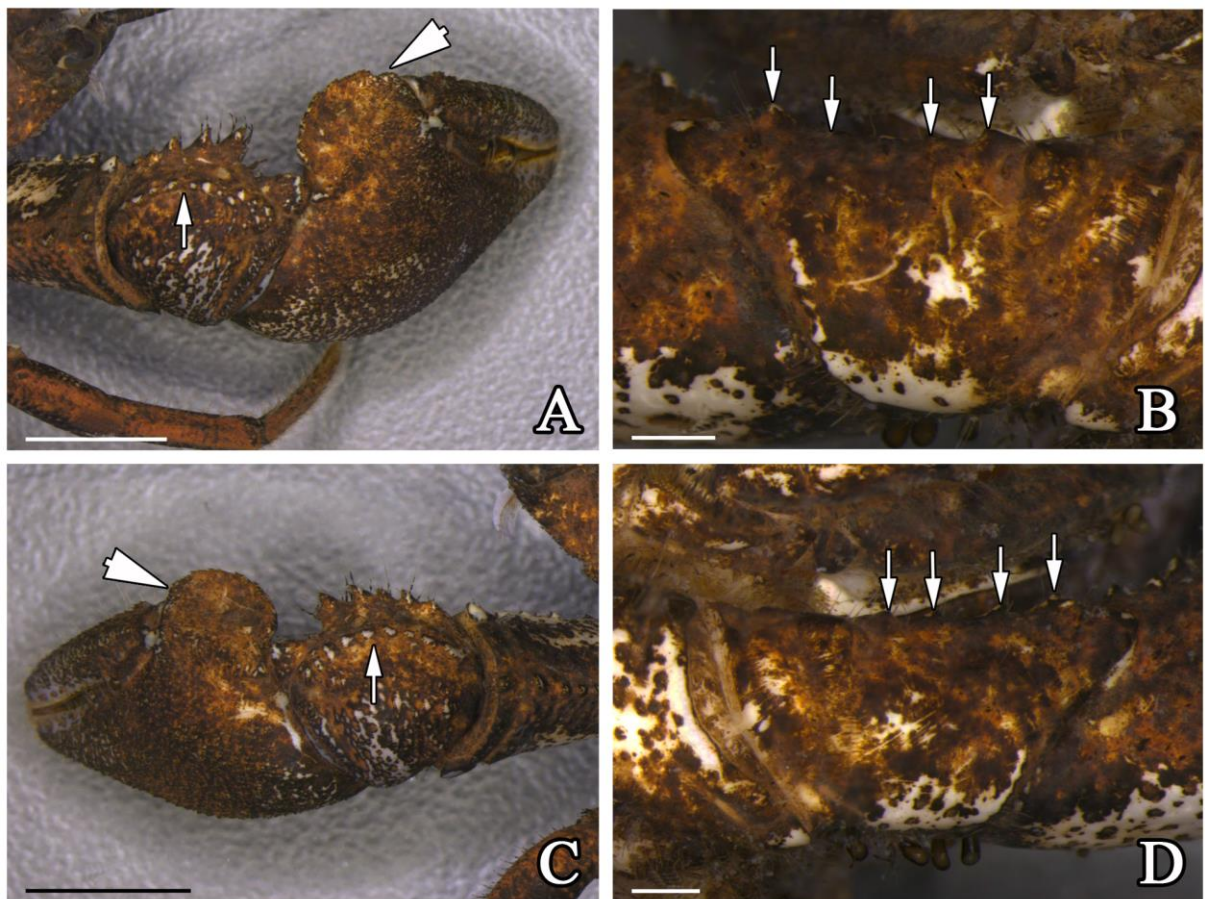
7
8 Epigastric prominences pronounced, with corneous scales. Protogastric lobes
9 pronounced, with corneous scales (Figure 3A). Gastric area elevated in relation to hepatic
10 lobes and rostrum in lateral view. Demarcation between the first and the second hepatic lobe
11 well defined, between the second and the third hepatic lobe weakly delimited. Lateral margins
12 of hepatic lobes with small corneous scales and small setae.

13 Cervical groove U-shaped (Figure 3B). Transverse dorsal linea sinuous along its
14 extension. Areola trapezoidal ($APM/AAD = 1.95$). Cardiac area trapezoidal ($TDL/PMC =$
15 1.39). Epibranchial area strongly elongated, anterolateral angle with corneous scale, lateral
16 margin with row of corneous scales and small setae (Figure 3B). Lateral margins of anterior
17 and posterior branchial areas with row of corneous scales and small setae.

18 Chelipeds unequal. Right cheliped largest (Figures 4A, B). Dactylus: dorsal margin
19 and outer surface with small corneous scales and small setae, inner surface with setal tufts and
20 scales. Proximal dorsal margin with moderate-sized lobe. Cutting margin with well-developed
21 lobular basal tooth, followed by row of corneous scales to distal end. Row of small tufts of
22 long setae next to cutting margin. Pre-dactylar lobe well developed, rounded, without
23 corneous scales. Propodus: outer surface granular, globose aspect. Palmar crest disciform with
24 outer surface excavated, margin poorly serrated, covered by corneous scales. Cutting margin
25 of fixed finger with well-developed lobular basal tooth, followed by row of corneous scales to
26 distal end. Inner and outer surfaces of fixed finger with rows of long setal tufts next to cutting

1 margin. Carpus: dorsal margin with 2 proximal tubercles, median spine, 2 distal spines, each
 2 tubercle or spine with small setae and terminal corneous scale, subterminal lobe well defined,
 3 pointed, with small corneous scales and setae. Inner surface with 3 tubercles, long setae next
 4 to dorsal margin. Outer surface with carpal ridge high, with small corneous scales. Merus:
 5 dorsolateral edge with distal tubercle, with corneous scale terminally, followed by row of
 6 tubercles decreasing in size proximally. Ventromesial edge with 2 distal spines, with corneous
 7 scale terminally, followed by 4 tubercles of similar size, with corneous scale. Ventrolateral
 8 border with distal tubercle, with terminal corneous scale, followed by several small tubercles
 9 proximally. Ischium: dorsolateral edge with spine, with corneous scale terminally.
 10 Ventromesial border with proximal tubercle, 2 small median tubercles and large distal
 11 tubercle, each with terminal corneous scale. Ventrolateral border smooth.

12



13

14 **Figure 4.** *Aegla* sp. n. 1, male holotype, CLE 19.9 mm (MZUEL 513). (a) dorsal view of the
 15 dactylus, propodus, and carpus of major cheliped (right) showing disciform palmar crest
 16 (thick arrow) and high carpal ridge (thin arrow). (b) ventral view of ischium of major cheliped
 17 (right) with four tubercles (arrows). (c) dorsal view of the dactylus, propodus, and carpus of
 18 minor cheliped (left) showing disciform palmar crest (thick arrow) and high carpal ridge (thin

1 arrow). (d) ventral view of ischium of minor cheliped (left) with four tubercles (arrows). Scale
2 bars: a, c = 5.0 mm; b, d = 1.0 mm.

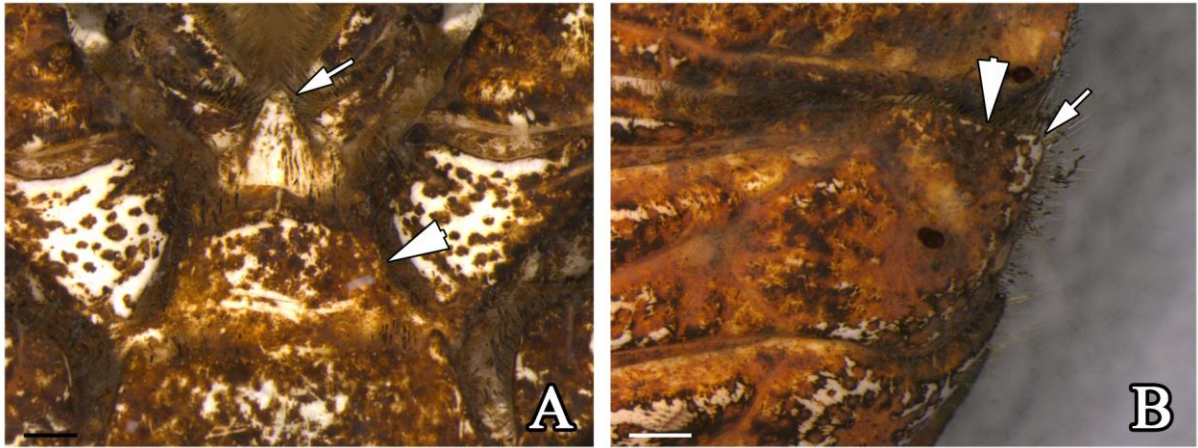
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4 Minor cheliped (left) similar to major cheliped except as noted hereafter (Figures 4C,
5 D). Dactylus: cutting margin with rudimentary lobular basal tooth. Propodus: cutting margin
6 with rudimentary lobular basal tooth. Carpus: dorsal margin with proximal tubercle, 3 median
7 spines, distal spine, double-tipped, each tubercle or spine with terminal corneous scale. Inner
8 surface with 5 tubercles, corneous scale terminally. Merus: ventromesial edge with distal
9 tubercle, double-tipped, followed by 5 tubercles, each with terminal corneous scale. Ischium
10 (Figure 2B): ventromesial border with 4 tubercles, each with terminal corneous scale, distal
11 tubercle double-tipped.

12 Second, third and fourth pereopods similar. Dactyli, propodi, carpi, meri and ischii
13 with several rows of setal tufts and small scales on surface. Carpi and meri with row of small
14 tubercles with terminal corneous scale along dorsal margin. Meri with row of small tubercles
15 with terminal corneous scale along ventral margin. Meri and ischii with long setae
16 concentrated along dorsal margin.

17 Anteromesial region of third thoracic sternite tapered, projecting between coxae of
18 third maxillipeds, with 2 terminal small corneous scales and scattered setae (Figure 2C).
19 Fourth thoracic sternite with anterolateral angles produced anteriorly, with scattered setae
20 (Figure 5A). Pleopods 2–5 rudimentary (Figure 2D). Anterolateral angle of second abdominal
21 epimeron well defined, unarmed (Figure 5B). Ventral angles of third and fourth abdominal
22 epimeron well defined, fourth abdominal epimeron with corneous scales apically. Anterior
23 margin of second abdominal epimeron almost straight (Figures 2E, 5B). Uropods well
24 developed, wide ($WU/HWT = 1.06$). Telson divided by longitudinal suture. Anterolateral and
25 posterolateral margins well differentiated.

26



1
2 **Figure 5.** *Aegla* sp. n. 1, male holotype, CLE 19.9 mm (MZUEL 513). (a) third (thin arrow)
3 and fourth (thick arrow) thoracic sternites. (b) dorsal view of second abdominal epimeron
4 (right side) showing almost straight anterior margin (thick arrow) and unarmed anterolateral
5 angle (thin arrow). Scale bars = 1.0 mm.

6
7 ***Variations***

8 The epigastric prominences may be poorly pronounced in some paratypes. The areola can be
9 trapezoidal (n = 9), rectangular (n = 3) or subrectangular (n = 2). The cardiac area varies from
10 trapezoidal (n = 11) to subrectangular (n = 3). The proximal lobe on the dorsal margin of the
11 dactylus of the major and minor chela may be less developed than in the holotype. The palmar
12 crest is rectangular instead of disciform in female paratypes. The ventromesial border of
13 ischium may present 5 tubercles instead of 4 as in the holotype. In some specimens, the
14 ventral angle of the fourth abdominal epimeron is devoid of corneous scales. The uropods are
15 narrow in a few specimens (n = 4). All measurements are summarized in Table 1.

16 ***Distribution***

17 The new species has been collected at two watercourses within the Tibagi River sub-basin and
18 the Paranapanema River basin. These watercourses are located in the city of São Jerônimo da
19 Serra, Paraná state, Brazil.

20 ***Conservation status***

21 The threatened category ‘Endangered’ (EN) is herein suggested for *Aegla* sp. n. 1 under
22 criteria B1, B2ab(iii) as defined by the IUCN (2019). *Aegla* sp. n. 1 has been recorded from
23 two localities only (B2a), the known extent of occurrence is estimated to be less than 100 km²
24 (B1), and these sites of occurrence are in agricultural and urbanized areas (B2b(iii)).

1 **Table 1.** Measurements (mm) and morphometric relationships of the type material of the new *Aegla* species. The measurements of the paratypes
 2 are shown as mean (standard deviation). AAD, areolar anterior demarcation; AH, areolar height; APM, areolar posterior margin; CL, carapace
 3 length including rostrum; CLE, carapace length excluding rostrum; CW, carapace width; HWT, half the maximum width of telson; LMR, lateral
 4 margin of rostrum; PCW, pre-cervical width; PMC, mesial region of the posterior margin of the cephalothorax; RBW, rostral base width; TDL,
 5 transversal dorsal linea length; WU, width of uropod.

	<i>Aegla</i> sp. n. 1		<i>Aegla</i> sp. n. 2		<i>Aegla</i> sp. n. 3	
	Holotype	Paratypes (n = 14)	Holotype	Paratypes (n = 13)	Holotype	Paratypes (n = 12)
CL	23.5	19.50(3.29)	19.6	18.25(3.82)	23.1	18.86(2.63)
CLE	19.9	16.50(2.80)	16.2	15.22(3.16)	19.3	15.77(2.12)
CW	20.0	16.97(2.95)	15.7	15.04(3.22)	20.0	16.03(2.18)
PCW	14.1	12.09(1.89)	11.8	11.15(2.13)	14.3	11.54(1.59)
RBW	3.9	3.09(0.43)	3.1	3.10(0.54)	4.1	3.24(0.44)
LMR	4.3	3.37(0.50)	3.9	3.45(0.75)	4.4	3.59(0.57)
APM	3.9	3.11(0.52)	3.0	2.97(0.53)	3.6	3.03(0.37)
AAD	2.0	1.79(0.26)	1.9	1.90(0.41)	1.8	1.56(0.27)
AH	6.9	5.72(1.11)	5.4	5.14(1.13)	7.0	5.48(0.77)
TDL	7.9	6.56(0.97)	6.4	6.15(1.10)	7.3	6.13(0.84)
PMC	5.7	4.74(0.77)	4.6	4.67(0.84)	5.9	4.57(0.56)
WU	3.6	3.05(0.51)	2.8	2.81(0.60)	3.6	2.98(0.35)
HWT	3.4	3.09(0.49)	2.7	2.75(0.52)	3.4	2.84(0.45)
CW/CLE	1.01	1.03(0.02)	0.97	0.99(0.03)	1.04	1.02(0.03)
PCW/CW	0.71	0.71(0.02)	0.75	0.74(0.02)	0.72	0.72(0.02)
RBW/LMR	0.91	0.92(0.05)	0.79	0.91(0.06)	0.93	0.91(0.06)
APM/AAD	1.95	1.75(0.19)	1.58	1.58(0.18)	2.00	1.96(0.20)
AH/[(APM+AAD)/2]	—	2.34(0.14)	2.20	2.12(0.19)	—	2.44(0.30)
TDL/PMC	1.39	1.39(0.07)	1.39	1.32(0.06)	1.24	1.35(0.14)
WU/HWT	1.06	0.99(0.06)	1.04	1.02(0.06)	1.06	1.06(0.10)

1 **Remarks**

2 The disciform palmar crest of *Aegla* sp. n. 1 is shared with *A. odebrechtii*, *A. castro*, *A.*
 3 *strinatii*, *A. schmitti*, *A. lata*, *A. jarai*, *Aegla jaragua* Moraes, Tavares and Bueno, 2016 and *A.*
 4 *jacutinga*. Notwithstanding, the new species can be differentiated from its congeners in
 5 having: subrostral process well developed (undeveloped in *A. strinatii*); orbital and extra-
 6 orbital sinuses deep (shallow in *A. odebrechtii*); protogastric lobes pronounced (poorly
 7 pronounced in *A. odebrechtii*, *A. lata*, *A. jarai* and *A. jaragua*); subterminal lobe of carpus
 8 well defined, pointed (poorly defined in *A. strinatii*); outer surface of carpus with carpal ridge
 9 high (low in *A. jacutinga*); dorsal margin of carpus and merus of second pereopods with
 10 small tubercles with terminal corneous scale (with distal spine followed by tubercles
 11 decreasing in size proximally in *A. jarai*); ventral margin of merus of second pereopods with
 12 small tubercles with terminal corneous scale (one or two small spines in *A. castro* and *A.*
 13 *schmitti*); uropods wide (narrow in *A. lata* and *A. jaragua*).

14 *Aegla* sp. n. 1 can be further differentiated from these species by the: cardiac area
 15 trapezoidal (subrectangular in *Aegla* sp. n. 2 and *Aegla* sp. n. 3); epibranchial area strongly
 16 elongated (shortened in *Aegla* sp. n. 2, slightly elongated in *A. jaragua* and *Aegla* sp. n. 3);
 17 proximal dorsal margin of dactylus with moderate-sized lobe (without lobe in *A. strinatii*,
 18 rudimentary in *Aegla* sp. n. 2, rudimentary or absent lobe in *A. jacutinga* and *Aegla* sp. n. 3,
 19 pronounced and surmounted by tubercles in *A. castro* and *A. schmitti*); anterolateral angle of
 20 second abdominal epimeron unarmed (with spine in *A. castro* and *A. schmitti*); anterior
 21 margin of second abdominal epimeron almost straight (concave in *A. castro* and *A. schmitti*
 22 and slightly concave in *A. jacutinga*).

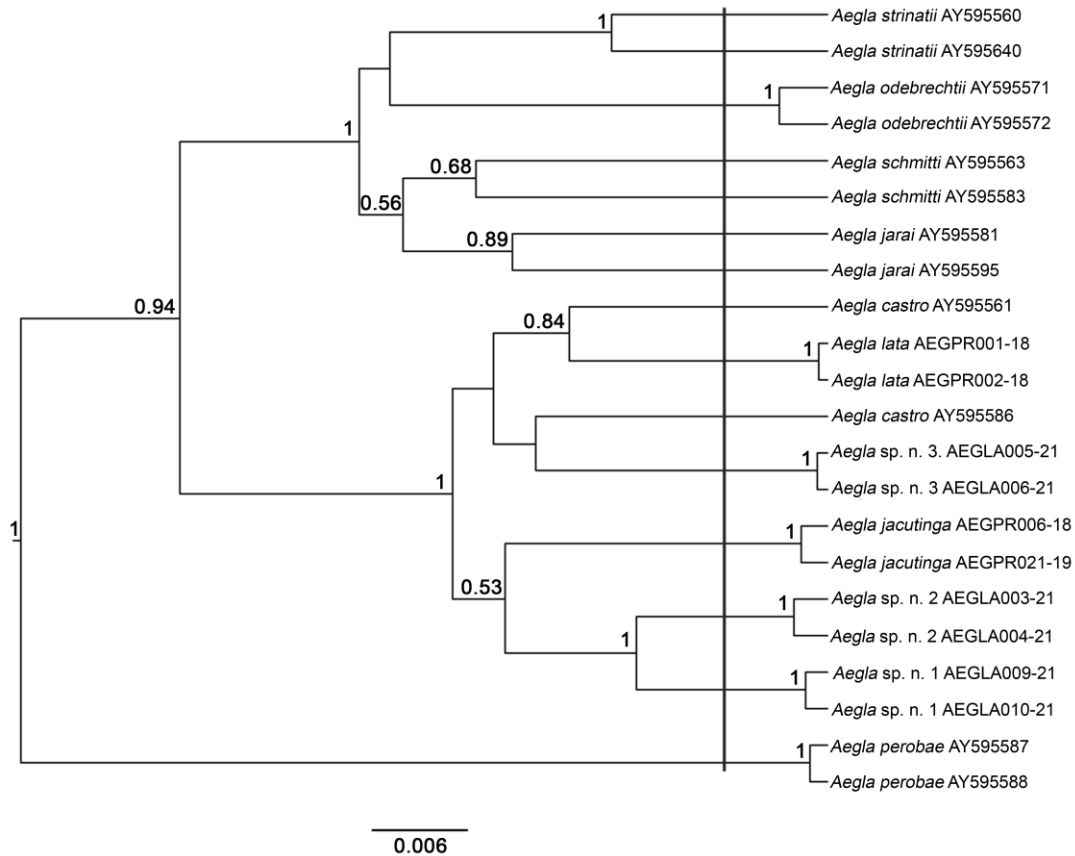
23 Another unusual character of *Aegla* sp. n. 1 is the presence of rudimentary pleopods in
 24 adult male specimens. Until now, this morphological trait has been described only for *A.*
 25 *perobae* (see Moraes and Bueno 2015) and partially developed pleopods 2-5 have been
 26 observed in adult males of *Aegla charon* Bueno and Moraes, 2017 (Bueno *et al.* 2017). *Aegla*
 27 sp. n. 1, however, differs from these species in having: subrostral process occupying proximal
 28 third of subrostral margin (on proximal half of subrostral margin in *A. charon*); protogastric
 29 lobes pronounced (rudimentary in *A. charon*); areola trapezoidal (rectangular in *A. perobae*);
 30 proximal dorsal margin of dactylus with moderate-sized lobe (without lobe in *A. perobae*);
 31 palmar crest disciform (rectangular in *A. charon* and subrectangular in *A. perobae*); outer
 32 surface of carpus with carpal ridge high (low in *A. perobae*); anteromesial region of third
 33 thoracic sternite tapered (abrupt in *A. charon*).

34 The genetic distance between *Aegla* sp. n. 1 and its congeners ranged from 1.2% to

1 5.8% (Table 2). *Aegla* sp. n. 2 showed the lowest divergence relative to *Aegla* sp. n. 1. As
 2 shown in Figure 6, most of the analyzed sequences grouped in a clade with high nodal
 3 support. This clade is composed of two major subclades, both maximally supported. The new
 4 species clustered in one of these subclades, along with *A. castro*, *A. lata* and *A. jacutinga*.
 5 Furthermore, our Bayesian tree suggests *Aegla* sp. n. 2 is the sister species to *Aegla* sp. n. 1.
 6

7 **Table 2.** Interspecific and intraspecific genetic distances based on mitochondrial gene
 8 cytochrome c oxidase I (COI). Values are shown as percentages. Intraspecific distances are in
 9 bold.

Species	1	2	3	4	5	6	7	8	9	10	11
1. <i>Aegla odebrechtii</i>	0.3										
2. <i>Aegla castro</i>	4.4	1.9									
3. <i>Aegla strinatii</i>	4.1	5.5	2.7								
4. <i>Aegla perobae</i>	6.3	6.5	7.3	0.1							
5. <i>Aegla schmitti</i>	2.9	4.2	3.9	6.4	2.7						
6. <i>Aegla lata</i>	6.0	3.0	6.9	7.4	5.3	0.0					
7. <i>Aegla jarai</i>	3.3	4.4	4.5	6.9	3.1	5.3	3.4				
8. <i>Aegla jacutinga</i>	4.2	1.8	5.5	5.9	3.7	3.2	4.1	0.1			
9. <i>Aegla</i> sp. n. 1	4.0	2.2	5.2	5.8	4.0	3.4	4.0	1.8	0.2		
10. <i>Aegla</i> sp. n. 2	4.4	2.2	5.6	6.3	4.3	3.6	4.1	1.7	1.2	0.2	
11. <i>Aegla</i> sp. n. 3	4.7	2.3	5.7	6.5	4.1	3.5	4.5	2.0	2.6	2.2	0.0



1

2 **Figure 6.** Bayesian tree (HKY+I+G) for *Aegla* species based on partial sequences of the COI
 3 gene. The numbers above the branches represent the posterior probability (values < 0.5 are
 4 not indicated), and the vertical line indicates the species delimitation assigned in the GMYC
 5 analysis.

6

7

Aegla sp. n. 2 Marçal and Teixeira

8

(Figures 7–10)

9

urn:lsid:zoobank.org:act:8DC448C9-6106-447A-90E0-9B143E120783

10 ***Holotype***

11 Male [CLE 16.2 mm], Brazil, Paraná, Ortigueira, Paranapanema River basin, Tibagi River
 12 sub-basin, Formiga River, 24°11'11.77"S, 50°56'28.60"W, altitude 725 m, G.M. Teixeira, I.C.
 13 Marçal and R.S. Vieira coll., 10 March 2020 (MZUEL 515).

14 ***Paratypes***

15 5 males [CLE 12.8–24.4 mm] and 8 females [CLE 12.5–18.2 mm], same data as holotype
 16 (MZUEL 499).

17 ***Additional material examined***

1 4 males [size not recorded] and 6 females [size not recorded], same data as holotype (MZUEL
 2 504, genetic vouchers: Bold Systems access AEGLA003-21, AEGLA004-21). 1 male [CLE
 3 16.7 mm], Brazil, Paraná, Ortigueira, Paranapanema River basin, Tibagi River sub-basin,
 4 tributary of the Formiga River, 24°10'56.50"S, 50°56'31.50"W, altitude 726 m, O.A. Shibatta
 5 coll., August 2014 (MZUEL 388). 1 male [CLE 20.1 mm] and 6 females [CLE 13.6–19.4
 6 mm], Brazil, Paraná, Ortigueira, Paranapanema River basin, Tibagi River sub-basin, Piquira
 7 River, coordinates and coll. unknown, 02 February 2001 (MZUEL 440). 1 male [CLE 20.1
 8 mm] and 1 female [CLE 19.2 mm], same locality, coordinates and coll. unknown, 25 April
 9 2002 (MZUEL 441).

10 *Diagnosis*

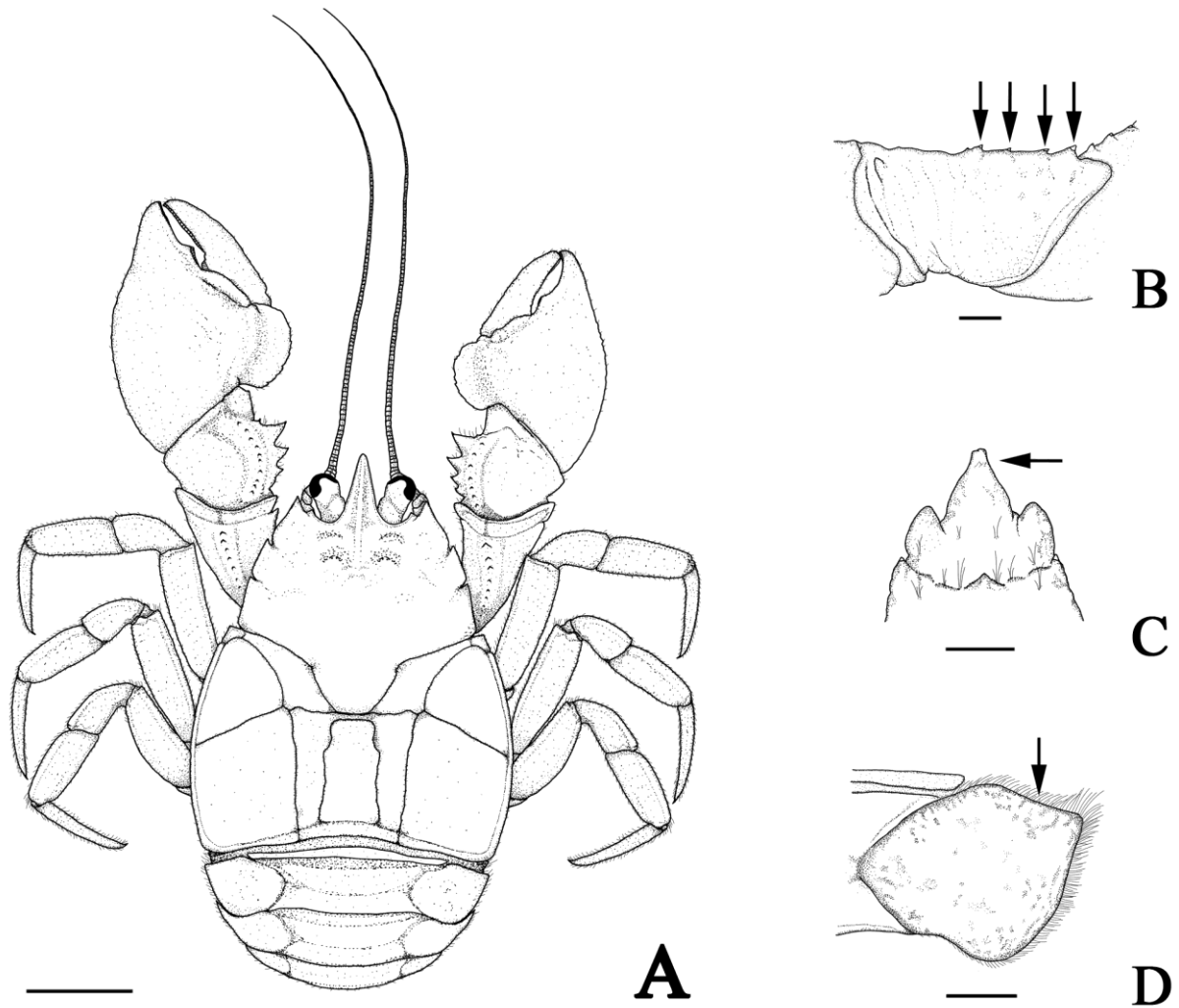
11 Rostrum triangular, narrow base, extending beyond distal apex of compound eyes, carinate
 12 along entire length. Subrostral process well developed, occupying proximal half of subrostral
 13 margin, anterior and posterior margins forming acute angle. Orbital and extra-orbital sinuses
 14 deep. Anterolateral spines reaching basal margin of cornea. Epigastric prominences
 15 pronounced. Protogastric lobes pronounced. Cervical groove trapezoidal. Areola
 16 subrectangular. Epibranchial area shortened. Lobe on proximal dorsal margin of dactylus
 17 rudimentary. Carpal ridge high on outer surface of carpus. Ventromesial border of cheliped
 18 ischium with 4 or 5 tubercles. Anteromesial region of third thoracic sternite abrupt. Anterior
 19 margin of second abdominal epimeron almost straight. Uropods wide.

