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Parasites of the invasive Atlantic Blue Crab *Callinectes sapidus* and native crabs *Carcinus maenas* and *Afruca tangeri* in Merja Zerga Lagoon, Moroccan Atlantic coast

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Introduction

The Atlantic blue crab, *Callinectes sapidus,* is a well-established invasive species along the Mediterranean and the Atlantic coasts of Morocco (Oussellam et al., 2023). The present study aims to (1) explore parasites of the invasive *C. sapidus,* and the native crabs *Carcinus maenas*, and *Afruca tangeri* in the Merja Zerga Lagoon (Atlantic, Morocco); (2) test the enemy release hypothesis in the invasive blue crab, and (3) detect potential parasite spillover or spillback between native and non-native species.

Material and Methods

Overall, 36 *Callinectes sapidus*, 10 *Carcinus maenas*, and 43 *Afruca tangeri* were collected from the Merja Zerga Lagoon **(Figure 1)** between March and April 2025 and then dissected **(Table 1)**. Hemolymph was microscopically screened for parasites belonging to *Hematodinium* and internal organs (hepatopancreas, gills, heart, stomach, and ganglion) were examined for other parasites. Genetic analysis of *Hematodinium* was performed using Sanger sequences from 13 *C. sapidus*, 3 *C. maenas*, and 17 *A. tangeri*. The haplotype network and the phylogenetic tree were created respectively by PopART using the Median-Joining algorithm and MEGA software, with the optimal model Kimura 2-Parameter and Neighbor-Joining method.

Results

Parasites identified are reported in **Figure 2,** their prevalences in **Figure 3** and the infected organs by species in **table 1**.

Genetic analysis, based on the ITS1 rDNA gene from *Hematodinium,* confirmed the sequences as being those of *Hematodinium perezi* (Lamkhalkhal et al., 2024). The haplotype network **(Figure 4)** and the phylogenetic tree **(Figure 5)** reveal that Moroccan *H. perezi* sequences are closer to those from England and Greece, but more distant from those in the USA.

Table 1: Morphometric measurements, parasites identified, and infected organs in *C. sapidus*, *C. maenas*, and *A. tangeri* collected from Merja Zerga Lagoon.

Species	CL (cm)		CW (cm)		W (g)		Parasites	Tissues / organs
	Min-Max	Mean±SD	Min- Max	Mean±SD	Min-Max	Mean±SD		
Callinectes sapidus	2.1 - 6.7	4.92 ± 0.48	4.1 - 15.3	10.36 ± 2.1	8.2 - 199.6	101.24±46.2	*H. perezi*	Hemolymph
							Digenean trematode	Gills - ganglion
							Microsporidian	Ganglion-stomach-hepatopancreas-heart
Carcinus maenas	2.2 - 3.6	2.8 ± 0.3	3 - 4.8	3.78 ± 0.3	5.35-25.45	13.16 ± 3.7	*H. perezi*	Hemolymph
							Digenean trematode	Gills- hepatopancreas- heart- ganglion
							Haplosporidian	Heart- ganglion
Afruca tangeri	1.1 - 3.7	2.36 ± 0.2	2 - 3.7	3.09 ± 0.3	6.4 - 30.8	17.56 ± 4.8	*H. perezi*	Hemolymph
							Haplosporidian	Ganglion- heart- gills

