

SPIXIANA	36	2	283–288	München, Dezember 2013	ISSN 0341–8391
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## *Papuadessus baueri* spec. nov. from Biak Island, Papua

(Coleoptera, Dytiscidae, Hydroporinae)

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Balke, M., Warikar, E., Toussaint, E. F. A. & Hendrich, L. 2013. *Papuadessus baueri* spec. nov. from Biak Island, Papua (Coleoptera, Dytiscidae, Hydroporinae). *Spixiana* 36 (2): 283–288.

*Papuadessus baueri* spec. nov. is described from Biak Island, Papua. The phylogenetic analysis of DNA sequence data suggested placement in that genus which otherwise contains *P. pakdjoko* Balke, 2001, a species widespread across mainland New Guinea. The new species seems to be endemic to Biak where it was collected from a limestone sinkhole. Important species characters (habitus, median lobe and paramere) are illustrated, and the habitat of *P. baueri* spec. nov. and its water beetle coenosis are briefly outlined.

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### Introduction

*Papuadessus* was described by Balke (2001) for the large and conspicuous New Guinea species *P. pakdjoko* (Fig. 1). Molecular phylogenetic investigations by Balke & Ribera (2004) and Ribera et al. (2008) established *Papuadessus* as a well delineated, isolated lineage within the Bidessini, but its closer relatives remain not well established. The species has been shown to be comparably widely distributed across New Guinea. Here, we add a second species to the genus. It appears morphologically rather divergent from *P. pakdjoko* and we decided to assign it to *Papuadessus* based on molecular phylogenetic inference, especially because the generic classification within the Bidessini using morphology is problematic (cf. Hendrich et al. 2009). We use the condensed descriptive format introduced by Riedel et al. (2013), integrating DNA sequencing, digital imaging and wiki publication of data.

### Material and methods

The specimens included in this study are deposited in the following collections:

- ANIC Australian National Insect Collection, Canberra, Australia
- CLH Collection Lars Hendrich, Berlin, Germany; property of the NHMW
- MZB LIPI Division of Zoology, Museum Zoologicum Bogoriense, Cibinong, Indonesia
- NMPC Národní Museum, Prague, Czech Republic
- NHMW Naturhistorisches Museum Wien, Vienna, Austria
- SAMA South Australian Museum, Adelaide, South Australia, Australia
- ZSM Zoologische Staatssammlung München, Munich, Germany

**Morphological observations.** Photographs were taken with a Leica Photar 1:2/25 on bellows attached to a Nikon D3X camera, an image stack was produced with a custom built robotic macro-rail and combined with Helicon Focus software ([www.heliconsoft.com](http://www.heliconsoft.com)). The principal setup is illustrated on our wiki: <http://zsmentomology.de/wiki/Dig->

ital imaging in the beetle lab. The male genitalia were studied in dry condition with a Leica M205C dissecting scope at 160×. Pencil sketches were produced with a drawing tube, scanned, and digitally inked using CorelDRAW 11.

**DNA extraction and amplification.** DNA extractions were carried out on fresh material kept in 96 % ethanol using the DNeasy Tissue Kit (Qiagen GmbH, Hilden, Germany). We sequenced fragments of the cytochrome oxidase subunit 1 (CO1, 611 bp) and ribosomal 16S (823 bp) using standard protocols ([http://zsm-entomology.de/wiki/The\\_Beetle\\_D\\_N\\_A\\_Lab](http://zsm-entomology.de/wiki/The_Beetle_D_N_A_Lab)). The DNA strands obtained after sequencing were eye-corrected and aligned under Geneious R6 (available from <http://www.geneious.com>).

**Phylogenetic analyses.** The phylogenetic relationships were inferred in a Bayesian framework using MrBayes 3.2 (Ronquist et al. 2012). We used three partitioning schemes, namely  $P_1$  with only one partition for both genes,  $P_2$  with one partition for each gene, and  $P_3$  including a partition for each coding position of the CO1 and one partition for the 16S. The substitution model for each partition was selected under jModelTest 0.1.1 (Posada 2008). The analyses consisted of two independent runs of 8 Markov Chain Monte Carlo running 20 million generations and sampling every 1000 cycles. The convergence of the runs was assessed under Tracer 1.5 (available at: <http://BEAST.bio.ed.ac.uk/Tracer>) by checking the log-likelihood curves and the Effective Sample Size values for each parameter of the analyses. We applied a conservative burnin consisting of 25 % of the topologies sampled, and used the remaining ones to generate a 50 % majority-rule consensus tree based on the best partitioning scheme selected under Tracer 1.5 on the basis of Bayes Factors ( $B_F$ ) calculated using 1000 Bootstrap replicates.