20 *Description of holotype*

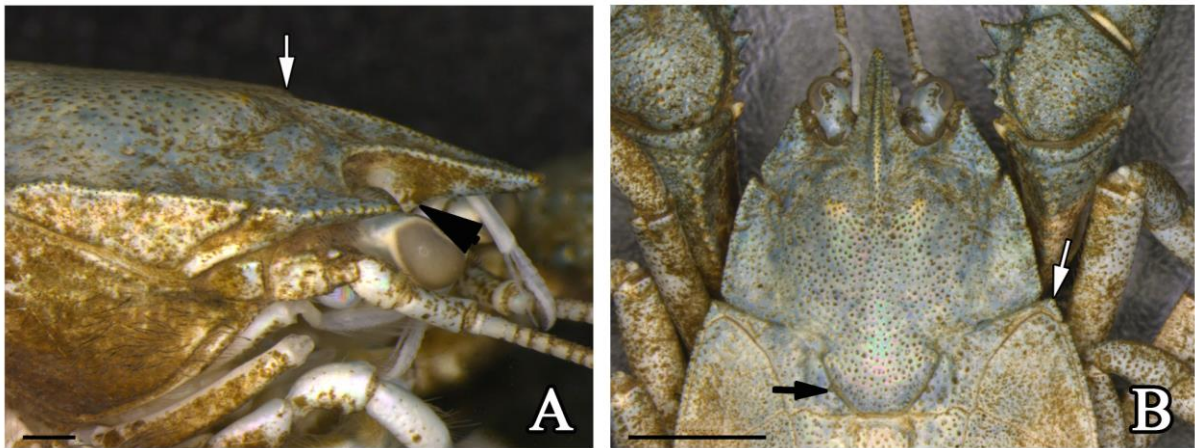
21 Carapace moderately convex, gastric region convex, dorsal surface scabrous, covered with
 22 punctations (Figure 7A). Rostrum triangular, narrow base ($RBW/LMR = 0.79$), extending
 23 beyond distal apex of compound eyes, carinate along entire length, small corneous scales on
 24 lateral margins and tip; ventral portion of rostrum much higher than dorsal in profile. Rostral
 25 carina beginning at level of protogastric lobes, with 2 rows of corneous scales extending next
 26 to apex. Subrostral process well developed, occupying proximal half of subrostral margin,
 27 triangular, tip rounded, anterior and posterior margins forming acute angle (88°) (Figure 8A).

28 Eyestalk and cornea well developed. Orbital and extra-orbital sinuses deep. Orbital
 29 sinus U-shaped. Orbital spines well developed, with small terminal corneous scale.
 30 Anterolateral spines acuminate apically with small corneous scales terminally, reaching basal
 31 margin of cornea.

32



1
 2 **Figure 7.** *Aegla* sp. n. 2, male holotype, CLE 16.2 mm, Formiga River, Ortigueira, Paraná,
 3 Brazil (MZUEL 515). (a) dorsal view of the cephalothorax and anterior portion of the
 4 abdomen. (b) ventral view of ischium of major cheliped (left) showing four tubercles
 5 (arrows). (c) third thoracic sternite abrupt (arrow). (d) dorsal view of second abdominal
 6 epimeron (right side) showing anterior margin almost straight (arrow). Scale bars: a = 5.0
 7 mm; b–d = 1.0 mm.
 8



1
2 **Figure 8.** *Aegla* sp. n. 2, male holotype, CLE 16.2 mm (MZUEL 515). (a) external surface
3 view of the anterior portion of the cephalothorax showing pronounced protogastric lobes
4 (white arrow) and well-developed subrostral process (black arrow). (b) dorsal view of the
5 anterior region of the cephalothorax showing trapezoidal cervical groove (black arrow) and
6 shortened epibranchial area (white arrow). Scale bars: a = 1.0 mm; b = 5.0 mm.

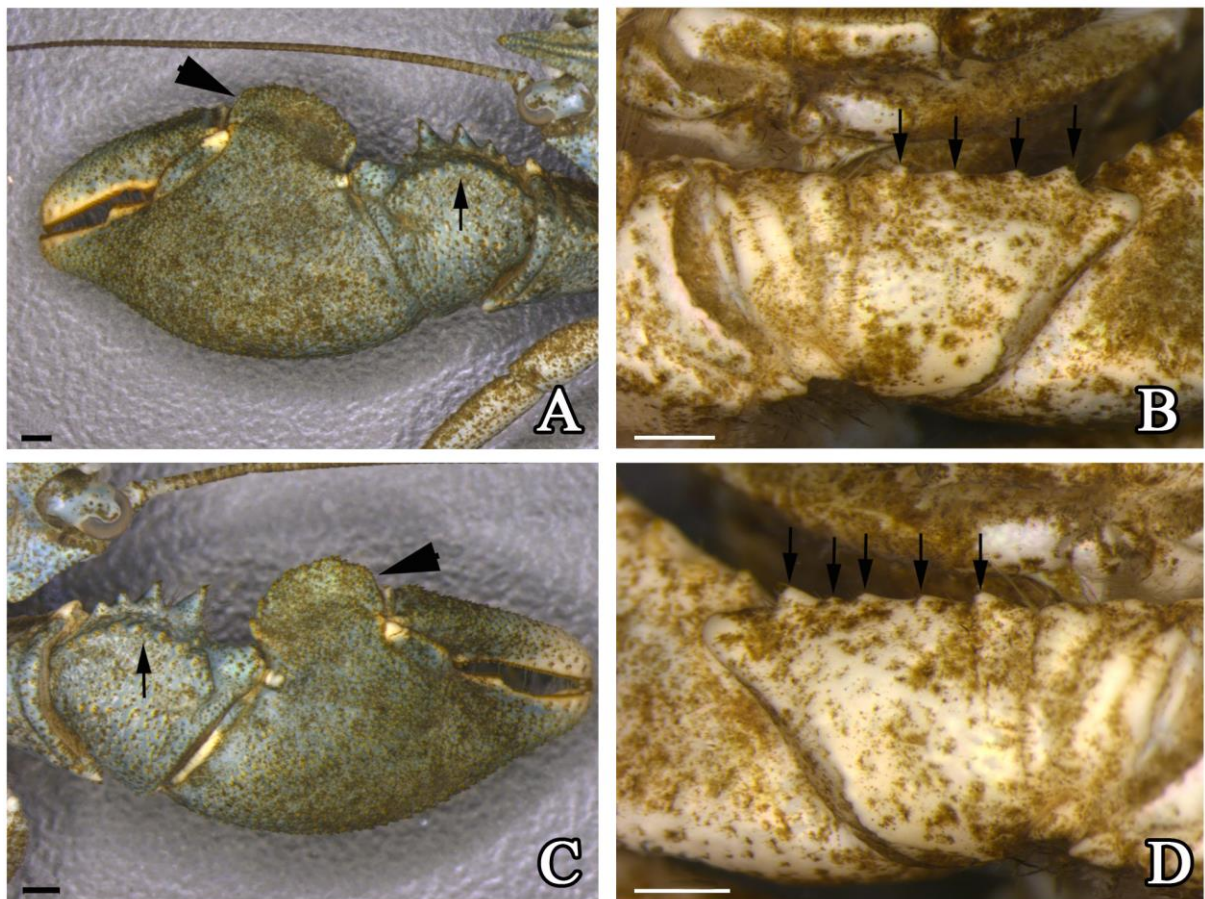
7
8 Epigastric prominences pronounced, with corneous scales. Protogastric lobes
9 pronounced, with corneous scales (Figure 8A). Gastric area elevated in relation to hepatic
10 lobes and rostrum in lateral view. Demarcation between the first and the second hepatic lobes
11 well defined, between the second and the third hepatic lobes weakly delimited. Lateral
12 margins of hepatic lobes with small corneous scales and small setae.

13 Cervical groove trapezoidal (Figure 8B). Transverse dorsal linea sinuous along its
14 extension. Areola subrectangular ($AH/[(APM+AAD)/2] = 2.20$). Cardiac area trapezoidal
15 ($TDL/PMC = 1.39$). Epibranchial area shortened, triangular, anterolateral angle with corneous
16 scale, lateral margin with row of corneous scales and small setae (Figure 8B). Lateral margins
17 of anterior and posterior branchial areas with row of corneous scales and small setae.

18 Chelipeds unequal. Left cheliped largest (Figures 9A, B). Dactylus: dorsal margin and
19 outer surface with small corneous scales, inner surface with setal tufts and scales. Proximal
20 dorsal margin with rudimentary lobe. Cutting margin with well-developed lobular basal tooth,
21 followed by row of corneous scales to distal end. Row of small tufts of long setae next to
22 cutting margin. Pre-dactylar lobe well developed, rounded, without corneous scales.
23 Propodus: outer surface granular, globose aspect. Palmar crest subdisciform with outer
24 surface excavated, margin poorly serrated, covered by acuminate corneous scales. Cutting
25 margin of fixed finger with well-developed lobular basal tooth, followed by row of corneous
26 scales to distal end. Inner and outer surfaces of fixed finger with rows of long setal tufts next

1 to cutting margin. Carpus: dorsal margin with 2 proximal tubercles, median spine, distal spine
 2 longest, each tubercle or spine with small setae and terminal corneous scale, subterminal lobe
 3 well defined, pointed, with small corneous scales and setae. Inner surface with large tubercle,
 4 long setae next to dorsal margin. Outer surface with carpal ridge high, with small corneous
 5 scales. Merus: dorsolateral edge with distal tubercle, with corneous scale terminally, followed
 6 by row of tubercles decreasing in size proximally. Ventromesial edge with distal spine, with
 7 corneous scale terminally, followed by 4 tubercles of similar size, with corneous scale.
 8 Ventrolateral border with distal tubercle, with terminal corneous scale, followed by row of
 9 small tubercles. Ischium (Figure 7B): dorsolateral edge with spine, with corneous scale
 10 terminally. Ventromesial border with proximal tubercle, 2 median tubercles and large distal
 11 tubercle, each with terminal corneous scale. Ventrolateral border smooth.

12



13

14 **Figure 9.** *Aegla* sp. n. 2, male holotype, CLE 16.2 mm (MZUEL 515). (a) dorsal view of the
 15 dactylus, propodus, and carpus of major cheliped (left) showing subdisciform palmar crest
 16 (thick arrow) and high carpal ridge (thin arrow). (b) ventral view of ischium of major cheliped
 17 (left) with four tubercles (arrows). (c) dorsal view of the dactylus, propodus, and carpus of
 18 minor cheliped (right) showing subdisciform palmar crest (thick arrow) and high carpal ridge

1 (thin arrow). (d) ventral view of ischium of minor cheliped (right) with five tubercles
 2 (arrows). Scale bars = 1.0 mm.

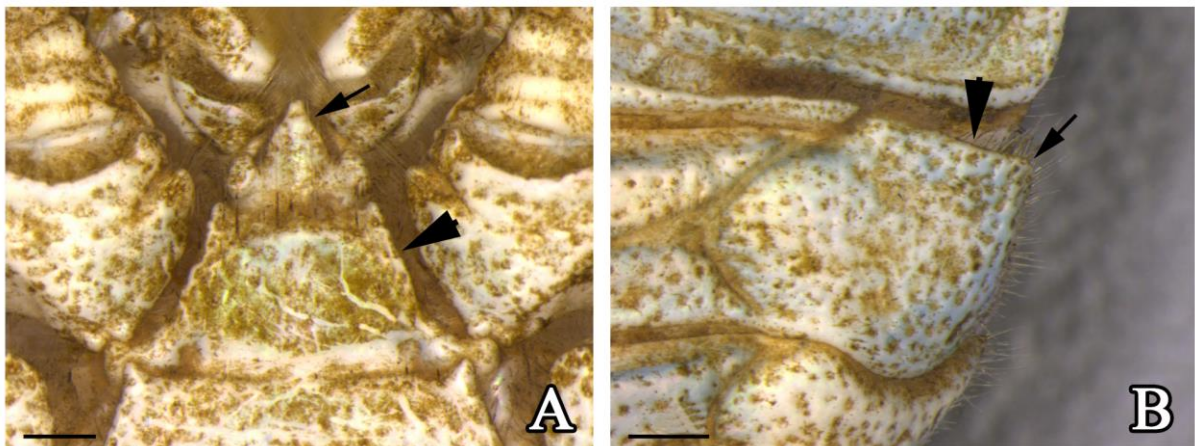
3

4 Minor cheliped (right) similar to major cheliped except as noted hereafter (Figures 9C,
 5 D). Dactylus: cutting margin with rudimentary lobular basal tooth. Propodus: cutting margin
 6 with rudimentary lobular basal tooth. Ischium: ventromesial border with proximal tubercle, 3
 7 small median tubercles and large distal tubercle, each with terminal corneous scale.

8 Second, third and fourth pereopods similar. Dactyli, propodi, carpi, meri and ischii
 9 with several rows of setal tufts and small scales on surface. Carpi and meri with row of small
 10 tubercles with terminal corneous scale along dorsal margin. Meri with row of small tubercles
 11 with terminal corneous scale along ventral margin. Meri and ischii with long setae
 12 concentrated along dorsal margin.

13 Anteromesial region of third thoracic sternite abrupt, projecting between coxae of third
 14 maxillipeds, with scattered setae (Figure 7C). Fourth thoracic sternite with anterolateral
 15 angles produced anteriorly, with scattered setae (Figure 10A). Pleopods 2–5 absent.
 16 Anterolateral angle of second abdominal epimeron well defined, unarmed (Figure 10B).
 17 Ventral angle of third abdominal epimeron well defined with small corneous scales apically.
 18 Ventral angle of fourth abdominal epimeron well defined, unarmed. Anterior margin of
 19 second abdominal epimeron almost straight (Figures 7D, 10B). Uropods well developed, wide
 20 ($WU/HWT = 1.04$). Telson divided by longitudinal suture. Anterolateral and posterolateral
 21 margins well differentiated.

22



23

24 **Figure 10.** *Aegla* sp. n. 2, male holotype, CLE 16.2 mm (MZUEL 515). (a) third (thin arrow)
 25 and fourth (thick arrow) thoracic sternites. (b) dorsal view of second abdominal epimeron
 26 (right side) showing almost straight anterior margin (thick arrow) and unarmed anterolateral

1 angle (thin arrow). Scale bars = 1.0 mm.

2

3 **Variations**

4 The areola can be subrectangular (n = 10), trapezoidal (n = 2) or rectangular (n = 1). The
5 cardiac area varies from subrectangular (n = 9) to trapezoidal (n = 4). The palmar crest may
6 appear rectangular instead of subdisciform. The anteromesial region of third thoracic sternite
7 can be abrupt (n = 8) or tapered (n = 5). The anterolateral angle of second abdominal
8 epimeron may present apical corneous scales instead of being naked as in the holotype. In
9 most specimens, the ventral angle of the third abdominal epimeron is devoid of corneous
10 scales. The uropods are narrow in a few specimens (n = 2). All measurements are summarized
11 in Table 1.

12 **Distribution**

13 The new species has been collected in three watercourses within the Tibagi River sub-basin,
14 Paranapanema River basin. These watercourses are located in the city of Ortigueira, Paraná
15 state, Brazil.

16 **Conservation status**

17 We suggest that *Aegla* sp. n. 2 be assigned as 'Vulnerable' (VU) under criteria B1, B2ab(iii)
18 as defined by the IUCN (2019). This species has been recorded in three localities (B2a) and
19 the known extent of occurrence is estimated to be less than 500 km² (B1). The streams where
20 the specimens of *Aegla* sp. n. 2 were found are in agricultural and urbanized areas (B2b(iii)).

21 **Remarks**

22 *Aegla* sp. n. 2 can be separated from its congeners, mainly by, among other characters,
23 subrostral process well developed (undeveloped in *A. strinatii*), occupying proximal half of
24 subrostral margin (on proximal third of subrostral margin in *A. lata*, *A. jacutinga*, *Aegla* sp. n.
25 3 and *Aegla* sp. n. 1, and occupying median portion of subrostral margin in *A. jaragua*);
26 anterior and posterior margins of subrostral process forming acute angle (right angle in *A. lata*
27 and *A. jacutinga*, and obtuse angle in *A. jaragua*, *Aegla* sp. n. 3 and *Aegla* sp. n. 1); orbital
28 and extra-orbital sinuses deep (shallow in *A. odebrechtii*); epigastric prominences pronounced
29 (poorly pronounced in *A. lata* and *A. jacutinga*); protogastric lobes pronounced (poorly
30 pronounced in *A. odebrechtii*, *A. lata*, *A. jarai* and *A. jaragua*); cervical groove trapezoidal
31 (U-shaped in *A. lata* and *Aegla* sp. n. 1); subterminal lobe of carpus well defined, pointed
32 (poorly defined in *A. strinatii*); outer surface of carpus with carpal ridge high (low in *A.*

1 *jacutinga*); dorsal margin of carpus and merus of second pereopods with small tubercles with
 2 terminal corneous scale (with distal spine followed by tubercles decreasing in size proximally
 3 in *A. jarai*); ventral margin of merus of second pereopods with small tubercles with terminal
 4 corneous scale (one or two small spines in *A. castro* and *A. schmitti*); anteromesial region of
 5 third thoracic sternite abrupt (tapered or truncate in *A. lata*, truncate in *A. jaragua*, and tapered
 6 in *A. jacutinga*, *Aegla* sp. n. 3 and *Aegla* sp. n. 1); anterior margin of second abdominal
 7 epimeron almost straight (concave in *A. castro* and *A. schmitti* and slightly concave in *A.*
 8 *jacutinga*); uropods wide (narrow in *A. lata* and *A. jaragua*).

9 Our Bayesian tree based on the COI mitochondrial gene (Figure 6) recovered *Aegla*
 10 sp. n. 2 as the sister species to *Aegla* sp. n. 1, and both clustered in the same subclade as *A.*
 11 *jacutinga*. The interspecific genetic distances (Table 2) reinforce the relationships evidenced
 12 in the Bayesian analysis.

13
 14 ***Aegla* sp. n. 3** Marçal and Teixeira

15 (Figures 11–14)

16 urn:lsid:zoobank.org:act:5751F246-51C1-4BC3-BBD5-CE21CB09CEC5

17 ***Holotype***

18 Male [CLE 19.3 mm], Brazil, Paraná, Telêmaco Borba, Paranapanema River basin, Tibagi
 19 River sub-basin, Codorna Branca stream, 24°15'06.70"S, 50°31'46.58"W, altitude 792 m,
 20 G.M. Teixeira, I.C. Marçal and P.F. da Silva coll., 11 March 2020 (MZUEL 511).

21 ***Paratypes***

22 5 males [CLE 13.4–20.9 mm] and 5 females [CLE 14.1–16.0 mm], same data as holotype
 23 (MZUEL 500). 1 male [CLE 17.0 mm] and 1 female [CLE 16.9 mm], same locality, J.F.M. da
 24 Silva, E.S. da Silva and S.T. Bennemann coll., 07 August 2014 (MZUEL 470).

25 ***Additional material examined***

26 7 males [size not recorded] and 3 females [size not recorded], same data as holotype (MZUEL
 27 505, genetic vouchers: Bold Systems access AEGLA005-21, AEGLA006-21). 1 male [CLE
 28 13.3 mm], Brazil, Paraná, Telêmaco Borba, Paranapanema River basin, Tibagi River sub-
 29 basin, Varanal stream, 24°19'59.70"S, 50°33'37.20"W, altitude 761 m, S.T. Bennemann coll.,
 30 19 May 2005 (MZUEL 183). 3 males [CLE 12.7–16.8 mm], same locality and coll., March
 31 2004 (MZUEL 349). 1 male [CLE 20.5 mm], same locality and coll., 24°20'12.70"S,
 32 50°32'03.20"W, altitude 802 m, 11 February 2005 (MZUEL 332). 1 male [CLE 16.4 mm],

1 same locality and coll., 24°20'13.40"S, 50°35'23.10"W, altitude 687 m, 9 November 2005
2 (MZUEL 344). 1 female [CLE 17.0 mm], Brazil, Paraná, Telêmaco Borba, Paranapanema
3 River basin, Tibagi River sub-basin, Harmonia stream, coordinates and coll. unknown, 20
4 June 2006 (MZUEL 414). 4 females [CLE 12.5–15.8 mm], same locality, coordinates and
5 coll. unknown, 16 March 2012 (MZUEL 415). 1 male [CLE 15.2 mm] and 1 female [CLE
6 15.4 mm], Brazil, Paraná, Telêmaco Borba, Paranapanema River basin, Tibagi River sub-
7 basin, Moinho Velho stream, 24°13'18.34"S, 50°37'42.42"W, altitude 739 m, S.T.
8 Bennemann coll., 7 August 2014 (MZUEL 426). 1 male [CLE 25.3 mm], same locality,
9 J.F.M. da Silva coll., 3 November 2014 (MZUEL 427). 2 females [CLE 14.4–15.0 mm],
10 Brazil, Paraná, Telêmaco Borba, Paranapanema River basin, Tibagi River sub-basin, Colônia
11 stream, 24°10'27.79"S, 50°37'28.45"W, altitude 736 m, S.T. Bennemann coll., 7 August 2014
12 (MZUEL 437).

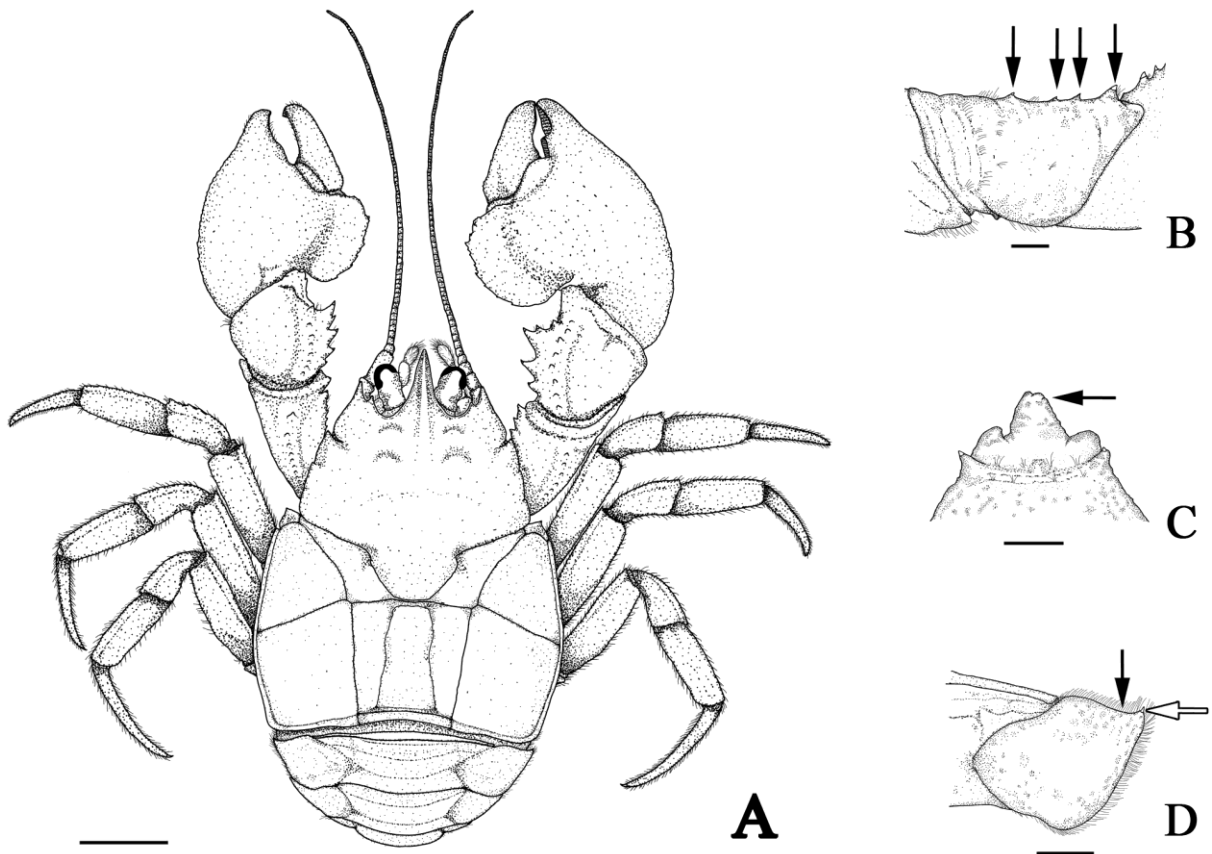
13 *Diagnosis*

14 Rostrum triangular, narrow base, extending beyond distal apex of compound eyes, carinate
15 along entire length. Subrostral process well developed, occupying proximal third of subrostral
16 margin, anterior and posterior margins forming obtuse angle. Orbital and extra-orbital sinuses
17 deep. Anterolateral spines reaching basal margin of cornea. Epigastric prominences
18 pronounced. Protogastric lobes pronounced. Areola trapezoidal. Cardiac area subrectangular.
19 Epibranchial area slightly elongated. Lobe on proximal dorsal margin of dactylus rudimentary
20 or absent. Carpal ridge high on outer surface of carpus. Ventromesial border of cheliped
21 ischium with 4 or 5 tubercles. Ventral angles of third and fourth abdominal epimeron with
22 corneous scales apically. Uropods wide.

23 *Description of holotype*

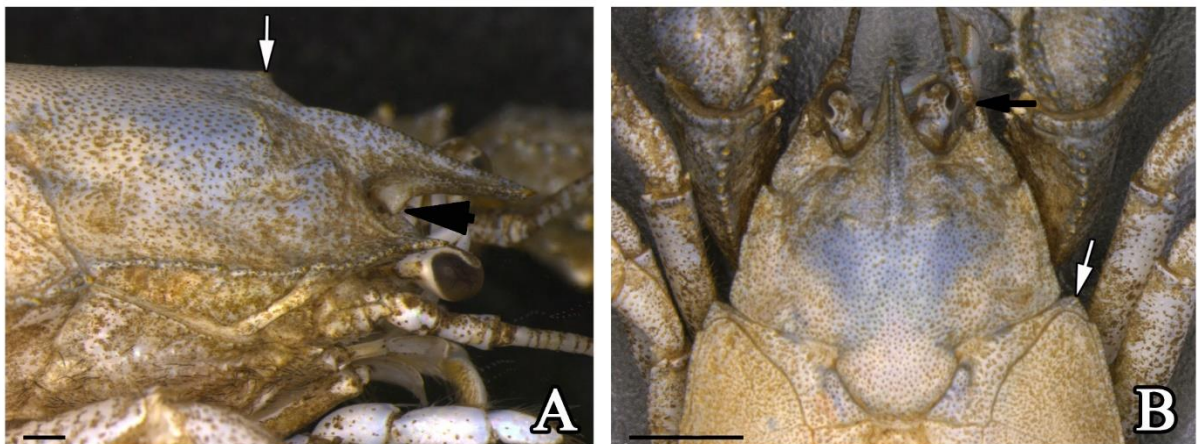
24 Carapace moderately convex, gastric region convex, dorsal surface scabrous, covered with
25 punctations (Figure 11A). Rostrum triangular, narrow base (RBW/LMR = 0.93), extending
26 beyond distal apex of compound eyes, carinate along entire length, small corneous scales on
27 lateral margins and tip; ventral portion of rostrum slightly higher than dorsal in profile.
28 Rostral carina beginning at level of protogastric lobes, with 2 rows of corneous scales
29 extending next to apex. Subrostral process well developed, occupying proximal third of
30 subrostral margin, produced ventrally, triangular, tip rounded, anterior and posterior margins
31 forming obtuse angle (95°) (Figure 12A).

