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Revealing the presence and genetic identification of the rare and critically endangered deep-sea Sandy skate (*Leucoraja circularis*) in the Adriatic Sea

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ABSTRACT

The sandy skate (*Leucoraja circularis*) is one of the rarest deep-sea batoids in the Mediterranean Sea and has long been considered absent or exceptionally rare in the Adriatic Sea. Here, we report seven confirmed records obtained through fishery-dependent monitoring along the upper continental slope of the southern Adriatic Sea off Vlorë, Albania. All individuals were captured at depths between 400 and 600 m, with six of seven records concentrated within a narrow depth interval (410–423 m) off the Karaburun Peninsula and Sazan Island. Both juvenile and adult specimens were documented, indicating the presence of multiple ontogenetic stages within the study area. These findings represent the first verified records from Albanian waters and constitute the largest dataset available for the species in the Adriatic Sea to date. All individuals were found dead upon retrieval, indicating alarmingly high at-vessel mortality for this critically endangered species. Molecular data confirmed species identification and provided new COI and NADH2 mtDNA sequences, representing the first regional molecular dataset for *L. circularis*, crucial for the establishing of a baseline for future assessments. Moreover, genetic analyses highlighted the occurrence of new private haplotypes in Albanian waters in both COI and NADH2 datasets, suggesting the presence of a possible resident population in the studied area. Together, these results confirm the occurrence of *L. circularis* in the southern Adriatic Sea and identify this region as a previously overlooked component of the species' Mediterranean range, with important implications for monitoring, management, and conservation of one of the Mediterranean's most threatened deep-sea skates.

1. Introduction

Deep-sea skates (Rajidae de Blainville, 1816) represent an ecologically important yet highly vulnerable component of bathydemersal ecosystems (Clark et al., 2016). As mesopredators, they contribute to the structuring of benthic communities through predation on invertebrates and small demersal fishes, while their foraging behavior causes sediment disturbances that further influence these habitats (Stevens et al., 2000). Like many other elasmobranchs, deep-sea skates exhibit conservative life-history traits, including slow growth, delayed sexual maturity, and long lifespans (Dulvy et al., 2014), which collectively result in low population productivity and a limited capacity for recovery following population declines (Simpfendorfer and Kyne, 2009). Consequently, deep-sea elasmobranchs are widely recognized as among the most extinction-prone marine vertebrates (Dulvy et al., 2021). The primary threat to deep-sea skates is fishing pressure, particularly from bottom trawl fisheries operating along the edges of continental shelves and upper slopes (Finucci et al., 2024). Although few deep-sea rays are directly targeted, many species are frequently captured as bycatch and may either be retained for commercial use or discarded at sea, often with unknown post-release survival (Ebert et al., 2013; Dulvy et al., 2017; Ellis et al., 2017; Gajić and Martin, 2025). The substantial spatial overlap between deep-sea fishing grounds and the depth distribution of large skates results in chronic exposure to fishing-induced mortality across much of their range (Clark et al., 2016). Additional emerging threats include climate change, habitat degradation and pollution; as well as potential future impacts associated with deep-sea mining, which are projected to overlap with the distribution of numerous threatened deep-sea elasmobranch species (Miller et al., 2018). Together, these pressures have driven widespread declines in deep-sea skate

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populations, many of which remain poorly documented due to limited survey coverage and inherently low encounter rates (Cashion et al., 2019; Johri et al., 2021).

