

Correspondence

Running title: *Meladema* of the Sahara

The *Meladema* Laporte, 1835 (Coleoptera, Dytiscidae) of the Sahara Desert

IGNACIO RIBERA¹, DAVID T. BILTON² & ANABELA CARDOSO¹

¹*Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Passeig Maritim de la Barceloneta 37-49, 08003 Barcelona, Spain. E-mails: ignacio.ribera@ibe.upf-csic.es, anabela.cardoso@ibe.upf-csic.es*

²*Marine Biology and Ecology Research Centre, University of Plymouth, Drake Circus, Plymouth PL4 8AA, UK. email: d.bilton@plymouth.ac.uk*

Meladema Laporte, 1835 is a genus of large diving beetles, found in the Western Palaearctic, from the Canary Islands and Madeira to western Turkey (Bilton & Ribera 2017). The genus currently contains four species: the widespread *M. coriacea* Laporte, 1835, distributed from the Canary Islands to Turkey and ranging from southern France and the central Balkans south to the central Sahara, two Atlantic Island endemics, *M. imbricata* (Wollaston, 1871) from the western Canary Islands and *M. lanio* (Fabricius, 1775) from the main island of Madeira, and a fourth, recently described species, *M. lepidoptera* Bilton & Ribera, 2017 from the Tyrrhenian Islands (Corsica, Sardinia, Elba, Montecristo) and parts of the Italian mainland (Bilton & Ribera 2017).

In a recent revision of the genus, Bilton & Ribera (2017) reported some museum specimens from the central Sahara, in the Hoggar, Tassili n'Ajjer (Algeria) and Tibesti mountains (Chad). These specimens had very dense, small and strongly curved crescentic striolae on the elytra, giving a somewhat tuberculate appearance to the elytral surface, particularly basally (Figs 1A, B; specimen with reddish elytra teneral), different to that typical of the otherwise similar *M. coriacea* and *M. lepidoptera* (Figs 1C, D). Bilton & Ribera (2017) reported a sequence from the nuclear gene Histone 3 (H3) of a specimen from Chad (voucher number IBE-AN739: 1 ♀ "KOUDOU// VERS 2000 m// 17 XI 49" "TIBESTI// MASSIF KOUSSE// PH. DE MIRÉ", "MUSÉUM PARIS" [blue label] (Muséum national d'Histoire naturelle, Paris). This H3 sequence was identical to that seen in all *M. coriacea* and *M. lepidoptera*, differing from *M. imbricata* and *M. lanio* in the single diagnostic position in this gene fragment (see Bilton & Ribera 2017 and Sýkora *et al.* 2017 for details). Bilton & Ribera (2017) assigned these beetles to *M. coriacea*, despite the deviating sculpture, in the absence of molecular data suggesting otherwise, but noted the possibility that these Saharan beetles may represent an additional cryptic lineage within the genus.

Subsequent to the publication of Bilton & Ribera (2017) we have obtained a 404 bp fragment of the 3' end of the gene Cytochrome Oxidase Subunit 1 (COI-3') of the IBE-AN739 specimen, using the primer pair chy-pat and the laboratory procedures to avoid contamination detailed in Bilton & Ribera (2017). We have included this new sequence in a matrix with the full COI-3' fragment (826 bp) of specimens reported in Bilton & Ribera (2017), and analysed it with a fast Maximum Likelihood heuristic algorithm in RAxML-HPC2 in the CIPRES Science Gateway (Miller *et al.* 2010), using a single

partition with a GTR+G evolutionary model and assessing node support with 100 pseudoreplicates of a rapid bootstrapping algorithm (Stamatakis *et al.* 2008).

The sequence of this specimen from the Tibesti Mountains was placed deep inside the *M. coriacea* clade (Fig. 2) with good bootstrap support (86%). Here it is grouped with some specimens from Morocco (Anti Atlas) and Gran Canaria, from which it differs in a single nucleotide (i.e. 0.25%), suggesting very recent divergence between these haplotypes. Our results confirm the inclusion of the morphologically deviating central Saharan populations within *M. coriacea*, and suggest that isolation between these populations and those elsewhere in North Africa occurred very recently, perhaps as a result of desert expansion in the Holocene (Tierney *et al.* 2017). Observed differences in elytral sculpture may have evolved as a result of population bottlenecks, something which could also have occurred during the evolution of other lineages of the genus *Meladema*.

Acknowledgements

We are grateful to Antoine Mantilleri (Muséum national d'Histoire naturelle, Paris) for loan of Saharan *Meladema*. Molecular work was funded by project CGL2013-48950-C2-1-P (AEI/FEDER, UE).

^a In Bilton & Ribera (2017) the geographical coordinates of the locality of the neotype of *M. coriacea* were given as 43°09'45.74"N 9°15'38.82"E in error. They should have been 43°09'45.74"N 6°15'38.82"E.

References

- Bilton, D.T. & Ribera, I. (2017) A revision of *Meladema* diving beetles (Coleoptera, Dytiscidae), with the description of a new species from the central Mediterranean based on molecules and morphology. *Zookeys*, 702, 45–112.
- Miller, M.A., Pfeiffer, W. & Schwartz, T. (2010) *Creating the CIPRES Science Gateway for inference of large phylogenetic trees*. In: Proceedings of the Gateway Computing Environments Workshop (GCE). New Orleans, pp. 1–8.
- Stamatakis, A., Hoover, P. & Rougemont, J. (2008) A rapid bootstrap algorithm for the RAxML web servers. *Systematic Biology*, 57, 758–771.
- Sýkora, V., García-Vázquez, D., Sánchez-Fernández, D. & Ribera, I. (2017) Range expansion and ancestral niche reconstruction in the Mediterranean diving beetle genus *Meladema* (Coleoptera, Dytiscidae). *Zoologica Scripta*, 46, 445–458 + 14 pp. electronic supp. material.
- Tierney, J.E., Pausata, F.S.R. & deMenocal, P.B. (2017) Rainfall regimes of the Green Sahara. *Science Advances*, 3, e1601503, 9 pp. + 20 pp. electronic supp. material.

Figure legends

FIGURE 1. *Meladema* species, elytral sculpture, shoulder and middle left and right, respectively; DNA vouchers where applicable. A) *M. coriacea* male, Chad, Tibesti, Koudou (teneral specimen); B) *M. coriacea* female, Chad, Tibesti, Bassin de Gorrom; C) *M. coriacea* neotype, France, Var, La-Londe-les-Maures (NHM-IRM11C)^a; D) *M. lepidoptera* holotype male, Corsica, Cap Corse (NHM-IRM12E). Scale bar = 0.5 mm.

FIGURE 2. Phylogram obtained from analysis of the COI-3' fragment in RAxML. Numbers on nodes, bootstrap support values. In brackets, potential hybrid specimens. See above and Ribera & Bilton (2017) for details and for specimen and locality codes.