32



1
2 **Figure 11.** *Aegla* sp. n. 3, male holotype, CLE 19.3 mm, Codorna Branca stream, Telêmaco
3 Borba, Paraná, Brazil (MZUEL 511). (a) dorsal view of the cephalothorax and anterior
4 portion of the abdomen. (b) ventral view of ischium of minor cheliped (left) showing four
5 tubercles (arrow). (c) third thoracic sternite truncate (arrow). (d) dorsal view of second
6 abdominal epimeron (right side) showing anterolateral angle with corneous scale (white
7 arrow) and anterior margin slightly concave (black arrow). Scale bars: a = 5.0 mm. b–d = 1.0
8 mm.

9



10

11 **Figure 12.** *Aegla* sp. n. 3, male holotype, CLE 19.3 mm (MZUEL 511). (a) external surface

1 view of the anterior portion of the cephalothorax showing pronounced protogastric lobes
2 (white arrow) and well-developed subrostral process (black arrow). (b) dorsal view of the
3 anterior region of the cephalothorax showing anterolateral spine reaching basal margin of the
4 cornea (black arrow) and slightly elongated epibranchial area (white arrow). Scale bars: a =
5 1.0 mm; b = 5.0 mm.

6

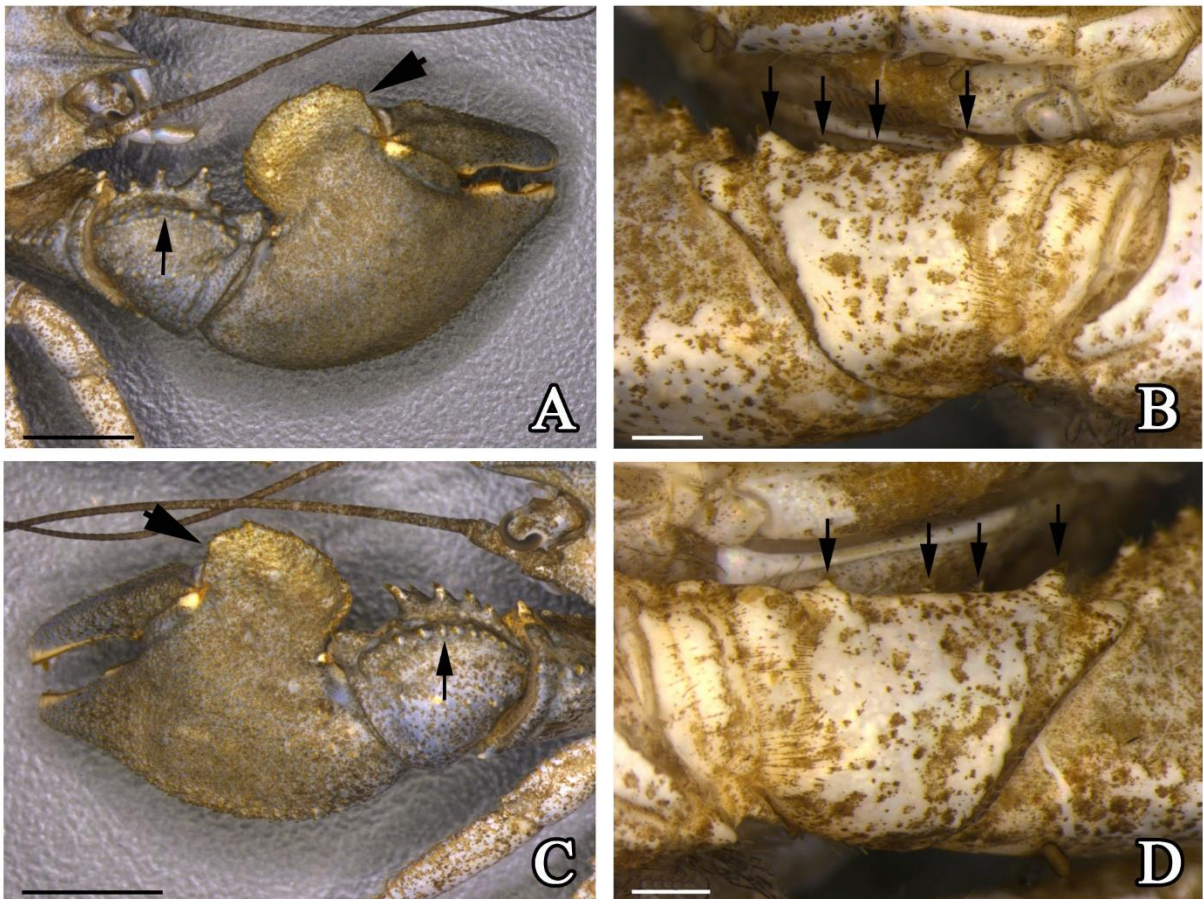
7 Eyestalk and cornea well developed. Orbital and extra-orbital sinuses deep. Orbital
8 sinus U-shaped. Orbital spines well developed, with small terminal corneous scale.
9 Anterolateral spines acuminate apically with small corneous scales terminally, reaching basal
10 margin of cornea (Figure 12B).

11 Epigastric prominences pronounced, with corneous scales. Protogastric lobes
12 pronounced, with corneous scales (Figure 12A). Gastric area elevated in relation to hepatic
13 lobes and rostrum in lateral view. Demarcation between hepatic lobes well defined. Lateral
14 margins of hepatic lobes with small corneous scales and small setae.

15 Cervical groove trapezoidal. Transverse dorsal linea sinuous along its extension.
16 Areola trapezoidal ($APM/AAD = 2.00$). Cardiac area subrectangular ($TDL/PMC = 1.24$).
17 Epibranchial area slightly elongated, triangular, anterolateral angle with corneous scale,
18 lateral margin with row of corneous scales and small setae (Figure 12B). Lateral margins of
19 anterior and posterior branchial areas with row of corneous scales and small setae.

20 Chelipeds unequal. Right cheliped largest (Figures 13A, B). Dactylus: dorsal margin
21 and outer surface with small corneous scales, inner surface with setal tufts and scales.
22 Proximal dorsal margin with rudimentary lobe. Cutting margin with well-developed lobular
23 basal tooth, followed by row of corneous scales to distal end. Row of small tufts of long setae
24 next to cutting margin. Pre-dactylar lobe well developed, rounded, without corneous scales.
25 Propodus: outer surface granular, globose aspect. Palmar crest disciform with outer surface
26 excavated, margin poorly serrated, covered by acuminate corneous scales. Cutting margin of
27 fixed finger with well-developed lobular basal tooth, followed by row of corneous scales to
28 distal end. Inner and outer surfaces of fixed finger with rows of long setal tufts next to cutting
29 margin. Carpus: dorsal margin with 2 proximal tubercles, median spine, distal spine longest,
30 double-tipped, each tubercle or spine with terminal corneous scale, subterminal lobe well
31 defined, pointed, with small corneous scales and setae. Inner surface with spine, long setae
32 next to dorsal margin. Outer surface with carpal ridge high, with small corneous scales.
33 Merus: dorsolateral edge with distal tubercle, with corneous scale terminally, followed by row
34 of tubercles decreasing in size proximally. Ventromesial edge with distal spine, with corneous

1 scale terminally, followed by 4 tubercles of similar size, with corneous scale. Ventrolateral
 2 border with distal tubercle, with terminal corneous scale, followed by row of tubercles
 3 decreasing in size proximally. Ischium: dorsolateral edge with spine, with corneous scale
 4 terminally. Ventromesial border with proximal tubercle, 2 small median tubercles and large
 5 distal tubercle, each with terminal corneous scale. Ventrolateral border smooth.
 6



7
 8 **Figure 13.** *Aegla* sp. n. 3, male holotype, CLE 19.3 mm (MZUEL 511). (a) dorsal view of the
 9 dactylus, propodus, and carpus of major cheliped (right) showing disciform palmar crest
 10 (thick arrow) and high carpal ridge (thin arrow). (b) ventral view of ischium of major cheliped
 11 (right) with four tubercles (arrows). (c) dorsal view of the dactylus, propodus, and carpus of
 12 minor cheliped (left) showing disciform palmar crest (thick arrow) and high carpal ridge (thin
 13 arrow). (d) ventral view of ischium of minor cheliped (left) with four tubercles (arrows). Scale
 14 bars: a, c = 5.0 mm; b, d = 1.0 mm.

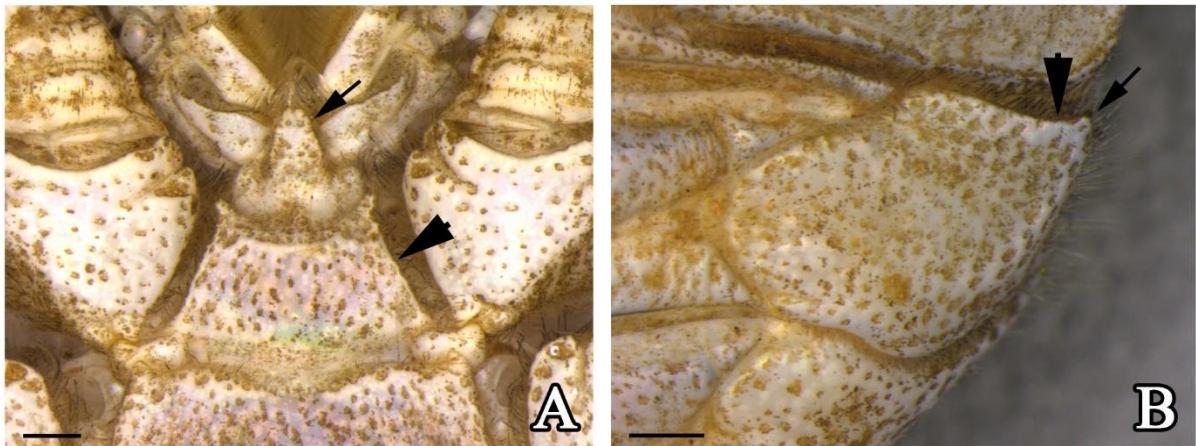
15

16 Minor cheliped (left) similar to major cheliped except as noted hereafter (Figures 11B,
 17 13C, D). Dactylus: proximal lobe on dorsal margin absent. Cutting margin with rudimentary
 18 lobular basal tooth. Propodus: cutting margin with rudimentary lobular basal tooth. Carpus:

1 dorsal margin with 2 proximal tubercles, median tubercle, distal spine longest, double-tipped,
 2 each tubercle or spine with small setae and terminal corneous scale. Inner surface with 2
 3 tubercles, largest tubercle with double-tipped, corneous scale terminally. Merus: ventromesial
 4 edge with 2 distal tubercles, followed by 4 tubercles, each with terminal corneous scale.

5 Second, third and fourth pereopods similar. Dactyli, propodi, carpi, meri and ischii
 6 with several rows of setal tufts and small scales on surface. Carpi and meri with row of small
 7 tubercles with terminal corneous scale along dorsal margin. Meri with row of small corneous
 8 scales along ventral margin. Meri and ischii with long setae concentrated along dorsal margin.

9 Anteromesial region of third thoracic sternite truncate, projecting between coxae of
 10 third maxillipeds, with 2 terminal small corneous scales and scattered setae (Figure 11C).
 11 Fourth thoracic sternite with anterolateral angles produced anteriorly, with scattered setae
 12 (Figure 14A). Pleopods 2–5 absent. Anterolateral angle of second abdominal epimeron and
 13 ventral angles of third and fourth abdominal epimeron well defined, with corneous scales
 14 apically. Anterior margin of second abdominal epimeron slightly concave (Figures 11D,
 15 14B). Uropods well developed, wide ($WU/HWT = 1.06$). Telson divided by longitudinal
 16 suture. Anterolateral and posterolateral margins well differentiated.



18
 19 **Figure 14.** *Aegla* sp. n. 3, male holotype, CLE 19.3 mm (MZUEL 511). (a) third (thin arrow)
 20 and fourth (thick arrow) thoracic sternites. (b) dorsal view of second abdominal epimeron
 21 (right side) showing slightly concave anterior margin (thick arrow) and anterolateral angle
 22 with corneous scales (thin arrow). Scale bars = 1.0 mm.

24 *Variations*

25 The areola can be trapezoidal ($n = 10$), rectangular ($n = 1$) or subrectangular ($n = 1$). The
 26 cardiac area varies from subrectangular ($n = 7$) to trapezoidal ($n = 5$). The palmar crest may

1 appear rectangular instead of disciform. The ventromesial border of ischium may present 5
 2 tubercles instead of 4 as in the holotype. In all paratypes, the third thoracic sternite is tapered
 3 instead of being truncate. The anterolateral angle of second abdominal epimeron is devoid of
 4 corneous scales in most specimens. Also, the anterior margin of second abdominal epimeron
 5 may be almost straight. The uropods are narrow in a few specimens (n = 3). All measurements
 6 are summarized in Table 1.

7 ***Geographical distribution***

8 The new species has been collected in five streams within the Tibagi River sub-basin,
 9 Paranapanema River basin. These streams are located in the city of Telêmaco Borba, Paraná
 10 state, Brazil.

11 ***Conservation status***

12 The conservation status of *Aegla* sp. n. 3 may, for the moment, be assessed as ‘Vulnerable’
 13 (VU) under criteria B1, B2ab(iii) as defined by the IUCN (2019). Since the known extent of
 14 occurrence is estimated to be less than 500 km², the record of occurrence is limited to ≤ 5
 15 locations, and the decline in quality of habitat is observed because of the agricultural matrix.

16 ***Remarks***

17 *Aegla* sp. n. 3 can be distinguished from its congeners because it has: rostrum carinate along
 18 entire length (without carina in the distal third in *A. odebrechtii*); subrostral process well
 19 developed (undeveloped in *A. strinatii*); orbital and extra-orbital sinuses deep (shallow in *A.*
 20 *odebrechtii*); anterolateral spines reaching basal margin of cornea (not reaching basal margin
 21 of cornea in *A. strinatii*, *A. jaragua*, *A. jacutinga* and *Aegla* sp. n. 1, and extending beyond
 22 basal margin of cornea in *A. odebrechtii*, *A. castro*, *A. schmitti* and *A. jarai*); epigastric
 23 prominences pronounced (poorly pronounced in *A. lata* and *A. jacutinga*); protogastric lobes
 24 pronounced (poorly pronounced in *A. odebrechtii*, *A. lata*, *A. jarai* and *A. jaragua*); areola
 25 trapezoidal (rectangular in *A. lata*, and subrectangular in *A. jaragua*, *A. jacutinga* and *Aegla*
 26 sp. n. 2); subterminal lobe of carpus well defined, pointed (poorly defined in *A. strinatii*);
 27 outer surface of carpus with carpal ridge high (low in *A. jacutinga*); dorsal margin of carpus
 28 and merus of second pereopods with small tubercles with terminal corneous scale (with distal
 29 spine followed by tubercles decreasing in size proximally in *A. jarai*); ventral margin of
 30 merus of second pereopods with small tubercles with terminal corneous scale (one or two
 31 small spines in *A. castro* and *A. schmitti*); ventral angles of third and fourth abdominal
 32 epimeron with corneous scales apically (unarmed in *Aegla* sp. n. 2); uropods wide (narrow in

1 *A. lata* and *A. jaragua*).

2 Based on the Bayesian tree (Figure 6), *Aegla* sp. n. 3 is the sister of *A. castro* and
3 *Aegla* sp. n. 3 + *A. castro* is the sister group of *A. lata* + *A. castro*.

4

5 DISCUSSION

6 In general, the aeglids are very similar to each other (Schmitt 1942). Notwithstanding, the
7 detailed analysis of the morphology allowed us to identify several morphological characters
8 that differentiate the new species from their congeners. Some structures, such as the rostrum
9 or the palmar crest, are more easily recognized and have been used as diagnostic characters
10 for many decades (Schmitt 1942; Jara 1977; Jara 1982; Bond-Buckup and Buckup 1994;
11 Santos *et al.* 2015; Jara *et al.* 2018; Páez *et al.* 2018; Trombetta *et al.* 2019; Marçal *et al.*
12 2020). Other structures, such as the epibranchial area, are more subtle and have been used to
13 compare species in more recent studies (Moraes *et al.* 2016; Moraes *et al.* 2017).

14 Considering all the species that occur in the Tibagi River basin, *Aegla* sp. n. 1 is
15 unique in having the following combination of characters: anterolateral spines not reaching
16 basal margin of the cornea, cervical groove U-shaped, cardiac area trapezoidal, epibranchial
17 area strongly elongated and rudimentary pleopods in adult male specimens. By the same
18 token, *Aegla* sp. n. 2 can be distinguished from its congeners by the following combination of
19 characters: subrostral process occupying proximal half of the subrostral margin, anterior and
20 posterior margins of subrostral process forming an acute angle, cervical groove trapezoidal,
21 epibranchial area shortened and anteromesial region of third thoracic sternite abrupt. *Aegla* sp.
22 n. 3 can be separated from its congeners by a unique combination of characters that includes
23 the subrostral process occupying the proximal third of the subrostral margin, the anterolateral
24 spines reaching the basal margin of the cornea, the cardiac area subrectangular, the
25 epibranchial area slightly elongated and the ventral angles of third and fourth abdominal
26 epimeron with corneous scales apically.

27 The diagnostic morphological characters listed here are clear in indicating that *Aegla*
28 sp. n. 1, *Aegla* sp. n. 2, and *Aegla* sp. n. 3 are new species. In addition, the maximum
29 nucleotide divergence values obtained in intraspecific comparisons do not overlap with the
30 lowest values found in interspecific comparisons (Table 2), clearly indicating an interval
31 between them. According to Meyer and Paulay (2005), if there is an interval between
32 intraspecific and interspecific distance, a cut value for species delimitation can be established
33 in the data. Similar values were observed for other species of *Aegla* (Jara *et al.* 2003; Páez *et*

1 *al.* 2018; Marçal *et al.* 2020). However, *A. castro*, *A. strinatii*, *A. schmitti* and *A. jarai*
2 exhibited intraspecific values that overlap with interspecific values. The GMYC analysis
3 indicated that these species correspond to non-monophyletic groups, as observed by Pérez-
4 Losada *et al.* (2004), Páez *et al.* (2018), Trombetta *et al.* (2019), and Marçal *et al.* (2020).
5 Molecular data also indicate a probable phylogenetic relationship among the species,
6 suggesting the new species belong to the same subclade as *A. castro*, *A. lata* and *A. jacutinga*
7 (see Figure 6). This subclade is strongly supported, and all these species have been recorded
8 in the Tibagi River basin. Furthermore, *A. castro*, *A. lata* and *A. jacutinga* are grouped in
9 clade C of the aeglid phylogeny as proposed by Pérez-Losada *et al.* (2004) (see Marçal *et al.*
10 2020). Thus, we can assume that the new species also belong to clade C, which includes
11 species from the Paraná River. However, to corroborate the phylogenetic relationships of the
12 new species, it is recommended to include more genes in the analysis, both mitochondrial and
13 nuclear genes.

14 The three new species of *Aegla* described here, all occurring in watercourses in the
15 Tibagi River basin, Paraná state, southern Brazil, expand the diversity of aeglids in this
16 hydrographic basin from four to seven species. Furthermore, our results raise the number of
17 known *Aegla* species to 93. Nevertheless, the new species have limited distributions and occur
18 in habitats impacted by urbanization or agriculture. The rivers of the Paraná state have been
19 degraded because of the intense deforestation in this region (Santos *et al.* 2015). According to
20 IAT (2020), approximately 60% of the state's area is used as pasture and agricultural
21 plantations. Despite the efforts of various groups of researchers, we believe that our
22 knowledge about the diversity, biology and ecology of *Aegla* species in this region is still
23 scarce. There is a vast field of work to be explored in future studies. Given these points, the
24 current study emphasizes the importance of the Tibagi River basin for the conservation of
25 aeglids and reinforces the high potential for finding new species in the Paraná state.

26

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2 No potential conflict of interest was reported by the authors.

3

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1 **3. CAPÍTULO 2**

2 **DIVERSITY AND GEOGRAPHICAL DISTRIBUTION OF AEGLIDS CRABS**
3 **(CRUSTACEA, ANOMURA, AEGLIDAE) FROM TIBAGI RIVER BASIN, PARANÁ**
4 **STATE, BRAZIL**

5

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1 ABSTRACT

2 This study updates the geographical distribution of the *Aegla* species from the Tibagi River
3 basin, Paraná state, Brazil. We analyzed specimens deposited at the Crustacean Collection of
4 the Museu de Zoologia of Universidade Estadual de Londrina (MZUEL). The taxonomic
5 determination was done following the identification keys and descriptions. New records of
6 occurrence were obtained for *Aegla castro* (10), *A. lata* (5), and *A. jacutinga* (10). The
7 collections also allowed us to identify two new species. Here *Aegla* n. sp. 4 and *Aegla* n. sp. 5
8 are described and differentiated from their congeners based on morphological and molecular
9 evidence (COI mitochondrial DNA). The conservation status of the new species is discussed
10 and a diagnostic key to all currently recognized species of *Aegla* from the Tibagi River basin
11 is provided. Our results reveal that most studied species have a restricted distribution and
12 occur in streams impacted by urbanization, industry, and agriculture. Of the nine species that
13 occur in the Tibagi River basin, seven are endemic to this basin. Given these points, this
14 hydrographic basin has a great diversity of aeglids and, therefore, needs to be protected.

15 ADDITIONAL KEYWORDS: *Aegla*, description, new records, Paraná River basin,
16 taxonomy

17

1 INTRODUCTION

2 Aeglidae is the only family that constitutes the superfamily Aegloidea (McLaughlin *et al.*,
3 2010). Of the 95 species that compound the Aeglidae family, 93 are species and subspecies of
4 the genus *Aegla* Leach, 1820 (Moraes *et al.*, 2017; Jara *et al.*, 2018; Páez *et al.*, 2018;
5 Trombetta *et al.*, 2019; Marçal *et al.*, 2020, 2021; Marçal *et al.*, in press) and two are fossils.
6 *Haumuriaegla glaessneri* Feldmann, 1984 was discovered in marine rocks in New Zealand
7 (Feldmann, 1984) while *Protaegla minuscula* Feldmann, Veja, Applegate & Bishop, 1998
8 was found in marine rocks in Mexico (Feldmann *et al.*, 1998). On the other hand, the
9 representatives of the genus *Aegla* are exclusively from continental waters of southern South
10 America, occurring in the hydrographic basins of Brazil, Chile, Argentina, Uruguay,
11 Paraguay, and Bolivia (Bond-Buckup & Buckup, 1994; Bond-Buckup & Buckup, 1999;
12 Bond-Buckup, 2003).

13 The fossil records (Feldmann, 1984; Feldmann *et al.*, 1998) suggest that the origin of
14 Aeglidae occurred in a marine environment and, later there was a dispersion towards the
15 freshwater environment. Different works debate about the direction of the dispersion of these
16 crustaceans in the freshwater habitats of southern South America. Some researchers
17 postulated that this dispersion occurred from the Atlantic Ocean (Schmitt, 1942; Ringuelet,
18 1948; Morrone & Loppreto, 1994). However, studies on distribution patterns (Ortmann,
19 1902), fossil evidence (Feldmann, 1984; Feldmann *et al.*, 1998), biogeography and molecular
20 systematics of *Aegla* (Pérez-Losada *et al.*, 2004) give greater support to the hypothesis that
21 this dispersion occurred from the Pacific Ocean.

22 Phylogenetic analysis of *Aegla* suggests that the colonization of southern South
23 America began at least 60 Mya (Pérez-Losada *et al.*, 2004). This analysis clustered *Aegla*
24 species into five large groups informally named clades A, B, C, D, and E. The species that
25 occur in the Paraná River basin (including those from the Tibagi River basin) are

1 encompassed in clade C, whose origin was estimated to be 33.2 ± 1.8 Mya. Pérez-Losada *et*
2 *al.* (2004) postulated that the primary radiation of the aeglids along this drainage occurred
3 before the formation of the Paranan Sea and the final uplift of the Serra do Mar (~12 Mya).
4 Existing studies recognize that the final uplift of Serra do Mar had dramatic effects on
5 drainage patterns because it altered the course of some tributaries of rivers (Potter, 1997;
6 Pérez-Losada *et al.*, 2004). Thus, more recent taxa probably speciated after the regression of
7 the Paranan Sea (Pérez-Losada *et al.*, 2004).

8 According to the literature, the distribution area of *Aegla* is limited to the north by the
9 record of *Aegla franca* Schmitt, 1942 in the city of Claraval, state of Minas Gerais, Brazil
10 ($20^{\circ}18'47''\text{S}$, $47^{\circ}16'37''\text{W}$) and to the south by the report of *Aegla alacaluñi* Jara & López,
11 1981 on the island of Duke of York, Chile ($50^{\circ}33'31''\text{S}$, $75^{\circ}19'17''\text{W}$) (Bueno *et al.*, 2007;
12 Oyanedel *et al.*, 2011). Although some species have been reported in more than one
13 hydrographic basin (Schmitt, 1942; Bond-Buckup & Buckup, 1994; Jara & Palacios, 1999;
14 Oyanedel *et al.*, 2011), most are known to occur in tributaries of the same river or only in its
15 type locality (Buckup & Rossi, 1977; Jara, 1982; Rocha & Bueno, 2011; Santos *et al.*, 2009,
16 2010, 2012, 2013, 2014, 2015; Moraes *et al.*, 2016, 2017; Bueno *et al.*, 2017; Jara *et al.*,
17 2018; Páez *et al.*, 2018; Trombetta *et al.*, 2019; Marçal *et al.*, 2020, 2021).

18 Current geographic distribution patterns of *Aegla* have been associated with historical
19 factors, such as marine transgressions, tectonic elevations (Pérez-Losada *et al.*, 2004),
20 glaciation, and the formation of glacial refuges (Xu *et al.*, 2009; Oyanedel *et al.*, 2011).
21 Trevisan *et al.* (2009) associated the distribution of *Aegla platensis* Schmitt, 1942 and *Aegla*
22 *singularis* Ringuelet, 1948 along the Jacutinga River basin, in the state of Rio Grande do Sul
23 (Brazil), to land use and occupation. These authors suggested that the predominance of *A.*
24 *platensis* in river and pasture springs and *A. singularis* in urban and agricultural areas may be
25 related to riparian coverage, degree of margin erosion, food availability, habitat diversity,

1 competition interspecific, among others. Tumini *et al.* (2016) attested that the distribution of
2 freshwater decapods in southern South America (Argentina) is strongly influenced by local
3 environmental variables, such as altitude, water body stability, annual temperature range, pH,
4 and conductivity. Furthermore, Gonçalves *et al.* (2018) used *Aegla* species distribution
5 modeling to identify and propose priority areas for conservation within four freshwater
6 ecoregions in South America, specifically in extreme south Brazil and adjacent areas in
7 Argentina and Uruguay.

8 Of the 61 species of *Aegla* recorded in Brazil, 19 occur in the Paraná River basin,
9 seven of which are reported for the Tibagi River basin (Santos *et al.*, 2017; Páez *et al.*, 2018;
10 Trombetta *et al.*, 2019; Marçal *et al.*, 2020, 2021; Marçal *et al.*, in press). The Tibagi River
11 basin covers approximately 25,000 km² of the state of Paraná (SEMA-PR, 2010). Despite the
12 large area and importance of this basin, the aeglids of this region have only recently begun to
13 be studied more extensively (Galves *et al.* 2007; Silva *et al.*, 2017; Marçal *et al.*, 2018;
14 Chaves *et al.*, 2019; Marçal *et al.*, 2020; Almeida *et al.*, 2021; Silva *et al.*, 2021; Marçal *et al.*,
15 in press). Probably aeglids are the most threatened freshwater decapod crabs in South
16 America (Bueno *et al.*, 2016), and knowledge about the number of species and their
17 geographic ranges is crucial to assess the risk of extinction of these crab species (Boos *et al.*,
18 2012).