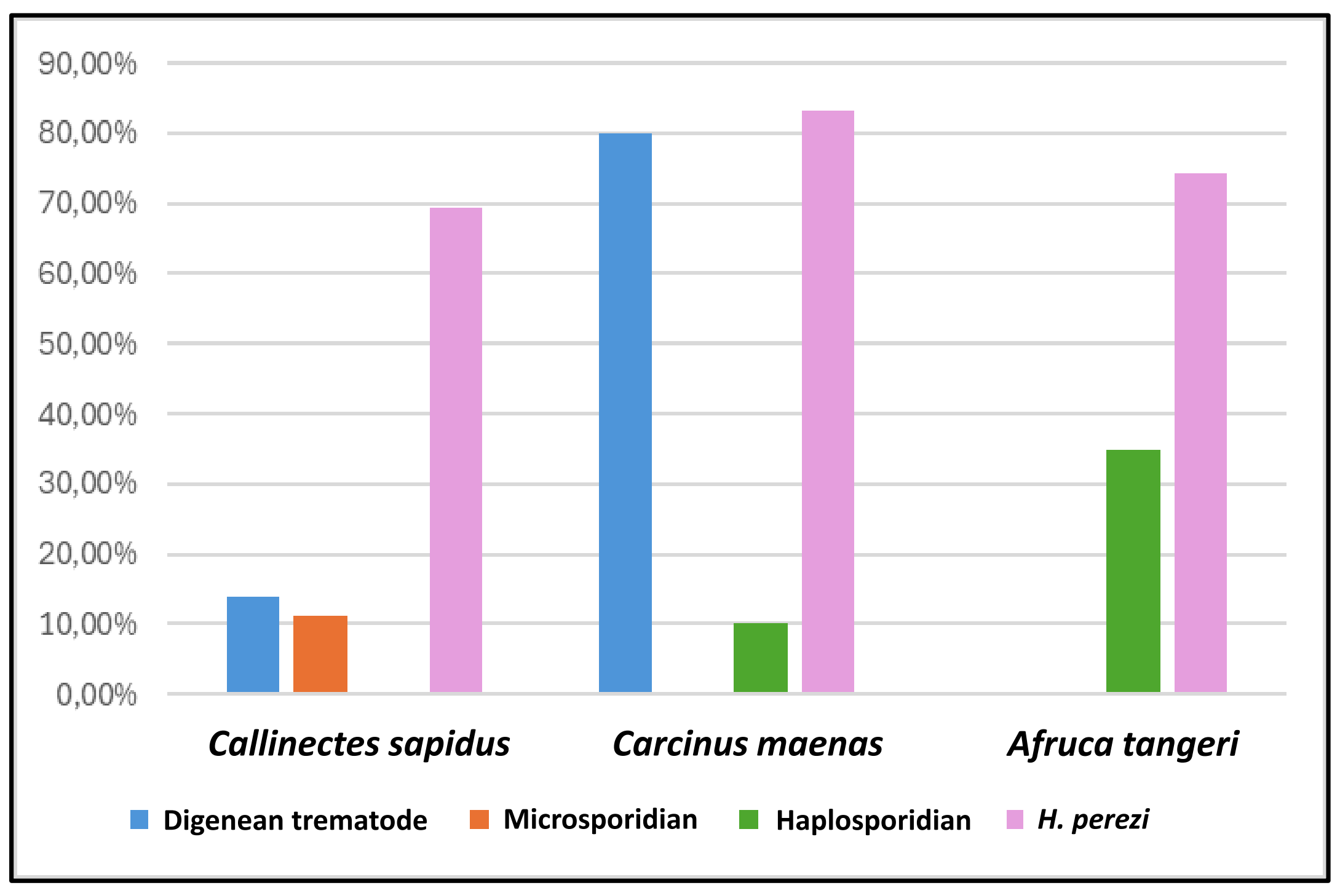

Figure 3: Comparison of parasite prevalence in *Callinectes sapidus*, *Carcinus maenas*, and *Afruca tangeri*.