## Results

### Phylogeny

The final matrix comprised 1434 bps with no stop codons, and the GTR+ $\Gamma$ +I model was selected as the best-fitting for all partitions under jModelTest 0.1.1. All the Bayesian analyses carried out based on the molecular dataset converged well, and the partitioning scheme  $P_3$  was selected under the  $B_F$  criterion. The topology resulting from this partitioning scheme is presented in Figure 7. Overall the phylogenetic tree is well to strongly supported, and two main clades were recovered. The first clade is strongly supported (PP=1.0) and includes the following genera: *Allodessus* Guignot, 1953, *Gibbidessus* Watts, 1978, *Kakadudessus* Hendrich & Balke, 2009, *Neobidessodes* Hendrich & Balke, 2009, and *Uvarus* Guignot, 1939. The second clade contains the genus *Clypeodytes*

Régimbart, 1894 along with the genera *Papuadessus* and *Hydroglyphus* Motschulsky, 1853 with a moderate support (PP=0.7). Within this group, *P. pakdjoko* is found sister to the specimen from Biak Island with strong support (PP=1.0). These two specimens are recovered in a sister position to *Hydroglyphus* with strong support (PP=1.0).

## Taxonomy

### Genus *Papuadessus* Balke, 2001

*Papuadessus* Balke, 2001: 108; Balke & Ribera 2004: 125.

**Type species.** *Papuadessus pakdjoko* Balke, 2001, by original designation.

**Online resource.** SpeciesID page: <http://species-id.net/wiki/Papuadessus>

### *Papuadessus baueri* spec. nov.

Figs 2–9

**Type locality.** Indonesia, Papua, Biak Island, road to Korim, 00°55.736' S 136°02.766' E

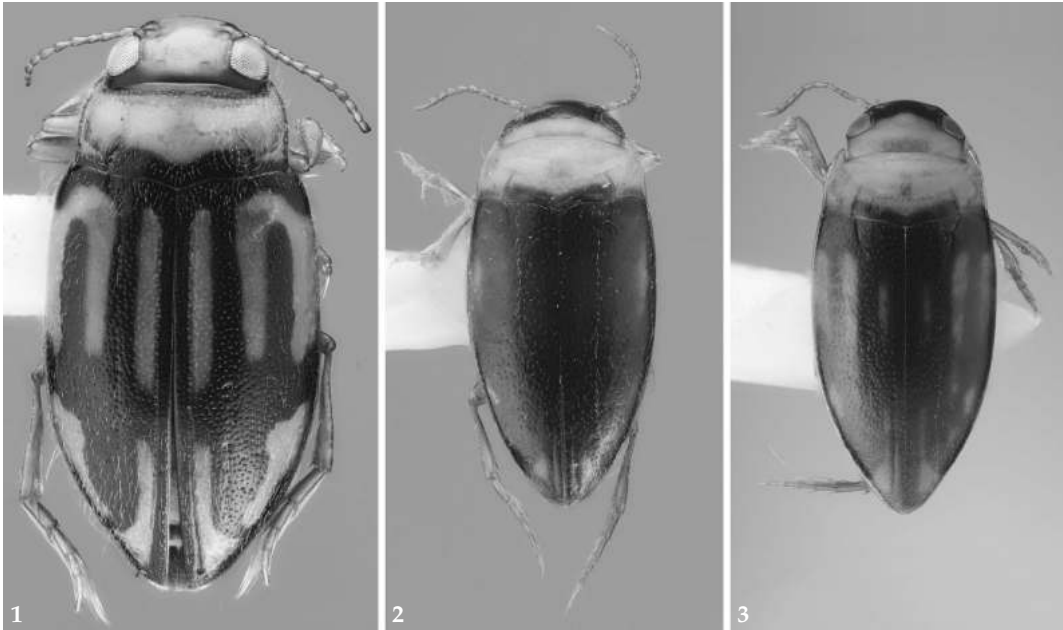
**Type material.** Holotype: ♂, Indonesia: “Indonesia/Biak 7 BIA 1 Lake betw. Biak & Korem, 80 m, 13.7.1991 leg. Balke & Hendrich”, “Holotype *Papuadessus baueri* sp. nov. Balke, Warikar, Toussaint & Hendrich des. 2013” [red printed label] (MZB). – Paratypes: 33 exs, same data as the holotype (ANIC, CLH, NHMW, NMPC, SAMA, ZSM); 12 exs, “Papua, Biak, road to Korim, sinkhole, 100 m, 24.x.2011, 00°55.736' S 136°02.766' E, Warikar, Surbakti & Balke leg. (PAP19) (MZB, ZSM)”, 2 exs with DNA extraction numbers MB4486 and MB4487 (vouchers as well as DNA aliquots in ZSM). All paratypes are provided with red printed paratype labels.

