The family Meloidae, the blister beetles, contains about 3000 species placed in about 130 genera (Ricci et al. 2020). The name of ‘blister’ remains into the ability of these insects to secrete cantharidin, a chemical fluid that causes irritation and blistering when it contacts with animal skins. Males produce this substance not only as a defensive tool but also as a copulatory gift for females during the mating process (Moed et al. 2001). Genetic information on this species is scarce and is limited to a cytogenetic study that included the analysis of a repetitive DNA family (Ruedena et al. 2021). Data from mitogenomes can be useful for future phylogenetic studies in this beetle group.

The specimens of *H. scutellatus* were collected in Alcudia de Guadix, Spain (37.79°N, 3.78°W). *H. scutellatus* is not an endangered or protected species thus we did not need any specific permission for its collection. Specimens of the analyzed population were stored in the RNM-924 Group collection (voucher 2006_HS_01; contact email: plorite@ujaen.es) in the University of Jaén, Spain. Genomic DNA was isolated using the Nucleospin Tissue kit (Machery-Nagel GmbH & Co.). Genomic DNA was used for the construction of a library with 750 bp fragments and sequenced using the HiSeq 2000 Illumina platform, with pair-ends reads (101 bp each) at Macrogen Japan Corp. (Tokyo, Japan). Graph-based clustering analysis was performed on RepeatExplorer, implemented within the Galaxy environment (http://repeatexplorer.org/) (Novák et al. 2010, 2013). Sequences corresponding to mtDNA were selected and assembled with CAP3 software using the *Hyleus cichorii* mitogenome (Wu et al. 2018) as reference. Two regions were not recovered using genome sequencing. These two gaps were closed by PCR amplification using a two pair of primers; ND1-F (TGAAATTGAGCCCGCCACGAGAA) and ND1-R (GTACCGTTCATCTTTATAGGAGCCG) for the first region and RControl-F (ATATAGGGGTCTCCTAATCCCCAGT) and the ARNt-Met primers (AGGGTATGAACCTAAWAGC) for the second one. The mitogenome was annotated using MITOS (http://mitos.bioinf.uni-leipzig.de/help.py) (Bernt et al. 2013) with manual curation for consistent start/stop codons. The complete mitogenome of *H. scutellatus* was 16,035 base pairs in length, being comparable to other blister beetles. The A + T content was high (71.7%) as a typical feature of insects. The mitogenome contained the typical 13 protein-coding genes (PCGs), two rRNAs genes and 22 tRNAs. All PCGs used typical ATN start codons: ATG (start of coII, nd1, nd2, nd3, nd4 and cytB), ATA (start of coI, coIII, nd5), ATT (start of atp6, nd4, nd6 and nd1) or ATC (start of atp8, nd5 and nd6). Eight out of the 13 PCGs have the TAA stop codon and one of them (nd3) the TAG stop codon. Four PCGs have incomplete T stop codons (coI, coII, nd5 and nd4). All tRNAs could be folded into the typical secondary structure, except for the tRNA-Ser (AGN), which lacks the DHU arm. The length of *rrnS* was 1,282 bp and the length of *rrn5* was 733 bp.

Complete mitogenomes from other species from the family Meloidae were recovered from GenBank and used for phylogenetic analysis (Figure 1). Sequences from the 13 PCGs were aligned using MAFFT and concatenated for phylogenetic analysis. The phylogenetic relationships were reconstructed using the Maximum-Likelihood method (Saitou and
Nei (1987) implemented in the program MEGA version 11 (Tamura et al. 2021). GTR + G + I was selected as the best model as it showed the lowest BIC (Bayesian Information Criterion) value. The nodes were assessed with 1000 bootstrap replicates. Phylogenetic analysis showed that Hycleus and Mylabris species appear clustered together in a very well-supported clade, which is in agreement with other studies that recovered the tribe Mylabrini as a monophyletic group (Bologna and Pinto 2001; Du et al. 2017). However, the species of both genera do not appear separately within the clade. Separation of Mylabris and Hycleus received strong support in other phylogenetic studies based on the 16S and ITS2 sequences (Bologna et al. 2005, 2008), although these studies included a limited number of species. Mylabris and Hycleus are the most speciose genera in the Meloidae family, their phylogenetic relationships are still understudied and some authors have highlighted the need of more phylogenetic analyses within the group (Pan and Bologna 2014; Salvi et al. 2019; Riccieri et al. 2020).

