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Genetics and ecology of an island endemic from Pantelleria: *Acheta pantescus* (Orthoptera Gryllidae)

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Abstract

The biology of the recently described stenoecious cricket *Acheta pantescus* is mostly unknown. This study includes an integrative systematics approach using ecology and barcode sequencing of the mtDNA NADH dehydrogenase subunits (ND1), the cytochrome c oxidase subunit 1 (COI) gene and the 16S ribosomal RNA region. A comparison with other species, including a discussion on the hypotheses about its origin, requires further work noting the lack of information currently available on GenBank. Two data loggers were placed at the Martingana locality, within the site where *A. pantescus* is known to occur and just outside it, to record temperatures and relative humidity; results show statistical differences between the area inhabited by the species and that immediately outside its habitat. Adults can be encountered between the end of April through to October; moreover, a broad range of life-cycle stages, from 1st instar to penultimate nymphal (sub-adult) phase were recorded in the month of May. Adults observed in May would have presumably been the result of eggs laid during the autumn and hatched around the latter part of February. Observations made during the night from a seacraft made it possible to identify locations on the island where the species is present, through its characteristic stridulatory 'song'.

Key Words

Coastal habitat conservation, insularity, Italy, Mediterranean biogeography, stenotopic

Introduction

The genus *Acheta* Fabricius, 1775 comprises seventeen extant species whose natural range broadly spans three biogeographic realms, the Palearctic, Afrotropical and Indomalayan, with concentrations in south-western Asia and the Mediterranean and Saharo-Arabian subregions (Udvardy 1975; Cigliano et al. 2025). One species, *Acheta domesticus* (Linnaeus, 1758), is essentially cosmopolitan, having expanded its distribution passively into North America and many parts of Europe including Macaronesia, among other locations worldwide, from semi-arid and arid regions of northern Africa, the Middle East and West Asia. Four species are known from within Italian territory, including *A. domesticus*, *A. gossypii* (Costa 1855), *A. hispanicus* Rambur, 1838 and *A. pantescus* Massa, Cusimano, Fontana, Brizio, 2022, although *A. gossypii* may require further investigation, given its uncertain status (Massa 1995; Massa et al. 2012; Iorio et al. 2019; Massa et al. 2022); it was described by Costa (1855) who portrayed its status as abundant on *Gossypium* cultivations in Apulia. However, it later transpired that this so-called new species was never recorded again, while to confound matters, the types were lost. Moreover, the specimens reported from other geographical areas are not supported by clear-cut identification. Indeed, the female identified as *A. gossypii* collected in Murcia (Spain) most likely belongs to a different species (Gorochov and Llorente 2001), while Chopard's (1967) record from Kenya was actually not collected and therefore there is

no voucher specimen that can be examined in support of such a claim. An additional three taxa occur in the central Mediterranean area, specifically from northern Africa, these being *A. chudeaui* (Chopard 1927), *A. confalonierii* (Capra 1929), and *A. meridionalis* (Uvarov 1921) (described from Sudan) (Cigliano et al. 2025).

The present paper aims to deepen our knowledge of *Acheta pantescus*, a species which was discovered in 2022 on the island of Pantelleria. It is an enigmatic species, discovered by chance while sifting through bioacoustic recordings of nocturnal fauna, and found to be closely linked to coastal cliff environments. In addition, its inability to fly, due to brachypterous hindwings, renders it a species with a somewhat restricted capacity to disperse widely. Only one other species of *Acheta* is known to occur on the island of Pantelleria, namely the widespread *A. domesticus*.

The island of Pantelleria, lies on the Siculo-Tunisian Strait and comprises a volcanic caldera with a number of monogenic clusters or vents whose sub-aerial history dates back more than 300,000 years (Villari 1974; Civetta et al. 1988; Rotolo et al. 2021). Pantelleria lies less than one hundred kilometres from the south-west coast of Sicily and seventy kilometres east of the Cap Bon promontory (Tunisia) on the north African coast (Fig. 1). It may be pertinent to add that its distance to the Sicilian coast during the Pleistocene lowstands (glacials) would have been markedly reduced as Adventure Bank and other otherwise submerged landmasses became exposed subaerially as eustatic sea-levels fell (Grasso et al. 1985).

The visits to Pantelleria related to the present work aimed to investigate the status of a selected suite of target species of biogeographical interest, amongst which, *A. pantescus*, a stenoecious species restricted to coastal rocky habitats along the southern segment of the island (Figs 2, 3), where the geomorphology is characterised by craggy sea-cliffs and boulder screes made up of volcanic rock features comprising crevices, fissures and shallow cave formations. The predominant stratigraphic exposure of the landform on this part of the coast consists of Green Tuff and pre-Green Tuff eruptive units (Corradino et al. 2024). This contribution focuses on two main aspects relating to *A. pantescus*, namely its habitat affinity and its genetics, with a view to draw comparisons with other *Acheta* species.