Such knowledge gaps are particularly pronounced in the Mediterranean Sea, where research effort has been unevenly distributed (Dulvy et al., 2016; Serena et al., 2020; Gajić and Sulikowski, 2024). The Mediterranean represents a global hotspot for elasmobranch biodiversity but simultaneously for elasmobranch decline, with a disproportionately high number of species classified as threatened (Scacco et al., 2023). Demersal trawl fisheries are widespread throughout the basin, exerting sustained pressure on shelf and slope habitats that overlap extensively with the distribution of deep-sea elasmobranchs (Ferretti et al., 2008, 2013). Data deficiency remains a major challenge as scientific monitoring has historically been limited or absent in certain regions and many species are known from only a few records (Consalvo et al., 2009; Alkusairy and Saad, 2018; Digenis et al., 2024). Despite the recognized vulnerability of deep-sea skates across the Mediterranean, their true distribution, frequency of occurrence, and interaction with fisheries remain poorly understood, particularly in the Adriatic Sea (Serena et al., 2020). Within this context, *Leucoraja circularis* (Couch, 1838) (commonly known as the sandy skate or sandy ray) stands out as one of the rarest and most threatened skate species in the Mediterranean Sea (Consalvo et al., 2009; Serena et al., 2020), where it is currently assessed as Critically Endangered (McCully et al., 2016). Likewise, its conservation status is worrying also at European and Global level, where it is assessed as Vulnerable (Finucci et al., 2025). The species has been reported sporadically across the western and central Mediterranean; however, records are typically limited to isolated captures, often separated by several decades (Alkusairy and Saad, 2018; Mulas et al., 2021). Despite well-defined morphological diagnostic features (Otero et al., 2019; Barone et al., 2022), the apparent rarity of *L. circularis* may be partly attributable to historical misidentification with *Leucoraja fullonica* (Linnaeus, 1758) (as described in Kousteni et al., 2019), leading to underreporting and uncertainty in fisheries statistics and scientific surveys (Chatzispyrou and Koutsikopoulos, 2023). Consequently, the species' true distribution, persistence, and conservation status across portions of its Mediterranean range remain unresolved (Cashion et al., 2019; Tsikliras and Dimarchopoulou, 2021). In the Adriatic Sea, *L. circularis* has long been regarded as either absent (Serena et al., 2020) or exceptionally rare and was previously known only from a small number of anecdotal or historical reports (Ferretti et al., 2013). Notably, Soldo and Bakiu (2021) explicitly stated that the species was not part of the Albanian ichthyofauna, and Soldo and Lipej (2022) postulated that the individuals are recorded only after prolonged absence of records, spanning decades. In terms of its ecology and habitat use, the sandy skate inhabits offshore continental shelves and upper slopes in the northeastern Atlantic and the Mediterranean Sea (Quignard and Tomasini, 2000; Quéro et al., 2003; Ellis et al., 2005; McCully et al., 2016). Although the species has been reported across a broad depth range, from approximately 10–800 m Weigmann, 2016), it is most commonly associated with depths below the 100 m isobath (Ellis et al., 2005) and has been recorded even below 400 m in the Ionian Sea (Mytilineou et al., 2005). *Leucoraja circularis* typically attains total lengths of 60–70 cm, with a maximum reported length of up to 120 cm (Stehmann, 1990). The species is oviparous, depositing egg cases on muddy and sandy substrates (Mnasri et al., 2009), and functions as an opportunistic predator feeding on a variety of benthic organisms (Stehmann and Bürkel, 1984).

Here, we document seven new records of *L. circularis* from the Adriatic Sea (2023–2024) and provide the first genetic data for the species from the region, alongside observations on fisheries interactions and post-capture outcomes. By addressing a long-standing knowledge gap, this study contributes critical baseline information for reassessing the regional status of one of the Mediterranean's rarest deep-sea skates and highlights the Adriatic Sea as a potentially overlooked area of conservation relevance.

2. Material and methods

2.1. Field work and sampling

Systematic fishery-dependent research on deep-sea elasmobranchs in this study was conducted between January 2023 and December 2024 off the coast of Vlorë, Albania. At-sea monitoring was carried out abroad three commercial bottom trawlers operating at depths ranging from 50 to 650 m within 3–12 NM off Vjose Delta, Sazan Island, and Karaburun Peninsula. Over this period, 150 fishing trips were monitored (41 in 2023 and 109 in 2024), each lasting one to four days, resulting in the examination of 831 individual tows (of which 224 in 2023 and 607 in 2024). Each tow lasted approximately 5–7 h, with an average trawling speed of 2–2.5 knots, covering transects of 10–14 NM. The authors did not interfere with fishing operations at any stage and acted solely as passive observers. In addition, land-based monitoring was opportunistically conducted at Triport Harbour Orikum (Vlorë, Albania), focusing mainly on bottom trawlers operating between 50 and 350 m. Landing surveys were performed upon vessel arrival and resulted in the examination of more than 4000 additional tows over the study period.

Catch per unit effort (CPUE) was quantified as the mean number of individuals per trawl tow (ind·tow^{-1}). This metric was obtained by dividing the total number of specimens observed during onboard monitoring by the total number of trawl tows monitored at sea. Encounter frequency at the fishing-trip level was calculated as the percentage of trips in which at least one individual was documented, derived by relating the number of trips with a positive record to the total number of monitored trips. Overall encounter frequency was estimated across the entire sampling effort, integrating both onboard and port-based observations, and expressed as the proportion (%) of hauls in which the species was detected, calculated by dividing the number of positive records by the total number of examined hauls and multiplying by 100. Additionally, encounter likelihood during port-based monitoring alone ($>$5000 inspected hauls) was assessed qualitatively using a presence–absence approach.

