



Article Cytochrome b Sequencing as a Tool for Identification of Morphologically Similar Mediterranean Gobies Gobius incognitus and Gobius bucchichi (Actinopterygii: Gobiidae)

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Abstract: Despite being one of the most speciose fish families in the Mediterranean Sea, knowledge about the diversity of gobies (Actinopterygii: Gobiidae) in this sea is still unsatisfactory, as documented by recent descriptions of a number of new species. Although very common in shallow water, Gobius incognitus Kovačić & Šanda, 2016, had escaped attention until 2016, when it was discovered. Due to its overall superficial morphological similarity, G. incognitus used to be confused with a much rarer species, Gobius bucchichi Steindachner, 1870, which was considered one of the most common shallow-water gobies in the Mediterranean Sea. In this work, we tested the suitability of the genetic data (mitochondrial gene encoding cytochrome b) for identifying and distinguishing between these two goby species, and assessed the congruency between the distribution records based on genetic data and those based on morphological identification. We analysed material of 304 specimens of G. incognitus and G. bucchichi from 49 localities covering a considerable part of the Mediterranean Sea, Black Sea, and the Atlantic Ocean near Gibraltar, representing 19 geographically well-separated areas. We detected 270 sequences of G. incognitus, and only 34 of G. bucchichi. In both species, a high haplotype variability was observed. The sequence species identity matched morphological identification for all specimens for which vouchers were available. The mean uncorrected p-distance between G. incognitus and G. bucchichi was 13%, while the mean intraspecific distances were much lower (0.63% and 0.68%, respectively). We found 79 fixed mutations between these two species. Data on distribution based on genetic identification are completely congruent with published results based on morphological identification. The results of this study support molecular methods as a reliable tool for distinguishing morphologically similar fish species, which is particularly useful when only tissue is available for determination.

Keywords: diversity; distribution; gobies; Mediterranean; genetic identification



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1. Introduction

Gobies (Gobiidae) are one of the most speciose fish families worldwide [1]. At the same time, they are one of the most species-rich families of the Mediterranean marine fishes [2]. Despite this fact, gobiid diversity in the Mediterranean Sea is still far from being completely known. At the family level, the native gobiid fishes from the Mediterranean Sea are considered either members of a single family, Gobiidae [1], or of two sister families, Gobiidae and Oxudercidae [3]. The knowledge about the diversity of the gobies in the Mediterranean Sea is still unsatisfactory, as documented by a description of a number of new species in the last years, e.g., [4-9]. Usually, new species were first discovered in a small geographic area, but subsequently, they were found in even geographically considerably distant localities [10–15], indicating that they are rather widespread, and that the knowledge about their distribution could be improved by increased research effort [16]. Furthermore, some of the new species were described from greater depths or are typical cryptobenthic species that are difficult to sample by conventional fishing methods, but also by SCUBA divers (e.g., by active sampling methods or by a photographic evidence). Thus, it is more difficult to record them despite their often widespread presence. However, one of the recently described species was discovered in a very shallow water, where it is very common and abundant, and its late discovery is only due to its overall superficial morphological similarity with another, well-known species, which used to be considered one of the most common shallow-water gobies in the Mediterranean Sea region [17]. This species pair is a long-time known Gobius bucchichi Steindachner, 1870 and a newly described Gobius incognitus Kovačić & Šanda, 2016. Although cursorily very similar (Figure 1), both species are in fact readily distinguishable by morphological character [18]; they can even be reliably identified from photographs [19]. Both species also seem to be genetically considerably distinct [4,18]. Data on the distribution of both species were recently comprehensively reviewed [20]. While the newly described G. incognitus is widespread throughout the Mediterranean Sea, reaching the Atlantic Ocean in the Gibraltar straight region [20], G. bucchichi was confirmed only in a few scattered areas in the northern part of the Mediterranean Sea (in the Adriatic, Ionian, and Aegean Seas), and the Marmara and Black Seas [20]. However, the studies differentiating both species and providing reliable data about the exact distribution of either of these species were based mostly on morphological evidence: either on morphological examination or on photographic evidence [18,20–27], while the genetic methods were used only scarcely and on very limited amounts of material [4,18,28]. Even though these two gobies have no economic value, their biogeography is of particular interest, especially in the case of G. bucchichi, which seems to have a unique distribution pattern among the Mediterranean gobies [20]. Moreover, the conservation status of both species needs an urgent update. In the international IUCN Red List of threatened species, only G. bucchichi is included, and is evaluated as Least Concern [29], while G. incognitus has not yet been evaluated. However, the conservation status of G. bucchichi [29] is based on data that include both species, and thus is no longer valid.