Materials and methods

Five entomological expeditions to the island of Pantelleria were conducted between 2023 and 2025. The first was undertaken in the last days of May 2023, the second and third visits were held in 2024, one at the end of February and the other at the end of summer/early autumn respectively, while the fourth visit took place towards the end of February 2025, and the fifth was held in late June-early July 2025. During the February 2024 field visit, two data loggers (Lascare Electronics, model EL-USB-2-PRO) were placed at the Martingana locality to record temperatures (°C) and relative humidity (%). These were set up to take readings every six hours for a whole year and withdrawn from the field in February 2025. One of the instruments was positioned above the cave at 23 m asl, among coastal vegetation, while the second was set up inside a fissure among the rocks (where coastal vegetation is sparse or virtually absent), at 16 m asl, where *A. pantescus* is known to occur. It should be noted that, as of 20th October 2024, one of the data loggers that was positioned above the cave at 23 m asl, no longer recorded data. To compensate for this mishap, however, missing data were extrapolated from the closest weather station (via https://www.wunderground.com/), using matching

Figure 1. The island of Pantelleria on the Siculo-Tunisian strait. Source of original basemap: IUCN webpage.

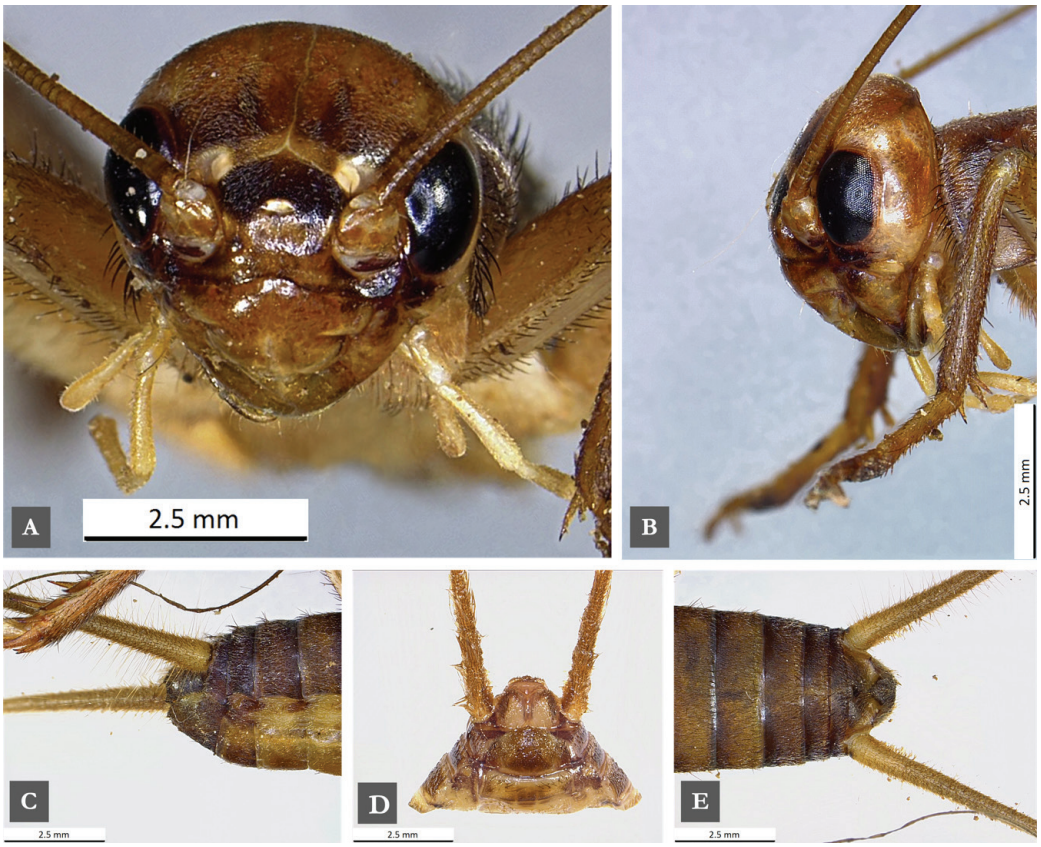

Figure 2. *Acheta pantescus* ♂ nymph detail of the head, anterior [**A**] and lateral view [**B**]. Male terminalia in lateral and dorsal view [**C, E**]; subgenital plate in ventral view [**D**].