2.2. Morphological examinations

All sandy skates encountered during the study were documented; individuals retrieved dead were retained for laboratory analyses. The skates were successfully identified based on a suite of diagnostic morphological characters, including a conspicuous large triangular patch of thorns on the nape–shoulder region, more than two longitudinal rows of thorns along the tail, a short snout with a well-defined and prominent rostrum, and a dorsal reddish-brown coloration marked by small white to cream-colored spots with dusky margins. This combination of features, as described by Otero et al. (2019), Ebert and Dando (2020), and Barone et al. (2022), clearly distinguishes *L. circularis* from morphologically similar species, particularly *L. fullonica*. For each individual, muscle tissue or fin clips were sampled and preserved at -20 °C in 96% ethanol for molecular analyses. The macroscopic pathomorphological examinations were performed following Crow (2004) to assess the trauma and injury from fisheries. Stomach content was removed and identified to the lowest possible taxonomic level using morphological keys and reference guides, such as FAO species identification guides. All the recorded individuals were measured for a full set of biometric characteristic following Alkusairy et al. (2014) and Gajić et al. (2023). Furthermore, morphometric (condition factor CF and hepatosomatic index HSI) were calculated to assess relative well-being (Logan et al., 2018) and indicators of nutritional status and energy reserves (Okoboshi et al., 2022). The condition factor (CF) was calculated as $CF = (TW \times 10^{3}) / TL^3$, where TW is the total weight (g) and TL is the total length (cm). The hepatosomatic index was calculated as $HSI = (LW / TW) \times 100$, where LW is liver weight (g) and TW is total weight (g).

All the recorded individuals were preserved frozen for future examination and are archived in the Sharklab ADRIA reference collection under catalogue numbers LEC/01/0505/23, LEC/02/2405/23, LEC/03/1606/23, LEC/04/0107/23, LEC/05/1307/23, LEC/06/0108/23 and LEC/07/1305/24.

2.3. Molecular analysis

Total genomic DNA (gDNA) was extracted following the Salting Out extraction protocol (Miller et al., 1988). The amplifications of COI and NADH2 mitocondrial genes were performed in a Mastercycler EP Gradient S Eppendorf.

A fragment of the COI was obtained using the FishF2 and FishR1 primers (Ward et al., 2005). Amplifications were performed with an initial denaturation of 3 min at 95 °C, followed by 35 cycles of 30 s at 95 °C, 30 s at 54 °C and 60 s at 72 °C, and a final extension step for 5 min at 72 °C. Similarly, a fragment of the NADH2 was amplified using the ND2-MetF and ND2-TrpR primers (Vella et al., 2017). PCR conditions consisted of an initial denaturation of 3 min at 94 °C, followed by 40 cycles of 30 s at 94 °C, 30 s at 53 °C and 45 s at 72 °C, and a final extension step for 5 min at 72 °C. PCR reactions were performed in 25 μL total volume containing 0.2 mM of dNTPs, 1.0 pmol of each primer, 1 × Wonder Taq Reaction buffer and 0.8 U of DreamTaq DNA polymerase (Thermo Fisher Scientific, Waltham, MA, USA). All the amplicons were Sanger-sequenced using the same forward primers used during the amplification by the external provider Macrogen Europe (Milan, Italy).

The newly obtained COI and NADH2 sequences were imported in MEGA 12 (Kumar et al., 2024), aligned using the CLUSTAL W algorithm (Thompson et al., 1994), and carefully checked for both quality and correct amino acidic translation (Song et al., 2008).

Haplotype diversity [Hd], nucleotide diversity [π], and number of haplotypes were obtained using DNASP v.6 (Rozas et al., 2017).

Specimen identification was confirmed by comparing newly produced sequences with sequences available on GenBank (National Center for Biotechnology Information; NCBI) (Federhen, 2012; Sayers et al., 2022) and Barcode of Life Data Systems (BOLD) (Ratnasingham et al., 2024) online databases. Furthermore, newly generated and publicly available sequences were used to infer relationships among haplotypes and to reconstruct haplotype networks of *L. circularis* using the TCS method (Clement et al., 2000), as implemented in the software Hapsolutely (Vences et al., 2024).