Molecular methods were used in numerous studies on gobies from the Mediterranean Sea and in general from Europe. Most of the studies focused on taxonomy or distribution, e.g., [4–9,11,12,14,15,18,28,30–32]. Several studies deal with phylogenetic relationships, e.g., [33–36], and also the population genetic structure and phylogeography were investigated for several species, e.g., [37–43].

The aims of this work were to test the suitability of the genetic data (mitochondrial marker *cytochrome b*) for the identification and distinguishing between the goby species *G. bucchichi* and *G. incognitus*, and to assess the congruency between the distribution records based on genetic data and those based on morphological identification, which are, for a large part, based on citizen science [20]. Genetics has been proven to be a useful tool for the identification of taxonomically complicated gobiid species complexes in the Mediterranean region [30]. Moreover, if proved to be reliable, this type of identification can be applied also



in the case when voucher material, apart from a tissue, is absent, or on specimens that are too damaged to be used for unambiguous morphological identification.

Figure 1. *Gobius incognitus* from Hvar Island, Sveta Nedjelja, Croatia (loc. 23 in Table 1) (upper) and *Gobius bucchichi* from Selce, Croatia (loc. 19 in Table 1) (lower) photographed in an aquarium. Both specimens are deposited in the collection of the National Museum of the Czech Republic in Prague and were morphologically determined. Photo: R. Šanda.

2. Materials and Methods

Tissue samples for molecular analyses (fin clips) were preserved in 96% ethanol. Genomic DNA was extracted with the Geneaid Genomic DNA Mini Kit (Tissue) (Geneaid Biotech, New Taipei City, Taiwan). Mitochondrial gene *cytochrome b* (*cyt b*) was used for the identification, considering the relatively high divergence between both species on this marker observed by Kovačić & Šanda [18]. *Cyt b* was confirmed to be a useful marker for species delimitation in gobies, e.g., [9,18,32], reconstruction of phylogenetic relationships between species e.g., [31,34–36], as well as for studying phylogeography and population genetics e.g., [37,38,40,42,43]. *Cyt b* was amplified by polymerase chain reaction (PCR) using PPP Master Mix (Top-Bio, Praha, Czech Republic) following primers and protocols described in Šanda et al. [44]. Sequencing was performed by Macrogen Inc using newly designed primers (GbuchR1: 5'-TGGGGGAAAAGAGGGCAAGG-3'; GbuchF1: 5'-GGCTTCTCCGTTGACAATGC-3'). These primers were designed based on previously published *cyt b* sequences of both species [18,34] using Geneious Prime 2021.1 (https://www.geneious.com, accessed on 20 January 2022).

In total, 304 sequences of *G. bucchichi* and *G. incognitus* originating from 49 localities were analysed (Table 1, Figure 2). Thirty-nine localities covered only new material, seven localities were based on published data supplemented by newly analysed specimens, while three localities were based solely on the published data (Table 1). The newly analysed material was morphologically identified following [2,18] if the voucher specimens were available (Table 1).