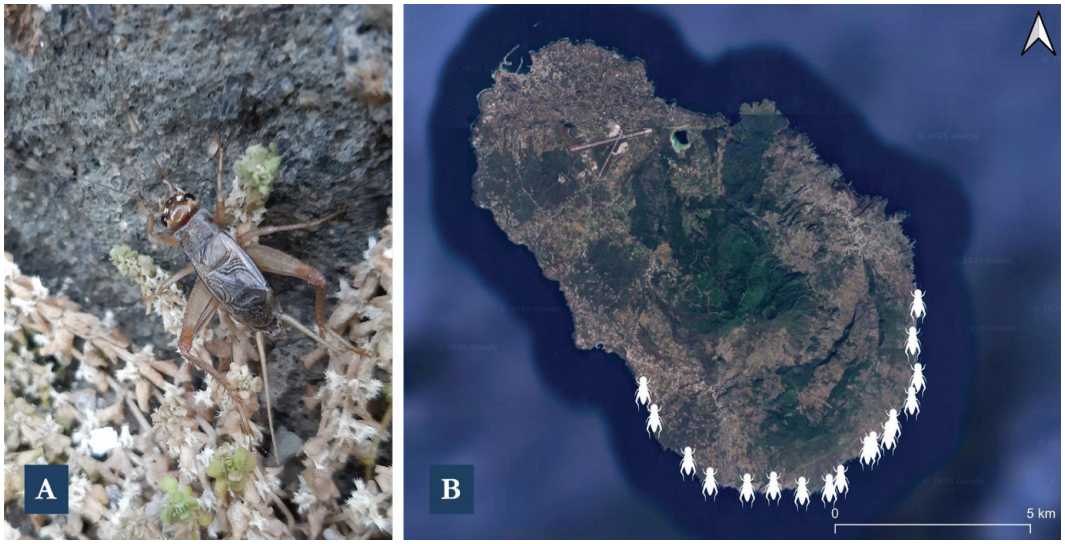

Figure 3. An adult ♂ (holotypus of the species) at Punta Limarsi, Balata dei Turchi [**A**] (photo: P. Fontana). An indication of sites where *Acheta pantescus* has so far been recorded [**B**] (source of basemap: Google Satellite on QGIS).

meteorological parameters, which in the months February-September produced data identical to that of our data loggers. The data from the data loggers were subsequently analysed and the t-test for unpaired parametric data was used for statistical comparison using free software for scientific data analysis (Past version 4.12, made available by the Natural History Museum of the University of Oslo). The climatic parameters taken into consideration for the analyses were the mean daily average of temperature and relative humidity between 7th February 2024 and 25th February 2025; in total, a sample of 3340 data points was analyzed.

During every visit, apart from those carried out in February 2024 and 2025, acoustic detection was carried out via the use of recorders ("Wildlife Acoustics" with an integrated microphone model "Song Meter Micro)", which

were positioned at Martingana, a locality where a population of this species is known to occur. These were set at a frequency of 44.1 kHz (Massa et al. 2022) and programmed to record an audio file remotely for a duration of 30 minutes every hour between sunset and sunrise. The data from the bioacoustic recorders were analysed with Audacity Software 3.3.1 (Audacity Team, 1999–2023) an open-source software application, the sole scope of which was to better understand the cricket's life cycle across the different months of the year, based on nocturnal activity, more specifically, stridulating adult males.

During the latter part of July 2022 and the initial days of July 2025, night-time searches along the entire coast of Pantelleria were carried out by boat. Each of these boat trips lasted some five hours, during which time a record was kept of geographical locations where stridulating males of *A. pantescus* were heard (Fig. 3). During the second field visit of 2024, thorough searches around the mouth of secluded coastal caves at Cala Rotonda, Martingana and the cliffs immediately above were carried out on three separate occasions. Loose rocks were carefully lifted or turned over in search of *A. pantescus* and subsequently placed in their original position (to ensure minimal disturbance to any fauna sheltering thereunder). Since during previous visits, it was ascertained that the crickets were attracted to bait, such as fresh fruit, between five and eight pitfall traps were set up at dusk and each one was baited with fresh fruit and unsalted anchovy; these were then inspected the following morning. The pitfalls were positioned just outside the shallow caves under the cliff overhang at the locality, as well as among the flotsam and within mounds of rocks and cliff face debris that accumulated at the foot of the cliffs consequent to spalling processes. At the time of survey, a handful of small boats, seemingly abandoned, lay within the area (Fig. 4). These boats and the assorted maritime items littering the area also provided shelter for a suite of invertebrates, including *A. pantescus*. Two male specimens were collected and used for the DNA analysis discussed in the present contribution; additional information is based on field observations during the various visits, which builds upon results published in Massa et al. (2022).