3. Results

3.1. Morphological analysis

Between January 2023 and December 2024, a total of seven individuals of *L. circularis* were recorded during the systematic fishery-dependent monitoring of commercial bottom trawl fisheries off the southern Albanian coast (Fig. 1; Table 1). All specimens were captured along the upper continental slope at depths ranging from 400 to 600 m. The majority of records (six of seven individuals) were concentrated within a narrow depth interval between 410 and 423 m, while a single individual was captured at approximately 600 m. All captures occurred over soft-bottom habitats within the operational depth range of the monitored trawl fishery. Despite continuous monitoring throughout the year, captures of *L. circularis* were restricted to late spring and summer months (May to August), with no records obtained outside this seasonal window. The recorded individuals included six females and one male. Female specimens comprised three juveniles and three adults, with total lengths ranging from 23.2 to 62.1 cm and body mass ranging from 81 g to 1.02 kg. The single male recorded was juvenile, measuring 50.8 cm in total length and weighing 0.53 kg. Overall, juvenile individuals spanned total lengths of 23.2–37.6 cm, whereas adult females ranged from 52.5 to 62.1 cm, indicating the presence of multiple life stages within the sampled population. Each individual was characterized by a well-defined triangular aggregation of thorns in the nape–shoulder region

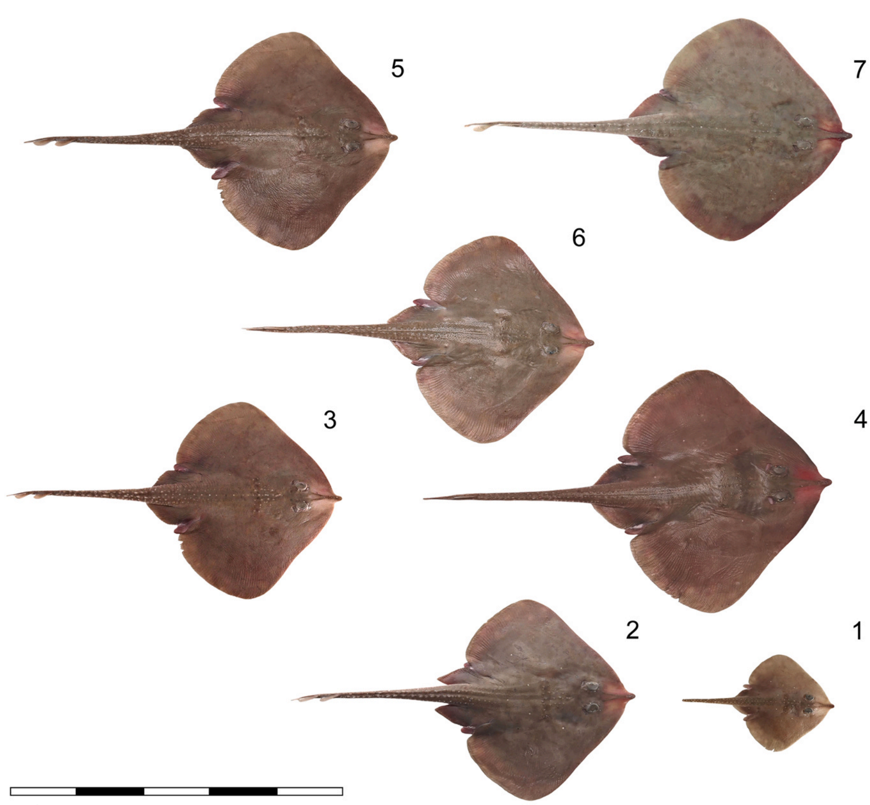

Fig. 1. Sandy skates (*Leucoraja circularis*) captured as by-catch in bottom trawling off Vlorë (Croatia), at the depths between 400 and 600 m. Numbers correspond to the Table 1. Photos: A. Gajić / Sharklab ADRIA.

Table 1
Overview of the records of the *Leucoraja circularis* in the southern Adriatic Sea off Albania 2023–2024 (Legend: TL – total length, DW – disc width, TW – total weight, CF – condition factor, HSI – hepatosomatic index). M and F in the sex column refer to male and female, respectively.

No.	DATE	COUNTRY	LOCATION	TOOL	DEPHT	CODE	SEX	TL	DW	TW	CF	HSI
1	05.05.2023.	Albania	Vlorë	Trawl	411 m	LEC/01	F	23.2 cm	14.6 cm	81 g	0.649	1.72
2	24.05.2023.	Albania	Vlorë	Trawl	400 m	LEC/02	F	53.5 cm	32.7 cm	660 g	0.431	3.85
3	11.06.2023.	Albania	Vlorë	Trawl	423 m	LEC/03	M	50.8 cm	28.0 cm	533 g	0.407	3.17
4	01.07.2023.	Albania	Vlorë	Trawl	411 m	LEC/04	F	61.5 cm	36.7 cm	1021 g	0.439	2.59
5	13.07.2023.	Albania	Vlorë	Trawl	410 m	LEC/05	F	56.2 cm	33.4 cm	803 g	0.452	4.00
6	01.08.2023.	Albania	Vlorë	Trawl	416 m	LEC/06	F	53.6 cm	32.1 cm	682 g	0.443	3.72
7	15.05.2024.	Albania	Vlorë	Trawl	600 m	LEC/07	F	58.9 cm	36.9 cm	1013 g	0.496	3.78

and multiple (>2) longitudinal thorn rows extending along the tail (Fig. 2). Full set of biometric data of all recorded specimens is presented in Table 2.

