Journal of the Marine Biological Association of the United Kingdom

cambridge.org/mbi

Research Article

Cite this article: Moraes IRR, Pasinatto K, Bochini GL, Horch AP, Almeida AO, Terossi M (2024). Shrimps from a marine biodiversity hotspot: new records and molecular analysis of alpheids from the Fernando de Noronha Archipelago (Decapoda: Caridea). *Journal of the Marine Biological Association of the United Kingdom* **104**, e73, 1–8. https://doi.org/ 10.1017/S0025315424000730

Received: 30 April 2024 Revised: 18 July 2024 Accepted: 12 August 2024

Keywords:

16S gene; Brazilian fauna; crustacean biodiversity; cytochrome oxidase subunit I; marine conservation

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Shrimps from a marine biodiversity hotspot: new records and molecular analysis of alpheids from the Fernando de Noronha Archipelago (Decapoda: Caridea)

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Abstract

The oceanic archipelago of Fernando de Noronha represents one of the most important regions for Brazilian marine biodiversity, and is considered a 'no-take' marine area under law. More than 130 crustacean species have already been registered in the archipelago, with a significant number of caridean shrimps. Almost half of these shrimps belong to the family Alpheidae, making them an important marker of the species composition of the region. This study provides five new records of alpheids for the archipelago. Samples were taken in 2019 and 2022 from six locations around Fernando de Noronha, using active search during low tide and SCUBA diving in subtidal zones. The new records are Alpheus agilis, A. angulosus, A. rudolphi, Automate dolichognatha sensu lato, and Salmoneus ortmanni, and their DNA sequences have been made available alongside geographical distribution, photographs, ecological notes, and species remarks. All DNA sequences (mitochondrial 16S and cytochrome oxidase I genes) generated were compared with sequences available in Genbank and, in some cases, our sequences are the first for the species. Through this update, a total of 46 species of caridean shrimps have been recorded from Fernando de Noronha. Here we highlight the importance of checklists as a tool to keep an updated record of species' distributions. Continuous study of the native fauna of one of the most important biodiversity hotspots on the Brazilian coast is essential to establish effective management and conservation plans for the region.

Introduction

The Fernando de Noronha Archipelago, along with Atol das Rocas, has been considered a World Heritage Site as part of the Brazilian Atlantic islands since 2001 (Unesco, 2001). It is an oceanic archipelago located 545 kilometres away from the Brazilian coast, and situated on top of volcanic peaks from an underwater mountain chain, whose consolidated base is more than four thousands metres deep (Unesco, 2001; Castro, 2010; Serafini *et al.*, 2010). The archipelago is represented by 21 volcanic islands, forming numerous beaches, coves, and coral reefs, among other marine microhabitats (Gillespie, 2001; Serafini *et al.*, 2010; Gove *et al.*, 2016).

The largest island of the archipelago, which shares the name of Fernando de Noronha and is more than 17 km in length, houses over 3000 people (IBGE, 2023), along with an increasing number of tourists throughout the year (Pereira *et al.*, 2024). Due to this fluctuating population, the main island deserves special attention, as the local environment may suffer direct anthropogenic and social disturbances (Pereira *et al.*, 2024).

Fernando de Noronha is one of the most representative sites of Brazilian biodiversity, from the tiniest invertebrates to the largest vertebrates (IBAMA, 2005; Fioravanso and Nicolodi, 2021). The peculiar aspects of its fauna, flora, and ecosystems, set the archipelago apart from other environments on Earth (Unesco, 2001). As a set of oceanic islands with a large quantity of endemic fauna, it is considered an ecological hotspot of biodiversity (Gillespie, 2001; Gove *et al.*, 2016). The archipelago is a no-take marine region under two different Brazilian conservation legislations: it is an 'Área de Proteção Ambiental (APA)' (i.e. Environmental Protection Area) and a 'Parque Nacional Marinho (PARNAMAR)' (i.e. National Marine Park) (Brasil, 1988; Fioravanso and Nicolodi, 2021).