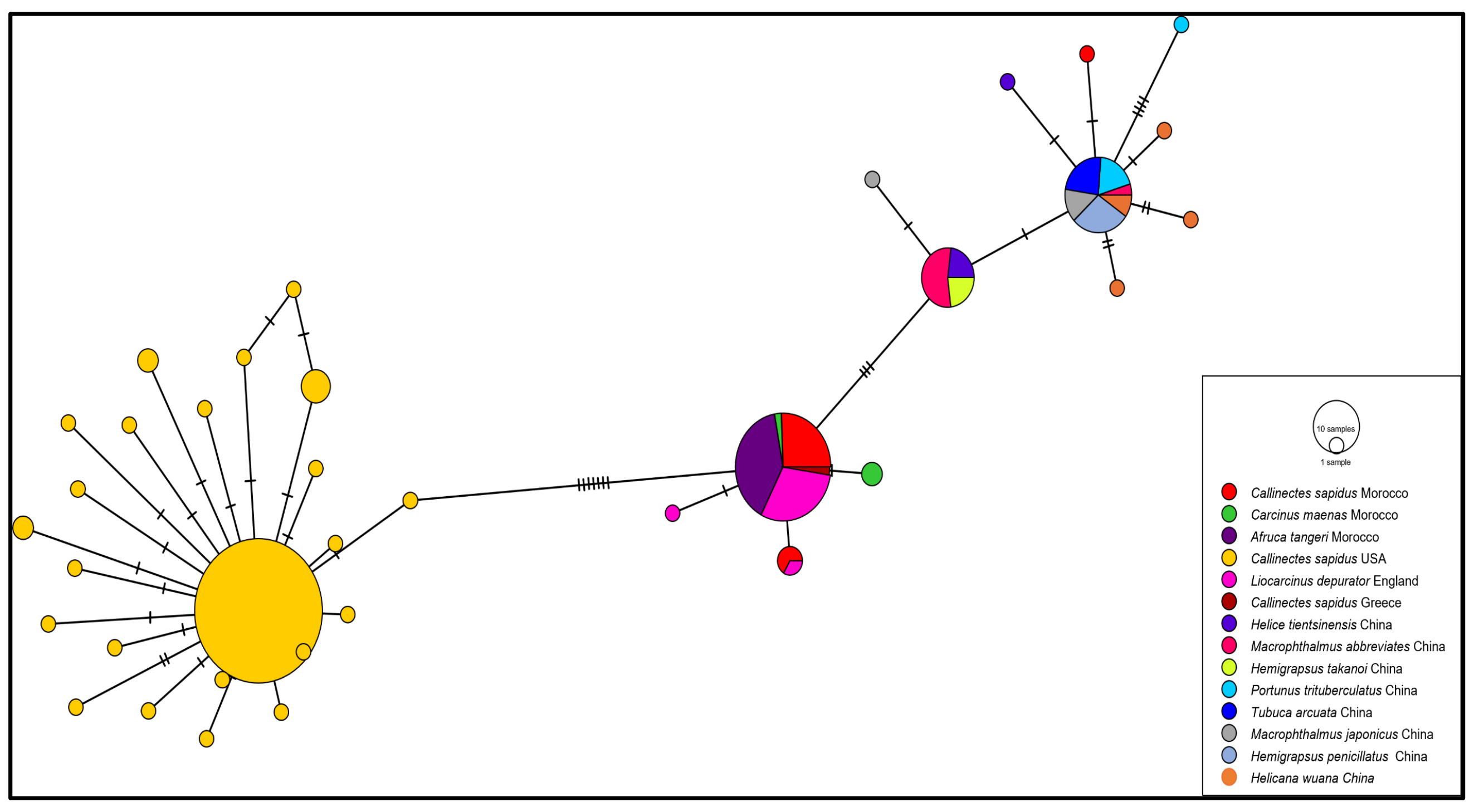

Figure 4: Haplotype network of *H. perezi* (ITS1 rDNA) from the crab species studied and GenBank sequences, grouped by host and country. Circle size indicates haplotype frequency; vertical lines represent the number of mutations.

Conclusion

These findings support the enemy release hypothesis, indicating that *C. sapidus* did not arrive in Morocco carrying its parasites but instead experienced parasite spillback from eastern Atlantic species.