All sequences were visually checked and manually edited using Chromas v.2.6.4, and aligned in Bioedit v.7.2.6.1 [45]. New sequences were collapsed to haplotypes in Fabox [46], and the haplotypes were deposited in GenBank under the accession numbers OR834513–OR834734. The dataset included three sequences, which were considerably shorter than most of the sequences due to problematic sequencing. These sequences were used only for the identification, which was unambiguous in each case, while for the analyses only the long sequences were used. The dataset was further extended by available

published sequences of *cyt b* of both species (FJ526784 [34] and KR811029-KR811059 [18]) (Table 1). Sequences of both species published by Kovačić & Šanda [18] were taken as a reference, because they include sequences of type material of *G. incognitus* and morphologically confirmed specimens of *G. bucchichi* based on redescription of this species.

Table 1. Overview of the analysed material of *G. incognitus* and *G. bucchichi*. For each included locality, geographic coordinates and sea subarea are provided. Sea subareas names follow Kovačić et al. [20]. Locality numbers correspond to the numbers of localities in Figure 2. Voucher specimens were available for all localities, where new material was included, except for the locality marked with * (loc. 43). NE—north-eastern, W Med—western Mediterranean. Published sequences originated from ^A [18] and ^B [34].

Detected Species on Locality	Sea Subarea	Locality	Country	Coordinates	No. in Map	New Sequences	Published Sequences
Gobius incognitus	NE Atlantic	Gale	Portugal	37.076972, -8.310722	1	7	
Gobius incognitus	NE Atlantic	Sesmarias, Praia de Evaristo	Portugal	37.074006, -8.303575	2	6	
Gobius incognitus	African W Med	Bou Ismail	Algeria	36.650767, 2.691153	3	4	
Gobius incognitus	African W Med	Tipaza	Algeria	36.594200, 2.449131	4	5	
Gobius incognitus	African W Med	Algiers, Sidi Fredj	Algeria	36.764291, 2.848401	5	17	
Gobius incognitus	African W Med	Algiers, Ain Benian	Algeria	36.802050, 2.898339	6	19	
Gobius incognitus	Spanish W Med	Benidorm	Spain	38.533982, -0.129395	7	4	
Gobius incognitus	Gulf of Lion	Banyuls-sur-Mer	France	42.481817, 3.136032	8	10	6 ^A
Gobius incognitus	Gulf of Lion	Banyuls-sur-Mer, Paulliles beach	France	42.505759, 3.123662	9	7	3 ^A
Gobius incognitus	Gulf of Lion	Port Vendres	France	42.523300, 3.109700	10	1	
Gobius incognitus	Corsican shelf	Corsica, Lumio	France	42.574444, 8.805278	11	25	
Gobius incognitus	Maltese shelf	Gozo Island, Ramla	Malta	36.061869, 14.284042	12	2	
Gobius incognitus	Ionian Sea	Sicily, Aci Castello	Italy	37.555419, 15.149383	13	9	
Gobius incognitus	Ionian Sea	Sicily, Aci Trezza	Italy	37.562758, 15.163661	14	9	
Gobius incognitus	Ionian Sea	Sicily, Capo Mulini	Italy	37.574014, 15.173408	15	8	
Gobius bucchichi	Adriatic Sea	Kraljevica	Croatia	45.267660, 14.562256	16	1	1 ^A