Since the end of the XIX century, efforts have been made to record the diversity of the decapod crustacean fauna (crabs, shrimps, lobsters, among others) inhabiting the archipelago (Pocock, 1890; Fausto-Filho, 1974; Coelho *et al.*, 2002, 2006; Coelho-Filho, 2006). More recently, two major checklists concerning this group have been published, recording more

Sampling site	Coordinate	Method
Praia do Porto de Santo Antônio	3°50′1.59″S 32°24′1.27″W	Active search – low tide
Praia Caieiras	3°50′12.80″S 32°23′59.42″W	Active nocturnal search – low tide
Pontinha	3°51′00.5″S 32°23′32.8″W	Active search – low tide
Abreus	3°51′45.72″S 32°24′53.73″W	Active search – low tide
Laje Dois Irmãos	3°50′40.2″S 32°26′34.6″W	SCUBA dive
Praia do Sueste	3°52′2.39″S 32°25′18.30″W	Active search – low tide

 Table 1. List of sampling sites of the Fernando de Noronha Archipelago,

 geographical coordinates and sampling methods applied in each area.

than 130 species in over 40 families, showing the importance of the region for Brazilian crustacean fauna (Alves *et al.*, 2008; Souza *et al.*, 2011).

Within the decapod species of the archipelago, the shrimps of the infraorder Caridea have great representativeness, with 41 records distributed into seven families. Most of this diversity is concentrated on species of the family Alpheidae Rafinesque, 1815, with almost half (21) of all caridean shrimps reported, followed by Palaemonidae Rafinesque, 1815, with eight species (Alves *et al.*, 2008). These records are not surprising, since Alpheidae is one of the richest families in the infraorder, and is ubiquitous in the shallow-waters of tropical marine and estuarine areas (Almeida *et al.*, 2018; Bauer, 2023). This study aims to provide five new records of alpheids for Fernando de Noronha, updating the number of species recorded for the region. It also provides molecular data alongside geographical distribution, photographs, ecological notes, and species remarks for the taxa sampled.

Material and methods

Two expeditions were conducted to the Fernando de Noronha Archipelago in June/July 2019 and 2022, with 10 days of sampling effort in each expedition. The specimens analysed here were captured by active search during low tide (day and night) and SCUBA diving (day) in six sampled sites (Table 1, Figures 1, 2). For the active search, specimens were sampled manually from under rocks, rubble, sand crevices, and inside biogenic substrates. Sample efforts were determined by the duration of the low tide and how long the substrate remained exposed. For SCUBA diving, the collection was performed by four divers, totalling 4 h of catching effort per expedition. The map of the Fernando de Noronha Archipelago with all sampled locations (Figure 1) was created using the QGIS software (Geographic Information System; http://www.qgis.org).

The criteria used to search for shrimps in the subtidal zone was based on knowledge of the lifestyle of the target species, as alpheids are often found on hard bottoms, seeking sheltered places and in association with other invertebrates. All specimens sampled were immediately stored individually in plastic flasks to preserve the morphological integrity of the specimens.

All shrimps were photographed and fixed in 80% alcohol, to be transferred to the laboratory and identified according to the literature. The specimens were sexed based on the presence or absence



Figure 1. Location of the Fernando de Noronha Archipelago off the coast of Brazil, and location of the sampling sites in the study area.



Figure 2. General view of each sampling site along the Fernando de Noronha Archipelago. (A) Abreus; (B) Praia Caieiras; (C) Pontinha; (D) Praia do Porto de Santo Antônio; (E) Praia do Sueste; (F) Laje Dois Irmãos.

of the *appendix masculina* on the endopod of the second pleopods, being designated as males or females, respectively (Bauer, 2023). Moreover, females were also identified by the presence of eggs attached to the pleopods and subsequently defined as ovigerous females. All specimens were deposited in the Coleção de Crustáceos do Departamento de Zoologia da Universidade Federal do Rio Grande do Sul (DZ/UFRGS).