A Leica DVM6 digital microscope with a FOV of 43.73 and Z-stacking capability was used to photograph selected structures of the *A. pantescus* specimens under examination. Moreover, the entire hind limb of each of the collected specimens was removed and preserved in molecular grade ethanol solution (95.6%).

DNA was extracted from the sample using the QIAamp DNA tissue microkit [Qiagen, Hilden, Germany] according to the manufacturer's protocol, and quantified using a Nanodrop 2000 spectrophotometer. A partial sequence of the mitochondrial 16S ribosomal RNA region was amplified with the primers 16S22 and 16SR21, while the cytochrome c oxidase subunit 1 (COI) gene was amplified using the primer pairs LCO1490 and HCO2198 (Folmer et al. 1994; Yeh and Yang 1997). The mitochondrial DNA (mtDNA) NADH dehydrogenase subunit 1 (ND1) was amplified using a nested PCR methodology by using the CA-CYTBJ and OR-12SN primers for the first PCR. Subsequently, the OR-ND1J

Figure 4. *Acheta pantescus* habitat; sea-cliffs and shallow caves at Martingana, where pitfall traps were employed (Photos: J.J. Borg).

and OR-12SN primers were used for the second PCR (Sheffield et al. 2010). PCR amplifications were then performed in a total volume of 50 µL, containing approximately 100 ng of DNA, a deoxynucleoside triphosphate mixture (0.2 mM each), supplemented to give a final concentration of 1.8 mM MgCl2, 0.625 U of OneTaq Quick Load 2× Master Mix with Standard Buffer [New England Biolabs, Inc.], 0.5 pmol of each primer and of 21 µL nuclease-free water. Amplifications were carried out in a GeneAmp thermocycler PCR system 2700 [Applied Biosystems, Foster City, USA] according to the PCR programmes as per Pradit et al. (2022) and Sheffield et al. (2020). PCR products were subsequently verified on 1% (w/v) agarose gel and purified using a Wizard® SV Gel and PCR Clean-Up System [Promega, Madison, USA]. Purified material was sequenced at Genewiz [Azenta Life Sciences] Leipzig, Germany. Sequences were then manually checked by inspecting the chromatograms and compared to published sequences via the Basic Local Alignment Search Tool (BLAST), specifically the BLASTN 2.17.0 with the standard algorithm parameters, housed at the United States National Center of Biotechnology Information (Zhang et al. 2000).

Multiple alignments of the COI, 16S and ND1 markers were performed using the MAFFT algorithm L-INS-I (Katoh and Standley 2013). Three datasets were analysed, the first based on COI (740 bp), which included 12 nucleotide sequences from GenBank, together with the newly produced sequences. The second dataset comprised 16S sequences (530 bp) that included 7 nucleotide sequences from GenBank, together with new sequences produced in this study, while the third dataset, based on ND1 (794 bp), included 6 nucleotide sequences from GenBank, together with a new sequence produced in this study. *Gryllus bimaculatus* and *G. veletis* were selected as outgroup taxa, while sequences of *A. domesticus* and *A. hispanicus*, the only sequences available for the genus of *Acheta* on GenBank, were used in the phylogeny. Additionally, other closely related genera available on GenBank and as per Chintauan-Marquier et al. (2016), were used, details of which can be found in Suppl. material 1.

Bayesian Inference (BI) was performed using MrBayes v. 3.2.7 (Ronquist et al. 2012) on the NGPhylogeny portal (Lemoine et al. 2019). Maximum Likelihood (ML) analyses were carried out using PhyML (Guindon et al. 2010), with the general time reversible + gamma distribution + invariable sites model (GTR + G + I) (Nei and Kumar 2000) with 1000 bootstrap replicates (Nei and Kumar 2000). BI analyses were run with the GTR + G + I model parameters estimated independently for each partition, with four Monte Carlo Markov Chains for 2 million generations. Nodal support was assessed by calculating the posterior probability (PP) values for each node of the resulting consensus tree after a burn-in value of 25% of the trees. Both ML and BI analyses produced trees with a similar topology. Viewing and editing of the phylogenetic trees were carried out in FigTree v. 1.4.4 (Rambaut 2012).

Results

Diffusion of the species on the island of Pantelleria

On the basis of the results obtained from the acoustic recordings and nocturnal excursions along the island's coastline, it can be concluded that *A. pantescus* is widespread along the sheer cliffs on the southern part of the island (Fig. 3B), including Faraglione dietro l'isola, where this cricket is closely associated with the south-facing coastal crags.