19 Based on our inventory and literature records of *Aegla* species (Schmitt, 1942; Bond-
20 Buckup & Buckup, 1994; Galves *et al.*, 2007; Trevisan & Masunari, 2010; Santos *et al.*,
21 2017; Marçal *et al.*, 2018; Chaves *et al.*, 2019; Marçal *et al.*, 2020; Marçal *et al.*, in press), the
22 present work aimed to update the geographical distribution of *Aegla* species from the Tibagi
23 River basin, adding new records and describing two new species. The conservation status of
24 the new species was assessed according to criteria established by the International Union for
25 Conservation of Nature (IUCN, 2019). Finally, a diagnostic key to all currently recognized

1 species of *Aegla* from this hydrographic basin is provided.

2

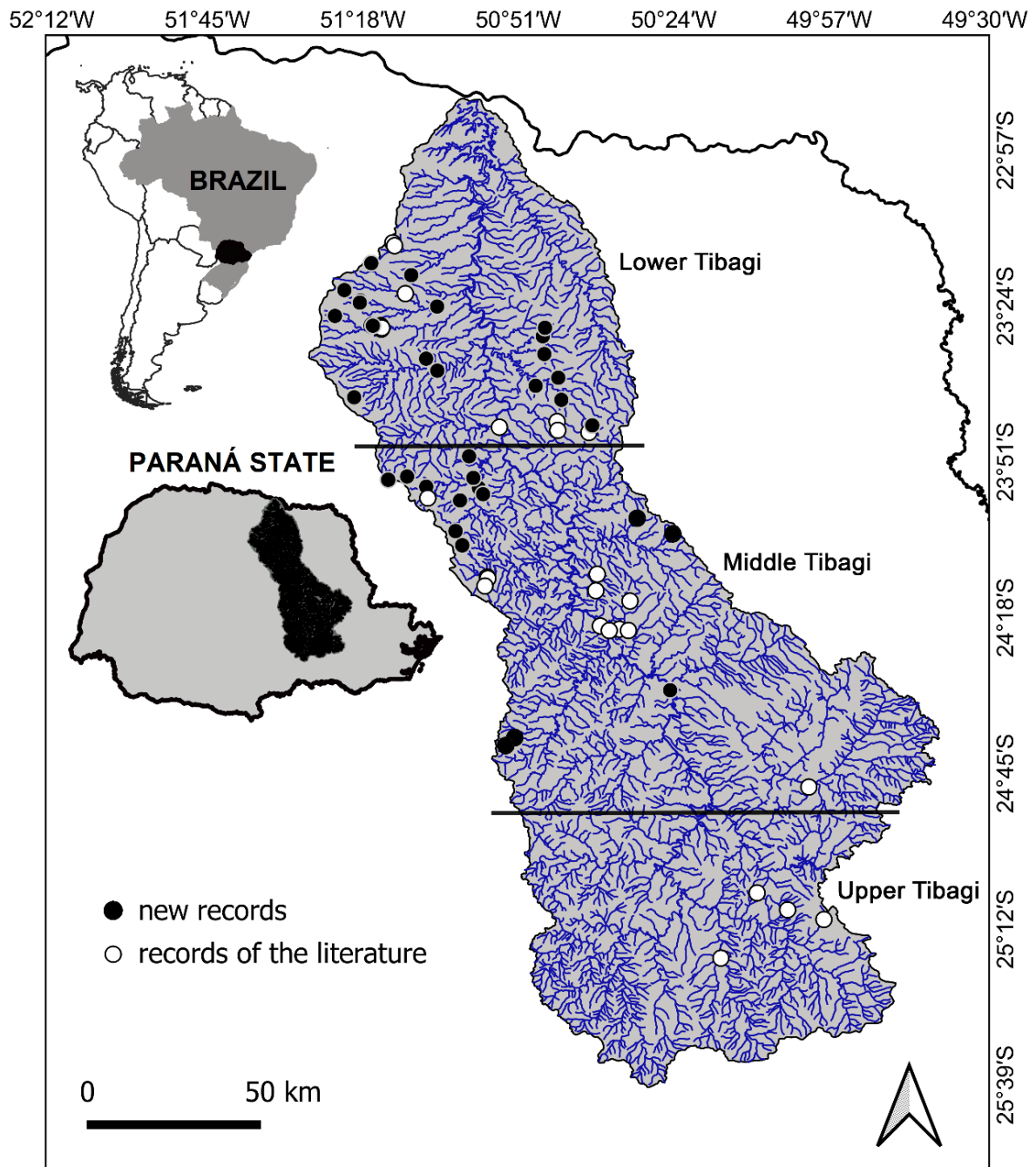
3 MATERIAL AND METHODS

4 Study Area And Data Collection

5 Tibagi River is a tributary of Paranapanema river, which in turn, drains into the Paraná River.
6 Its main tributaries on the right bank are the Iapó, São Jerônimo, and Congonhas rivers, while
7 on the left bank are the Taquara, Apertados, and Três Bocas rivers (SEMA-PR, 2010).
8 According to Mendonça & Danni-Oliveira (2002), the Tibagi River integrates the region of
9 the Paraná River basin in an area of transition between subtropical and tropical climates.
10 Surprisingly, the Tibagi River has an altitude drop of about 792 m, from its source in Serra
11 das Almas (1.100 m above sea level) until it flows into the Paranapanema River (298 m above
12 sea level) (Maack, 2002; Parolin *et al.*, 2010). Because of variations in altitude, climate, and
13 type of vegetation, the Tibagi River basin has been traditionally divided into Upper, Middle,
14 and Lower Tibagi (Anjos *et al.*, 1997; Medri *et al.*, 2002). Upper Tibagi is the southernmost
15 region of the basin (> 800 m above sea level), where there is a predominance of grassy-woody
16 steppe vegetation and the average annual temperature is lower (Anjos *et al.*, 1997; Torezan,
17 2002). The intermediate region, Middle Tibagi is constituted of the mixed ombrophilous
18 forest (or Aracauria forest) (Torezan, 2002). Finally, the Lower Tibagi, the northernmost
19 region (600–300 m above sea level), is characterized by the seasonal semideciduous forest and
20 the highest average annual temperature (Anjos *et al.*, 1997; Torezan, 2002).

21 Streams and tributary rivers of the Tibagi River (between 23°13'01.24"S,
22 51°12'58.19"W and 24°40'09.00"S, 50°53'20.80"W), central-eastern portion of Paraná state,
23 Brazil were sampled (Fig. 1). Aeglids deposited in the Crustacean Collection of the Museu de
24 Zoologia, Universidade Estadual de Londrina (MZUEL) were analyzed and identified.
25 Additional collections were made at the type localities of the new species to obtain fresh

1 material for molecular analysis. Specimens were collected by a hand net (90 cm diameter, 4
 2 mm mesh size) and fixed in 70% or absolute alcohol. Sampled specimens are deposited in the
 3 Crustacean Collection of the MZUEL.



4
 5 **Figure 1.** Map of the records of occurrence of *Aegla* in the Tibagi River basin, Paraná state,
 6 Brazil. Black circles represent the new records of occurrences, while white correspond to the
 7 records reported in the literature.

1 Morphological Analysis

2 The taxonomic determination was done following the identification keys (Bond-Buckup &
3 Buckup, 1994) and descriptions (Schmitt, 1942; Santos *et al.*, 2015; Moraes *et al.* 2016, 2017;
4 Páez *et al.*, 2018; Trombetta *et al.*, 2019; Marçal *et al.*, 2020, 2021; Marçal *et al.*, in press).
5 Sex was recognized by the presence (females) or absence (males) of pleopods and by the
6 position of the gonopore openings (coxa of the third pair of pereopods in females and of the
7 fifth pair in males) (Martin & Abele, 1988).

8 Descriptions of the new species use the standard terminology for the carapace and
9 pleon (Martin & Abele, 1988; Bond-Buckup & Buckup, 1994; Moraes *et al.*, 2016).
10 Characters of the carapace, chelipeds, thoracic sternite and epimeron were examined in detail,
11 and photographs were taken using a Leica stereomicroscope (model M205, Leica Biosystems,
12 Wetzlar, Germany). The following abbreviations are used: areolar anterior demarcation
13 (AAD), areolar height (AH), areolar posterior margin (APM), carapace length including
14 rostrum (CL), carapace length excluding rostrum (CLE), carapace width (CW), half the
15 maximum width of telson (HWT), lateral margin of rostrum (LMR), pre-cervical width
16 (PCW), mesial region of the posterior margin of the cephalothorax (PMC), rostral base width
17 (RBW), transversal dorsal linea length (TDL), width of uropod (WU). All measurements (in
18 mm) were taken using a 0.01 mm precision caliper. The morphometric ratios RBW/LMR,
19 APM/AAD, $AH/[(APM+AAD)/2]$, TDL/PMC, and WU/HWT were calculated according to
20 Moraes *et al.* (2016).

21

22 Molecular Analysis

23 DNA was extracted from muscle tissues following the protocol described by Marçal *et al.* in
24 press. Amplification of partial sequences of the COI gene was carried out by polymerase
25 chain reaction (PCR) using the primers of van Syoc (1995), following the PCR method

1 proposed by Pérez-Losada *et al.* (2002). Prior to sequencing PCR products were cleaned with
2 ExoSAP IT® (Prodimol Biotecnologia, Belo Horizonte, MG, Brazil). Purified PCR products
3 were sequenced in both directions on an ABI 3500xL automated sequencer using ABI Big
4 Dye Terminator v 3.1. Sequences were assembled into contigs using Electropherogram
5 Quality Analysis software (Togawa & Brigido, 2003). Contigs were aligned using ClustalW
6 implemented in MEGA 6.0 (Tamura *et al.*, 2013). We adjusted our dataset with the sequences
7 available in the GenBank or BOLD database for *Aegla* species that are morphologically
8 similar to the new species or occur in the Tibagi River basin. Genetic distances (intra and
9 interspecific) were calculated in MEGA 6.0 based on Kimura-2-parameter model (Kimura,
10 1980). The HKY+I model (proportion of invariant sites = 0.802) was selected by jModelTest2
11 (Darriba *et al.*, 2012) as the most adequate mutation model for the data. Bayesian analysis
12 was then conducted in BEAST 2.6.2 (Bouckaert *et al.*, 2019), sampling one tree every 1,000
13 generations per 100,000,000 generations. Posterior probabilities were calculated with a burn-
14 in of 25%. Finally, the Generalized Mixed Yule Coalescent (GMYC) model was carried out
15 in Splits package (Fujisawa & Barraclough, 2013; Pons *et al.*, 2006) with R 3.5.1. program,
16 using the unique threshold method to delimit the species.

17

18 Geographical Distribution

19 We researched data on the occurrence of aeglids in the Tibagi River basin from four scientific
20 collections of crustaceans (MN/UFRJ, MZUSP, MHNCI, UFRGS) and one invertebrate
21 zoology collection (NMNH). We used data from the collections because they include the
22 records not published and those cited in the literature. These records were added to those
23 obtained in the present work to make maps of species geographic distribution. Localities were
24 georeferenced using Google Earth® software. If the collection site coordinates were not
25 available, we used the city coordinate as the reference point. We obtained the city coordinates

1 using GeoNames (<http://www.geonames.org/>). The geographic distribution maps of the
2 species were prepared using the free software QGIS v.3.10.7
3 (https://www.qgis.org/pt_BR/site/).

4

5 RESULTS

6 Surveys resulted in 51 records of Aeglidæ crabs in the study area (Table 1), comprising nine
7 species, of which two are morphologically and genetically distinct new species. Considering
8 the Tibagi River basin regions, three species are present in the Upper Tibagi (*Aegla castro*
9 Schmitt, 1942, *Aegla schmitti* Hobbs, 1979, and *Aegla lata* Bond-Buckup & Buckup, 1994),
10 five in the Middle Tibagi (*A. castro*, *Aegla* n. sp. 2 Marçal & Teixeira in press, *Aegla* n. sp. 3
11 Marçal & Teixeira in press, *Aegla* n. sp. 4, and *Aegla* n. sp. 5) and four species occur in the
12 Lower Tibagi (*A. castro*, *A. lata*, *Aegla jacutinga* Marçal & Teixeira, 2020, and *Aegla* n. sp. 1
13 Marçal & Teixeira in press). In addition, 25 new records of occurrence of three aeglidæ
14 species, previously described, were added (Fig. 2). One of them is *A. castro*, species widely
15 distributed throughout the Tibagi River basin, occurring from the Apucararinha River
16 (Londrina city) to the Guaraúna Creek (Ponta Grossa city). However, the ten new records are
17 within the already known geographical distribution (Fig. 2A). It is worth mentioning that Fig.
18 2A does not represent all the distribution sites of *A. castro*, as this species also occurs on the
19 right bank of the Paranapanema River. *Aegla lata*, in turn, is known from the southeastern and
20 northwestern portions of the Tibagi River basin, occurring in streams in the cities of Ponta
21 Grossa and Londrina. The five new records extend its range towards the city of Califórnia,
22 north of Paraná state (Fig. 2C). Finally, *A. jacutinga* is known from the northwestern portions
23 of the Tibagi River basin. Although this species had already been recorded in streams in the
24 city of Londrina, its distribution was described only for two streams. Herein, we report five
25 new populations found in Londrina and surrounding cities. Besides, five localities in the cities

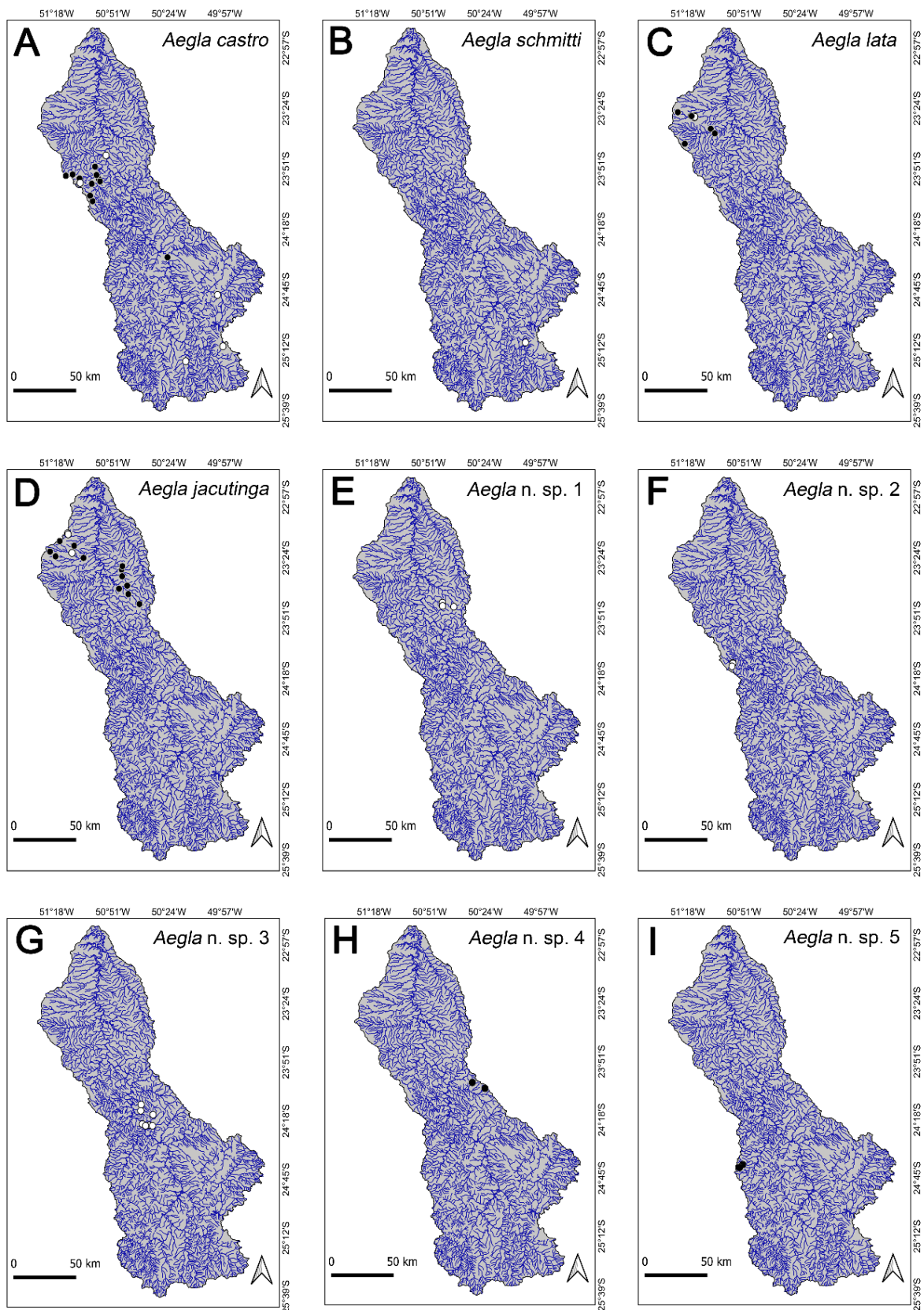
1 of São Sebastião da Amoreira, Nova Santa Bárbara, and São Jerônimo da Serra are new
2 records and broaden the geographical distribution of *A. jacutinga* towards the northeastern of
3 the Tibagi basin (Fig. 2D). The specimens examined are very similar to those described by
4 Marçal *et al.* (2020), notwithstanding they can present more pronounced epigastric
5 prominences and an almost straight anterior margin of the second abdominal epimeron. We
6 believe, however, that such differences are subtle and can be considered as intraspecific
7 variability.

1 **Table 1.** Records of occurrence of *Aegla* species in the Tibagi River basin, Paraná state, Brazil.

Species	Region	City	Locality	Geographical coordinates
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁷	LT	Londrina	<u>Jacutinga stream</u>	23°13'31.05"S, 51°12'39.47"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Cambé	Tributary of the Cafezal stream	23°16'33.00"S, 51°16'42.00"W*
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Londrina	Lindóia stream	23°18'37.00"S, 51°09'46.00"W*
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Rolândia	Cavalaris stream	23°21'12.90"S, 51°21'22.50"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁷	LT	Londrina	Tributary of the Cafezal stream	23°21'48.90"S, 51°10'47.10"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Rolândia	Três Bocas Creek	23°22'59.90"S, 51°18'37.60"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Londrina	Tributary of the Três Bocas Creek	23°23'23.00"S, 51°18'41.80"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	São Sebastião da Amoreira	Três Barras stream	23°29'12.83"S, 50°46'55.74"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Nova Santa Bárbara	José Maria River	23°32'17.54"S, 50°46'39.76"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	Nova Santa Bárbara	Tigre stream	23°36'24.28"S, 50°44'13.82"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	São Jerônimo da Serra	Matão stream	23°37'47.93"S, 50°48'9.49"W
<i>Aegla jacutinga</i> Marçal & Teixeira, 2020 ⁹	LT	São Jerônimo da Serra	São Jerônimo River	23°44'39.16"S, 50°38'19.98"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ³	LT	Londrina	Tributary of the Apertados Creek	23°25'41.60"S, 51°23'00.20"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ⁶	LT	Londrina	Bule stream	23°27'20.86"S, 51°16'32.44"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ⁹	LT	Londrina	Coqueiros River	23°27'22.08"S, 51°16'25.07"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ⁴	LT	Londrina	Stream 1 of the MGSP	23°27'23.50"S, 51°15'05.50"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ⁴	LT	Londrina	Stream 2 of the MGSP	23°27'45.60"S, 51°14'52.30"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ⁹	LT	Londrina	Tributary of the Taquara River	23°33'06.10"S, 51°07'10.80"W
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ⁹	LT	Londrina	Marrequinha stream	23°35'11.00"S, 51°05'14.00"W*
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ³	LT	Califórnia	Jacucaca stream	23°39'48.00"S, 51°19'41.00"W*
<i>Aegla lata</i> Bond-Buckup & Buckup, 1994 ²	UT	Ponta Grossa	<u>Pinto River</u>	25°5'42.00"S, 50°9'43.00"W*
<i>Aegla</i> n. sp. 1 Marçal & Teixeira in press ⁸	LT	São Jerônimo da Serra	<u>Tigre River</u>	23°44'00.50"S, 50°44'26.74"W
<i>Aegla</i> n. sp. 1 Marçal & Teixeira in press ⁸	LT	São Jerônimo da Serra	Pilões stream	23°45'31.25"S, 50°44'19.70"W
<i>Aegla castro</i> Schmitt, 1942 ²	LT	Londrina	Apucarantina River	23°44'58.62"S, 50°54'27.01"W*
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Tamarana	Encontro stream	23°50'01.10"S, 50°59'43.70"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Mauá da Serra	Recanto Pinhão stream	23°53'31.19"S, 51°10'29.54"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Mauá da Serra	Unnamed stream	23°54'05.00"S, 51°13'46.00"W*
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Tamarana	Água Branca River	23°55'30.91"S, 50°58'01.32"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Mauá da Serra	Meio River	23°55'17.10"S, 51°07'09.80"W

<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Tamarana	Água do Anta River	23°56'35.97"S, 50°57'17.81"W
<i>Aegla castro</i> Schmitt, 1942 ⁵	MT	Mauá da Serra	Couro River	23°57'15.60"S, 51°06'53.80"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Mauá da Serra	Preto River	23°57'23.10"S, 51°06'50.30"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Tamarana	Água Boa stream	23°57'40.43"S, 51°01'17.46"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Ortigueira	Apucarana River	24°05'26.82"S, 51°00'54.66"W
<i>Aegla castro</i> Schmitt, 1942 ⁹	MT	Tibagi	Rosas stream	24°30'34.00"S, 50°24'49.00"W*
<i>Aegla castro</i> Schmitt, 1942 ¹	MT	Castro	<u>Iapó River</u>	24°47'21.00"S, 50°0'44.00"W*
<i>Aegla castro</i> Schmitt, 1942 ²	UT	Ponta Grossa	Quebra-Perna River	25°10'18.33"S, 49°58'6.64"W*
<i>Aegla castro</i> Schmitt, 1942 ³	UT	Ponta Grossa	Guaraúna Creek	25°17'00.00"S, 50°16'00.00"W
<i>Aegla</i> n. sp. 4 ⁹	MT	Curiúva	Unnamed stream	24°00'45.39"S, 50°30'32.44"W
<i>Aegla</i> n. sp. 4 ⁹	MT	Curiúva	<u>Água das Pombas stream</u>	24°03'27.84"S, 50°24'20.34"W
<i>Aegla</i> n. sp. 2 Marçal & Teixeira in press ⁸	MT	Ortigueira	Tributary of the Formiga River	24°10'56.50"S, 50°56'31.50"W
<i>Aegla</i> n. sp. 2 Marçal & Teixeira in press ⁸	MT	Ortigueira	<u>Formiga River</u>	24°11'11.77"S, 50°56'28.60"W
<i>Aegla</i> n. sp. 2 Marçal & Teixeira in press ⁸	MT	Ortigueira	Piquira River	24°12'30.00"S, 50°56'58.00"W*
<i>Aegla</i> n. sp. 3 Marçal & Teixeira in press ⁸	MT	Telêmaco Borba	Colônia stream	24°10'27.79"S, 50°37'28.45"W
<i>Aegla</i> n. sp. 3 Marçal & Teixeira in press ⁸	MT	Telêmaco Borba	Moinho velho stream	24°13'18.34"S, 50°37'42.42"W
<i>Aegla</i> n. sp. 3 Marçal & Teixeira in press ⁸	MT	Telêmaco Borba	<u>Codorna Branca stream</u>	24°15'06.70"S, 50°31'46.58"W
<i>Aegla</i> n. sp. 3 Marçal & Teixeira in press ⁸	MT	Telêmaco Borba	Harmonia stream	24°19'26.00"S, 50°36'56.00"W*
<i>Aegla</i> n. sp. 3 Marçal & Teixeira in press ⁸	MT	Telêmaco Borba	Varanal stream	24°20'12.70"S, 50°32'03.20"W
<i>Aegla</i> n. sp. 5 ⁹	MT	Reserva	<u>Tributary of the Tibagi River</u>	24°38'47.70"S, 50°51'48.10"W
<i>Aegla</i> n. sp. 5 ⁹	MT	Reserva	Maromba stream	24°40'09.00"S, 50°53'20.80"W
<i>Aegla schmitti</i> Hobbs, 1979 ²	UT	Ponta Grossa	Roça Velha River	25°08'38.00"S, 50°04'25.00"W*

- 1 LT, Lower Tibagi; MGSP, Mata dos Godoy State Park; MT, Middle Tibagi; UT, Upper Tibagi. The number above species name indicates the
2 reference: 1 = Schmitt (1942); 2 = Bond-Buckup & Buckup (1994); 3 = Pérez-Losada *et al.* (2004); 4 = Galves *et al.* (2007); 5 = Marçal *et al.*
3 (2018); 6 = Chaves *et al.* (2019); 7 = Marçal *et al.* (2020); 8 = Marçal *et al.* in press; 9 = Present work. Underlined localities are the type
4 localities. The type locality of *Aegla schmitti* is in the Iguaçu River basin. The asterisk represents the use of city coordinate as the reference point.



1

2 **Figure 2.** Distribution map of *Aegla* species in the Tibagi River basin. A, *Aegla castro*. B,
 3 *Aegla schmitti*. C, *Aegla lata*. D, *Aegla jacutinga*. E, *Aegla n. sp. 1*. F, *Aegla n. sp. 2*. G,
 4 *Aegla n. sp. 3*. H, *Aegla n. sp. 4*. I, *Aegla n. sp. 5*. Black circles represent the new records of

1 occurrences, while white correspond to the records reported in the literature.

2

3

TAXONOMY

4

Family Aeglidae Dana, 1852

5

Genus *Aegla* Leach, 1820

6

***Aegla* n. sp. 4**

7

(FIGS 3–6)

8 *Type material:* Holotype. male, Brazil, Paraná, Curiúva, Tibagi River basin, Água das
9 Pombas stream, 24°03'27.84"S, 50°24'20.34"W, 769 m, 26 June 2014, coll. unknown
10 (MZUEL 512). Paratypes. 2 males, same data as the holotype (MZUEL 390); 2 males and 3
11 females, same locality as holotype, 11 March 2020, G.M. Teixeira, I.C. Marçal & P.F. da
12 Silva coll. (MZUEL 506, genetic vouchers: Bold Systems access AEGLA001-21,
13 AEGLA002-21).

14 *Additional material examined:* 1 male and 1 female, Brazil, Paraná, Curiúva, Tibagi River
15 basin, Unnamed stream, 24°00'45.39"S, 50°30'32.44"W, 697 m, 19 August 2014, J.F.M. da
16 Silva, F.C. Jerep & R.H.C. Nascimento coll. (MZUEL 391).

17 *Diagnosis:* Rostrum triangular, extending beyond distal apex of compound eyes, carinate
18 along entire length. Subrostral process well developed, occupying proximal half of subrostral
19 margin, anterior and posterior margins forming obtuse angle. Orbital sinus deep, extra-orbital
20 sinus shallow. Epigastric prominences pronounced. Protogastric lobes pronounced.
21 Epibranchial area strongly elongated. Proximal dorsal margin of dactylus with moderate size
22 lobe. Palmar crest rectangular, outer surface slightly excavated, margin serrated. Outer surface
23 of carpus with carpal ridge high. Ventromesial border of cheliped ischium with 3 to 5
24 tubercles. Anteromesial region of third thoracic sternite tapered. Anterolateral angle of second
25 abdominal epimeron unarmed. Ventral angles of third and fourth abdominal epimeron with

1 corneous scales apically. Anterior margin of second abdominal epimeron almost straight.

2 Uropods wide.

3 *Description of holotype:* Carapace moderately convex, gastric region convex, dorsal surface
4 scabrous, covered with punctations (Fig. 3). Rostrum triangular, wide base (RBW/LMR =
5 1.00), reaching distal apex of compound eyes, carinate along entire length, small corneous
6 scales on lateral margins and tip; ventral portion of rostrum much higher than dorsal in
7 profile. Rostral carina beginning at level of protogastric lobes, with 2 rows of corneous scales
8 extending next to apex. Subrostral process well developed, occupying proximal half of
9 subrostral margin, produced ventrally, triangular shaped, tip rounded, anterior and posterior
10 margins forming obtuse angle (113°) (Fig. 4A).

11 Eyestalk and cornea well developed. Orbital sinus deep, extra-orbital sinus shallow
12 (Fig. 4B). Orbital sinus U-shaped. Orbital spines well developed, with small terminal
13 corneous scale. Anterolateral spines acuminate apically with small corneous scales terminally,
14 extending beyond basal margin of cornea (Fig. 4B).