Gobius bucchichi	Adriatic Sea	Krk İsland, Omišalj	Croatia	45.218911, 14.550908	17		2 ^A
Gobius bucchichi	Adriatic Sea	Krk Island, Glavotok	Croatia	45.094134, 14.436694	18		1 ^B
Gobius bucchichi	Adriatic Sea	Selce	Croatia	45.152293, 14.718928	19	6	1 ^A
Gobius incognitus	Adriatic Sea	Krk Island, Sveti Marak	Croatia	45.105944, 14.668500	20	2	
Gobius bucchichi + Cobius incognitus	Adriatic Sea	Brač Island, Sumartin	Croatia	43.285934, 16.878829	21	10 (5xG. inc., 5xC. buc)	6 ^A (G. inc.)
Gobius incognitus Gobius incognitus	Adriatic Sea	Hvar Island, Smočiguzica	Croatia	43.233889, 16.574722	22	1	
Gobius incognitus	Adriatic Sea	Hvar Island, Sveta Nedjelja	Croatia	43.134433, 16.591381	23	14	
Gobius bucchichi	Adriatic Sea	Boka Kotorska, Kostanjica	Montenegro	42.485403, 18.669678	24	6	
Gobius bucchichi	Adriatic Sea	Boka Kotorska, Strp	Montenegro	42.503989, 18.669453	25	4	
Gobius incognitus	Adriatic Sea	Budva, Jaz beach	Montenegro	42.283836, 18.809034	26	1	2 ^A
Gobius incognitus	Adriatic Sea	Kamenovo	Montenegro	42.273917, 18.887667	27	5	
Gobius incognitus	Adriatic Sea	Sveti Stefan	Montenegro	42.257180, 18.892118	28		5 ^A
Gobius bucchichi	Ionian Sea	outflow of Butrint lagoon	Albania	39.743614, 20.018654	29	1	5 ^A
Gobius incognitus	Ionian Sea	Sivota	Greece	39.399800, 20.234664	30	2	
Gobius incognitus	Ionian Sea	Romanos, Peloponnesos	Greece	36.985361, 21.651634	31	1	
Gobius incognitus	Ionian Sea	Petalidi, Peloponnesos	Greece	36.959142, 21.934967	32	1	
Gobius incognitus	Aegean Sea	Euboia Island, Petalii Islands	Greece	38.014764, 24.280875	33	3	
Gobius incognitus	Aegean Sea	Euboia Island, Marmari	Greece	38.048808, 24.318328	34	4	
Gobius incognitus	Aegean Sea	Euboia Island, Kalamitsi beach	Greece	37.971372, 24.365764	35	2	
Gobius incognitus	Aegean Sea	Euboia Island, Mnima penninsula	Greece	37.978775, 24.399581	36	4	
Gobius incognitus	Aegean Sea	Euboia Island, Agia Pelagia Islet	Greece	37.997008, 24.398186	37	1	
Gobius incognitus	Aegean Sea	Euboia Island, Karystos	Greece	38.009667, 24.430804	38	3	
Gobius incognitus	Aegean Sea	Euboia Island, Kastri Beach	Greece	37.973022, 24.537658	39	1	
Gobius incognitus	Aegean Sea	Euboia Island, Mirmigia rocks	Greece	37.972336, 24.548042	40	1	
Gobius incognitus Cobius incognitus	Aegean Sea	Raches	Greece	38.876144, 22.785700	41 42	3 18	
Gobius incognitus	Aegean Sea	between Geyikli and	Turkev	39.789722. 26.156111	43	22	
Cobine incomitue	Lovantino Soa	Dalyan * Akamas Fontana	Cuprus	35 000108 22 202844	44	3	
Cobius incognitus	Levantino Sea	Akamaa Coorgo Island	Cyprus	25.074058 22.202044	15	8	
Cobius incognitus	Levantine Sea	Akamas, George Island	Cyprus	33.074930, 32.3332222 34.062503, 34.072079	45	7	
Cobius incognitus	Levantino Sea	Cavo Greco, runnel—cave	Cyprus	34 976053 34 076791	-10 17	, 2	
Cohius incognitus	Levantine Sea	Cavo Greco, Ciclope cavo	Cyprus	34 985631 34 076028	48	<u>-</u> 1	
Gobius bucchichi	Black Sea	Sevastopol	Ukraine	44.494094, 33.533650	49	1	