Phenology and ecology

During field surveys in which the first individuals of *A. pantescus* were collected, namely in May 2022, a number of very small nymphs (in their early development phase) were observed at the Martingana coastal site, a few meters from the rock cavities where the first female was discovered and stridulation of male individuals was recorded. As a consequence, these nymphs were attributed to the species under study. During the field visit of May 2023, four nymphs in various stages of development were collected in baited traps at Martingana and reared in captivity. They eventually reached their adult phase between September and October of the same year, although it transpired that each individual's wings failed to develop properly. During the 2024 field visit, an adult female was found at the site in Cala Rotonda, Martingana, under rocky debris at the mouth of one of the shallow caves. The elusive specimen, however, managed to scurry into a debris mound, because of which, it was not collected. Meanwhile, two nymphs, both males, were collected from different pitfall traps containing similar bait from the same site (details in relation to date, locality and stages of metamorphosis are shown in Table 1). These were both transported back to the laboratory alive where they were kept in netted vivaria under observation for over seven weeks prior to preparation. One reason for attempting to rear the nymphs was because the biology of the recently described *A. pantescus* is still

Table 1. List of observations detailing dates, localities and stages of metamorphosis.

Month (date)	Location	Development stage of metamorphosis
May (14, 2022)	Punta Limarsi, Balata dei Turchi	1 adult ♂
May (15, 2022)	Martingana	1 sub-adult ♀; some 1st instar nymphs
May (29–30, 2023)	Martingana	4 nymphs – various life stages
July (15, 2022)	Martingana	1 sub-adult ♀
September (13–16, 2024)	Martingana	1 adult ♀ and 2 juv. ♂♂ with minute wing buds
October (4–5, 2022)	Martingana	Juvenile stages without wing buds
November (1–3, 2022)	Martingana	Juvenile stages with wing buds

insufficiently known. Although the nymphs were relatively quite large in comparison to the adult form, the wing buds were quite small and underdeveloped and, as a result, quite inconspicuous to the naked eye. In captivity, the nymphs were fed dry fish food pellets and fresh vegetable kitchen scraps, which they readily consumed. However, ecdysis (moulting of the outer cuticle or exoskeleton) did not occur.

Site-selection of the two stations within which monitoring of temperature and relative humidity was based, respectively, on (*i*) recorded presence of *A. pantescus* and (*ii*) a vegetated area on the sea-cliff where no sightings were made, thus, assumed to be beyond the cricket's ecological area of diffusion. The habitat of *A. pantescus* evidently retains warmer temperatures and lower humidity percentages during the winter season, and lower temperatures and higher humidity in the summer season (labelled "on site"). Conversely, *A. pantescus* was not present within the more vegetated section of the sea-cliff (to-date, this area has been shown to be beyond the habitat typically occupied by the cricket), where cooler temperatures and high rates of humidity were registered in winter, and higher temperatures with accompanying low percentages of humidity were recorded in summer. Parametric data analysed included both temperature and humidity. In the case of temperature data recorded for the two stations, it transpired that the difference between the variances (two monitored points on the sea-cliff) were not statistically significant (t-test = 0.86, p-value = 0.39); however, differences in the means of parameters involving relative humidity were highly significant (t-test = 3.94, p-value < 0.001) (Fig. 5). With regard to bioacoustic recordings that were carried out from February to October, with the exclusion of the month of March, it appears that *A. pantescus* males begin to stridulate from the end of April and continue, uninterrupted, through to September/October. During the warmer months, stridulation attains greater intensity, while from October onwards, when temperatures begin to drop, the male cricket's stridulatory activity decreases markedly (observations across months of the year are shown in Table 2).