Recorded individuals were retrieved dead upon the retrieval. Gross macroscopic examination revealed only minor superficial bruising, small lacerations, and localized hemorrhaging consistent with contact with trawl gear. No severe traumatic lesions were observed, and there were no gross pathological signs indicative of compromised health status prior to capture. Among the examined individuals, five contained prey remains in their stomachs: four had consumed shrimp, while one contained a partially digested teleost together with a shrimp; the remaining two individuals had empty stomachs. The condition factor (CF) varied between 0.407 and 0.649 (mean 0.474 ± 0.08), whereas the hepatosomatic index (HSI) ranged from 1.71 to 4.00 (mean 3.26 ± 0.85) across all examined individuals. The smallest juvenile (23.2 cm TL) displayed the highest CF (0.649) but the lowest HSI (1.72), potentially reflecting greater allocation of energy toward somatic growth rather than hepatic reserves during early ontogeny. Larger individuals (50.8–61.5 cm TL) exhibited relatively consistent CF values, with a mean of 0.445, whereas HSI showed greater variability. The highest HSI was recorded in an adult female measuring 57.1 cm TL (HSI = 4.00), while the lowest HSI among subadult and adult individuals occurred in the largest specimen (61.5 cm TL; HSI = 2.59). The single male specimen (50.8 cm TL) had the lowest CF (0.407) and an intermediate HSI value (3.17). Variability in HSI may reflect differences in reproductive stage and hepatic energy storage rather than body size alone, whereas the relatively stable CF values of larger individuals may be consistent with the reduced somatic growth expected as individuals approach asymptotic size. Collectively, CF and HSI values (Table 1) indicate size- and life-stage-related variation in body condition within the examined sample.

Overall encounter frequency across the entire sampling effort, integrating both onboard and port-based monitoring, was very low. Catch per unit effort (CPUE) was estimated at 0.008 ind·tow^{-1}, while encounter frequency at the fishing-trip level was 4.7%, and haul-level encounter frequency during onboard monitoring was 0.84%. During port-based monitoring alone, which included inspections of more than 4500 hauls, no individuals of *L. circularis* were recorded. This absence of detections likely reflects the lack of commercial value of the species and its routine discarding at sea, resulting in limited availability for landings-based observation.

3.2. Molecular analysis

DNA was successfully extracted, amplified and sequenced for the *L. circularis* specimen obtaining new COI and NADH2 sequences (deposited in GenBank; Accession Number upon acceptance). The COI dataset (n = 70; length 628 base pairs) showed 11 polymorphic and seven parsimony sites, for a total of nine haplotypes. At the same time, the NADH2 dataset (n = 25; length 1016 base pairs) showed 11 polymorphic and three parsimony sites, for a total of nine haplotypes. Both dataset showed moderate haplotype diversity (COI: Hd = 0.624; NADH2: Hd=0.643) coupled with low nucleotide diversity (COI: π = 0.00351; NADH2: π = 0.00128), indicating the presence of multiple