The 'Ecological notes' included in the results section provides habitat and ecological details for each species based on observations made during the collections. These are descriptions of the locations where the specimens were found, if symbiosis was observed, and substrate distribution along the sampling sites.

Obtaining genetic data (tissue DNA extraction, PCR amplification, PCR product cleanup, sequencing, and consensus sequence) was conducted following Soledade *et al.* (2019). An ~500-bp region of the mitochondrial 16S gene and ~650-bp region of the barcode region of cytochrome oxidase subunit I (COI) gene were amplified using the primers (melting temperature of 46–48°C): 1472 (5'–AGATAGAAACCAACCTGG–3') and 16SL2 (5'–TGCCTGTTTATCAAAAACAT–3') (Crandall and Fitzpatrick, 1996; Schubart *et al.*, 2002) for 16S, and COH6 (5'-TADACTTCDGGRTGDCCAAARAAYCA-3'), COL6B2 (5'-ACAAATCATAAAGATATYGG-3'), COIAH2 m (5[']- GACCR AAAAATCARAATAAATGTTG-3') and COIAL20 (5[']-ACGC AACGATGATTATTTTCTAC-3') (Schubart and Huber, 2006; Mantelatto *et al.*, 2016) for COI.

Sequences were edited and the consensus sequences were obtained by using the BioEdit v7.0.9.0 software (Hall, 1999). All consensus sequences were confirmed by using the application BLASTn available at the NCBI database (http://blast.ncbi.ncbi. nlm.nih.gov/blast.cgi). A phylogram was generated for sequences of mitochondrial 16S gene based on the new sequences from Fernando de Noronha and the closest sequences according to BLASTn, which were downloaded from Genbank and included in the analysis. Also, a sequence of *Leptalpheus* Williams, 1965 retrieved from Genbank was used as an outgroup. Genbank sequence accession numbers were included in the phylogram (Figure 3) and cited in the text.

Sequence alignment was performed in MUSCLE (Multiple Sequence Comparison by Log-Expectation) (Edgar, 2004), available on the platform Cyberinfrastructure for Phylogenetic Research (CIPRES) (Miller *et al.*, 2010). The maximum likelihood analysis (ML) was conducted with RAxML 8.2.12 (Stamatakis, 2014) using the online version at CIPRES. ML was conducted with the default parameters for RAxML for the GTR model of evolution, using the option to automatically determine the number of bootstraps to be run in RAxML (Stamatakis *et al.*, 2008), thus, 950 bootstrap pseudo-replicates were run, and only confidence values >50% are reported.

Results and discussion

Family Alpheidae Rafinesque, 1815 Genus Alpheus Fabricius, 1798 Alpheus agilis Anker, Hurt and Knowlton, 2009 (Figure 4A, B) Alpheus agilis Anker, Hurt and Knowlton, 2009: 12, Figs 4, 5F.

Material examined: 1 ovigerous female and 1 male, Praia do Porto de Santo Antônio, 1 July 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6961); 1 female, Praia do Porto de Santo Antônio, 3 July 2022, coll. A. Horch & K. Pasinatto (DZ/UFRGS #6962); 1 male, Praia do Porto de Santo Antônio, 3 July 2022, coll. A. Horch & K. Pasinatto (DZ/ UFRGS #6965); 2 females and 4 males, Praia Caieiras, 28 June



Figure 3. Phylogram of the new records from the Fernando de Noronha Archipelago (in bold) and some specimens of alpheid shrimps from Genbank, using the ML analysis of mitochondrial 16S gene sequences. Numbers are support values for 950 bootstraps; values < 50% were not included. AR, Atol das Rocas; Atl, Atlantic Ocean; BA, Bahia; FN, Fernando de Noronha; GM, Gulf of Mexico; SP, São Paulo.