**Online resources.** Genbank accession numbers: HG 327112 and HG327113. SpeciesID page: [http://species-id.net/wiki/Papuadessus\\_baueri](http://species-id.net/wiki/Papuadessus_baueri), where dorsal punctation and microreticulation can be examined based on high resolution images.

**Etymology.** To Jakob Bauer, volunteer in the Coleoptera section who visits us every week to mount specimens with a “thank you – your help is greatly appreciated”!

### Description of the holotype

Sculpture and structure. Beetle with continuous body outline in dorsal view, narrowly oval and body rather narrowed towards apex. Head and pronotum with fine microreticulation, regularly and fine punctate, punctures smaller and weaker anteriorly and basally. Elytra with coarse microreticulation, regularly and coarsely punctured. Punctures on elytra not forming rows. Head without cervical line; pronotum and



**Figs 1- 3.** Habitus of *Papuadessus* species. 1. *P. pakdjoko* Balke (length 3.2 mm). 2. *P. baueri* spec. nov. (length 2.2 mm), with darker elytra. 3. *P. baueri* spec. nov., with more extensive pale elytral bands.

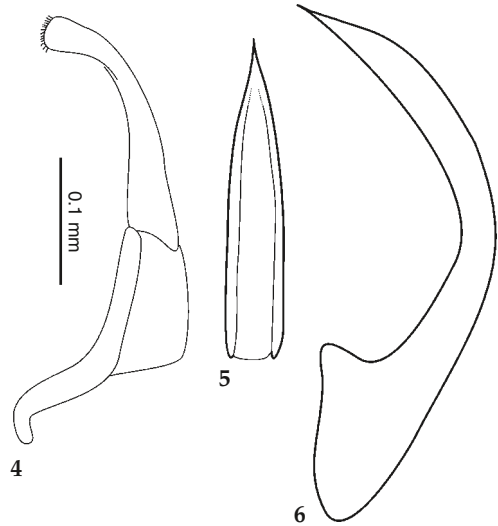
elytron with distinct basal plica; elytron without distinct sutural line (as in *Hydroglyphus* species) but apically with rather faint sutural impression. Epipleuron without basal pit or carina. Ventral side of elytron laterally with two distinct lamellae, as in *P. pakdjoko*, one caudad and one in a median position. Meta- and mesoventrites coarsely and densely punctured, punctures on all abdominal ventrites weaker and smaller.

**Colour.** Head dark brown, with yellow vertex and a lighter spot on each side of head above clypeus; pronotum yellow, with dark brown median patch at base of pronotum between the pronotal plicae; elytron dark brown with paler longitudinal markings discally, laterally and one distally (Fig. 3), ventrally yellow, head appendages and legs yellow.

**Male.** Pro- and mesotarsi not expanded. Median lobe of aedeagus in lateral view gently curved, produced into a very fine, acute tip, in ventral view also with pointed tip; parameres two-segmented (Figs 4-6).

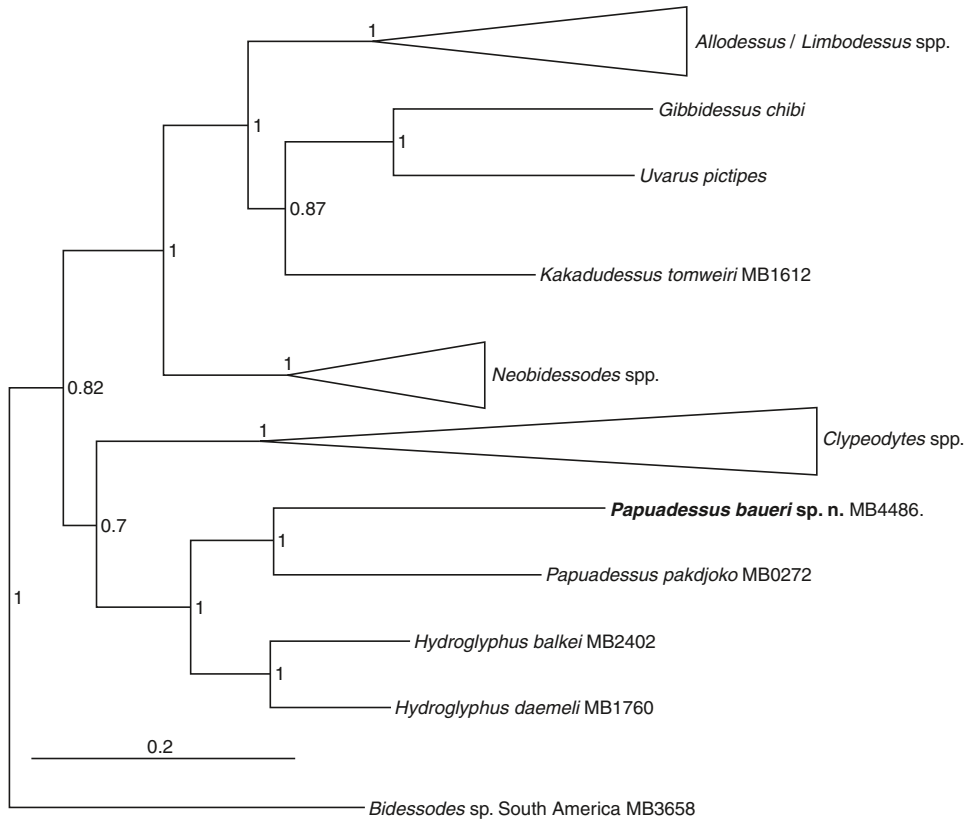
**Variability.** The extend of the pale elytral markings varies, the surface can be mostly dark or the paler areas are more extended (Fig. 3). In the latter case, the general configuration of pale bands then agrees well with that of *P. pakdjoko* (Fig. 1).