References

- ❖ Oussellam et al. 2023. Bioinvasions Rec. 12: 403–416
- ❖ Lamkhalkhal et al. 2024. J. Mar. Sci. Eng. 12: 1045.

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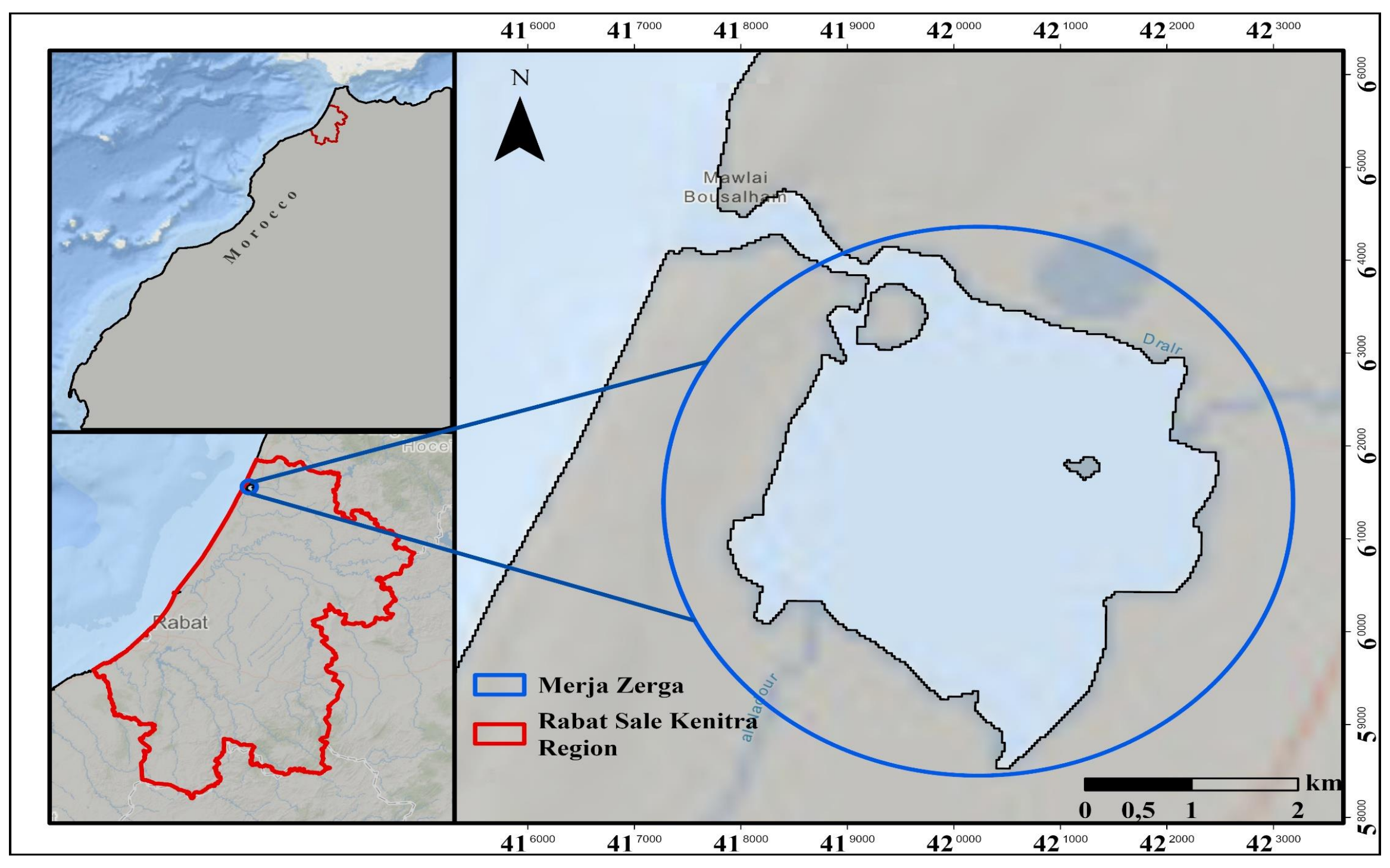
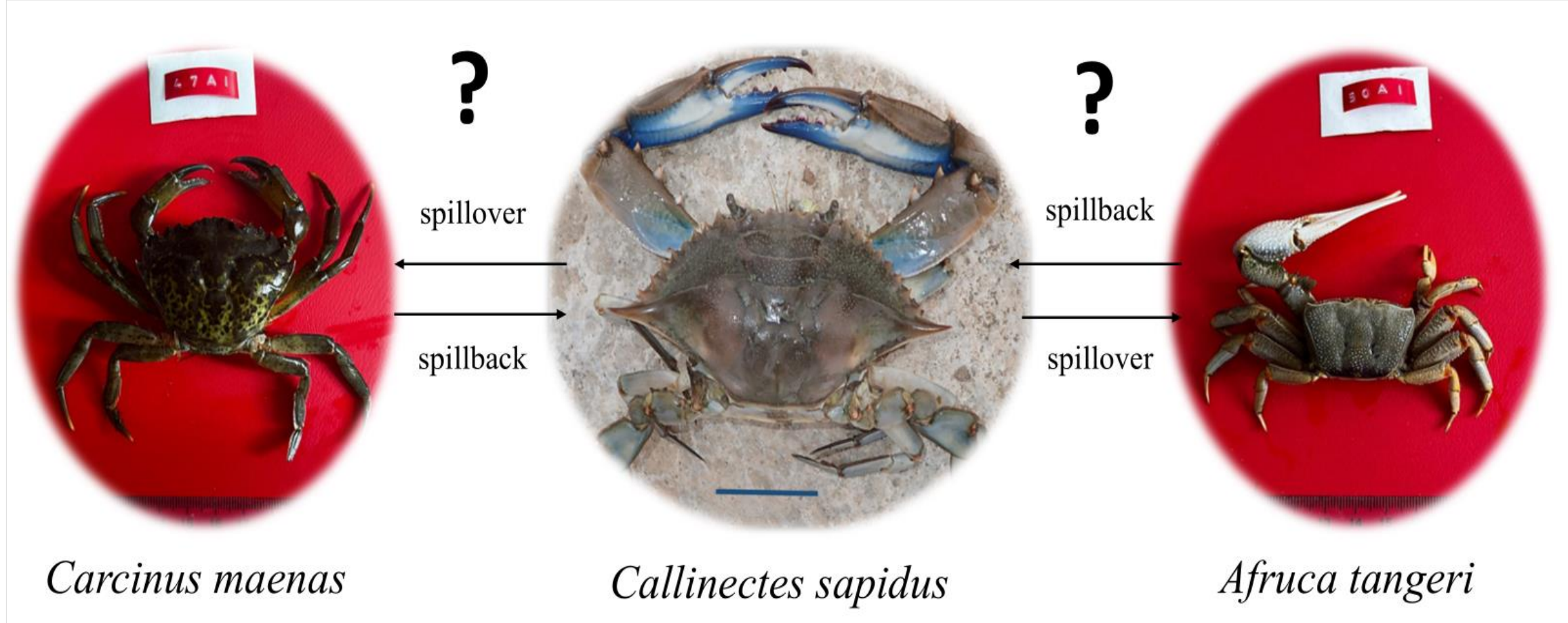