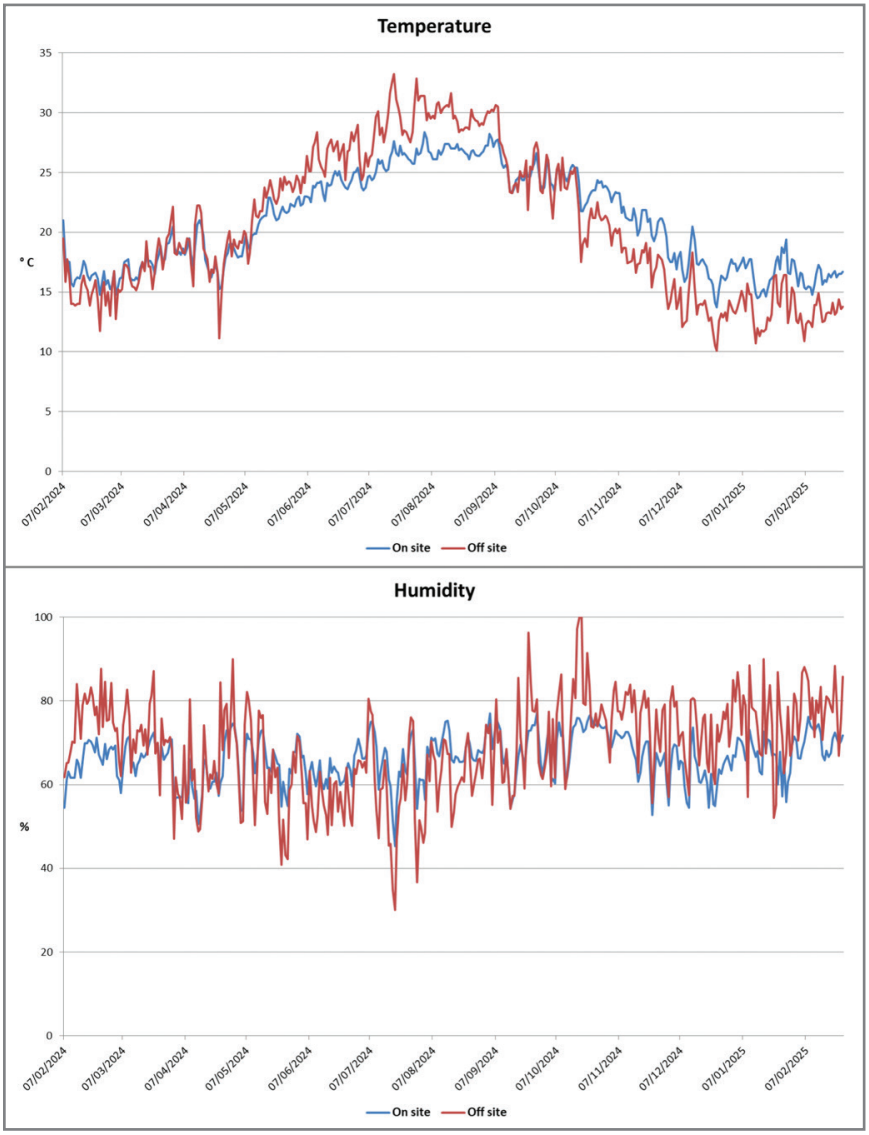

Figure 5. Temperature and relative humidity trends at the two sites over a one-year monitoring period (On site: presence of the cricket; Off site: absence of the cricket).

Table 2. Observations made across the different months of the year.

Observations / Development Stage	Detection											
Stridulation (indicatating presence of adults)	–	N	–	Y	Y	Y	Y	Y	Y	Y	–	–
Adults (observed during fieldwork)	–	N	–	–	Y	N	N	–	Y	N	N	–
Nymphs with wing buds	–	N	–	–	Y	N	Y	–	Y	N	Y	–
Nymphs without wing buds	–	N	–	–	Y	N	N	–	N	Y	N	–
1st instar nymphs	–	N	–	–	Y	N	N	–	N	N	N	–
Month of the Year	January	February	March	April	May	June	July	August	September	October	November	December

Genetics

In total, five COI, 16S and ND1 sequences were obtained during this study. These were submitted to GenBank and assigned the accession numbers listed in Table 3. The COI sequences for specimens Ap29Pnl and Ap30Pnl (644 and 623 bp) of the two male specimens of *Acheta pantescus*, did not result in a close hit on GenBank. The two sequences were only 91.6% identical to GenBank sequences OR974517 of *Acheta hispanicus* from Portugal (Beja, Mertola, Herdade de Alagaes) and 90% identical to OR974511 and OR974760 of *Acheta domesticus*, both from Portugal (Beja, Mertola, Bombeira do Guadiana and Castelo Branco, Idanha-a-Nova, Segura) (Pina et al. 2024). The 16S sequences for Ap29Pnl and Ap30Pnl (487 and 480 bp) of the two specimens also did not result in any close hits on GenBank. The two *A. pantescus* sequences were 94.3–94.6% identical to *A. domesticus* specimens with GenBank accession numbers MZ440654 purchased in Tokyo (complete mitochondrial genome in Sanno et al. 2021) and OK504623 from Thailand (complete mitochondrial genome in Homchan et al. 2024). There are no *A. hispanicus* sequences of 16S on GenBank. Similarly, the ND1 sequence for Ap30Pnl (794 bp) was 91% identical to *A. domesticus* specimens with GenBank accession numbers MZ440654 purchased in Tokyo (complete mitochondrial genome in Sanno et al. 2021) and OK504623 from Thailand (complete mitochondrial genome in Homchan et al. 2024). There are no *A. hispanicus* sequences of ND1 on GenBank.

Table 3. List of barcode sequences produced in this study, with the corresponding NCBI accession numbers.