2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6959); 1 male, Praia da Pontinha, 27 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6957); 1 female, Praia da Pontinha, 28 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6958); 1 female and 6 males, Praia Sueste, 29 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6960); 1 specimen of unidentified sex, Praia Sueste, 29 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6960); 1 specimen of unidentified sex, Praia Sueste, 29 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6963); 1 female, Praia Sueste, 29 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6964), genetic voucher).

Geographical distribution: Amphi-Atlantic. Eastern Atlantic – Cape Verde Archipelago and São Tomé & Príncipe. Western Atlantic – Brazil (Atol das Rocas, Fernando de Noronha and Trindade Island) (Anker *et al.*, 2009, 2016; present study).

Ecological notes: In tide pools, mostly under rocks in the intertidal.

Remarks: Alpheus agilis was described to the Eastern Atlantic Ocean (São Tomé) and reported in Brazil (Atol das Rocas) by Anker *et al.* (2009). The second record of the species in Brazil occurred in 2016, at Trindade Island (Anker *et al.*, 2016). Now we record the species for the first time in Fernando de Noronha. So far, all Brazilian records have been made at oceanic islands. No information about the biological and ecological features of this species is provided in the literature.

Genetic data: Here we provide the first mitochondrial 16S sequence of the species (GenBank access PQ041197). In the phylogram (Figure 3), *A. agilis* from Fernando de Noronha was close to *Alpheus bouvieri* A. Milne-Edwards, 1878. This was expected, considering that both belong to the same species complex and are

closely related on the phylogeny proposed by Anker *et al.* (2009). Unfortunately, no COI sequence was obtained for this species.

Alpheus angulosus McClure, 2002 (Figure 4C, D) Alpheus angulosus McClure, 2002: 368.

Material examined: 6 females (3 ovigerous) and 8 males, Praia do Porto de Santo Antônio, 1 July 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6975); 9 females (6 ovigerous) and 3 males, Praia do Porto de Santo Antônio, 3 July 2022, coll. A. Horch & K. Pasinatto (DZ/UFRGS #6976); 1 male, Praia do Porto de Santo Antônio, 3 July 2022, coll. A. Horch & K. Pasinatto (DZ/UFRGS #6977); 1 male, Praia Caieiras, 28 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6978); 4 females (2 ovigerous) and 1 male, Praia da Pontinha, 27 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6980); 1 male, Praia da Pontinha, 28 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6979); 6 females (4 ovigerous) and 7 males, Praia Sueste, 29 June 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6974, genetic voucher).

Geographical distribution: Western Atlantic – USA (North Carolina to Florida), Gulf of Mexico, Caribbean Sea, French Guyana, Brazil (Atol das Rocas, Fernando de Noronha, Maranhão, Ceará, Paraíba, Pernambuco, Bahia, Rio de Janeiro, São Paulo, Santa Catarina, Rio Grande do Sul) (Anker, 2012; Tracey *et al.*, 2013; Almeida *et al.*, 2018; Costa-Souza *et al.*, 2019, 2022; Teles and Mantelatto, 2023; present study).

Ecological notes: In tide pools, mostly under rocks in the intertidal. **Remarks:** Although the occurrence of *A. angulosus* in Fernando de Noronha has been registered by Anker (2012), the



Figure 4. Lateral and dorsal view of the alpheid shrimps recorded for the first time in the Fernando de Noronha Archipelago. (A–B) Alpheus agilis Anker, Hurt and Knowlton, 2009; (C–D); Alpheus angulosus McClure, 2002; (E–F); Alpheus rudolphi Almeida and Anker, 2011.

author did not provide any material examined from this region, nor does it provide a previous reference for the occurrence of the species there. In the present study, we confirmed the occurrence of *A. angulosus* in the archipelago.