15 Epigastric prominences pronounced, with corneous scales. Protogastric lobes
16 pronounced, with corneous scales (Fig. 4A). Gastric area elevated in relation to hepatic lobes
17 and rostrum in lateral view. Demarcation between the first and the second hepatic lobe well
18 defined, between the second and the third hepatic lobe weakly delimited. Lateral margins of
19 hepatic lobes with small corneous scales and small setae.

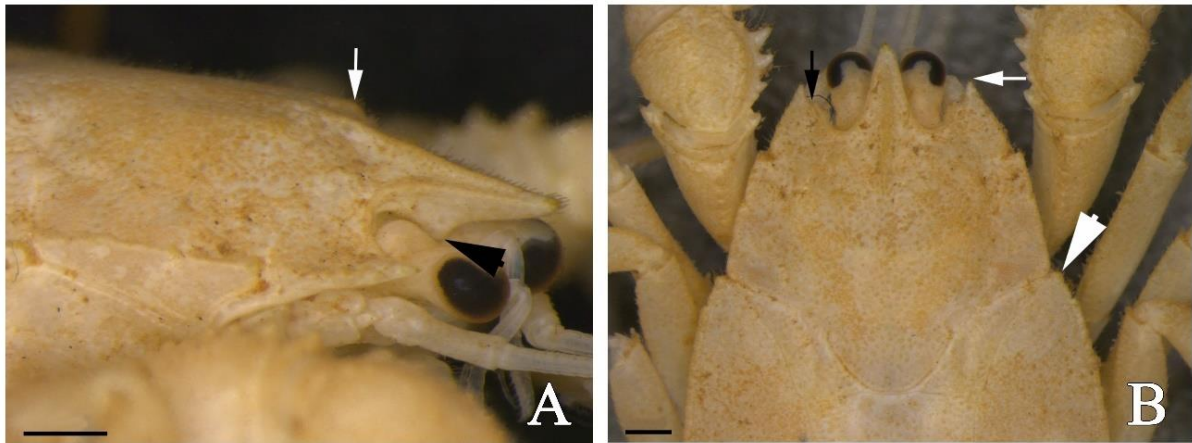
20 Cervical groove trapezoidal. Transverse dorsal linea sinuous along its extension.
21 Areola trapezoidal (APM/AAD = 2.00). Cardiac area subrectangular (TDL/PMC = 1.31).
22 Epibranchial area strongly elongated, anterolateral angle with corneous scale, lateral margin
23 with row of corneous scales and small setae (Fig. 4B). Lateral margins of anterior and
24 posterior branchial areas with row of corneous scales and small setae.



1

2 **Figure 3.** *Aegla* n. sp. 4, male holotype, MZUEL 512. Specimen collected in the Água das
3 Pombas stream, Curiúva, Paraná, Brazil. Dorsal view of the cephalothorax and abdomen.
4 Scale bar = 5.0 mm.

5

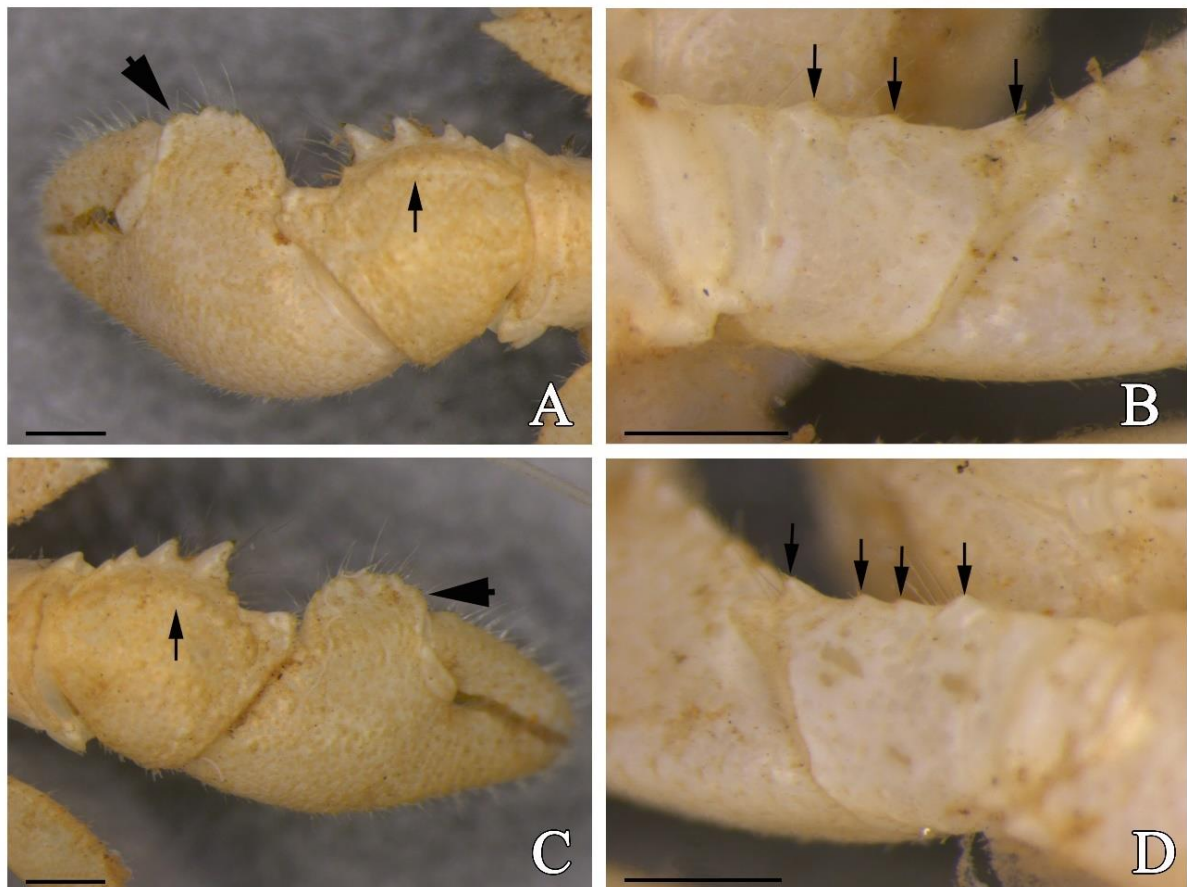


1
2 **Figure 4.** *Aegla* n. sp. 4, male holotype, MZUEL 512. A, external surface view of the anterior
3 portion of the cephalothorax showing pronounced protogastric lobes (white arrow) and well
4 developed subrostral process (black arrow). B, dorsal view of the anterior region of the
5 cephalothorax showing shallow extra-orbital sinus (black arrow), anterolateral spine
6 extending beyond basal margin of cornea (thin white arrow) and strongly elongated
7 epibranchial area (thick white arrow). Scale bars = 1.0 mm.

8

9 Chelipeds unequal. Left cheliped largest (Figs 5A, B). Dactylus: dorsal margin and
10 outer surface with small corneous scales, inner surface with setal tufts and scales. Proximal
11 dorsal margin with moderate size lobe. Cutting margin with well-developed lobular basal
12 tooth, followed by row of corneous scales up to distal end. Row of small tufts of long setae
13 next to cutting margin. Pre-dactylar lobe well developed, without corneous scales. Propodus:
14 outer surface granular, globose aspect. Palmar crest rectangular with outer surface slightly
15 excavated, margin serrated, covered by acuminate corneous scales. Cutting margin of fixed
16 finger with well-developed lobular basal tooth, followed by row of corneous scales up to
17 distal end. Inner and outer surfaces of fixed finger with rows of long setae tufts next to cutting
18 margin. Carpus: dorsal margin with proximal tubercle and 3 spines, distal spine longest, each
19 spine with small setae and terminal corneous scale, subterminal lobe well defined, pointed,
20 with small corneous scales and setae. Inner surface with 2 small tubercles, long setae next to
21 dorsal margin. Outer surface with carpal ridge high, with small corneous scales. Merus:

1 dorsolateral edge with distal tubercle, with corneous scale terminally, followed by row of
 2 tubercles decreasing in size proximally. Ventromesial edge with distal spine, with corneous
 3 scale terminally, followed by 3 tubercles of similar size, with corneous scale. Ventrolateral
 4 border with distal tubercle, with terminal corneous scale, followed by row of tubercles
 5 decreasing in size proximally. Ischium: dorsolateral edge with tubercle, with corneous scale
 6 terminally. Ventromesial border with proximal tubercle, small median tubercle and large
 7 distal tubercle, each with terminal corneous scale. Ventrolateral border smooth.

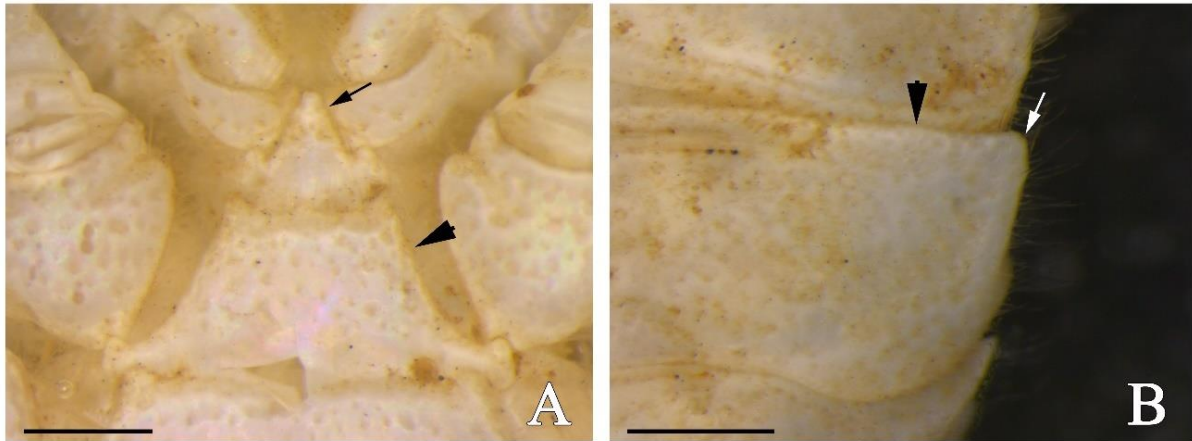


8
 9 **Figure 5.** *Aegla* n. sp. 4, male holotype, MZUEL 512. A, dorsal view of the dactylus,
 10 propodus, and carpus of major cheliped (left) showing rectangular palmar crest (thick arrow)
 11 and high carpal ridge (thin arrow). B, ventral view of ischium of major cheliped (left) with
 12 three tubercles (arrows). C, dorsal view of the dactylus, propodus, and carpus of minor
 13 cheliped (right) showing rectangular palmar crest (thick arrow) and high carpal ridge (thin
 14 arrow). D, ventral view of ischium of minor cheliped (right) with four tubercles (arrows).
 15 Scale bars = 1.0 mm.

1 Minor cheliped (right) similar to major cheliped except as noted hereafter (Figs 5C,
2 D). Dactylus: proximal dorsal margin with rudimentary lobe. Cutting margin with
3 rudimentary lobular basal tooth. Propodus: cutting margin with rudimentary lobular basal
4 tooth. Carpus: dorsal margin with 2 proximal tubercles, median tubercle, distal spine longest,
5 each tubercle or spine with small setae and terminal corneous scale. Merus: ventromesial edge
6 with distal spine, followed by 4 tubercles, each with terminal corneous scale. Ischium:
7 ventromesial border with proximal tubercle, 2 small median tubercles and large distal
8 tubercle, each with terminal corneous scale.

9 Second, third, and fourth pereopods morphologically similar. Dactyli, propodi, carpi,
10 meri and ischii with several rows of setal tufts and small scales on surface. Carpi and meri
11 with row of small tubercles with terminal corneous scale along dorsal margin. Meri with row
12 of small tubercles with terminal corneous scale along ventral margin. Meri and ischii with
13 long setae concentrated along dorsal margin.

14 Anteromesial region of third thoracic sternite tapered, projecting between coxae of
15 third maxillipeds, with scattered setae. Fourth thoracic sternite with anterolateral angles
16 produced anteriorly, with scattered setae (Fig. 6A). Pleopods 2–5 absent. Anterolateral angle
17 of second abdominal epimeron well defined, unarmed (Fig. 6B). Ventral angles of third and
18 fourth abdominal epimeron well defined, with corneous scales apically. Anterior margin of
19 second abdominal epimeron almost straight (Fig. 6B). Uropods well developed, wide
20 ($WU/HWT = 1.06$). Telson divided by longitudinal suture. Anterolateral and posterolateral
21 margins well differentiated.



1

2 **Figure 6.** *Aegla* n. sp. 4, male holotype, MZUEL 512. A, third (thin arrow) and fourth (thick

3 arrow) thoracic sternites. B, dorsal view of second abdominal epimeron (right side) showing

4 almost straight anterior margin (black arrow) and unarmed anterolateral angle (white arrow).

5 Scale bars = 1.0 mm.

6

7 *Variations:* The base of the rostrum can be narrow ($n = 3$) or wide ($n = 3$). The areola can be8 trapezoidal ($n = 3$), subrectangular ($n = 3$), or rectangular ($n = 1$). The cardiac area varies from9 trapezoidal ($n = 5$) to subrectangular ($n = 2$). The ventromesial border of ischium may present

10 five tubercles instead of three or four as in the holotype. In most specimens, the anteromesial

11 region of third thoracic sternite is bifurcated, with two corneous scales terminally.

12 Measurements and morphometric relationships of the type series specimens are summarized

13 in Table 2.

14

15

16

17

18

1 **Table 2.** General measurements and morphometric ratios of the type material of *Aegla* n. sp. 4
 2 and *Aegla* n. sp. 5.

	<i>Aegla</i> n. sp. 4		<i>Aegla</i> n. sp. 5	
	Holotype	Paratypes (n = 7)	Holotype	Paratypes (n = 6)
CL	11.6	14.04(2.26)	13.7	17.40(3.94)
CLE	9.6	11.90(2.22)	11.5	14.63(3.17)
CW	9.3	11.90(2.28)	11.2	14.63(3.50)
PCW	7.0	8.93(1.69)	8.2	10.47(2.46)
RBW	2.2	2.50(0.37)	2.5	2.95(0.60)
LMR	2.2	2.50(0.39)	2.7	3.22(0.74)
APM	2.0	2.20(0.56)	2.0	2.82(0.86)
AAD	1.0	1.29(0.29)	1.1	1.43(0.42)
AH	3.2	3.84(0.72)	4.0	5.20(1.11)
TDL	3.8	4.86(0.79)	4.4	5.92(1.33)
PMC	2.9	3.41(0.76)	3.0	4.32(1.30)
WU	1.8	2.30(0.37)	2.2	2.92(0.71)
HWT	1.7	2.17(0.35)	1.9	2.70(0.78)
CW/CLE	0.97	0.99(0.04)	0.97	1.00(0.03)
PCW/CW	0.75	0.75(0.02)	0.73	0.72(0.01)
RBW/LMR	1.00	0.97(0.03)	0.93	0.92(0.04)
APM/AAD	2.00	1.71(0.18)	1.82	1.97(0.18)
AH/[(APM+AAD)/2]	—	2.25(0.27)	—	—
TDL/PMC	1.31	1.44(0.10)	1.47	1.40(0.12)
WU/HWT	1.06	1.06(0.03)	1.16	1.09(0.07)

3 All measurements in mm. The measures of the paratypes are shown as mean (standard
 4 deviation). AAD, areolar anterior demarcation; AH, areolar height; APM, areolar posterior
 5 margin; CL, carapace length including rostrum; CLE, carapace length excluding rostrum;
 6 CW, carapace width; HWT, half the maximum width of telson; LMR, lateral margin of
 7 rostrum; PCW, pre-cervical width; PMC, mesial region of the posterior margin of the
 8 cephalothorax; RBW, rostral base width; TDL, transversal dorsal linea length; WU, width of
 9 uropod.

10

11 *Remarks:* *Aegla* n. sp. 4 can be easily differentiated from its congeners from the Tibagi River
 12 basin by several morphological characteristics. The new species have a rectangular palmar
 13 crest, diverging from the subdisciform to the disciform palmar crest of *A. castro*, *A. schmitti*,
 14 *A. lata*, *A. jacutinga*, and *Aegla* n. sp. 1. Moreover, the subrostral process occupies the
 15 proximal half of the subrostral margin in *Aegla* n. sp. 4 whereas in *A. lata*, *A. jacutinga*, *Aegla*
 16 n. sp. 1, and *Aegla* n. sp. 3 is on the proximal third of subrostral margin. The pronounced
 17 protogastric lobes of *Aegla* n. sp. 4 are shared with *A. castro*, *A. schmitti*, *A. jacutinga*, *Aegla*

1 n. sp. 1, *Aegla* n. sp. 2, and *Aegla* n. sp. 3. However, the new species can be differentiated
2 from *A. castro*, *A. schmitti*, and *A. jacutinga* by present the anterior margin of the second
3 abdominal epimeron almost straight. The epigastric prominences and the carpal ridge of *A.*
4 *jacutinga* are poorly pronounced and low, distinguishing it from *Aegla* n. sp. 4. Besides, *A.*
5 *castro* and *A. schmitti* exhibit a spine on the anterolateral angle of the second abdominal
6 epimeron while this structure is unarmed in the new species. An unusual feature that
7 discriminates the new species from *Aegla* n. sp. 1 is the presence of rudimentary pleopods in
8 adult male specimens of the latter species. Morphologic characters that distinguish *Aegla* n.
9 sp. 4 from *Aegla* n. sp. 2 are the shortened epibranchial area, the rudimentary lobe on the
10 proximal dorsal margin of the dactylus, and the anteromesial region of the third thoracic
11 sternite of the abrupt format in *Aegla* n. sp. 2. Similarly, *Aegla* n. sp. 4 can be separated from
12 *Aegla* n. sp. 3 by the slightly elongated epibranchial area and the rudimentary or absent lobe
13 on the proximal dorsal margin of the dactylus in *Aegla* n. sp. 3. *Aegla* n. sp. 4 and *A. lata*
14 share the presence of corneous scales in the ventral angles of the third and fourth abdominal
15 epimeron. Notwithstanding, the new species differs from *A. lata* in having pronounced
16 epigastric prominences, pronounced protogastric lobes, and wide uropods. Another
17 morphological characteristic, the shallow extra-orbital sinus of *Aegla* n. sp. 4, is not reported
18 for other species of the same basin.

19 Although they occur in different hydrographic basins, *Aegla parva* Bond-Buckup &
20 Buckup, 1994, *Aegla meloi* Bond-Buckup & Santos, 2015, *Aegla okora* Páez & Teixeira,
21 2018, and *Aegla nebeccana* Trombetta, Páez, Santos & Teixeira, 2019 resemble the new
22 species in the shape of the palmar crest of cheliped. Nevertheless, *Aegla* n. sp. 4 can be
23 distinguished from these species especially by the: 1) epigastric prominences absent in *A.*
24 *meloi*, poorly pronounced in *A. parva* and inconspicuous in *A. nebeccana*; 2) proximal dorsal
25 margin of dactylus without lobe in *A. parva*, *A. meloi*, *A. okora*, and *A. nebeccana*; 3)

1 ventromesial border of cheliped ischium with a distal tubercle in *A. meloi*; 4) anterolateral
2 angle of second abdominal epimeron with a spine in *A. parva*; 5) anterior margin of second
3 abdominal epimeron slightly concave in *A. parva*, *A. okora*, and *A. nebeccana*; and 6) narrow
4 uropods in *A. nebeccana*.

5 *Geographical distribution*: The new species has been collected in two streams within the
6 Tibagi River basin. Both streams are located in the city of Curiúva, Paraná state, Brazil (Fig.
7 2H).

8

9

***Aegla* n. sp. 5**

10

(FIGS 7–10)

11 *Type material*: Holotype. male, Brazil, Paraná, Reserva, Tibagi River basin, tributary of the
12 Tibagi River, 24°38'47.70"S, 50°51'48.10"W, 901 m, 10 March 2020, G.M. Teixeira, I.C.
13 Marçal & R.S. Vieira coll. (MZUEL 514). Paratypes. 2 males and 2 females, same data as for
14 holotype (MZUEL 503, genetic vouchers: Bold Systems access AEGLA007-21, AEGLA008-
15 21); 1 male and 1 female, same locality as holotype, 09 April 2015, A.C. Hoffmann coll.
16 (MZUEL 463).

17 *Additional material examined*: 6 males and 4 females, Brazil, Paraná, Reserva, Tibagi River
18 basin, Maromba stream, 24°40'09.00"S, 50°53'20.80"W, 911 m, 09 April 2015, A.C.
19 Hoffmann coll. (MZUEL 462).

20 *Diagnosis*: Rostrum triangular, narrow base, extending beyond distal apex of compound eyes,
21 carinate along entire length. Subrostral process well developed, occupying proximal half of
22 subrostral margin, anterior and posterior margins forming obtuse angle. Orbital and extra-
23 orbital sinuses deep. Epigastric prominences pronounced. Protogastric lobes pronounced.
24 Cervical groove U-shaped. Areola trapezoidal. Epibranchial area slightly elongated. Proximal
25 dorsal margin of dactylus with rudimentary lobe. Palmar crest rectangular, outer surface

1 slightly excavated, margin poorly serrated. Outer surface of carpus with carpal ridge high.
2 Ventromesial border of cheliped ischium with 4 tubercles. Anterolateral angle of second
3 abdominal epimeron unarmed. Ventral angles of third and fourth abdominal epimeron with
4 corneous scales apically. Anterior margin of second abdominal epimeron almost straight.
5 Uropods wide.

6 *Description of holotype:* Carapace moderately convex, gastric region convex, dorsal surface
7 scabrous, covered with punctations (Fig. 7). Rostrum triangular, narrow base ($RBW/LMR =$
8 0.93), extending beyond distal apex of compound eyes, carinate along entire length, small
9 corneous scales on lateral margins and tip; ventral portion of rostrum much higher than dorsal
10 in profile. Rostral carina beginning at level of protogastric lobes, with 2 rows of corneous
11 scales extending next to apex. Subrostral process well developed and covered by small setae,
12 occupying proximal half of subrostral margin, tip rounded, anterior and posterior margins
13 forming obtuse angle (126°) (Fig. 8A).

14 Eyestalk and cornea well developed. Orbital and extra-orbital sinuses deep. Orbital
15 sinus U-shaped. Orbital spines well developed, with small terminal corneous scale.
16 Anterolateral spines acuminate apically with small corneous scales terminally, reaching basal
17 margin of cornea.

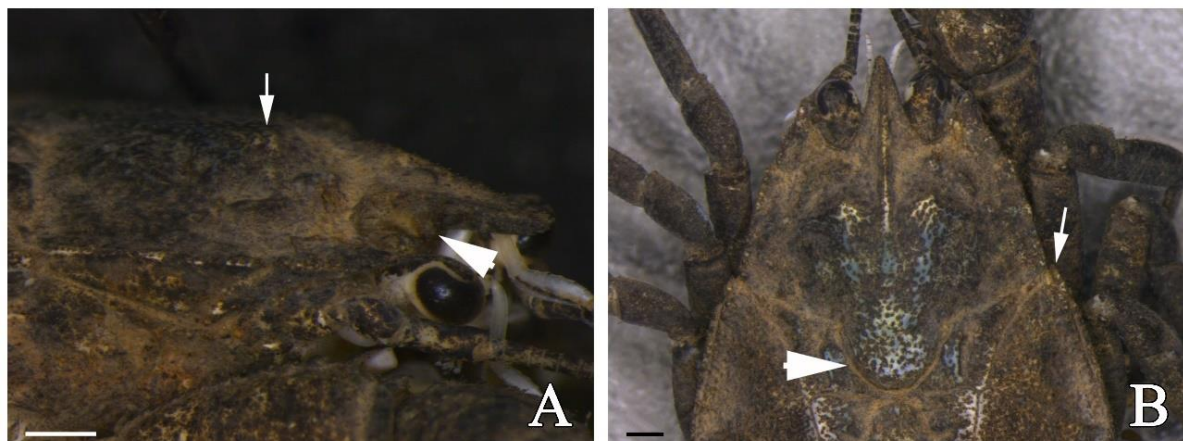
18 Epigastric prominences pronounced, with corneous scales. Protogastric lobes
19 pronounced, with corneous scales (Fig. 8A). Gastric area elevated in relation to hepatic lobes
20 and rostrum in lateral view. Demarcation between the first and the second hepatic lobe well
21 defined, between the second and the third hepatic lobe weakly delimited. Lateral margins of
22 hepatic lobes with small corneous scales and small setae.

23 Cervical groove U-shaped (Fig. 8B). Transverse dorsal linea sinuous along its
24 extension. Areola trapezoidal ($APM/AAD = 1.82$). Cardiac area trapezoidal ($TDL/PMC =$
25 1.47). Epibranchial area slightly elongated, triangular shaped, anterolateral angle with

- 1 corneous scale, lateral margin with row of corneous scales and small setae (Fig. 8B). Lateral
2 margins of anterior and posterior branchial areas with row of corneous scales and small setae.



- 3
4 **Figure 7.** *Aegla* n. sp. 5, male holotype, MZUEL 514. Specimen collected in the tributary of
5 the Tibagi River, Reserva, Paraná, Brazil. Dorsal view of the cephalothorax and abdomen.
6 Scale bar = 5.0 mm.
7

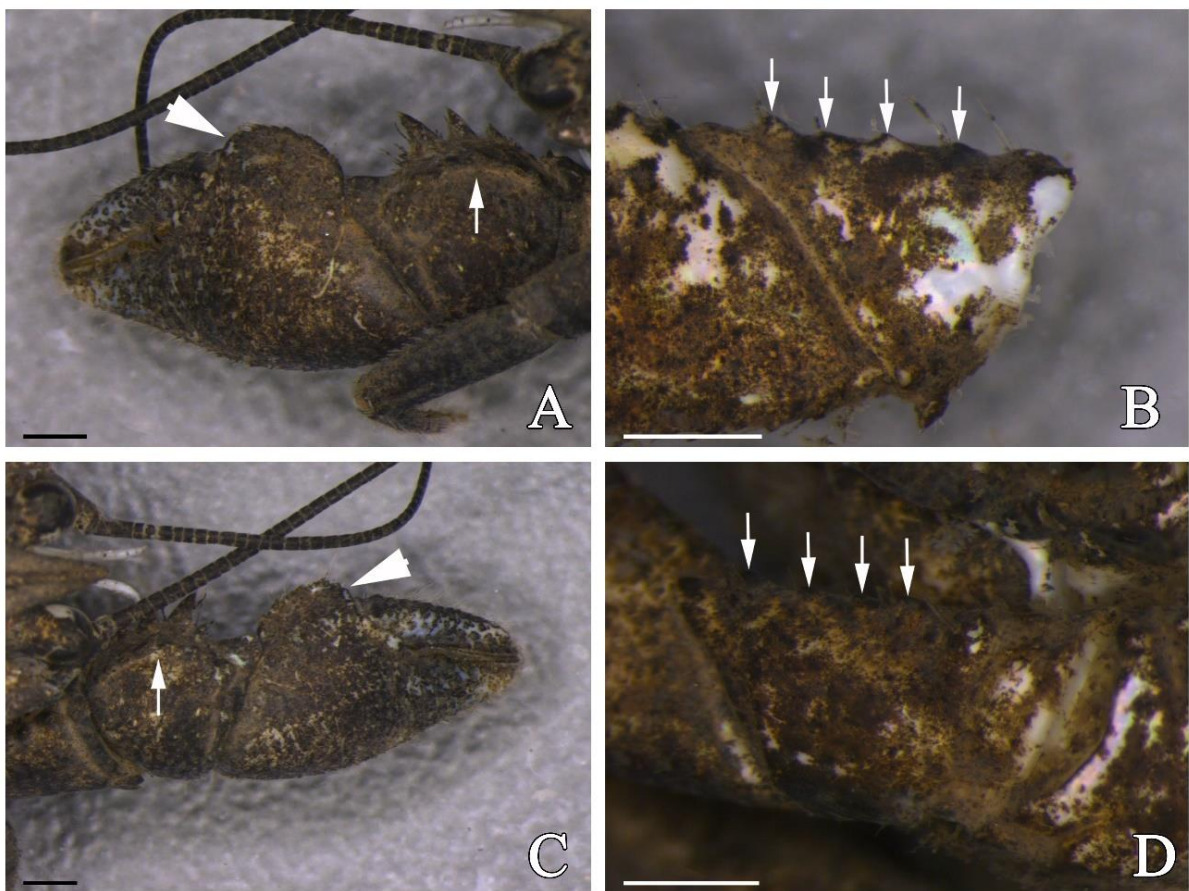


1
2 **Figure 8.** *Aegla* n. sp. 5, male holotype, MZUEL 514. A, external surface view of the anterior
3 portion of the cephalothorax showing pronounced protogastric lobes (thin arrow) and well
4 developed subrostral process (thick arrow). B, dorsal view of the anterior region of the
5 cephalothorax showing U-shaped cervical groove (thick arrow) and slightly elongated
6 epibranchial area (thin arrow). Scale bars = 1.0 mm.