**Female.** No sexual dimorphism observed.



**Figs 4- 6.** Aedeagus of *Papuadessus baueri* spec. nov. 4. Paramere (lateral lobe) inner view. 5. Median lobe in ventral view. 6. Median lobe in lateral view.

**Measurements.** Total length of beetle 2.0-2.2 mm (holotype 2.1 mm), total length of beetle without head 1.8-2.0 mm (holotype 1.9 mm); width of beetle 0.9-1.0 mm (holotype 0.9 mm).



**Fig. 7.** Bayesian inference tree including Australasian Bidessini, node support are Bayesian posterior probabilities. Where applicable, our DNA extraction and voucher numbers stated after taxon name. Other sequences are from genbank, and for details on multiple species sequenced in the collapsed genera see Hendrich & Balke 2009.

**Placement.** Assigned to the genus *Papuadessus* based on the analysis of mitochondrial DNA sequence data (Fig. 7).

**Collection circumstances.** The beetles were collected from shallow water, where they were swimming around coarse limestone gravel, at the edge of a limestone sinkhole (doline), ca. 100 meters in diameter (Fig. 8). The species was collected in association with the following Dytiscidae: *Cybister sugillatus* Erichson, 1834 and *Laccophilus heidia* Brancucci, 1983 (Balke et al. 1997).

**Distribution.** Only known from the type locality (Fig. 9).

### *Papuadessus paktjoko* Balke

Figs 1, 7, 9

*Papuadessus paktjoko* Balke, 2001: 108; Balke & Ribera 2004: 125.

**Online resources.** Genbank accession numbers: 16S rRNA-AY368225; 3' cox1-AY368229. SpeciesID page: [http://species-id.net/wiki/Papuadessus\\_paktjoko](http://species-id.net/wiki/Papuadessus_paktjoko)

**Notes.** This species (Fig. 1) inhabits gravel banks of large lowland rivers and was also collected from smaller streams. It was described from West Papua, south of Nabire and later reported from Simbu Province (Crater Mountain) in Papua New Guinea (Balke & Ribera 2004). Here, we report additional localities:

4 exs, Papua New Guinea: Sandaun, Mianmin, 670 m, 20.x.2008, 4°53.292' S 141°34.118' E, Ibalim (PNG 191); 2 exs, Papua New Guinea: Sandaun, Mianmin area, >1000 m, 23.xii.2009, near 4°54.540' S 141°36.953' E, Ibalim & Pius (PNG232); 3 exs, Papua New Guinea: Sandaun, Mianmin area, >1000 m, 26.xii.2009, near 4°54.540' S 141°36.953' E, Ibalim & Pius (PNG233); 2 exs,



Fig. 8. Habitat of *Papuadessus baueri* spec. nov.

Papua New Guinea: Sandaun, Mianmin area, >600 m, 13.i.2010, 4°54.540' S 141°36.953' E, Ibalim & Pius (PNG 236) (all in MZB, ZSM).

### Acknowledgements

We thank the staff of the Biology Department of the Cendrawasih University for help with the fieldwork, conducted during a training course on aquatic Coleoptera. Thanks are also due to Sentiko Ibalim and Pius (Binatang Research Center, Madang, PNG) for helping with the PNG fieldwork.

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Fig. 9. Distribution of *Papuadessus* spp. (●: *P. paktjoko*, ■: *P. baueri* spec. nov.).

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