Reconstruction of the phylogenetic relationships of the analysed material was estimated by Bayesian Inference (BI). Only unique haplotypes collapsed in Fabox [46] were used for the phylogenetic reconstruction. Sequences of Gobius niger Linnaeus, 1758 (FJ526782 [34]), Gobius fallax Sarato, 1889 (FJ526785 [34]), and Gobius couchi Miller & El-Tawil, 1974 (FJ389196 [47]) were used for comparison as well, while *Pomatoschistus minutus* (Risso, 1810) (FJ526776 [34]) and Economidichthys pygmeus (Holly, 1929) (KF415544 [33]) were used as outgroup. The appropriate model of nucleotide substitution was determined in jModeltest v.2.1.9 [48] based on Bayesian information criterion (BIC). BI was assessed in MrBayes v.3.2.2 [49] under the GTR+I+G model selected by JModeltest. Two independent runs, each consisting of four Markov Chain Monte Carlo (MCMC) methods, were simultaneously run for 5 million generations. Sampling of the trees was performed every 1000 generations. TRACER v.1.7.0 [50] was used to analyse the trace files generated by MCMC runs and visualise the convergence of chains. The first 25% of trees were discarded as burn-in and kept trees were used for the construction of a 50% majority-rule consensus tree. The final tree was visualised in FigTree v.1.4.4 [51] and edited in Inkscape version 0.92.3 [52]. Program MEGA 10 [53] was used to calculate genetic distance (uncorrected p-distances) between and within the species. Fabox [46] was used to visualise the variable sites and assess fixed mutations between the two species.





3. Results

3.1. Genetic Distinctiveness

In this work, we used altogether 304 sequences of *cyt b*, of which 272 were new and 32 were published. For *G. incognitus*, there were 270 sequences, of which 22 were published and 248 were newly obtained. Two new sequences of *G. incognitus* were shorter and were used only for identification. The remaining 258 sequences were 1077 base pairs long and represented 208 different haplotypes. For *G. bucchichi*, there were 34 sequences, of which 10 were published and 24 were new. A single new sequence of *G. bucchichi* was shorter and was used only for the identification. The remaining 33 sequences were 1077 base pairs long and they represented 29 different haplotypes. Altogether, 79 sites with fixed mutations discriminating between both species were detected.

The phylogenetic reconstruction analysis showed each of the included *Gobius* species as very distinct (Figure 3). The sequence species identity matches the morphological identification for all specimens, for which vouchers were available. All calculated genetic divergences are summarized in Table 2. The mean uncorrected p-distance between *G. incognitus* and *G. bucchichi* was 13% ($\pm 0.8\%$ S.E.), while the mean intraspecific distances were much lower (*G. incognitus* 0.63% \pm 0.086 S.E.; *G. bucchichi* 0.68% \pm 0.11% S.E.). The maximum observed intraspecific genetic distance between *G. incognitus* sequences was 1.76%, while for *G. bucchichi* it was 1.21%.



Figure 3. The 50% majority-rule consensus Bayesian phylogenetic reconstructions based on mitochondrial *cytochrome b* sequence data. Numbers on branches represent posterior probabilities.

Table 2. Genetic distance (uncorrected p-distances, in %) based on *cytochrome b* sequences for the analyzed *Gobius* species. Mean genetic distances between species are below diagonal, S.E. above diagonal. On the diagonal, mean intraspecific genetic divergence is shown, with S.E. in parentheses. Numbers in parentheses after species name in the first column are numbers of analyzed sequences for species. N/A—not applicable.

	G. incognitus	G. bucchichi	G. couchi	G. falax	G. niger
G. incognitus (258)	0.63 (±0.086)	0.8	0.9	1.1	1.1
G. bucchichi (30)	13	0.68 (±0.11)	1	1.1	1.2
G. couchi (1)	16.7	14.9	N/A	1.1	1.1
<i>G. falax</i> (1)	16.6	15.3	14.3	N/A	1.2
<i>G. niger</i> (1)	19.4	18	18.9	19.7	N/A

3.2. Distribution

We analyzed material of *G. incognitus* and *G. bucchichi* from 49 localities covering considerable parts of the Mediterranean Sea, Black Sea, and the Atlantic Ocean near Gibraltar (Figure 2, Table 1). Some localities are close to each other, within a distance of only a few km, and the samples cover 19 geographically well-separated areas (Figure 2).