7

8 Chelipeds unequal. Left cheliped largest (Figs 9A, B). Dactylus: dorsal margin and
9 outer surface with small corneous scales, inner surface with setal tufts and scales. Proximal
10 dorsal margin with rudimentary lobe. Cutting margin with well-developed lobular basal tooth,
11 followed by row of corneous scales up to distal end. Row of small tufts of long setae next to
12 cutting margin. Pre-dactylar lobe well developed, rounded, without corneous scales.
13 Propodus: outer surface granular, globose aspect. Palmar crest rectangular with outer surface
14 slightly excavated, margin poorly serrated, covered by acuminate corneous scales. Cutting
15 margin of fixed finger with well-developed lobular basal tooth, followed by row of corneous
16 scales up to distal end. Inner and outer surfaces of fixed finger with rows of long setae tufts
17 next to cutting margin. Carpus: dorsal margin with proximal tubercle, 2 median spines, distal
18 spine longest, each tubercle or spine with small setae and terminal corneous scale, subterminal
19 lobe well defined, pointed, with small corneous scales and setae. Inner surface with large
20 tubercle, long setae next to dorsal margin. Outer surface with carpal ridge high, with small
21 corneous scales. Merus: dorsolateral edge with distal tubercle, with corneous scale terminally,

1 followed by row of tubercles decreasing in size proximally. Ventromesial edge with 2 distal
 2 spines, with corneous scale terminally, followed by 3 tubercles of similar size, with corneous
 3 scale. Ventrolateral border with distal tubercle, with terminal corneous scale, followed by row
 4 of tubercles decreasing in size proximally. Ischium: dorsolateral edge with large tubercle,
 5 with corneous scale terminally. Ventromesial border with 3 similar size tubercles and large
 6 distal tubercle, each with terminal corneous scale. Ventrolateral border smooth.



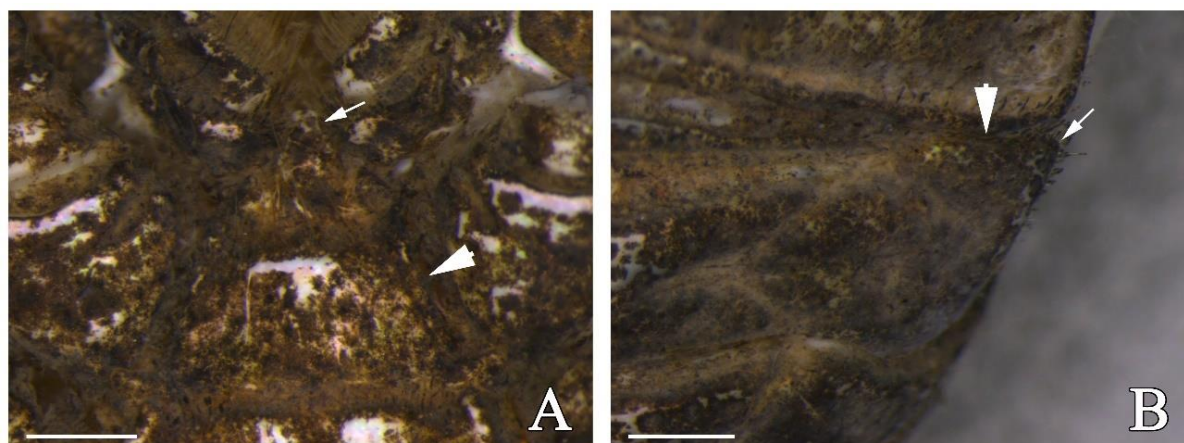
7
 8 **Figure 9.** *Aegla* n. sp. 5, male holotype, MZUEL 514. A, dorsal view of the dactylus,
 9 propodus, and carpus of major cheliped (left) showing rectangular palmar crest (thick arrow)
 10 and high carpal ridge (thin arrow). B, ventral view of ischium of major cheliped (left) with
 11 four tubercles (arrows). C, dorsal view of the dactylus, propodus, and carpus of minor
 12 cheliped (right) showing rectangular palmar crest (thick arrow) and high carpal ridge (thin
 13 arrow). D, ventral view of ischium of minor cheliped (right) with four tubercles (arrows).
 14 Scale bars = 1.0 mm.

15

1 Minor cheliped (right) similar to major cheliped except as noted hereafter (Figs 9C,
2 D). Dactylus: cutting margin with rudimentary lobular basal tooth. Propodus: cutting margin
3 with rudimentary lobular basal tooth. Merus: ventromesial edge with distal spine, followed by
4 3 tubercles, each with terminal corneous scale.

5 Second, third, and fourth pereopods morphologically similar. Dactyli, propodi, carpi,
6 meri and ischii with several rows of setal tufts and small scales on surface. Carpi and meri
7 with row of small tubercles with terminal corneous scale along dorsal margin. Meri with row
8 of small tubercles with terminal corneous scale along ventral margin. Meri and ischii with
9 long setae concentrated along dorsal margin.

10 Anteromesial region of third thoracic sternite tapered, projecting between coxae of
11 third maxillipeds, with scattered setae. Fourth thoracic sternite with anterolateral angles
12 produced anteriorly, with scattered setae (Fig. 10A). Pleopods 2–5 absent. Anterolateral angle
13 of second abdominal epimeron well defined, unarmed (Fig. 10B). Ventral angles of third and
14 fourth abdominal epimeron well defined, with corneous scales apically. Anterior margin of
15 second abdominal epimeron almost straight (Fig. 10B). Uropods well developed, wide
16 (WU/HWT = 1.16). Telson divided by longitudinal suture. Anterolateral and posterolateral
17 margins well differentiated.



18
19 **Figure 10.** *Aegla* n. sp. 5, male holotype, MZUEL 514. A, third (thin arrow) and fourth (thick
20 arrow) thoracic sternites. B, dorsal view of second abdominal epimeron (right side) showing

1 almost straight anterior margin (thick arrow) and unarmed anterolateral angle (thin arrow).

2 Scale bars = 1.0 mm.

3

4 *Variations:* In some specimens, the anterolateral spines can extend beyond the basal margin

5 of the cornea. The area cardiac varies from trapezoidal (n = 3) to subrectangular (n = 3). The

6 anteromesial region of third thoracic sternite can be tapered (n = 4) or abrupt (n = 2).

7 Measurements and morphometric relationships of the type series specimens are summarized

8 in Table 2.

9 *Remarks:* Several morphological features differentiate *Aegla* n. sp. 5 from the species that

10 occur in the Tibagi River basin. For example, the subrostral process occupies the proximal

11 half of the subrostral margin in *Aegla* n. sp. 5 whereas *A. lata*, *A. jacutinga*, *Aegla* n. sp. 1,

12 and *Aegla* n. sp. 3 is on the proximal third of the subrostral margin. The lobe on the proximal

13 dorsal margin of the dactylus is rudimentary in *Aegla* n. sp. 5 but of moderate size in *Aegla* n.

14 sp. 1 and *Aegla* n. sp. 4, and pronounced and surmounted by tubercles in *A. castro* and *A.*

15 *schmitti*. *Aegla* n. sp. 5 has a cervical groove U-shaped whereas *A. jacutinga*, *Aegla* n. sp. 2,

16 and *Aegla* n. sp. 3 has a cervical groove trapezoidal-shaped. The anterior margin of the second

17 abdominal epimeron is almost straight in *Aegla* n. sp. 5, slightly concave in *A. jacutinga*, and

18 concave in *A. castro* and *A. schmitti*. The new species can be further separated from *A.*

19 *jacutinga* by the pronounced epigastric prominences and the high carpal ridge on the outer

20 surface of the carpus. Epibranchial area is slightly elongated in *Aegla* n. sp. 5, shortened in

21 *Aegla* n. sp. 2, and strongly elongated in *Aegla* n. sp. 1 and *Aegla* n. sp. 4. *Aegla* n. sp. 5 has a

22 trapezoidal areola while *A. lata* has a rectangular areola and *Aegla* n. sp. 2 has a

23 subrectangular areola. *Aegla* n. sp. 5 can be also distinguished from *A. lata* in having

24 pronounced epigastric prominences, pronounced protogastric lobes, and wide uropods. The

25 anterolateral angle of the second abdominal epimeron is inermis in *Aegla* n. sp. 5, while in *A.*

1 *castro* and *A. schmitti* is projected in a spine. In *Aegla* n. sp. 5, the ventral angles of the third
2 and fourth abdominal epimeron are marked by corneous scales apically, while in *Aegla* n. sp.
3 2 is unarmed. Moreover, the margin of the palmar crest is poorly serrated in *Aegla* n. sp. 5 but
4 serrated in *Aegla* n. sp. 4.

5 The rectangular palmar crest of the new species is shared with *A. parva*, *A. meloi*, *A.*
6 *okora*, and *A. nebeccana*. Notwithstanding, *Aegla* n. sp. 5 differs from these species in having
7 a rudimentary lobe on the proximal dorsal margin of the dactylus. The epigastric prominences
8 are pronounced in *Aegla* n. sp. 5, absent in *A. meloi*, poorly pronounced in *A. parva*, and
9 inconspicuous in *A. nebeccana*. Furthermore, the anterior margin of the second abdominal
10 epimeron is almost straight in *Aegla* n. sp. 5, whereas in *A. parva*, *A. okora*, and *A. nebeccana*
11 is slightly concave. *Aegla* n. sp. 5 has four tubercles on the ventromesial border of cheliped
12 ischium while *A. meloi* has only a distal tubercle. The anterolateral angle of the second
13 abdominal epimeron is inermis in *Aegla* n. sp. 5 but is marked by a spine in *A. parva*. In
14 *Aegla* n. sp. 5, the uropods are wide, whereas in *A. nebeccana* are narrow.

15 *Geographical distribution:* The new species has been collected in two streams within the
16 Tibagi River basin. Both streams are located in the city of Reserva, Paraná state, Brazil (Fig.
17 2D).

18

19

MOLECULAR DATA

20 Altogether we analyzed 1231 base pairs (bp) of the mitochondrial gene COI. The mean base
21 frequencies were: A = 0.2954, C = 0.1403, G = 0.1479, T = 0.4164. The
22 transition/transversion ratio was 3.1669. The genetic distances ranged from 1.4% to 5.9%
23 among species of *Aegla* and 0% to 2.8% within species (Table 3). Concerning the new
24 species, *Aegla* n. sp. 4 showed the smallest genetic distance relative to *A. lata* and the highest
25 with *A. okora*. *Aegla* n. sp. 5 presented the lowest and highest divergence relative to *A.*

1 *jacutinga* and *A. okora*, respectively. Our Bayesian inference tree (Fig. 11) shows that *A. lata*
 2 is the sister species of *Aegla* n. sp. 4. Furthermore, both are grouped in the same subclade as
 3 *A. castro* with high nodal support. The *Aegla* n. sp. 5 specimens formed a clade sister related
 4 to *A. jacutinga* (Pp = 0.57). Based on the estimated phylogenetic tree, *Aegla* n. sp. 5 + *A.*
 5 *jacutinga* is the sister group of *Aegla* n. sp. 1 + *Aegla* n. sp. 2. The GMYC analysis indicated
 6 the presence of 15 independent strains within the analyzed samples. Moreover, all species
 7 were separated from each other by this species delimitation analysis.

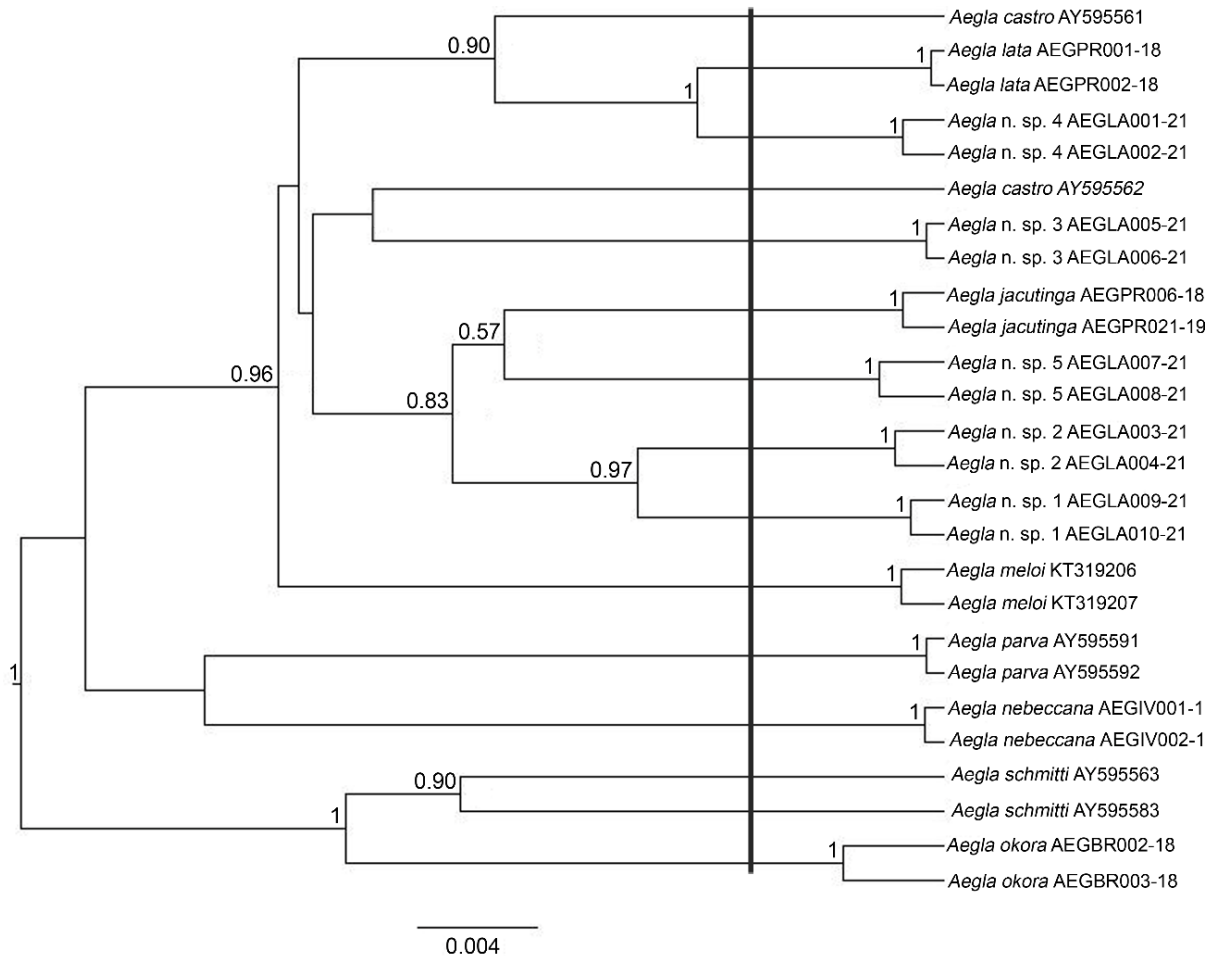
8

9 **Table 3.** Genetic distances (%) of the COI partial sequences of species of *Aegla*.

Species	1	2	3	4	5	6	7	8	9	10	11	12	13
1. <i>Aegla castro</i>	2.8												
2. <i>Aegla schmitti</i>	4.0	2.4											
3. <i>Aegla lata</i>	3.9	5.3	0.0										
4. <i>Aegla jacutinga</i>	2.2	3.5	3.8	0.2									
5. <i>Aegla parva</i>	3.1	2.8	4.7	2.3	0.0								
6. <i>Aegla meloi</i>	3.3	3.6	4.8	2.4	2.3	0.2							
7. <i>Aegla okora</i>	4.2	3.2	5.6	3.4	3.1	4.3	0.4						
8. <i>Aegla nebeccana</i>	4.7	4.3	5.6	4.1	3.5	5.0	5.9	0.0					
9. <i>Aegla</i> n. sp. 1	3.2	3.6	4.3	2.2	3.2	3.1	4.6	4.3	0.2				
10. <i>Aegla</i> n. sp. 2	3.1	4.0	4.6	1.8	3.7	3.2	4.7	4.9	1.4	0.4			
11. <i>Aegla</i> n. sp. 3	2.9	3.7	4.0	2.1	3.7	3.2	4.5	4.7	3.2	2.4	0.0		
12. <i>Aegla</i> n. sp. 4	2.3	3.6	1.7	2.1	3.3	3.0	4.5	4.2	2.7	2.8	2.2	0.0	
13. <i>Aegla</i> n. sp. 5	2.8	3.8	3.3	1.7	3.0	3.1	4.2	3.9	2.8	2.7	2.7	2.3	0.4

10 The intraspecific distances are in bold.

11



1

2 **Figure 11.** Bayesian inference tree of the *Aegla* spp. analyzed in this study. Numbers at the
 3 corresponding nodes represent the posterior probability (values < 0.5 are not indicated). The
 4 vertical line indicates the species delimitation assigned by the single-threshold method in
 5 GMYC analysis.

6

7 DISCUSSION

8 For over 70 years, researchers have carried out surveys in the Tibagi River basin, generating
 9 information on aeglids' taxonomy and distribution. The first report came in 1942, with the
 10 description of *A. castro* from Iapó River, Castro city (Schmitt, 1942). More than 50 years
 11 later, Bond-Buckup & Buckup (1994) described *A. lata* from Pinto River, Ponta Grossa city.
 12 These authors also reported new records of occurrence for *A. castro* and *A. schmitti* in this
 13 hydrographic basin. Several other works recorded the presence of these three species in
 14 tributaries of the Tibagi River (Swiech-Ayoub & Masunari, 2001; Galves *et al.*, 2007;

1 Trevisan & Masurani, 2010; Silva *et al.*, 2017; Marçal *et al.*, 2018; Chaves *et al.*, 2019).
2 Later, Marçal *et al.* (2020) described *A. jacutinga* from specimens collected in two streams in
3 Londrina city. More recently, one new species from the Lower Tibagi region and two from
4 the Middle Tibagi region have been described (Marçal *et al.*, in press).

5 *Aegla castro* and *A. schmitti* have wide geographical distribution in the sub-basins of
6 the Paraná River, southeastern and southern Brazil. The known localities of *A. castro* are
7 concentrated in tributaries of the Tibagi River basin (Paraná state), including its type locality
8 (Schmitt, 1942; Bond-Buckup & Buckup, 1994; Swiech-Ayoub & Masunari, 2001; Silva *et*
9 *al.*, 2017; Marçal *et al.*, 2018; Almeida *et al.*, 2021; Silva *et al.*, 2021). Besides, there are
10 several records of *A. castro* in the south of São Paulo state, on the right bank of the
11 Paranapanema River (Bond-Buckup & Buckup, 1994; Fransozo *et al.*, 2003; Takano *et al.*,
12 2016). Similarly, *A. schmitti* is mainly distributed in the Paraná state (Trevisan & Masunari,
13 2010; Trevisan *et al.*, 2021). However, the northern limit of the geographic distribution of *A.*
14 *schmitti* is in the Iporanga city, São Paulo state, and the southern limit is in the municipality
15 of Canoinhas, Santa Catarina state (Bond-Buckup & Buckup, 1994; Trevisan & Masunari,
16 2010). Interestingly, molecular studies indicate that *A. castro* and *A. schmitti* are cryptic
17 species complexes (Páez *et al.*, 2018; Trombetta *et al.*, 2019; Marçal *et al.*, 2020, 2021;
18 Marçal *et al.*, in prep). Therefore, its geographic distribution ranges must be interpreted with
19 caution as they may be narrower than currently recognized.

20 *Aegla lata*, *A. jacutinga*, *Aegla* n. sp. 1, *Aegla* n. sp. 2, *Aegla* n. sp. 3, *Aegla* n. sp. 4,
21 and *Aegla* n. sp. 5, on the other hand, have a restricted distribution and are probably endemic
22 to the Tibagi River basin. Literature reveals that *A. lata* is distributed in rivers and small
23 streams that drain into the Tibagi River (Bond-Buckup & Buckup, 1994; Galves *et al.*, 2007;
24 Chaves *et al.*, 2019; Marçal *et al.*, 2020), and it is extinct in the type locality (Pérez-Losada *et*
25 *al.*, 2004, Pérez-Losada *et al.*, 2009). The new records reported on here place *A. lata* in the

1 tributaries of the Tibagi River that drain waters of the Califórnia city (23°39'S, 51°19'W), in
2 north Paraná. Although this species occurs between Londrina city (23°25'S, 51°23'W) and
3 Ponta Grossa city (25°5'S, 50°9'W), its distribution can be considered as fragmented, since
4 there is no record of occurrence in the Middle Tibagi region (see Fig. 2C). Similarly, *A.*
5 *jacutinga* has been recorded along the left bank of the Tibagi River basin (Marçal *et al.*,
6 2020). Our data extend the known distribution of this species to the right bank of the Tibagi
7 River but maintain records only in the Lower Tibagi region (see Fig. 2D).

8 SYSTEMATICS

9 The Bayesian inference tree depicts *A. lata* as sister species to *Aegla* n. sp. 4 and places *Aegla*
10 n. sp. 5 in a subclade with *A. jacutinga* (Fig. 11). Both species belong to clade C of the
11 phylogeny presented in Pérez-Losada *et al.* (2004) (see Marçal *et al.*, 2020). Therefore, it is
12 likely that the new species also belong to clade C. Furthermore, molecular evidence clearly
13 shows that *Aegla* n. sp. 4 and *Aegla* n. sp. 5 are distinct phylogenetic lineage, supporting the
14 morphological differentiation observed. In future investigations, analyzes with other
15 mitochondrial and nuclear genes may be carried out to confirm our hypothesis on the
16 phylogenetic position of the new species.

17 CONSERVATION AND DIVERSITY

18 Regarding the conservation status of the new species, we suggest that *Aegla* n. sp. 4 and
19 *Aegla* n. sp. 5 be classified as “Endangered” (EN) under criteria B1, B2abiii as defined by the
20 International Union for Conservation of Nature (IUCN, 2019). Both species have been
21 recorded in only two localities (B2a) and the known extent of occurrence is estimated to be
22 less than 100 km² (B1). The streams where the specimens of *Aegla* n. sp. 5 were found are
23 located in agricultural and urbanized areas (B2biii). Moreover, in a recent sampling at the
24 type-locality of *Aegla* n. sp. 4 we did not find adult specimens and noticed that the stream is
25 heavily impacted, with hogs being raised next to the watercourse (B2biii).

1 According to our results and extensive literature research, the Tibagi River basin hosts
2 nine species of *Aegla*. This basin, therefore, has a greater number of aeglids species compared
3 to other hydrographic basins in Paraná state, such as Iguaçu (five species), Ivaí (four species),
4 and Cinzas (one species). Raio & Bennemann (2010) revealed that the Middle Tibagi region
5 has the highest fish biodiversity in the state of Paraná and recommend that all tributaries in
6 this region be inventoried, as each one has a different composition. Pérez-Losada *et al.* (2009)
7 assessed the conservation priority of 18 freshwater ecoregions in southern South America
8 based on the diversity and genetic distribution of *Aegla*. This study supports that the
9 Paranapanema River (Upper Paraná ecoregion) contains high biodiversity and identifies it as
10 one of the top priorities for conservation. Considering recent descriptions (Marçal *et al.*, 2020,
11 2021; Marçal *et al.*, in press), the number of *Aegla* species for the Paranapanema River basin
12 increased from 4 to 11. In contrast, most streams sampled in the present study have only small
13 remnants as a riparian forest. Santos *et al.* (2015) reported that the rivers in this region are
14 being degraded by intense deforestation of the banks and the dumping of residues from
15 lumber industries. As a consequence, most species that occur in this basin are under some
16 degree of extinction threat. Given the above considerations, it can be said that the Tibagi
17 River basin is essential for the conservation of the neotropical freshwater biota and, therefore,
18 must be protected.

19 In summary, we have improved the knowledge of the aeglids of the Tibagi River
20 basin. The distributions of *A. castro*, *A. lata*, and *A. jacutinga* were reviewed and extended.
21 Besides, we described two new *Aegla* species from the Middle Tibagi. Of the nine species that
22 occur in the Tibagi River basin, seven are endemic to this basin. Although morphologically
23 conservative, the detailed analysis of the morphology allowed the distinction of the species as
24 well as the construction of a diagnostic key. We emphasize that, for comparison purposes, it is
25 important to have adult male specimens because the full development of chelipeds, spines,

1 and tubercles in these individuals allows a safer interpretation of the diagnostic characters of
 2 the species. Despite several watercourses of the Middle and Lower Tibagi River were
 3 sampled in this study, many parts of the Upper Tibagi have either only a few or no records of
 4 aeglids. We recognize that this inventory represents a small fraction of what remains to be
 5 sampled within the Paraná River basin. However, it is hoped that the data provided by our
 6 research will contribute to revealing the real diversity and distribution patterns of aeglids from
 7 the Paraná River basin.

8

9

KEY TO THE SPECIES OF *AEGLA* FROM TIBAGI RIVER BASIN

- 10 1. Palmar crest of the chelipeds rectangular 2
 11 - Palmar crest of the chelipeds subdisciform to disciform 3
 12 2. Extra-orbital sinus shallow. Epibranchial area strongly elongated. Proximal dorsal margin
 13 of dactylus with moderate size lobe..... *Aegla* n. sp. 4
 14 - Extra-orbital sinus deep. Epibranchial area slightly elongated. Proximal dorsal margin of
 15 dactylus with rudimentary lobe..... *Aegla* n. sp. 5
 16 3. Protogastric lobes poorly pronounced. Uropods narrow *Aegla lata*
 17 - Protogastric lobes pronounced. Uropods wide 4
 18 4. Anterolateral spines not reaching basal margin of cornea 5
 19 - Anterolateral spines reaching or extending beyond basal margin of cornea 6
 20 5. Cervical groove U-shaped. Areola trapezoidal in shape. Rudimentary pleopods in adult
 21 male specimens *Aegla* n. sp. 1
 22 - Cervical groove trapezoidal. Areola subrectangular in shape. Pleopods absent in adult male
 23 specimens..... *Aegla jacutinga*
 24 6. Proximal dorsal margin of dactylus with pronounced lobe 7
 25 - Proximal dorsal margin of dactylus with rudimentary or absent lobe 8

- 1 7. Epigastric prominences poorly pronounced. Chelipeds broadly ovate and inflated. Palmar
2 crest dorsally excavate *Aegla schmitti*
- 3 - Epigastric prominences pronounced. Chelipeds moderately inflated, somewhat elongated.
4 Palmar crest shallowly impressed or excavate *Aegla castro*
- 5 8. Subrostral process occupying proximal half of subrostral margin. Areola subrectangular in
6 shape. Epibranchial area shortened..... *Aegla* n. sp. 2
- 7 - Subrostral process occupying proximal third of subrostral margin. Areola trapezoidal in
8 shape. Epibranchial area slightly elongated..... *Aegla* n. sp. 3

9

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17

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1 **4. CAPÍTULO 3**

2 **THE EFFECTIVENESS OF DNA BARCODING AS A TOOL IN *AEGLA* DIVERSITY**
3 **(CRUSTACEA, AEGLIDAE)**

4

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1 ABSTRACT

2 The barcode region of the cytochrome c oxidase I gene (COI) has been widely used to
3 identify animal taxa. Here, we examine the effectiveness of the COI barcode in discriminating
4 *Aegla* species, freshwater crustacean's endemic to southern South American. We calculated
5 the intra- and interspecific genetic distances based on the Kimura 2-parameter (K2P) model.
6 The Generalized Mixed Yule Coalescent (GMYC) model was also employed to delimit the
7 species. K2P genetic distances were on average 0.2% within species and 5.8% between
8 species. Species that exhibited high intraspecific divergence (>2%) were split into at least two
9 clusters by GMYC analysis, suggesting the presence of cryptic genetic diversity. The levels of
10 nucleotide divergence among the species were from 5 to 29 times greater than the
11 intraspecific divergences. Of the 74 species analyzed, 68 (92%) were correctly identified by
12 their barcode sequences. Thus, our results confirm the effectiveness of the COI barcode in
13 identifying *Aegla* species. In addition, possible cryptic taxa and genetically divergent lineages
14 were revealed in 22 investigated species. This study provides the first comprehensive
15 assessment of the genetic distances of aeglids species and therefore lays the groundwork for
16 future research. Given the richness, ecological relevance, high degree of endemism, and threat
17 of the *Aegla* genus, the validation, and standardization of tools such as the DNA barcode are
18 essential for the correct interpretation of diversity and the conservation of these crustaceans.