Figure 1: Geographical location of Merja Zerga Lagoon



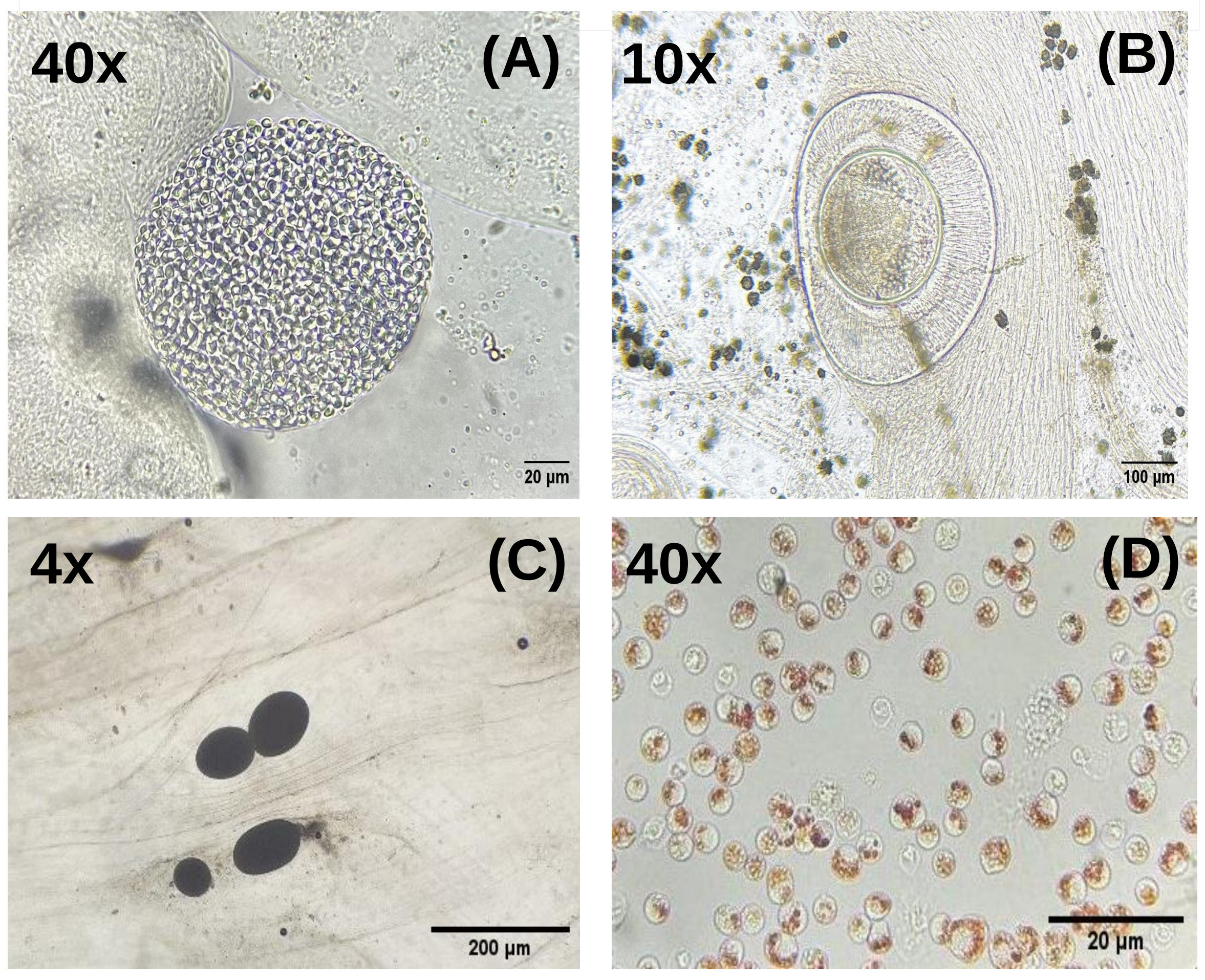


Figure 2: Haplosporidian (A) observed in the ganglion of *Afruca tangeri*, metacercaria (B) and microsporidian (C) in the ganglion of *Callinectes sapidus*; *Hematodinium perezi* (D) in the hemolymph of *C. sapidus*.