Genetic data: The mitochondrial 16S sequence of *A. angulosus* from Fernando de Noronha (GenBank accession PQ041199) is almost identical to the sequences of *A. angulosus* from Florida (USA, near type locality) and Atol das Rocas (Brazil) (Figure 3), within the *Alpheus armillatus* H. Milne Edwards, 1837 species complex (see Anker, 2012). The COI sequence of *A. angulosus* from Fernando de Noronha (GenBank accession PQ041234) is almost identical to a sequence of *A. angulosus* from Bahia (Brazil, GenBank accession KU312996).

Alpheus rudolphi Almeida and Anker, 2011 (Figure 4E, F) Alpheus rudolphi Almeida and Anker, 2011: 3, Figs. 1–22.

Material examined: 1 male, Laje Dois Irmãos, 30 June 2022, coll. I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6948, genetic voucher); 1 female (parental with larvae), Laje Dois Irmãos, 30 June 2022, coll. I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6949).

Geographical distribution: Western Atlantic – Brazil (Fernando de Noronha, Trindade Island, Ceará, Pernambuco, Alagoas, Bahia, Espírito Santo) (Almeida and Anker, 2011; Hurt *et al.*, 2013; Cunha *et al.*, 2015; Anker *et al.*, 2016; present study).

Ecological notes: At a depth of 15 m, on a bottom with corals and other invertebrates, associated with unidentified sea anemones.

Remarks: This species belongs to the *Alpheus armatus* Rathbun, 1901 species complex. Since the species description (Almeida and Anker, 2011), the population density appears to be low, with no more than seven specimens recorded in the literature (Cunha *et al.*, 2015; Anker *et al.*, 2016). *Alpheus rudolphi* has only been recorded in Brazilian waters so far. The species is generally found in continental islands or near the coast, but was registered in the Trindade and Martin Vaz Archipelago at a depth of 16 m (Anker *et al.*, 2016). Here we record the occurrence of *A. rudolphi* in Fernando de Noronha for the first time.

Genetic data: Here we provide the first mitochondrial 16S sequence of *A. rudolphi* (GenBank accession PQ041198). It also represents the first mitochondrial 16S sequence from a species of the *A. armatus* complex, making genetic comparisons with closely related species difficult. In the BLAST analysis, the closest sequence belongs to *Alpheus lobidens* De Haan, 1849, with only 86% similarity, and this was included in the phylogram (Figure 3). The COI sequence of *A. rudolphi* from Fernando de Noronha (GenBank accession PQ041233) is identical to a sequence of *A. rudolphi* from Ceará (Brazil, GenBank accession KF131534).

Genus Automate De Man, 1888 Automate dolichognatha sensu lato De Man, 1888 (Figure 5A, B)

Automate dolichognatha De Man, 1888: 529, Fig. 5, pl. 22.

Material examined: 1 female and 1 specimen of unidentified sex, Praia do Porto de Santo Antônio, 1 July 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/ UFRGS #6951, genetic voucher); 4 specimens of unidentified



Figure 5. Lateral and dorsal view of the alpheid shrimps recorded for the first time in the Fernando de Noronha Archipelago. (A–B) Automate dolichognatha sensu lato De Man, 1888; (C–D); Salmoneus ortmanni (Rankin, 1898).

sex, Abreus, 2 July 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6952).

Geographical distribution: Worldwide. Eastern Pacific – from USA (California) to Peru, including Cocos Island and Galapagos. Indo-West Pacific – from the Red Sea to Japan, Australia and French Polynesia. Eastern Atlantic – Cape Verde and Ascension Island. Western Atlantic – USA (from North Carolina to Florida), Mexico (Gulf of Mexico and Yucatan Peninsula), Virgin Islands, Antigua Island, Barbados, and Brazil (Atol das Rocas, Fernando de Noronha, Trindade Island, Bahia and Rio de Janeiro) (Holthuis, 1951; Chace, 1972 as *Automate gardineri*; Banner and Banner, 1973; Williams, 1984; Chace, 1988; Manning and Chace, 1990; Christoffersen, 1998; Wicksten and Hendrickx, 2003; Almeida *et al.*, 2013; Anker *et al.*, 2016; present study).