19

20 KEYWORDS: COI, cryptic species, genetic distance, species identification, molecular
21 taxonomy

22

1 INTRODUCTION

2 *Aegla* Leach, 1820 is currently represented by 90 species and subspecies (Trombetta et al.,
3 2019; Marçal et al., 2020, 2021) exclusively from freshwater of the temperate and subtropical
4 regions of southern South America (Schmitt, 1942a). The first described species was named
5 *Galathea laevis* Latreille, 1818, among marine crustaceans (Schmitt, 1942a). Through a more
6 accurate examination of the specimens deposited at the Muséum National D'Histoire
7 Naturelle in 1820, Leach proposed the genus *Aegla* for the species of Latreille (Bond-Buckup
8 & Buckup, 1994). For many years, several authors argued that the genus *Aegla* would have a
9 single species with wide distribution, occurring in watercourses in southern Brazil, Argentina,
10 and Chile (Bond-Buckup & Buckup, 1994). However, in 1942, Schmitt described 17 new
11 species and validated two other species, in addition to *Aegla laevis* (Latreille, 1818) (see
12 Schmitt 1942a, 1942b), demonstrating that the morphological differences noted in the
13 analyzed specimens could not be attributed to variations in a single species. Since then,
14 several studies have shown subtle differences in the morphological characters of the aeglids
15 (Buckup & Rossi, 1977; Jara, 1977, 1982; Jara & López, 1981; Bond-Buckup & Buckup,
16 1994; Jara & Palacios, 1999).

17 For more accurate discrimination of many aeglid species, several taxonomists have
18 used molecular techniques along with morphological data (Jara et al., 2003; Bond-Buckup et
19 al., 2010; Santos et al., 2009, 2010, 2012, 2013, 2015; Moraes et al., 2016; Jara et al., 2018;
20 Páez et al., 2018; Trombetta et al., 2019; Marçal et al., 2020, 2021). According to Hillis
21 (1987), molecular techniques can potentially reveal levels of genetic differentiation hidden in
22 morphologically similar populations. The phylogeny presented by Pérez-Losada et al. (2004),
23 for example, indicates that *Aegla cholchol* Jara & Palacios, 1999, *Aegla jarai* Bond-Buckup &
24 Buckup, 1994, *Aegla parana* Schmitt, 1942, *Aegla marginata* Bond-Buckup & Buckup, 1994,
25 *Aegla platensis* Schmitt, 1942 and *Aegla franciscana* Buckup & Rossi, 1977 form non-

1 monophyletic groups. Pérez-Losada et al. (2002) had already made similar observations for *A.*
2 *cholchol*. Under Cracraft's (1983) species concepts, populations that do not form
3 monophyletic groups qualify as distinct species. Thus, according to Pérez-Losada et al.
4 (2004), the conflict between alpha taxonomy and the results of gene trees may represent
5 unrecognized species (cryptic species). This assumption was later confirmed with the
6 description of *Aegla quilombola* Moraes, Tavares & Bueno, 2017, from one of the
7 populations formerly designated as *A. marginata* (Moraes et al., 2017).

8 There are various other examples of cryptic species within aeglids. For example,
9 morphological and molecular analyses showed that *Aegla paulensis* Schmitt, 1942 was a
10 complex with at least seven different species (Santos et al., 2015; Moraes et al., 2016). The
11 Ribeira de Iguape basin population was described as *Aegla lancinhas* Bond-Buckup &
12 Buckup, 2015 in Santos et al., 2015, and four populations of the Tietê basin were described as
13 new species (Moraes et al., 2016). Crivellaro et al. (2017) analyzed 17 populations attributed
14 to *Aegla longirostri* Bond-Buckup & Buckup, 1994, using two species delimitation methods,
15 and identified at least 14 potential species. Jara et al. (2018) described *Aegla chilota* Jara,
16 Pérez-Losada & Crandall, 2018 from a population preliminary designate as *Aegla*
17 *araucaniensis* Jara, 1980. Overlooked species were also reported between populations of *A.*
18 *platensis* and *Aegla uruguayana* Schmitt, 1942 (Zimmermann et al., 2018, 2021).
19 Furthermore, *Aegla jacutinga* Marçal & Teixeira, 2020 was described from populations
20 morphologically similar to *Aegla lata* Bond-Bukup & Buckup, 1994 (Marçal et al., 2020).

21 A molecular technique commonly used in species identification is DNA barcode, in
22 which each taxon would be identified by having a unique DNA sequence (Hebert et al.,
23 2003). Surveys such as that conducted by Hebert et al. (2003) have shown that the barcode
24 region of the cytochrome c oxidase I gene (COI) is a successful taxonomic tool for
25 identifications of known animal species and the recognition of undescribed ones. This

1 technique has been effectively used to discriminated species of lepidopterans (Hebert et al.,
2 2003; Janzen et al., 2005), birds (Hebert et al., 2004), spiders (Barrett & Hebert, 2005), ants
3 (Smith et al., 2005), fishes (Ward et al., 2005; Pereira et al., 2011, 2013; Souza-Shibatta et al.,
4 2018), crustaceans (Lefébure et al., 2006; Costa et al., 2007; Havermans et al., 2011; Matzen
5 da Silva et al., 2011) and others. The predominant approach used to analyze diversity patterns
6 with the COI barcode region is the classic pairwise distance method based on the Kimura 2-
7 parameter (K2P) model (Matzen da Silva et al., 2011). This method premise that genetic
8 distance between individuals of the same species (intraspecific divergence) is smaller than the
9 variation between different species (interspecific divergence) (Hebert et al., 2004; Ribolli et
10 al., 2017). Thus, a standard sequence threshold of ten times the mean intraspecific variation
11 was proposed by Hebert et al. (2004) and has been successfully employed in the delimitation
12 of some groups (Hebert et al., 2004; Witt et al., 2006; Ferri et al., 2009). Matzen da Silva et
13 al. (2011), assuming an intraspecific barcode threshold of a maximum of 2%, had success
14 around 98% in recognizing marine decapods. Lefébure et al. (2006) analyzed Aeglidae COI
15 sequences with another 17 different families of Crustacea and proposed a molecular threshold
16 to help species delimitation. However, this threshold was calculated excluding *Aegla* genus
17 sequences from the analysis. Thus, no study has evaluated genetic distances and proved the
18 success of the COI barcode for delimiting aeglids. Currently, 74 of the 90 morphologically
19 described species of *Aegla* have at least one COI sequence deposited in GenBank or BOLD
20 databases. Therefore, the present study aims to examine the effectiveness of the COI barcode
21 for species recognition in *Aegla*. We tested whether the 2% genetic distance threshold can
22 also be applied for *Aegla* delimitation.

23

24

25

1 MATERIAL AND METHODS

2 COI Profile

3 *Aegla* species COI sequences were accessed from the GenBank and BOLD databases. At least
4 five sequences per species were determined to maximize the recovery of high intraspecific
5 variation (Meyer & Pauley, 2005). Nevertheless, to avoid an imbalance in the representation
6 of some taxa, the maximum limit of ten sequences per species was established (Lefébure et
7 al., 2006). Sixteen species of *Aegla* (*Aegla charon* Bueno & Moraes, 2017, *A. expansa* Jara,
8 1992, *A. intermedia* Girard, 1855, *A. japi* Moraes, Tavares & Bueno, 2016, *A. jaragua*
9 Moraes, Tavares & Bueno, 2016, *A. jundiai* Moraes, Tavares & Bueno, 2016, *A. leachi* Bond-
10 Buckup & Buckup, 2012, *A. microphthalma* Bond-Buckup & Buckup, 1994, *A. muelleri*
11 Bond-Buckup & Buckup, 2010, *A. oblata* Bond-Buckup & Santos, 2012, *A. occidentalis* Jara,
12 Pérez-Losada & Crandall, 2003, *A. pomerana* Bond-Buckup & Buckup, 2010, *A. renana*
13 Bond-Buckup & Santos, 2010, *A. rosanae* Campos Jr., 1998, *A. saltensis* Bond-Buckup &
14 Jara, 2010, and *A. vanini* Moraes, Tavares & Bueno, 2016) do not have COI sequences
15 available and were not included in the analyses. Overall, 263 DNA sequences were selected to
16 establish a COI profile referred to here as dataset A.

17 Data Analysis

18 DNA sequences were aligned using the ClustalW algorithm in the MEGA v6 software
19 (Tamura et al., 2013). Genetic distances within species (intraspecific) and between species
20 (interspecific) were calculated based on the Kimura-2-parameter model (Kimura, 1980).
21 Histograms of the frequency distribution of intra- and interspecific distances from dataset A
22 were made. A Neighbor-joining (NJ) tree was created to provide a graphic representation of
23 the relationships among specimens.

24 The second method used to detect the transition point between intra- and interspecific
25 relations was the Generalized Mixed Yule Coalescent (GMYC) approach based on single-

1 locus data, a relatively robust tool for species delimitation (Pons et al., 2006; Fujisawa &
2 Barraclough, 2013). First, an ultrametric tree was generated using Bayesian inference. Then,
3 Bayesian analysis was conducted in BEAST 2.6.2 (Bouckaert et al., 2019) with a strict
4 molecular clock, a Birth-Death model, and a sequence evolution model estimated by
5 jModelTest2 (Darriba et al., 2012). If the best-fit model is not implemented in BEAST, we
6 replaced it with the closest over-parameterized model following Lecocq et al. (2013). A run of
7 10,000,000 generations, sampling one tree every 1,000 generations, was performed. The
8 subsequent probability of sufficient minimum effective sample size ($ESS > 200$) was verified
9 in TRACER 1.6. The TREEANNOTATOR 2.6.2 summarized the trees, with a burn-in of
10 25%. Finally, GMYC was performed from the ultrametric tree in the “Splits” package (Pons
11 et al., 2006; Fujisawa & Barraclough, 2013) with the R 3.5.1 program.

12 We identified the sequences of possible cryptic species, i.e., those that formed non-
13 monophyletic clades and/or presented intraspecific distances values \geq of 2%. Then, we
14 calculated the genetic distances considering each cryptic species as an independent genetic
15 unit. This dataset is here called B. In dataset B, the species delimitation performed by GMYC
16 analysis was considered. Therefore, species that were grouped with congeners were treated as
17 being only one.

18

19 RESULTS

20 COI sequences ranged in length from 615 to 1045 base pairs (bp), comprising 1292 bp in
21 alignment. No stop codons, deletions, or insertions were observed. A few species (*Aegla*
22 *bahamondei* Jara, 1982, *A. carinata* Bond-Buckup & Loureiro, 2014, *A. spectabilis* Jara,
23 1986, *A. franca* Schmitt, 1942, *A. singularis* Ringuelet, 1948, and *A. inconspicua* Bond-
24 Buckup & Buckup, 1994) had only one sequence available in the databases. However, two to
25 four sequences were obtained for most species (56) and five or more for 12 species.

1 Analysis Of The Molecular Dataset A

2 The genetic distance matrix of dataset A (Table 1) showed that the divergences between
 3 conspecific individuals were usually small, ranging from 0.0% to 8.9% (mean = 1.1%). The
 4 frequency distribution graph of K2P divergence values showed that 74% of the intraspecific
 5 comparisons were less than 2% (Figure 1). In contrast, 21 species exhibited intraspecific
 6 distance values that exceeded 2%, suggesting the presence of cryptic genetic diversity (Table
 7 1). GMYC analysis confirmed at least two different strains among these species. These cases
 8 raise the global mean intraspecific divergence and are responsible for the slight overlap
 9 between intra- and interspecific variations (Figure 1). Moreover, of the 17 species that formed
 10 non-monophyletic groups in the Neighbor-joining tree (Figure 2), 16 presented high within-
 11 species distances (values > 2%). The exception is *Aegla brevipalma* Bond-Buckup & Santos,
 12 2012, with a maximum intraspecific K2P distance of 1.5%.

13

14 **TABLE 1.** Pairwise COI barcode nucleotide divergences for *Aegla* species using K2P
 15 distances (%). N represents the number of analyzed sequences.

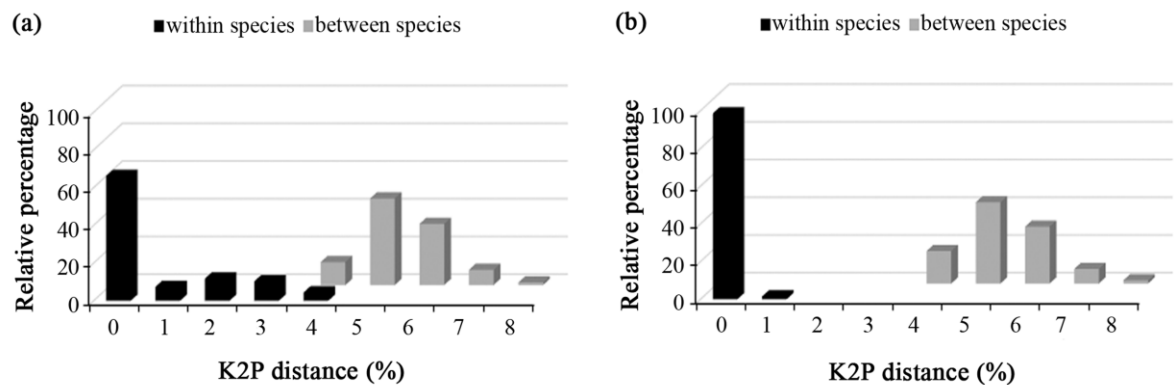
Species	N	Intraspecific distance			Interspecific distance		
		Min.	Mean	Max.	Min.	Mean	Max.
<i>Aegla abtao</i>	8	0.0	2.2	3.7	1.5	5.7	9.6
<i>Aegla affinis</i>	4	0.0	0.2	0.3	3.3	6.2	9.8
<i>Aegla alacalufi</i>	10	0.0	0.2	0.6	1.5	5.4	8.8
<i>Aegla araucaniensis</i>	2	0.9	0.9	0.9	2.1	4.8	9.5
<i>Aegla bahamondei</i>	1	–	–	–	2.7	5.4	7.9
<i>Aegla brevipalma</i>	2	1.5	1.5	1.5	0.9	4.5	8.5
<i>Aegla buenoi</i>	4	0.0	0.0	0.0	0.9	5.2	9.6
<i>Aegla camargoi</i>	4	0.3	2.7	3.7	2.1	5.6	10.2
<i>Aegla carinata</i>	1	–	–	–	3.0	5.1	7.9
<i>Aegla castro</i>	3	2.1	2.8	3.6	1.2	5.7	10.2
<i>Aegla cavernicola</i>	2	0.0	0.0	0.0	1.5	4.6	8.5
<i>Aegla chilota</i>	10	0.0	0.1	0.6	2.7	6.1	9.3
<i>Aegla chochol</i>	10	0.0	1.5	3.7	2.4	5.9	9.5
<i>Aegla concepcionensis</i>	2	0.3	0.3	0.3	2.7	5.5	8.6
<i>Aegla denticulata denticulata</i>	2	0.0	0.0	0.0	0.0	5.6	8.5
<i>Aegla denticulata lacustris</i>	2	0.0	0.0	0.0	0.0	5.6	8.5

<i>Aegla franca</i>	1	–	–	–	3.4	5.9	9.6
<i>Aegla franciscana</i>	3	0.6	2.0	3.0	0.9	5.0	9.2
<i>Aegla georginae</i>	10	0.0	2.9	4.9	4.3	7.3	11.4
<i>Aegla grisella</i>	4	0.6	3.3	4.6	2.7	6.0	10.6
<i>Aegla hueicollensis</i>	2	0.0	0.0	0.0	2.7	6.5	9.2
<i>Aegla humahuaca</i>	2	0.0	0.0	0.0	2.4	5.5	8.5
<i>Aegla inconspicua</i>	1	–	–	–	3.7	6.6	9.2
<i>Aegla inermis</i>	2	0.3	0.3	0.3	3.0	6.5	10.9
<i>Aegla intercalata</i>	3	3.0	3.1	3.3	2.1	5.3	8.9
<i>Aegla itacolomiensis</i>	3	0.0	0.0	0.0	3.3	5.5	10.6
<i>Aegla jacutinga</i>	4	0.0	0.2	0.3	0.9	5.6	10.2
<i>Aegla jarai</i>	10	0.0	2.4	4.0	0.0	4.8	9.6
<i>Aegla jujuyana</i>	2	0.6	0.6	0.6	2.1	6.7	10.2
<i>Aegla laevis</i>	2	0.0	0.0	0.0	2.4	5.1	8.8
<i>Aegla lancinhas</i>	2	0.9	0.9	0.9	2.1	5.5	9.3
<i>Aegla lata</i>	4	0.0	0.0	0.0	3.3	7.2	11.6
<i>Aegla leptochela</i>	2	0.0	0.0	0.0	0.0	6.2	10.2
<i>Aegla leptodactyla</i>	2	0.9	0.9	0.9	3.0	5.7	9.5
<i>Aegla ligulata</i>	3	0.0	0.6	0.9	0.9	6.0	9.5
<i>Aegla longirostri</i>	10	0.0	4.5	8.9	2.4	6.6	12.0
<i>Aegla loyolai</i>	3	0.0	0.0	0.0	2.4	5.6	8.9
<i>Aegla ludwigi</i>	10	0.0	0.2	0.6	4.0	6.4	10.7
<i>Aegla manni</i>	3	0.0	1.4	2.1	1.8	5.7	9.3
<i>Aegla manuinflata</i>	3	0.0	0.2	0.3	3.0	5.0	7.8
<i>Aegla marginata</i>	2	0.0	0.0	0.0	4.6	6.4	8.9
<i>Aegla meloi</i>	3	0.0	0.2	0.3	2.4	5.1	8.5
<i>Aegla nebeccana</i>	2	0.0	0.0	0.0	3.6	6.7	10.6
<i>Aegla neuquensis</i>	2	0.0	0.0	0.0	2.4	6.5	9.9
<i>Aegla obstipa</i>	2	0.3	0.3	0.3	3.7	6.5	9.9
<i>Aegla odebrechtii</i>	2	0.9	0.9	0.9	1.8	4.6	7.9
<i>Aegla okora</i>	4	0.0	0.0	0.0	3.0	5.8	9.5
<i>Aegla papudo</i>	2	0.0	0.0	0.0	4.7	7.4	11.1
<i>Aegla parana</i>	2	4.6	4.6	4.6	1.2	5.5	10.2
<i>Aegla parva</i>	2	0.0	0.0	0.0	2.1	5.0	8.9
<i>Aegla paulensis</i>	2	1.2	1.2	1.2	2.1	5.0	9.9
<i>Aegla perobae</i>	2	0.3	0.3	0.3	4.0	7.5	11.4
<i>Aegla pewenchaе</i>	3	0.0	0.0	0.0	3.7	6.4	10.3
<i>Aegla plana</i>	2	0.0	0.0	0.0	2.7	5.8	9.2
<i>Aegla platensis</i>	10	0.0	3.8	6.8	0.6	7.4	12.0
<i>Aegla prado</i>	2	0.0	0.0	0.0	4.0	6.6	9.6
<i>Aegla quilombola</i>	2	0.3	0.3	0.3	0.0	6.3	10.2
<i>Aegla ringueleti</i>	2	0.3	0.3	0.3	4.6	7.6	10.3
<i>Aegla riolimayana</i>	4	0.0	0.0	0.0	1.5	4.6	7.9
<i>Aegla rossiana</i>	2	0.0	0.0	0.0	2.4	5.6	7.9

<i>Aegla rostrata</i>	10	0.0	0.1	0.3	3.0	6.1	9.2
<i>Aegla sanlorenzo</i>	2	3.0	3.0	3.0	2.1	6.7	10.9
<i>Aegla scamosa</i>	3	0.3	3.3	4.9	3.7	6.3	9.2
<i>Aegla schmitti</i>	2	2.1	2.1	2.1	1.5	4.6	8.5
<i>Aegla septentrionalis</i>	2	0.0	0.0	0.0	3.7	6.4	10.5
<i>Aegla serrana</i>	3	1.2	3.5	4.6	2.7	5.9	9.3
<i>Aegla singularis</i>	1	–	–	–	4.0	8.5	11.1
<i>Aegla spectabilis</i>	1	–	–	–	1.8	4.6	8.2
<i>Aegla spinipalma</i>	4	0.0	0.3	0.6	3.3	6.5	11.6
<i>Aegla spinosa</i>	2	0.3	0.3	0.3	0.0	4.6	8.9
<i>Aegla strinatii</i>	3	0.3	1.8	2.7	1.5	5.5	9.9
<i>Aegla talcahuano</i>	3	1.2	3.5	5.2	2.4	5.7	9.6
<i>Aegla uruguayana</i>	10	0.0	4.2	7.4	0.6	6.5	9.6
<i>Aegla violacea</i>	5	0.0	2.2	3.7	2.4	5.6	9.2

1

2



3

4 **Figure 1.** Frequency distribution of mean intraspecific (black bars) and interspecific (gray
5 bars) distances for *Aegla* species: (a) dataset A; (b) dataset B.

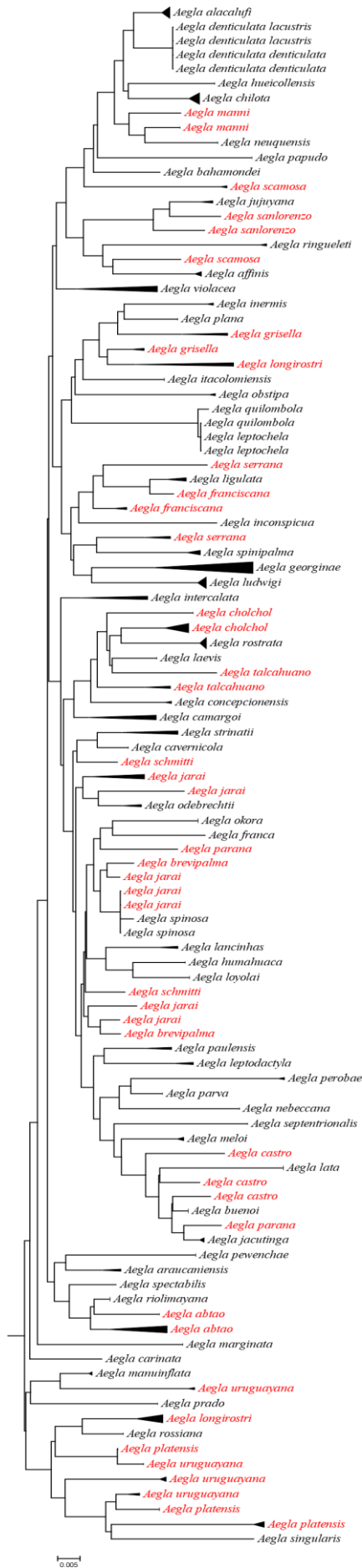


Figure 2. Neighbor-joining tree based on analysis of 263 COI sequences from 74 species of *Aegla*. Clusters with sequences of the same species are collapsed. Non-monophyletic taxa are colored in red. The branch length represents the Kimura 2-Parameter (K2P) distances.

1 The K2P genetic distance between species ranged from 0.0% to 12.0% (mean = 5.9%),
2 about five times greater than the intraspecific variation. Most species had a minimum
3 interspecific distance above 2%, which allowed correct discrimination of 92% of analyzed
4 species (68 of 74). In three exceptional cases, the interspecific distances were 0.0%. They
5 included the divergence between *Aegla denticulata denticulata* Nicolet, 1849 and *A.*
6 *denticulata lacustris* Jara, 1986; two sequences of *A. jarai* (AY595594, AY595595) and *A.*
7 *spinosa* Bond-Buckup & Buckup, 1994; *A. leptochela* Bond-Buckup & Buckup, 1994 and *A.*
8 *quilombola*. GMYC analysis joined these sequences into three clades as if they represented
9 only three species instead of six. Additionally, two sequences of *A. platensis* (AY595627,
10 AY595628) and *A. uruguayana* (MT489799, MT489800) presented 0.6% of the genetic
11 distance between them and were grouped by the delimitation analysis. Another 16 species
12 showed low divergences (0.9–1.8%) with some congeners. Nevertheless, in all cases, they
13 were delimited from their congeners by the GMYC method.

14 The model of sequence evolution applied in dataset A was GTR + I + G ($\alpha = 0.6480$,
15 proportion of invariant sites = 0.5570). Mean base frequencies were A: 0.2864, C: 0.1279, G:
16 0.1455, T: 0.4402. Transition/transversion rates were AC: 2.6831, AG: 19.2160, AT: 1.4111,
17 CG: 1.6919, CT: 16.2188, GT: 1.0000. Concerning species delimitation, the GMYC analysis
18 indicated the presence of 116 independent strains. Twenty-three species were split into two
19 clusters or even more (Figure 3). Surprisingly, the ten *A. jarai* sequences were separated into
20 nine strains. Data analysis in R is available as Supporting information Text S1.



Figure 3. Bayesian tree based on COI sequences of *Aegla*. Numbers above branches are posterior probabilities (values < 0.5 are not indicated). The vertical line indicates species delimitation assigned in GMYC analysis. Split species are colored in red. Grouped species are colored in blue.

1 Analysis Of The Molecular Dataset B

2 The average K2P distance within species was only 0.2%, while congeneric divergence
3 averaged 5.8% (Table S1). Considering these values, the barcode gap among congeneric and
4 intraspecific comparisons increases to 29 times. Furthermore, intraspecific divergences were
5 below 1% for 99% of the within-species comparisons in this dataset (Figure 1B). By contrast,
6 more than 82% of interspecific distance values exceeded 5%. As shown in Figure 1, there was
7 no overlap between the intra- and interspecific distance values for dataset B, contrary to
8 dataset A.

9

10 DISCUSSION

11 This study provides the first comprehensive assessment of the genetic distances of aeglids
12 species and includes sequences from 263 individuals in 74 supposed taxa, representing about
13 82% of the aeglids species recognized to date. Observed divergences were below 1% within
14 species of *Aegla* for 66% of analyzed taxa in dataset A. This finding is consistent with those
15 of Costa et al. (2007) for species of decapods (87%), *Gammarus* (75%), and *Daphnia* (59%).
16 However, with the approach used in dataset B, the intraspecific distance was less than 1% in
17 99% of cases. The average intraspecific distance calculated for dataset A was 1.1%. In some
18 cases, this divergence between individuals of the same species was greater than 2%. We
19 believe these high values are due to the presence of unrecognized cryptic species. When these
20 cryptic species complexes are considered independent genetic units (dataset B), the mean K2P
21 intraspecific divergence is 0.2%. These results align with data reported for other crustaceans
22 (Costa et al., 2007; Havermans et al., 2011; Matzen da Silva et al., 2011).

23 Extensive research has shown that several *Aegla* species represent in fact complexes of
24 morphologically similar (cryptic) species with restricted distribution (Pérez-Losada et al.,
25 2002, 2004; Santos et al., 2015; Moraes et al., 2016, 2017; Crivellaro et al., 2017; Jara et al.,

1 2018; Marçal et al., 2020; Zimmermann et al., 2021). Our study supports evidence from
2 previous observations. For example, the deep divergence observed combined with
3 phylogenetic and geographic distribution data (Pérez-Losada et al., 2002) reinforces the
4 possibility of overlooked species within *A. cholchol* and *A. talcahuano* Schmitt, 1942. Based
5 on the high intraspecific distances and the separation into two clusters by GMYC analysis, the
6 *A. franciscana*, *A. parana*, and *A. schmitti* Hobbs, 1979 complexes seem to consist of two
7 different species. These results corroborate the findings of Pérez-Losada et al. (2004), Páez et
8 al. (2018) and Marçal et al. (2020). Under the present results, previous molecular analyzes
9 have demonstrated the non-monophyly of *A. brevipalma*, *A. castro* Schmitt, 1942, *A. grisella*
10 Bond-Buckup & Buckup, 1994, and *A. jarai* (Pérez-Losada et al., 2004; Trombetta et al.
11 2019). The deep barcode divergences within *A. longirostri*, *A. platensis*, and *A. uruguayana*
12 members suggest the presence of overlooked species, confirming similar observations of
13 Crivellaro et al. (2017), Zimmermann et al. (2018), and Zimmermann et al. (2021).
14 Additionally, possible cryptic taxa and genetically divergent lineages were revealed in *A.*
15 *abtao* Schmitt, 1942, *A. camargoi* Buckup & Rossi, 1977, *A. georginae* Santos & Jara, 2013,
16 *A. intercalata* Bond-Buckup & Buckup, 1994, *A. manni* Jara, 1980, *A. sanlorenzo* Schmitt,
17 1942, *A. scamosa* Ringuelet, 1948, *A. serrana* Buckup & Rossi, 1977, *A. strinatii* Türkay,
18 1972, and *A. violacea* Bond-Buckup & Buckup, 1994.