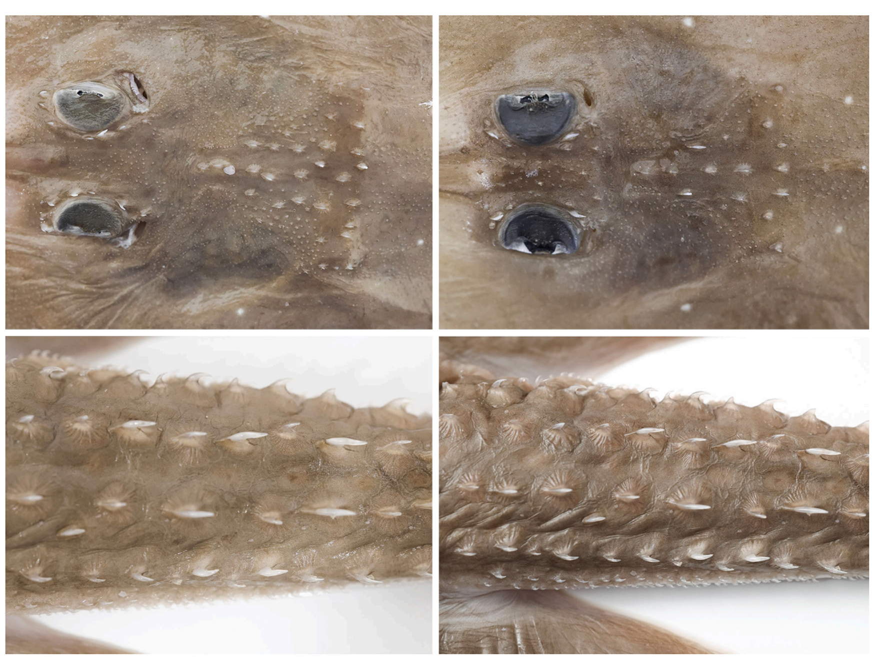

Fig. 2. Principal morphological diagnostic feature of the *Leucoraja circularis*, highlighting the triangular nape–shoulder thorn patch with creamy spots and multiple longitudinal caudal thorn rows. Photos: A. Gajić / Sharklab ADRIA.

Table 2
Biometric measurements of *Leucoraja circularis* individuals recorded during fishery-dependent monitoring of commercial bottom-trawl fisheries off southern Albania (in mm). A dash (–) indicates an injured individual or a missing body part.

Morphological feature	LEC/01/0505/23	LEC/02/2405/23	LEC/03/1606/23	LEC/04/0107/23	LEC/05/1307/23	LEC/06/0108/23	LEC/07/1305/24
Total Length	232	535	508	615	562	536	589
Disc Width	146	327	280	367	334	320	369
Disc Length	133	283	255	320	285	270	301
Snout, Preorbital	35	66.5	60	76	65	66	73
Snout, Preoral	36	71	67	82.5	71.5	66.5	76
Snout, Prenasal	31	57	52	63	56	50.5	60.5
Interorbital Width	12	19	20.5	23	21	21	23
Orbital Diameter	11.5	20	18	20	17.5	17.5	18
Interspiracular Distance	17	32	30	36.5	32.5	33	35
Spiracle Length	4.5	7	7	9.5	7.5	7	9.5
Head Length, Ventral	66.5	144	133	162	145	139	151
Mouth Width	19	41	40	50	42	39.5	45
Internarial Width	17	33	31	37	32.5	34	34
First Gill Slit, Length	-	8.5	6.5	6	9	6.5	10
Third Gill Slit, Lenght	-	10	7	6.5	10	7.5	12
Fifth Gill Slit, Length	-	7	4.5	5	7	6	8.5
Distance between 1st Gill Slits	34	73	70	89	70	73.5	81
Distance between 5th Gill Slits	27	47	45	55	46	48.5	52
From 1st to 5th	16	40	33.5	42	37	37	42.5
Pectoral Fin (Disc) Anterior Margin	113	235	215	260	230	225	245
Pectoral Fin (Disc) Posterior Margin	61	152	115	175	155	130	173
Pectoral Fin (Disc) Inner Margin	15	39	40	35	39	40	37
Pelvic Fin Height	14	34	28	40	36	31	32
Pelvic Fin Anteriror Margin	31	64	56	63	62	58	67
Pelvic Fin Posterior I m.	11.5	24	19.5	29	20	18	22
Pelvic Fin Posterior II m.	30	67	56	75	74	71	79
Pelvic Fin Inner Margin	14.5	35	31	32	42	39	44
First Dorsal Fin Height	-	13	13.5	11.5	12	12	11
First Dorsal Fin Base Length	-	29	27	35	29	28	33
Second Dorsal Fin Height	-	13	11	-	11	12.5	12.5
Second Dorsal Fin Base Length	-	26	27	-	32	31.5	37
Interdorsal Space	-	2	1.5	2	2	3	3
First Dorsal Fin to End of the Tail	-	-	43.5	47	47	44	49
Second Dorsal Fin to End of the Tail	-	-	12	-	16	11	17.5
Tail, Width at Pelvic Rare Tips	10	17	17	22	21	20	17.5
Pelvic Fin Length	41	98	81.5	109	100	89	106
Snout to Mid-cloaca	116	243	220	275	247	-	-
Snout to Dorsal 1 Origin	-	475	432	529	479	455	503
Snout to Dorsal 2 Origin	-	550	462	564	510	487	541
Mid-cloaca to Dorsal 1 Origin	-	227	210	252	230	225	-
Mid-cloaca to Dorsal 2 Origin	-	256	240	287	264	-	-
Mid-cloaca to Tail End	111	285	285	334	315	-	-

haplotypes separated by few mutational differences.

The *L. circularis* haplotype networks (Fig. 3) showed a star-like and geographically structured pattern, with haplotypes separated by a small number of mutational steps, revealing low overall genetic divergence. A limited number of high-frequency haplotypes occupied central positions in the network and were shared among multiple regions, whereas several low-frequency haplotypes were restricted to single geographic areas.