Gobius incognitus is widespread, occurring throughout the Mediterranean, and in the Atlantic Ocean near Gibraltar (Figure 2, Table 1). However, the documented distribution of *G. bucchichi* is much more restricted (Figure 2, Table 1). Genetic data confirmed its presence from three areas in the northern coastal region of the Adriatic Sea, one in the north-western part of the Ionian Sea, and from the Crimean region of the Black Sea. Both species were recorded sympatrically in four areas (Figure 2), though mostly from different localities

within the area (Table 1, Figure 2). However, a syntopic presence (i.e., at the same locality) of both species was revealed at a single locality (Table 1, Figure 2).

4. Discussion

The mitochondrial marker *cyt b* was confirmed to be a highly reliable tool for the genetic identification of morphologically similar and often confused gobies G. incognitus and G. bucchichi. Both species showed very high haplotype variability, relatively uncommon in coastal species, whose dispersal capability is limited by local oceanographic patterns [54]. However, G. incognitus and G. bucchichi can be genetically easily unambiguously identified, given that the average interspecific genetic divergence between them is almost 20 times higher than the average intraspecific divergence, and the number of fixed mutations between species on *cyt* b sequence data is nearly 80. Even the highest observed value of intraspecific distance (1.76% in *G. incognitus*) is six to seven times lower than the lowest interspecific genetic distance between both studied species. In general, gobies of the genus Gobius are easily identifiable by mtDNA markers, as proved by Iglésias et al. [4], where many species were analyzed by *cytochrome c oxidase*, and minimum genetic distance between species was 8–9% (with the only exception of the *Gobius auratus* complex), while the intraspecific distance was always several times lower. The overall high genetic divergence between species of the genus *Gobius* could be a result of the considerably long evolutionary history of this genus; the oldest paleontological record of *Gobius* based on complete skeleton fossil is dated to 20 MY ago [55]. It is probable that the evolution of the lineages leading to the extant species started in the very early diversification of the genus, allowing many mutations to accumulate over time. Nevertheless, the intraspecific genetic distance within the Mediterranean gobies on mtDNA markers can also be relatively high, commonly reaching 1.5-2% [15,18,37], and rarely even 5% [4,9], so molecular identification of genetically more similar species of gobies may be challenging. However, as this is not a case of G. bucchichi and G. incognitus, even the advanced genetic methods for identification of the species presence from environmental samples (eDNA approach) are applicable to these species, but also actually to most of the gobies from the Mediterranean Sea. The data from eDNA could potentially fill in the gaps in the knowledge on distribution of many goby species. A limitation of the use of the mtDNA markers for the species identification is that potential hybrids or mito-nuclear discordance cannot be detected, as mtDNA is uniparentally inherited. *Gobius incognitus* and *G. bucchichi* occur sympatrically, even syntopically, this work, [20]); their natural hybridisation, although not reported, cannot be a priori excluded. So far, the hybridisation of gobies from the European seas was reported only in the genus *Pomatoschistus* [56,57]. The hybridisation between European marine gobies can be assumed to be rare owing to their complex mating system, which includes nest building and species-specific sound production [58,59], which can serve as important prezygotic barrier through strong auditory-based assortative mating.

Gobius bucchichi was for a long time considered a widespread species in the Mediterranean and Black seas, present also in the European Atlantic near the Gibraltar strait up to Algarve coast of Portugal [17]. However, this assumption was actually based on the distribution of two morphologically similar species. After the discovery and description of *G. incognitus* by Kovačić & Šanda [18], the distribution of both species was questioned. Almost a decade after the description of *G. incognitus*, we can state that only several publications have provided unambiguous distribution data, accompanied by appropriate identification [4,18,20–28], while other works, even those recently published, continue to report only *G. bucchichi* [60–62], probably being unaware of the description of *G. incognitus*.