19 Our genetic distance matrix also indicated that divergence values between species are
20 ordinarily greater than 2%. When this value was employed as a threshold for species
21 diagnosis, 50 out of the 74 species were recognized. The exceptions comprise six species that
22 showed 0.0% of the minimum interspecific distance, two species that presented 0.6% of the
23 distance between some specimens, and 16 congeneric pairs that were genetically distinct but
24 showed low (0.9–1.8%) divergences. In the first case, the COI barcode grouped the two
25 subspecies *A. denticulata denticulata* and *A. denticulata lacustris*, with 0.0% distance. Such

1 genetic similarity indicates that these subspecies should be maintained as a single species.
2 Together, their similar morphological characteristics and the lack of barcode divergence
3 suggest that *A. denticulata lacustris* is a synonym of *A. denticulata denticulata*. The 0.0%
4 distance was also observed between *A. leptochela* and *A. quilombola*. Morphologically, *A.*
5 *quilombola* can be distinguished from related species *A. leptochela* by the well-developed
6 cornea, whereas *A. leptochela* possesses reduced cornea, an adaptation to obligatory cave-
7 dwelling (Bond-Buckup & Buckup, 1994; Moraes et al., 2017). However, both species were
8 collected in the same cave, “Caverna dos Paiva”, Ribeira do Iguape, Brazil (see Pérez-Losada
9 et al., 2004), and do not show genetic divergence, suggesting that they are a single species.
10 Likewise, we point out that one population of *A. jarai* (AY595594, AY595595) and *A.*
11 *spinosa* (AY595576, AY595577) are synonymous. Furthermore, there was confirmation of a
12 single species, through GMYC analysis, in both cases. It is noteworthy that the sequences
13 referred to here as *A. quilombola* were deposited in GenBank as *A. marginata* and later
14 described as *A. quilombola* (see Moraes et al., 2017).

15 *Aegla uruguayana* and *A. platensis* have a wide distribution, occurring in streams in
16 Argentina, Brazil, and Uruguay (Schmitt, 1942a). Most *A. platensis* populations belong to a
17 single species, but two potentially new species were reported (Zimmermann et al., 2018). On
18 the other hand, *A. uruguayana* was suggested as a complex of at least ten cryptic species
19 (Zimmermann et al., 2021). Thus, in addition to occurring in the same hydrographic basins,
20 both species were suggested as a species complex (Zimmermann et al., 2018, 2021). In our
21 study, only two sequences of each species showed a low genetic distance (0.6%) and were
22 grouped in the GMYC analysis. It may be the case, therefore, that these sequences represent a
23 cryptic species not yet described. However, detailed morphological and molecular analyzes
24 are needed to support this hypothesis.

25 The low interspecific divergences presented by the 16 congeneric pairs may indicate

1 more recent speciation. According to a phylogenetic study of *Aegla*, the radiation of aeglids
2 towards the freshwater habitats began at least 60 Mya, but some taxa show a more recent age
3 than their sister relatives (Pérez-Losada et al., 2004). Interestingly, these species have low
4 interspecific distances with congeners that belong to the same clade. For example, *A.*
5 *riolimayana* Schmitt, 1942, and *A. abtao* have 1.5% K2P distance, and both are grouped in
6 clade A of the phylogeny presented in Pérez-Losada et al. (2004). Similar values of low
7 divergence between closely related *Aegla* species were observed by Jara et al. (2003) and
8 Páez et al. (2018).

9 Several studies have demonstrated that genetic divergence is much lower within
10 species than among species (Hebert et al., 2003; Hebert et al., 2004; Lefébure et al., 2006;
11 Costa et al., 2007; Ferri et al., 2009; Tang et al., 2009; Havermans et al., 2011; Matzen da
12 Silva et al., 2011; Pereira et al., 2011, 2013). In particular, studies with crustaceans have
13 reported nucleotide sequence divergence levels from 6 to 48 times greater among congeneric
14 than in intraspecific variation (Costa et al., 2007; Havermans et al., 2011; Matzen da Silva et
15 al., 2011). Consistent with the literature, the divergence between closely related *Aegla* species
16 was 5 to 29 times higher than the genetic distances within species.

17 In general, our results based on DNA barcoding show that genetic divergences do not
18 correspond to all currently morphological classifications of the *Aegla* species. Some species
19 formed non-monophyletic groups in the NJ tree and showed unusually high intraspecific
20 distances, comprising a complex of cryptic species. When considering species complexes
21 (dataset A), it is possible to observe an overlap between intra- and inter-specific divergences,
22 but a barcoding gap exists between independent genetic units (dataset B). By the way, the
23 occurrence of cryptic species can change species richness, endemism, and, consequently, the
24 importance of a given region for conservation. Therefore, recognize the cryptic species is
25 crucial to understanding the diversity and distributional patterns of *Aegla*.

1 In summary, accurate discrimination of 92% of the analyzed species confirms the
2 effectiveness of the COI barcode in identifying *Aegla* species. Furthermore, the application of
3 the 2% threshold revealed many overlooked species. Our analyses suggest that the 74
4 supposed taxa possibly represent 116 species, pointing to at least 40 candidates for new
5 species. Nevertheless, caution must be taken to establish that value as a threshold to delimit
6 *Aegla* species, as a few species exhibit low interspecific divergences. According to Hebert et
7 al. (2003), an identification system based on COI provides a higher taxonomic resolution than
8 morphological studies achieve. However, this does not mean that DNA barcoding should be
9 considered a substitute for conventional taxonomic approaches (Costa et al., 2007; Havermans
10 et al., 2011). On the contrary, this tool should collaborate with morphological and ecological
11 data in an integrative taxonomic framework to delimit species. Considering the above, we
12 conclude that the barcode region of COI has considerable potential as a species identification
13 system for *Aegla* and recommend a critical examination of the morphology of the specimens
14 belonging to the species complexes recognized here to define new species.

15

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2

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```
1 SUPPORTING INFORMATION
2 S1 Text. Statistical analyses in R.
3
4 > library(splits)
5 Loading required package: ape
6 Loading required package: MASS
7 Loading required package: paran
8 Warning messages:
9 1: package 'ape' was built under R version 3.5.3
10 2: package 'MASS' was built under R version 3.5.3
11 3: package 'paran' was built under R version 3.5.3
12 > setwd("C:/Users/Ingrid/Desktop/ANALISES/datasetA")
13 > list.files()
14 [1] "datasetA.fas"          "datasetA.fas.jmodeltest.console"
15 [3] "datasetA.log"         "datasetA.tre"
16 [5] "datasetA.trees"       "datasetA.xml"
17 [7] "datasetA.xml.state"
18 > tree<-read.nexus("datasetA.tre")
19 > plot(tree)
20 > result<-gmyc(tree)
21 node T loglik
22 2 -0.05602779 2081.693
23 3 -0.05511339 2082.087
24 4 -0.05275027 2079.416
25 5 -0.05243123 2080.026
26 6 -0.05172594 2083.238
27 7 -0.05122257 2083.74
28 8 -0.04819222 2091.224
29 9 -0.04755885 2092.846
30 10 -0.04745702 2094.322
31 11 -0.04734627 2097.092
32 12 -0.04657236 2096.316
33 13 -0.04621604 2094.516
```

1	14	-0.04493611	2098.331
2	15	-0.04293636	2097.82
3	16	-0.04277671	2097.051
4	17	-0.04254546	2098.444
5	18	-0.04222827	2110.291
6	19	-0.04197059	2109.367
7	20	-0.04150058	2109.998
8	21	-0.03909064	2109.126
9	22	-0.03896916	2112.115
10	23	-0.03895294	2114.617
11	24	-0.03885646	2115.453
12	25	-0.03850913	2115.352
13	26	-0.03816218	2115.665
14	27	-0.03786279	2115.993
15	28	-0.03732883	2116.557
16	29	-0.03703917	2123.372
17	30	-0.03652243	2122.82
18	31	-0.03518532	2124.554
19	32	-0.03483764	2125.017
20	33	-0.03462127	2124.114
21	34	-0.03447047	2124.108
22	35	-0.03435416	2126.673
23	36	-0.03399086	2128.402
24	37	-0.03389817	2128.821
25	38	-0.03326683	2128.274
26	39	-0.03315082	2129.011
27	40	-0.03288373	2129.49
28	41	-0.03267097	2129.224
29	42	-0.0323704	2129.427
30	43	-0.03224613	2130.403
31	44	-0.03147891	2130.196
32	45	-0.03114129	2130.065
33	46	-0.03113334	2132.491
34	47	-0.03091816	2137.498

1 48 -0.03070205 2139.041
2 49 -0.03024998 2137.515
3 50 -0.03014661 2137.511
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5 52 -0.02955245 2137.993
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14 61 -0.02813398 2140.529
15 62 -0.02812204 2140.644
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18 65 -0.02764868 2132.24
19 66 -0.0272275 2133.007
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29 76 -0.02201123 2137.335
30 77 -0.0214402 2137.733
31 78 -0.02100443 2139.05
32 79 -0.02062045 2139.785
33 80 -0.02039419 2140.112
34 81 -0.02015052 2140.564

1 82 -0.01999971 2144.693
2 83 -0.01994574 2146.019
3 84 -0.01923904 2145.762
4 85 -0.01908057 2151.33
5 86 -0.01901551 2151.755
6 87 -0.01856439 2152.312
7 88 -0.01823988 2153.451
8 89 -0.01686373 2154.055
9 90 -0.01682902 2155.157
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12 93 -0.0149447 2157.316
13 94 -0.01463296 2157.162
14 95 -0.01417129 2157.686
15 96 -0.01294575 2158.227
16 97 -0.01286689 2158.511
17 98 -0.0127169 2159.097
18 99 -0.01267388 2159.73
19 100 -0.01202392 2160.382
20 101 -0.01186094 2161.139
21 102 -0.0113388 2162.227
22 103 -0.01097384 2162.96
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28 109 -0.007946611 2166.897
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33 114 -0.005377145 2168.577
34 115 -0.005291607 2168.627

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3	118	-0.005022691	2167.862
4	119	-0.004703982	2167.746
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6	121	-0.00449762	2167.726
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8	123	-0.00419344	2167.781
9	124	-0.004103798	2168.166
10	125	-0.004031266	2167.691
11	126	-0.003957583	2167.367
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16	131	-0.003082397	2164.635
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18	133	-0.002966112	2162.333
19	134	-0.002851943	2161.519
20	135	-0.002789063	2159.636
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22	137	-0.0026708	2156.702
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27	142	-0.002502989	2150.748
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29	144	-0.002363059	2147.916
30	145	-0.002319079	2146.442
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20 169 -0.001545323 2117.58
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24 173 -0.001449012 2114.869
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6	223	-0.0008193528	2075.727
7	224	-0.0008191383	2075.558
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8 259 -0.0003746216 2078.461
9 260 -0.0003492908 2079.07
10 261 -0.0003460862 2079.737
11 262 -0.0003382677 2080.471
12
13 Wed Jul 21 17:48:33 2021
14 finish.
15 > summary(result)
16 Result of GMYC species delimitation
17
18     method: single
19     likelihood of null model:    2079.694
20     maximum likelihood of GMYC model:    2168.666
21     likelihood ratio:    177.943
22     result of LR test:    0***
23
24     number of ML clusters: 68
25     confidence interval: 67-72
26
27     number of ML entities: 116
28     confidence interval: 109-127
29
30     threshold time: -0.005222857
31
32 > plot(result)
33 Waiting to confirm page change...
34 Waiting to confirm page change...
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2  > spec.list(result)
3      GMYC_spec          sample_name
4  1      1      AY050077_Aegla_papudo
5  2      1      AY050078_Aegla_papudo
6  3      2      AY595656.1_Aegla_ringueleti
7  4      2      AY595657.1_Aegla_ringueleti
8  5      3      AY050079.1_Aegla_affinis
9  6      3      AY050080.1_Aegla_affinis
10 7      3      AY050081.1_Aegla_affinis
11 8      3      AY050082.1_Aegla_affinis
12 9      4      AY050102.1_Aegla_hueicollensis
13 10     4      AY050103.1_Aegla_hueicollensis
14 11     5      FJ471847.1_Aegla_chilota
15 12     5      FJ471855.1_Aegla_chilota
16 13     5      FJ471856.1_Aegla_chilota
17 14     5      FJ471853.1_Aegla_chilota
18 15     5      FJ471854.1_Aegla_chilota
19 16     5      FJ471848.1_Aegla_chilota
20 17     5      FJ471850.1_Aegla_chilota
21 18     5      FJ471849.1_Aegla_chilota
22 19     5      FJ471851.1_Aegla_chilota
23 20     5      FJ471852.1_Aegla_chilota
24 21     6      AY050116.1_Aegla_manni
25 22     6      AY050118.1_Aegla_manni
26 23     7      FJ471822.1_Aegla_alacalufi
27 24     7      FJ471826.1_Aegla_alacalufi
28 25     7      FJ471823.1_Aegla_alacalufi
29 26     7      FJ471824.1_Aegla_alacalufi
30 27     7      FJ471825.1_Aegla_alacalufi
31 28     7      FJ471827.1_Aegla_alacalufi
32 29     7      FJ471830.1_Aegla_alacalufi
33 30     7      FJ471831.1_Aegla_alacalufi
34 31     7      FJ471828.1_Aegla_alacalufi
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24	89	26	KT319211_Aegla_loyolai
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21	222	75	AY595560.1_Aegla_strinatii
22	223	76	AY595561_Aegla_castro
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25	226	79	AY595564_Aegla_parana
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18	253	106	AY595655.1_Aegla_sanlorenzo
19	254	107	AY595664.1_Aegla_intercalata
20	255	108	AY595665.1_Aegla_intercalata
21	256	109	AY595666.1_Aegla_intercalata
22	257	110	FJ360706.1_Aegla_lancinhas
23	258	111	FJ360707.1_Aegla_lancinhas
24	259	112	HQ236289.1_Aegla_cholchol
25	260	113	MH998634.1_Aegla_brevipalma
26	261	114	MH998635.1_Aegla_brevipalma
27	262	115	MH998636.1_Aegla_carinata
28	263	116	MH998637.1_Aegla_franca

1 **TABLE S1.** Average pairwise divergences within and between each cryptic species of *Aegla* identified in dataset B. The asterisk after taxon
 2 names indicates the species grouped by the GMYC analysis. N represents the number of analyzed sequences. ** Accession numbers correspond
 3 to the BOLD System database. Genetic distances values are shown as percentages.

Species	N	Genbank accession number	Intraspecific distance	Interspecific distance
<i>Aegla abtao</i> species complex 1	2	AY050112, AY050113	0.0	5.5
<i>Aegla abtao</i> species complex 2	2	AY050108, AY050109	0.0	5.7
<i>Aegla abtao</i> species complex 3	2	AY050110, AY050111	0.3	5.1
<i>Aegla abtao</i> species complex 4	2	KX910287, KX910288	0.0	6.0
<i>Aegla affinis</i>	4	AY050079-AY050082	0.2	6.3
<i>Aegla alacalufi</i>	10	FJ471822-FJ471831	0.2	5.5
<i>Aegla araucaniensis</i>	2	AY050088, AY050089	0.9	4.7
<i>Aegla bahamondei</i>	1	AY050090	–	5.4
<i>Aegla brevipalma</i> species complex 1	1	MH998634	–	4.6
<i>Aegla brevipalma</i> species complex 2	1	MH998635	–	4.2
<i>Aegla buenoi</i>	4	AEGPR016-18-AEGPR020-18**	0.0	5.1
<i>Aegla camargoi</i> species complex 1	2	AY595589, AY595590	0.3	6.0
<i>Aegla camargoi</i> species complex 2	1	AY595580	–	5.4
<i>Aegla camargoi</i> species complex 3	1	AY595620	–	4.6
<i>Aegla carinata</i>	1	MH998636	–	5.0
<i>Aegla castro</i> species complex 1	1	AY595561	–	5.4
<i>Aegla castro</i> species complex 2	1	AY595562	–	6.0
<i>Aegla castro</i> species complex 3	1	AY595586	–	5.6
<i>Aegla cavernicola</i>	2	AY595635, AY595636	0.0	4.5
<i>Aegla chilota</i>	10	FJ471847-FJ471856	0.1	6.3
<i>Aegla cholchol</i> species complex 1	7	HQ236287, HQ236290-HQ236292, HQ236294- HQ236296	0.2	5.9
<i>Aegla cholchol</i> species complex 2	2	HQ236288, HQ236293	0.0	5.8
<i>Aegla cholchol</i> species complex 3	1	HQ236289	–	5.5

<i>Aegla conceptionensis</i>	2	FJ360704, FJ360705	0.3	5.4
<i>Aegla denticulata denticulata/lacustris</i> *	4	AY050106, AY050107, AY050114, AY050115	0.0	5.7
<i>Aegla franca</i>	1	MH998637	–	5.9
<i>Aegla franciscana</i> species complex 1	2	AY595603, AY595606	0.6	4.6
<i>Aegla franciscana</i> species complex 2	1	AY595605	–	5.6
<i>Aegla georginae</i> species complex 1	4	MG581889-MG581892	0.0	7.1
<i>Aegla georginae</i> species complex 2	4	MH212137, MH212138, MH998638, MH998639	0.0	7.0
<i>Aegla georginae</i> species complex 3	2	MH212139, MH998640	0.0	7.9
<i>Aegla grisella</i> species complex 1	2	AY595613, AY595616	0.6	5.0
<i>Aegla grisella</i> species complex 2	1	AY595611	–	6.9
<i>Aegla grisella</i> species complex 3	1	AY595612	–	6.7
<i>Aegla hueicollensis</i>	2	AY050102, AY050103	0.0	6.6
<i>Aegla humahuaca</i>	2	AY595660, AY595661	0.0	5.4
<i>Aegla inconspicua</i>	1	AY595604	–	6.6
<i>Aegla inermis</i>	2	AY595621, AY595622	0.3	6.5
<i>Aegla intercalata</i> species complex 1	1	AY595664	–	4.7
<i>Aegla intercalata</i> species complex 2	1	AY595665	–	5.4
<i>Aegla intercalata</i> species complex 3	1	AY595666	–	5.3
<i>Aegla itacolomiensis</i>	3	AY595598-AY595600	0.0	5.5
<i>Aegla jacutinga</i>	4	AEGPR006-18, AEGPR010-18, AEGPR021-19, AEGPR022-19**	0.2	5.5
<i>Aegla jarai</i> species complex 1	1	AY595568	–	4.4
<i>Aegla jarai</i> species complex 2	1	AY595569	–	4.7
<i>Aegla jarai</i> species complex 3	1	AY595570	–	4.8
<i>Aegla jarai</i> species complex 4	1	AY595573	–	5.5
<i>Aegla jarai</i> species complex 5	1	AY595578	–	4.5
<i>Aegla jarai</i> species complex 6	1	AY595579	–	5.0
<i>Aegla jarai</i> species complex 7	1	AY595581	–	5.3

<i>Aegla jarai</i> species complex 8	1	AY595582	–	4.0
<i>Aegla jujuyana</i>	2	AY595652, AY595653	0.6	6.6
<i>Aegla laevis</i>	2	AY050083, AY050084	0.0	5.0
<i>Aegla lancinhas</i> species complex 1	1	FJ360706	–	5.2
<i>Aegla lancinhas</i> species complex 2	1	FJ360707	–	5.5
<i>Aegla lata</i>	4	AEGPR001-18-AEGPR004-18**	0.0	7.2
<i>Aegla leptochela/quilombola*</i>	4	AY595637, AY595638, AY595641, AY595642	0.1	6.3
<i>Aegla leptodactyla</i>	2	AY595618, AY595619	0.9	5.6
<i>Aegla ligulata</i>	3	AY595555- AY595557	0.6	5.9
<i>Aegla longirostri</i> species complex 1	5	KX910280, KX910281, KX910283, KX910285, KX910286	0.0	6.3
<i>Aegla longirostri</i> species complex 2	2	KX910282, KX910284	0.0	6.4
<i>Aegla longirostri</i> species complex 3	1	AY595608	–	6.9
<i>Aegla longirostri</i> species complex 4	1	AY595609	–	7.0
<i>Aegla longirostri</i> species complex 5	1	AY595610	–	6.9
<i>Aegla loyolai</i>	3	KT319209-KT319211	0.0	5.6
<i>Aegla ludwigi</i>	10	MG581884-MG581887, MH212140-MH212142, MH998641-MH998643	0.2	6.4
<i>Aegla manni</i> species complex 1	2	AY050116, AY050118	0.0	5.8
<i>Aegla manni</i> species complex 2	1	AY050117	–	5.8
<i>Aegla manuinflata</i>	3	MF442423-MF442425	0.2	5.0
<i>Aegla marginata</i>	2	AY595558, AY595559	0.0	6.4
<i>Aegla meloi</i>	3	KT319206-KT319208	0.2	5.1
<i>Aegla nebeccana</i>	2	AEGIV001-19, AEGIV002-19**	0.0	6.6
<i>Aegla neuquensis</i>	2	AY595667, AY595668	0.0	6.6
<i>Aegla obstipa</i>	2	AY595645, AY595646	0.3	6.5
<i>Aegla odebrechtii</i>	2	AY595571, AY595572	0.9	4.5
<i>Aegla okora</i>	4	AEGBR001-18-AEGBR004-18**	0.0	5.7
<i>Aegla papudo</i>	2	AY050077, AY050078	0.0	7.5

<i>Aegla parana</i> species complex 1	1	AY595564	–	5.8
<i>Aegla parana</i> species complex 2	1	AY595565	–	5.1
<i>Aegla parva</i>	2	AY595591, AY595592	0.0	4.9
<i>Aegla paulensis</i>	2	AY595584, AY595585	1.2	5.0
<i>Aegla perobae</i>	2	AY595587, AY595588	0.3	7.5
<i>Aegla pewenchaе</i>	3	AY050099, AY050100, AY050101	0.0	6.4
<i>Aegla plana</i>	2	AY595601, AY595602	0.0	5.7
<i>Aegla platensis/uruguayana*</i>	4	AY595627, AY595628, MT489799, MT489800	0.4	5.8
<i>Aegla platensis</i> species complex 1	5	AY595662, AY595663, MF448838-MF448840	0.4	8.7
<i>Aegla platensis</i> species complex 2	3	MF448831-MF448833	0.0	6.3
<i>Aegla prado</i>	2	AY595633, AY595634	0.0	6.5
<i>Aegla ringueleti</i>	2	AY595656, AY595657	0.3	7.7
<i>Aegla riolimayana</i>	4	AY595548, AY050098, KX910289, KX910290	0.0	4.5
<i>Aegla rossiana</i>	2	AY595623, AY595624	0.0	5.5
<i>Aegla rostrata</i>	10	HQ236248-HQ236257	0.1	6.0
<i>Aegla sanlorenzo</i> species complex 1	1	AY595654	–	6.4
<i>Aegla sanlorenzo</i> species complex 2	1	AY595655	–	6.8
<i>Aegla scamosa</i> species complex 1	2	AY595648, AY595649	0.3	6.7
<i>Aegla scamosa</i> species complex 2	1	AY595647	–	5.8
<i>Aegla schmitti</i> species complex 1	1	AY595583	–	4.4
<i>Aegla schmitti</i> species complex 2	1	AY595563	–	4.5
<i>Aegla septentrionalis</i>	2	AY595650, AY595651	0.0	6.4
<i>Aegla serrana</i> species complex 1	1	AY595593	–	5.6
<i>Aegla serrana</i> species complex 2	1	AY595607	–	6.3
<i>Aegla serrana</i> species complex 3	1	AY595617	–	5.6
<i>Aegla singularis</i>	1	AY595614	–	8.4
<i>Aegla spectabilis</i>	1	AY050097	–	4.6
<i>Aegla spinipalma</i>	4	AY595615, KX910291-KX910293	0.3	6.4

<i>Aegla spinosa/jarai</i> *	4	AY595576, AY595577, AY595594, AY595595	0.1	4.4
<i>Aegla strinatii</i> species complex 1	2	AY595639, AY595640	0.3	5.1
<i>Aegla strinatii</i> species complex 2	1	AY595560	–	6.2
<i>Aegla talcahuano</i> species complex 1	1	AY050085	–	6.2
<i>Aegla talcahuano</i> species complex 2	1	AY050086	–	4.9
<i>Aegla talcahuano</i> species complex 3	1	AY050087	–	5.9
<i>Aegla uruguayana</i> species complex 1	4	AY595631, AY595632, MT489834, MT489835	0.2	6.5
<i>Aegla uruguayana</i> species complex 2	2	MT489824, MT489825	0.3	7.1
<i>Aegla uruguayana</i> species complex 3	2	MT489826, MT489827	0.6	5.9
<i>Aegla violacea</i> species complex 1	3	AY595552-AY595554	0.0	6.0
<i>Aegla violacea</i> species complex 2	2	AY595625, AY595626	0.0	5.0

1 5. CONCLUSÃO GERAL

2 A análise de uma grande quantidade de amostras de diferentes períodos e regiões da
3 bacia do rio Tibagi, tanto de coleção quanto amostras recém coletadas, possibilitou aprimorar
4 o conhecimento da diversidade e padrões de distribuição dos eglídeos desta região. As
5 distribuições de *A. castro*, *A. lata* e *A. jacutinga* foram revisadas e ampliadas. Além disso,
6 descrevemos cinco espécies novas; uma da região do Baixo Tibagi e as outras quatro da
7 região do Médio Tibagi. Com isso, a diversidade de eglídeos nesta bacia hidrográfica passa de
8 4 para 9 espécies e o número de espécies de *Aegla* conhecidas aumenta para 95. No entanto,
9 as espécies novas têm distribuições limitadas e ocorrem em habitats impactados pela
10 urbanização ou agricultura.

11 Das nove espécies de *Aegla* que ocorrem na bacia do rio Tibagi, sete são endêmicas
12 dessa bacia. Embora morfologicamente conservativos, a análise minuciosa da morfologia
13 permitiu a distinção das espécies bem como a construção de uma chave de identificação.
14 Ressaltamos que, para efeito de comparação, é importante ter espécimes machos adultos, pois
15 nestes indivíduos o desenvolvimento completo dos quelípodos, espinhos e tubérculos permite
16 uma interpretação mais segura dos caracteres diagnósticos das espécies.

17 Apesar de vários cursos de água do Médio e Baixo Rio Tibagi terem sido amostrados
18 neste estudo, muitas partes do Alto Tibagi têm apenas alguns ou nenhum registro de eglídeos,
19 indicando uma área prioritária a ser explorada em estudos futuros. Assim, os nossos
20 resultados demonstram a importância da bacia do rio Tibagi para a conservação dos eglídeos e
21 reforçam o alto potencial de descoberta de espécies novas no estado do Paraná.

22 A discriminação precisa de 92% das espécies analisadas confirma a eficácia da região
23 barcode do COI na identificação de espécies *Aegla*. Nossa matriz de distância genética
24 indicou que os valores de divergência entre as espécies são normalmente maiores que 2%.
25 Poucos pares de espécies (16 pares) asseguradas como válidas, tanto pela análise morfológica

1 quanto pelo GMYC, apresentaram divergências interespecíficas inferiores a 2%,
2 provavelmente em decorrência de especiações recentes. Desta forma, ressaltamos o cuidado
3 ao estabelecer esse valor como um limiar para delimitar as espécies de *Aegla*. Nossas análises
4 sugerem que os 74 supostos táxons possivelmente representam 116 espécies, apontando para
5 pelo menos 40 candidatos para espécies novas. Contudo, recomendamos um exame crítico da
6 morfologia dos espécimes pertencentes a estes complexos para dar suporte à identificação de
7 novas espécies com base no DNA barcode.