In the COI haplotype network, Norway was characterised by the presence of two haplotypes, one rare and one very common, not shared with Portugal and the other areas. In Mediterranean multiple private haplotypes were detected in several regions (i.e., Albania, Sardinia, and Spain). In Portuguese sequences were found two haplotypes not shared with other areas and closer to Mediterranean haplotypes than to Norway ones. Similarly, in the NADH2 haplotype network the occurrence of a central high-frequency haplotype was observed, shared among all the areas and several low-frequency and private haplotypes from Albanian and Sardinian specimen.

4. Discussion

This study provides the first dataset for *L. circularis* from the Adriatic Sea to date and delivers the first genetic and biometric data for the species in this basin, including the first confirmed records from Albanian waters. Although the species had never been recorded in Albania (Soldo and Bakiu, 2021) and was regarded as absent from the Adriatic Sea by some authors (Serena et al., 2020), the records presented here demonstrate a verifiable and previously overlooked presence of *L. circularis* in the southern Adriatic. All individuals reported in this study were recorded within a narrow spatial sector off Vlorë, predominantly between 410 and 430 m depth, consistent with the species' documented association with upper continental slope habitats in the eastern Ionian Sea (Mytilineou et al., 2005). The morphological identification of the seven new records was confirmed down to species level (i.e., *L. circularis*) using molecular analyses. Although the limited sample size precludes robust inference on habitat preference or fine-scale spatial structuring, the repeated detection of *L. circularis* within the same depth range and geographic area over two consecutive years and suggests that suitable habitat persists along the southern Adriatic slope.

Given the extreme rarity of *L. circularis* across the Mediterranean, where records are often limited to isolated captures separated by several decades (Mnasri et al., 2009), these findings represent a significant extension of current knowledge and confirm the occurrence of this critically endangered skate within the broader basin. More broadly, the results underscore the importance of targeted investigation of poorly surveyed deep-sea habitats, where historical data gaps and absent or

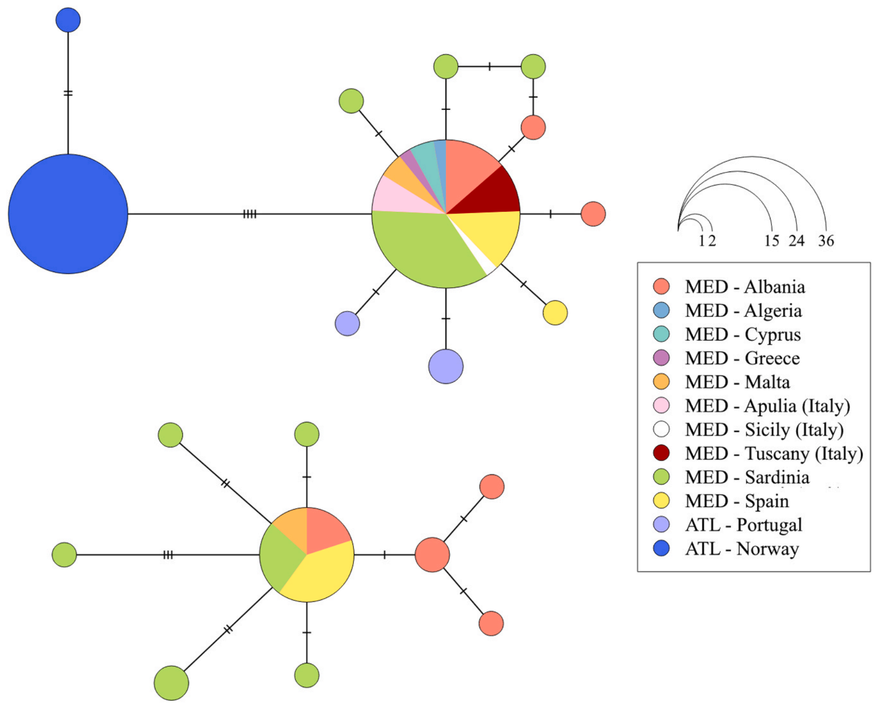

Fig. 3. Graphical representation of TCS haplotype network showing the results obtained for the COI (top) and NADH2 (bottom) datasets. Each bar represents a mutation event.