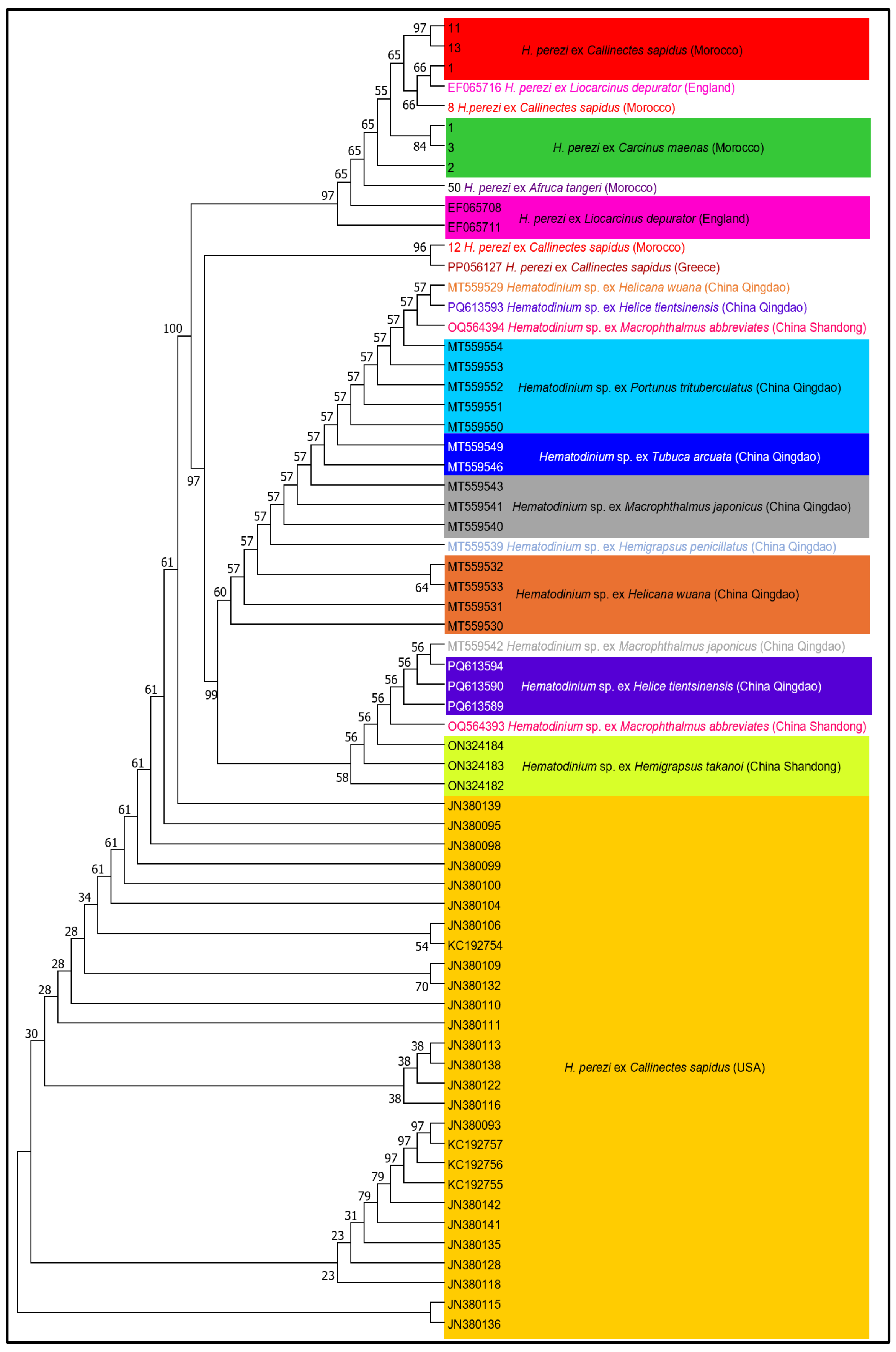


Figure 5: Midpoint-rooted phylogenetic tree of *H. perezi* (ITS1 rDNA) based on sequences from the studied crabs and GenBank data.