Specimen	Species name	COI	16S	ND1
Ap29PnI	*Acheta pantescus*	PV347106	PV348941	–
Ap30PnI	*Acheta pantescus*	PV347107	PV348942	PV344512

The consensus COI tree (Fig. 6) shows that specimens Ap29Pnl and Ap30Pnl clustered together, and this is supported by both BI and ML (1.00 and 100). Sister to this grouping is the *A. domesticus* cluster with specimen MZ440654 and OK504623, supported by both BI and ML analysis (0.89 and 76). This was an anticipated outcome since the species of *A. pantescus* had not been DNA barcoded previously. Our consensus 16S tree (Fig. 7) also shows that specimens Ap29Pnl and Ap30Pnl clustered together. Sister to this cluster is the *A. domesticus* and the *A. hispanicus* grouping, supported by both BI and ML (1.00 and 100). The ND1 phylogenetic tree (Fig. 8) also shows similar results, with Ap30Pnl forming part of the *Acheta* cluster and this is supported by both BI and ML (1.00 and 96).

Discussion

From the biogeographical point of view, the occurrence of an endemic species on a volcanic island, particularly one that has never been physically connected subaerially to other landmasses via terrestrial corridors throughout its entire geological history, is especially interesting. Evidently, the primary habitat of *A. pantescus* comprises natural fissures and shallow caves within the craggy coastal sea-cliffs, as well as cavities beneath loose lava rocks at the base of the cliffs. However, it remains to be seen if the cricket also exhibits a propensity for synanthropic environments, such as the dimly lit and humid surroundings within the 'voids' (bilges and other sections of the lower, inside hull) of the dilapidated seacraft at Cala Rotonda, Martingana. Nevertheless, there is no doubt that this stenoecious cricket's habitat is strictly confined to a considerably narrow strip of the coast, where it exploits clefts within the rugged sea-cliff environment. The species' habitat preference is undoubtedly bound to its ecological niche, a space that provides for its continued survival, including a refuge from predators, as also an adaptation to a microclimate that relies, above all, on specific humidity conditions, amenable to its physiology and/or its food resources, yet unknown. The shelter afforded by natural fissures and crevices in the craggy sea-cliffs also provides a means for temperature control within its habitat, although the cricket, like all poikilotherms, will in all likelihood be less active during the winter months due to lower temperatures. Indeed, it is recognised that this environmental parameter influences metabolism in crickets, as is amply demonstrated by studies on *Acheta domesticus* and *Gryllus bimaculatus* (Booth and Kiddell 2007; Weidlich et al. 2012). While a census of the species' precise range and population numbers would benefit any conservation effort, more field observations are required to better understand this stenoecious species' ecology.

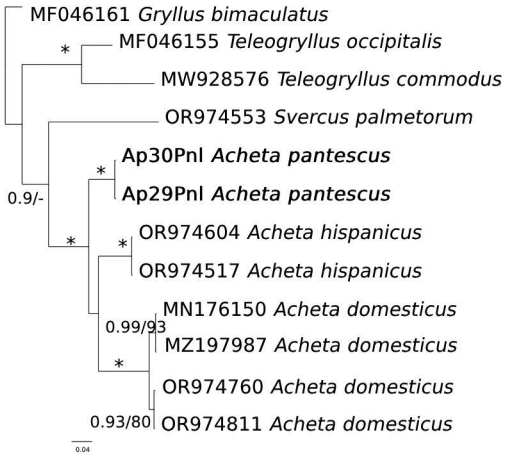

Figure 6. Consensus phylogenetic tree of species of *Acheta* together with other related species within the Gryllidae family inferred from COI sequences. The numbers on branches are Bayesian posterior probabilities (BPP) and bootstrap (BS) values (> 0.7 and 70% respectively). An asterisk (*) indicates full support (= 1.00 and 100%). The scale bar represents number of substitutions per site.

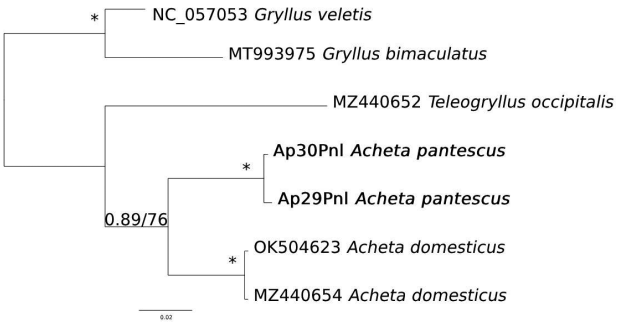

Figure 7. Consensus phylogenetic tree inferred from 16S sequences. The numbers on branches are Bayesian posterior probabilities (BPP) and bootstrap (BS) values (> 0.7 and 70% respectively). An asterisk (*) indicates full support (= 1.00 and 100%). The scale bar represents number of substitutions per site.