Kovačić et al. [20] have summarized the available information on the distribution of both *G. incognitus* and *G. bucchichi* and confirmed that distribution range of *G. incognitus* covers a considerable part of the Mediterranean Sea coastal region, and the European Atlantic near the Gibraltar strait up to Algarve (Figure 2), as previously suggested by Kovačić & Šanda [18]. In contrast, *G. bucchichi* was confirmed for a very restricted and scattered area (Figure 2). It has been reported only from the northern part of the Adriatic Sea, from Italy to Montenegro, from a few localities in the northern Ionian Sea in Albania and Greece, from one locality in the south-western Aegean Sea in Greece, south-eastern and south-western part of the Aegean Sea in Turkey, from the Sea of Marmara, and from the two areas of the northern Black Sea in Ukraine and Russia [20]. The range of both species in the Mediterranean Sea completely overlaps, while for the Black Sea and Marmara Sea, only the presence of *G. bucchichi* was confirmed [20]. Our results for distribution based on genetic data, often including a considerable number of analyzed specimens per locality/geographic area, are completely congruent with the revision of Kovačić et al. [20]. In our data, *G. bucchichi* was recorded only from the northern Black Sea (Figure 2, Table 1), while *G. incognitus* was detected throughout the whole Mediterranean Sea and the southern Portuguese Atlantic Ocean coast (Figure 2, Table 1).

However, for the large areas of the previously reported range of *G. bucchichi* [17], respectively for large portions of the Mediterranean coastal region in general, we are still awaiting clarification on which of the two species is present (Figure 2). This applies to almost all of African Mediterranean coastal region, as G. bucchichi was reported only from Libya [63] and Egypt [64], but this was not supplemented by morphological or molecular evidence; moreover, G. bucchichi had been previously reported from Morocco [65] and was recently confirmed to be *G. incognitus* instead [20]. Data are missing also for part of the Levantine coastal region of Turkey [20] and the coastal regions of Syria and Lebanon, from where neither of the species was reported (Syria [66]), or only *G. bucchichi* was listed (Lebanon [60,62]). The Black Sea is another area with unsatisfactory data on the presence of G. incognitus and G. bucchichi. Gobius bucchichi is the only unambiguously confirmed species from this region and, moreover, only from a small part of the northern coast [20] (our data). Nevertheless, at least one of these species is apparently widespread around the Black Sea, as there are reports on *G. bucchichi* from Turkey [67], Russia [68,69], Ukraine [70,71], as well as Bulgaria [72]. Finally, the lack of distribution data for the Italian Adriatic coastal region (Figure 2) is surprising, as it was considered a part of the distribution range of *G. bucchichi* by Miller [17]. Kovačić et al. [20] assumed that this gap in distribution may be real, as the area is well studied, and it could be a result of lack of suitable habitats in this region.

Further research should focus not only on the clarification of the distribution of both species, but especially on their ecology, including microhabitat use of each species and their niche separation, since nothing is known about how the species coexist/interact in areas of sympatric and syntopic occurrence.

The results of this study suggest an alternative, easier, and reliable identification method of morphologically similar fish species. A high divergence in *cyt b* between *G. incognitus* and *G. bucchichi*, including numerous sites with fixed mutations (79 in total), enables clear distinctions between the two goby species at the mtDNA level. This relatively fast and low-cost method complements an array of molecular methods, such as multiplex PCR assays, melt curve analysis real-time PCR, or restriction fragment length polymorphism, which are successfully used for fish identification [73]. Importantly, molecular tools could also aid potential conservation efforts of less common species, for example, in this particular case, of *G. bucchichi*. At the same time, our results demonstrate how insufficient our knowledge on the life in the Mediterranean Sea remains, and point to the great potential of molecular methods to achieve even a partial improvement.

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