limited monitoring effort may have contributed to erroneous assumptions of species absence, particularly for rare elasmobranchs (Gajić and Sulikowski, 2024; Gajić, 2024, 2025). Nevertheless, the extremely low CPUE and overall encounter frequencies observed in this study further confirm the exceptional rarity of *L. circularis* within the study area, consistent with patterns reported across the Mediterranean Sea (Consalvo et al., 2009; Mnasri et al., 2009; Alkusairy and Saad, 2018; Kousteni et al., 2019). Additionally, the absence of detections during extensive port-based monitoring (>4500 inspected hauls) indicates that the species is effectively undetectable through landings-based surveys. This likely reflects its very low abundance, lack of commercial value, and routine discarding at sea rather than true absence from fishing grounds. Consequently, onboard fishery-dependent monitoring and targeted scientific surveys are essential for documenting the species' occurrence; without such approaches, its true distribution and conservation status are likely to remain underestimated, potentially undermining effective management efforts (Gajić, 2025). The consistent retrieval of individuals already dead indicates that post-capture mortality of *L. circularis* following trawl capture is likely extremely high, suggesting that reliance on the release of incidentally caught individuals may provide little to no conservation benefit and may even impede effective management unless species-specific survival rates and mitigation measures are rigorously assessed through targeted research. Nevertheless, the absence of gross pathological findings, together with generally stable condition factor and hepatosomatic index values, suggests that all recorded individuals were in relatively good health prior to capture.

Molecular data indicates the occurrence of a reciprocally monophyletic lineages (sensu Jenkins et al., 2018), revealing two distinct groups within the species: one from Norway and one from the Mediterranean region, including Portugal. Regarding the latter, our data underline shallow genetic divergence, as observed in other Mediterranean chondrichthyans (Di Crescenzo et al., 2022; Melis et al., 2023; Barbato et al., 2025). The presence of widely shared central haplotypes likely reflects historical connectivity, possibly associated with past oceanographic conditions or demographic expansion from ancestral populations. However, the accumulation of multiple private haplotypes in several areas could suggest that present-day connectivity may be to some extent restricted (Pasolini et al., 2011; Jenkins et al., 2018).

For a demersal elasmobranch such as *L. circularis*, characterized by low fecundity, benthic egg deposition, and limited dispersal capacity (Villagra et al., 2022), the observation of geographically restricted haplotypes may be compatible with the presence of resident or semi-resident populations (Jenkins et al., 2018; Bellodi et al., 2024; Di Crescenzo et al., 2025). However, given the limited sampling size, this interpretation should be considered preliminary, and broader geographic and genomic sampling will be required to robustly assess population connectivity and residency patterns. In light of the Critically Endangered status of *L. circularis* (McCully et al., 2016), future studies aimed at resolving population structure and identifying important areas will be crucial for conservation prioritization, since local population losses may lead to the irreversible erosion of unique genetic diversity documented in other marine species (Domingues et al., 2018; Di Crescenzo et al., 2022; Iacovelli et al., 2025; Crobe et al., 2026).

Taken together, the results of this study demonstrate that *L. circularis* likely persists in the southern Adriatic Sea despite decades of apparent absence from confirmed records. The combination of repeated detections, depth-specific occurrence, and the presence of multiple life stages indicates that the region represents a previously overlooked component of the species' Mediterranean range. Given the intensity of demersal trawl fisheries operating along the Adriatic slope, these findings underscore the need for continued fishery-dependent monitoring and targeted documentation of rare deep-sea elasmobranchs. Improved reporting, combined with genetic verification, will be essential for refining the conservation status of *L. circularis* and for informing future management and protection measures in the Mediterranean Sea. Ultimately, effective conservation of *L. circularis* and many other deep-sea elasmobranchs in the Adriatic Sea and wider Mediterranean will require the integration of targeted fishery-dependent monitoring, species-specific post-capture survival research, and the development of mitigation measures aimed at reducing trawl-related mortality, as reliance on anectodal reports and incidental release alone is unlikely to prevent further decline.

CRediT authorship contribution statement

Chiara Pani: Writing – review & editing, Visualization, Software, Methodology. **Rita Cannas:** Writing – review & editing, Validation, Supervision, Resources. **Emina Karalić:** Writing – review & editing, Project administration, Methodology, Investigation. **Andrej A. Gajić:** Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Simone Di Crescenzo:** Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization.

Ethical approval

All specimens included in this study were obtained exclusively through monitoring of commercial bottom-trawl fisheries. No animals were captured, harmed nor killed specifically for the purposes of this research. Sampling was limited to individuals incidentally caught and retrieved dead as fisheries bycatch and examined post-capture.

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Declaration of Competing Interest

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

SM1 and highlighted in bold. Further inquiries can be directed to the corresponding authors.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.rsma.2026.105277.

Data availability

NCBI Accession Numbers of deposited COI and NADH2 sequences are reported in Table SM1 and highlighted in bold. Further inquiries can be directed to the corresponding authors.

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