Another characteristic that ought to be highlighted is that this species is practically flightless due to its atrophic hindwings, a trait that is akin to other Mediterranean species of *Acheta*, which similarly comprise vestigial hindwings. Such morphological attribute would naturally restrain the species from any form of long-haul mobility and subsequent active dispersal, rendering the taxon more responsive to evolutionary mechanisms influenced by reproductive isolation and genetic divergence; such would be the basis for endemism. The resultant morphometric configuration of the endemic *A. pantescus*, undoubtedly, also had a bearing on the species' unique song, which was found to be different from that of other related taxa (Massa et al. 2022). However, other species of insects that are unable to fly occur on Pantelleria, some of which are also present in North Africa and Sicily, while others are considered endemic taxa (Massa 1995); although it is difficult to fully understand how some of these species could have arrived and established a foothold on the island, it is

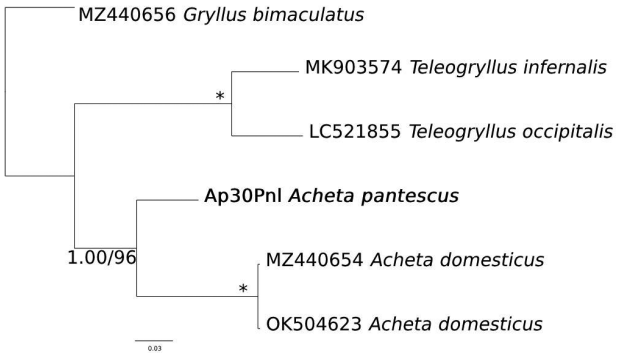

Figure 8. Consensus phylogenetic tree inferred from ND1 sequences. The numbers on branches are Bayesian posterior probabilities (BPP) and bootstrap (BS) values (> 0.7 and 70% respectively). An asterisk (*) indicates full support (= 1.00 and 100%). The scale bar represents number of substitutions per site.

presumed that passive dispersal, even through the importation by human agency, contributed greatly. The present authors refer to Massa et al. (2022) for possible interpretations on the origin of *A. pantescus*.

In addition to the species' strong preference for craggy quasi-vertical cliffs overlooking the sea (as already expounded above), *A. pantescus* is also partial to coastal rocky areas with sparse or no vegetation. The results obtained for temperature and relative humidity following a year of monitoring within Martingana but at two different stations with discernibly varying environmental conditions demonstrate a trend, illustrated in the graphs presented (Fig. 5). Although our knowledge of the species' phenology is still somewhat limited, observations gathered during the various field visits, nonetheless shed some light on the species' development. These preliminary findings, which are presented in tabular form, also need to be considered together with the timing of bioacoustic data gathered (for bioacoustics of the species, refer to Massa et al. 2022). However, so far, it is evident that adults can be encountered between the end of April through to October, although this is by no means conclusive, given it is based on short-visit snapshot data. Moreover, a broad range of life-cycle stages, from 1st instar to penultimate nymphal (sub-adult) phase were recorded in the month of May, over the years 2022 and 2025. Adults observed in May would have presumably been the result of eggs laid in Autumn and hatched around the onset of ecological spring, which in the Mediterranean typically commences towards the latter part of February. Given that advanced nymphal stages were also encountered between mid-September and early November, it may be plausible to assume that *A. pantescus* may indeed overwinter as an adult (potentially, along with advanced instar phases of the species). As ambient temperatures fall in winter, the cricket could well exploit the shelter provided by the rocky fissures on the sea-cliffs. Clearly, more field monitoring, particularly during the wet season, is warranted.

From the genetic standpoint, *Acheta pantescus* clustered together with other *Acheta* sequences of the genus available in databases, including *A. domesticus* and

A. hispanicus. However, a comparison with other species, including a discussion on hypotheses about its origin, requires further work noting the lack of information currently available on GenBank. For example, for *A. hispanicus*, only the partial COI gene was available for comparative purposes and, therefore, the phylogenetic trees of 16S (Fig. 7) and ND1 (Fig. 8) do not include this species. Thus, it is highly recommended that further research involving other related species and other genes is carried out to complement the findings of the present contribution. As also discussed in Bartolo et al. (2025), recent DNA work conducted on other gryllid species from the Mediterranean region (Cassar et al. 2025) has revealed that DNA barcoding of such taxonomic group from this geographical area is greatly lacking; this knowledge gap has implications for future studies and conservation, hence the significance of publishing such genetic data. In fact, populating databases with additional information is crucial for future barcoding and metabarcoding studies, especially in scientific fields where genetic studies have been somewhat lacking (Bartolo et al. 2020). It is augured that this first genetic data for *Acheta pantescus* presented herein spearheads other scientific inquires that will shed more light on the species and on the biogeography of the central Mediterranean area.

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Supplementary material 1

Species and GenBank accession numbers for the sequences included in the COI, 16S and ND1 datasets

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