Ecological notes: Under rocks and rubble, sometimes in burrows, mostly in the intertidal.

Remarks: Due to its pantropical distribution and variations in morphology and coloration, this species is considered in the literature as a species complex (Almeida et al., 2013; Anker et al., 2016). According to Anker et al. (2016), all western Atlantic records should be assigned to A. dolichognatha sensu lato. In Brazilian waters, the species has been recorded in both continental (Rio de Janeiro by Christoffersen, 1998, without figures; Bahia by Almeida et al., 2013, with photographs) and insular areas (Atol das Rocas and Trindade Island by Anker et al., 2016, without figures; Fernando de Noronha by the present study). We confirm the difficulty of registering the colour pattern for this species, mainly due to the translucent condition seen in all six specimens sampled. Despite that, we were able to photograph a female with an ovary showing bright yellow developed oocytes (Figure 5A, B), a characteristic that is likely an important coloration trait for this species.

Genetic data: Here we provide the first sequences from Brazilian material of *A. dolichognatha sensu lato* (GenBank accession – 16S: PQ041196; COI: PQ041232). In the mitochondrial 16S gene phylogram (Figure 3), the specimen from Fernando de Noronha was very similar to a specimen sampled in Bocas del Toro (Panama) and well separated from one specimen sampled in French Polynesia, giving support to the hypothesis of a species complex under the name *A. dolichognatha*. In the BLAST analysis, the COI sequence from Fernando de Noronha had 99% similarity with a sequence from Bocas del Toro, Panama (GenBank accession MN184105). A detailed morphological analysis of the material sampled in Brazil is ongoing, along with additional molecular analyses.

Genus Salmoneus Holthuis, 1955 Salmoneus ortmanni (Rankin, 1898) (Figure 5C, D) Athanas ortmanni Rankin, 1898: 251, Fig. 7, pl. 30.

Material examined: 3 specimens of unidentified sex, Praia do Porto de Santo Antônio, 21 June 2019, coll. G. Bochini & K. Pasinatto (DZ/UFRGS #6973); 2 females, Praia do Porto de Santo Antônio, 1 July 2022, coll. A. Horch, I. Moraes, K. Pasinatto & M. Terossi (DZ/UFRGS #6950); 1 specimen of unidentified sex, Praia da Pontinha, 20 June 2019, coll. G. Bochini & K. Pasinatto (DZ/UFRGS #6972, genetic voucher).

Geographical distribution: Western Atlantic – Bahamas, Aruba, Mexico (Yucatan Peninsula), Costa Rica, Panama, Venezuela, Bermuda; Brazil (Atol das Rocas, Fernando de Noronha, São Paulo) (Rankin, 1898; Verrill, 1922; Chace, 1972; Rodríguez, 1986; Anker, 2007, 2010; Anker *et al.*, 2013, present study).

Ecological notes: In tide pools, mostly under rocks in the intertidal.

Remarks: The taxonomic status of *S. ortmanni* was revised by Anker (2007), along with a redescription of the species and additional illustrations. *Salmoneus ortmanni* was previously considered a transisthmian species, occurring in both the Western Atlantic and the Eastern Pacific Oceans, but all Eastern Pacific specimens have been assigned to other species, keeping *S. ortmanni* exclusively in the Atlantic (Anker and Lazarus, 2015). As described by Anker *et al.* (2013), this species presents a semitransparent bright orange-yellow colour, which can be seen in the specimens collected in the present study (Figure 5C, D).

Genetic data: Here we provide the first sequences of the species (GenBank accession – 16S: PQ041195; COI: PQ041231). Salmoneus ortmanni from Fernando de Noronha was well separated from other species of the genus in the mito-chondrial 16S gene phylogram (Figure 3). Regarding COI, the only other sequence available is from Salmoneus carvachoi Anker, 2007, which showed 86% similarity in the BLAST analysis.