**Acknowledgments**

We thank Dr. Antonio Sánchez (Universidad de Jaén, Spain) for providing us with some of the samples used in this study. We thank Dr. Rafael Obregón (Universidad de Córdoba, Spain) for the taxonomical identification of the analyzed material.

**Author contributions**

PM, TP and PL conceived and designed the experiment; EEM and PM performed the experiment; PM, EEM, TP and PL analyzed the data; TP and PL acquired the funds; PM, EEM, TP and PL wrote the draft. All
authors have read and agreed to the published version of the manuscript.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

The study was supported by the Universidad de Jaén (through the program 'Plan de Apoyo a la Investigación 2019–2020').

**ORCID**

Pablo Mora [http://orcid.org/0000-0001-7967-3379]
Eugenia E. Montiel [http://orcid.org/0000-0002-2461-9268]
Teresa Palomeque [http://orcid.org/0000-0002-7144-4931]
Pedro Lorite [http://orcid.org/0000-0002-9692-5870]

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov) under the accession no. MN207126. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA791791, SRR17319087, and SAMN24345222 respectively.

**References**

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 986–319.

Bologna MA, D’Inzillo B, Cervelli M, Oliverio M, Mariottini P. 2005. Molecular phylogenetic studies of the Mylabrini blister beetles (Coleoptera, Meloidae). Mol Phylogenet Evol. 37(1):306–311.

Bologna MA, Oliverio M, Pitzalis M, Mariottini P. 2008. Phylogeny and evolutionary history of the blister beetles (Coleoptera, Meloidae). Mol Phylogenet Evol. 48(2):679–693.

Bologna MA, Pinto JD. 2001. Phylogenetic studies of the Meloidae (Coleoptera), with emphasis on the evolution of phoresy. Syst Entomol. 26(1):33–72.

Du C, Zhang L, Liu T, Ma J, Zeng C, Yue B, Zhang X. 2017. Mitochondrial genomes of blister beetles (Coleoptera, Meloidae) and two large intergenic spacers in Hylecus genera. BMC Genomics. 18(1):698.

Moed L, Shwayder TA, Chang MW. 2001. Cantharidin revisited: a blistering defense of an ancient medicine. Arch Dermatol. 137(10): 1357–1360.

Naz F, Wu Y, Zhang N, Yang Z, Yu C. 2020. Anticancer attributes of cantharidin: involved molecular mechanisms and pathways. Molecules. 25(14):3279.

Novák P, Neumann P, Macas J. 2010. Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data. BMC Bioinformatics. 11:378.

Novák P, Neumann P, Pech J, Steinhaisl J, Macas J. 2013. RepeatExplorer: a Galaxy-based web server for genome-wide characterization of eukaryotic repetitive elements from next-generation sequence reads. Bioinformatics. 29(6):792–793.

Pan Z, Bologna MA. 2014. Taxonomy, bionomics and faunistics of the nominate subgenus of Mylabris Fabricius, 1775, with the description of five new species (Coleoptera: Meloidae: Mylabrin). Zootaxa. 3806(1):1–78.

Riccieri A, Mancini E, Salvi D, Bologna MA. 2020. Phylogeny, biogeography and systematics of the hyper-diverse blister beetle genus Hylecus (Coleoptera: Meloidae). Mol Phylogenet Evol. 144:106706.

Ruiz-Torres L, Mora P, Ruiz-Mena A, Vela J, Mancebo FJ, Montiel EE, Palomeque T, Lorite P. 2021. Cytogenetic analysis, heterochromatin characterization and location of the rDNA genes of Hylecus scutellatus (Coleoptera, Meloidae); a species with an unexpected high number of rDNA clusters. Insects. 12(5):385.

Saitou N, Nei M. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol. 4(4):406–425.

Salvi D, Maura M, Pan Z, Bologna MA. 2019. Phylogenetic systematics of Mylabris blister beetles (Coleoptera, Meloidae): a molecular assessment using species trees and total evidence. Cladistics. 35(3):243–268.

Tamura K, Stecher G, Kumar S. 2021. MEGA11: molecular evolutionary genetics analysis version 11. Mol Biol Evol. 38(7):3022–3027.

Trotta-Moreu N, García-París M. 2001. The Iberian species of Hylecus Latreille, 1829 (Coleoptera: Meloidae): Geographic ranges and elytral variability. GRAELLSIA. 57(1):99–111.

Wu Y, Liu Y, Chen X. 2018. The complete mitochondrial genomes of Hylecus cichorii and Hylecus phaleratus (Coleoptera: Meloidae). Mitochondrial DNA B Resour. 3(1):159–160.