Conclusion

In this study, we record five additional alpheid species for the Fernando de Noronha Archipelago. Together with the previous records, it brings the total species of alpheid and caridean shrimps known from the archipelago to 26 and 46, respectively. Our results indicate that despite the previous efforts made to evaluate the decapod fauna of Fernando de Noronha (Pocock, 1890; Fausto-Filho, 1974; Coelho *et al.*, 2002, 2006; Coelho-Filho, 2006; Alves *et al.*, 2008; Souza *et al.*, 2011), our knowledge regarding the biodiversity of this important invertebrate group is still incomplete.

Preserved areas aim primarily to conserve biodiversity and manage natural resources. Therefore, the creation and application of legislations for no-take marine regions depend on in-depth knowledge of the local biota (Hendrickx, 1995; Gerhardinger *et al.*, 2011; Gamarra *et al.*, 2019). Considering the caridean shrimps, it is known that they are geographically and ecologically diverse in their distribution, and participate directly in the balance of aquatic food webs since they feed on lower trophic levels and transfer energy into food for other major predators (Wenner and Boesch, 1979; Amaral and Nallin, 2011).

Moreover, this is the first study with decapods from Fernando de Noronha that includes molecular data and records the colour pattern of the species. Some alpheid shrimps are difficult to identify based solely on the morphology of material preserved in ethanol (Knowlton and Mills, 1992; Anker, 2001). Thus, genetic and colour data can help in this process, which are now available for these species and can be used for comparisons in future studies. Finally, we highlight the importance of continuous biodiversity surveys to properly describe the biodiversity of the archipelago, employing different collection methods, recording colour and molecular data, and focusing on subsampled microhabitats. The data we provide here are essential for the continuous conservation and management of this important hotspot of Brazilian marine fauna.

Acknowledgements. Thanks are due to Leonardo Lopes Gonçalves da Silva for all the help during the scuba diving, to Angélica Viana e Silva and Pedro Augusto Mendes de Castro Melo, for Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio NGI Noronha), Autarquia Territorial Distrito Estadual de Fernando de Noronha - ATDEFN, and Dive Operator Atlantis for all logistical support during the fieldwork. We are also grateful to the two anonymous reviewers for the suggestions and corrections that improved the manuscript.

Author Contributions. IRRM: Sampling, main text writing, bibliography survey, specimen photography, and editing.

KP: Sampling and organization of the samples, identification, main text revision, and bibliography survey.

GLB: Sampling, bibliography survey, and taxonomy comments.

APH: Sampling and organization of the samples, production of map, main text revision, English grammar correction.

AOA: Identification, main text revision, taxonomic comments, and taxonomic revision.

MT: Research conception and design, coordinated the financial grants that supported the project (sampling and laboratory costs), sampling and organization of the samples, text writing and full text revision, genetic analyses.

Financial Support. This study was supported by Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) Research Grants to MT (Universal 421193/2018-2, PQ 311340/2021-0), AOA (PQ 311217/2022-2), APH (PhD fellowship 140920/2021-8), and KP (PhD fellowship 140066/2021-7).

Competing interests. The authors declare that they have no known competing financial interest or personal relationships that could have appeared to influence the work reported in this paper.

Ethical Standards. All samplings in this study were conducted according to applicable state and federal laws, license no. 66478 MMA/IBAMA/SISBIO granted to MT.

Data Availability. All specimens presented here were deposited and are now available for consultation in the Coleção de Crustáceos do Departamento de Zoologia da Universidade Federal do Rio Grande do Sul (DZ/UFRGS). The genetic sequences provided for each species are available on GenBank (https://www.ncbi.nlm.nih.gov/genbank/) and the access numbers can be found in the text and in the phylogram (Figure 3).

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