A global invader or a complex of regionally distributed species? Clarifying the status of an invasive calcareous tubeworm *Hydroides dianthus* (Verrill, 1873) using barcoding

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A calcareous tube worm *Hydroides dianthus* (Verrill, 1873) is a common fouling invader. Originally described from off Massachusetts, USA, this species has been reported along the East coast of North America down to Florida and Grand Caribbean, and nowadays extends its distribution range to Brazil, China, Europe, Japan, and West Africa (Fig. 1). Unlike most congeners, *H. dianthus* has tolerance for a wide temperature range occurring from temperate to subtropical waters, which casts doubts on the status of *H. dianthus*.

Aims

- to assess whether these populations comprise a single species or a species complex using barcoding gene cytochrome c oxidase subunit I (COI)
- provide insight into the native range and invasive routes of *H. dianthus*

← *H. dianthus* specimens removed from their tubes

Fig. 1 *Hydroides dianthus* distribution. Black spots indicate sampling locations. Dark grey shadow indicates known distribution of the species. Pie charts on the map represent haplotype frequencies for each locality; the pie size is proportional to sample size. AN: Ancona, Italy; CT: Old Saybrook, Connecticut, USA; FL: Tampa, Florida, USA; IZ: Izmir, Turkey; LI: Livorno, Italy; MA: Woods Hole, Massachusetts, USA; OT: Olbia-Tempio, Italy; QD: Qingdao, Shandong, China; RA: Ravenna, Italy; RJ: Cabo Frio, Rio de Janeiro, Brazil; RO: Rome, Italy; SV: Sevastopol, Crimea, Ukraine; TX: Galveston, Texas, USA; TY: Tokyo, Japan; VA: Hampton, Virginia, USA; VE: Venice, Italy; VM: Village Marina, Florida, USA. H: HaplotypePhoto of *H. dianthus* is from Google by M.Taru.

Results

- Twenty haplotypes from all 17 localities detected based on COI gene, the highest genetic diversity (nine of ten haplotypes) observed in the Mediterranean (Fig. 1)
- Two clades (A & B) supported by both haplotype network analysis and phylogenetic reconstruction (Fig. 2 & 3)
- High genetic homogeneity present at the continental scales in each clade (Fig. 1)

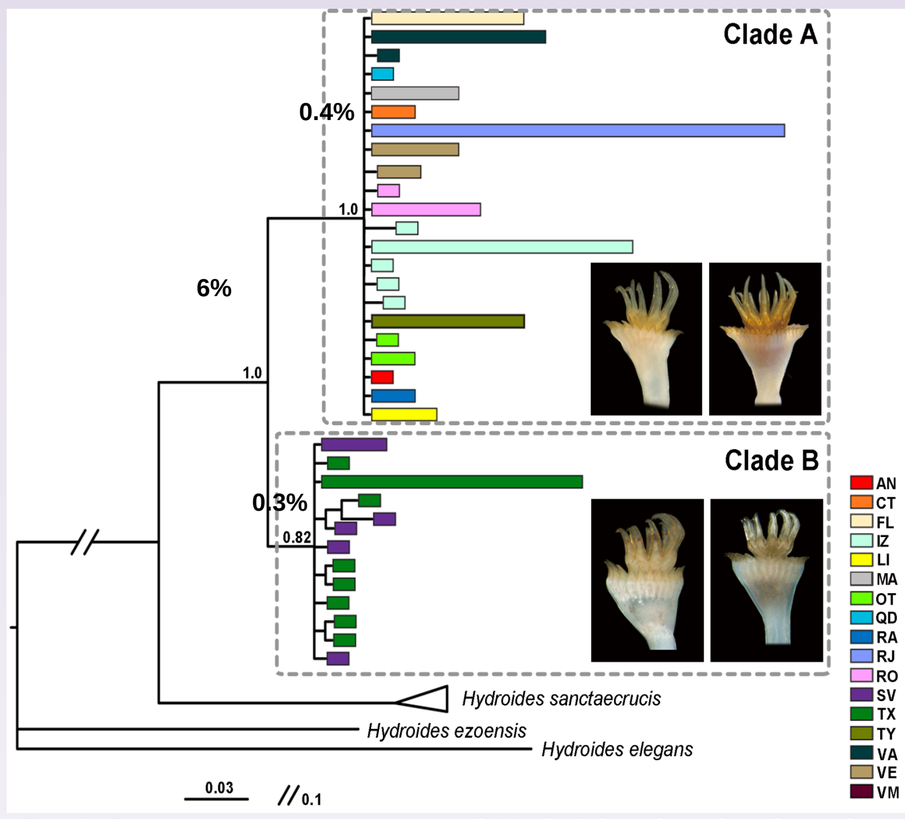

Fig. 2 Bayesian consensus tree of *Hydroides dianthus* based on COI sequences. Two main clades are highlighted. Values represent posterior probabilities (pp) > 0.7. Bar length after branches indicate numbers of individuals in that branch.

Conclusions

- *Hydroides dianthus* is a species-complex consisting of two cryptic species with high invasive potential.
- The native range of *H. dianthus sensu stricto* is the Mediterranean rather than the United States.
- Human-mediated transport plays an important role in *H. dianthus* dispersal. With increasing shipping activity, *H. dianthus* is likely to extend its distribution range to new localities such as e.g., south Africa and Australia.
- Further attention should be directed towards the establishment adequate monitoring and mitigation policies on a global scale to reduce further potential introductions of *H. dianthus*.

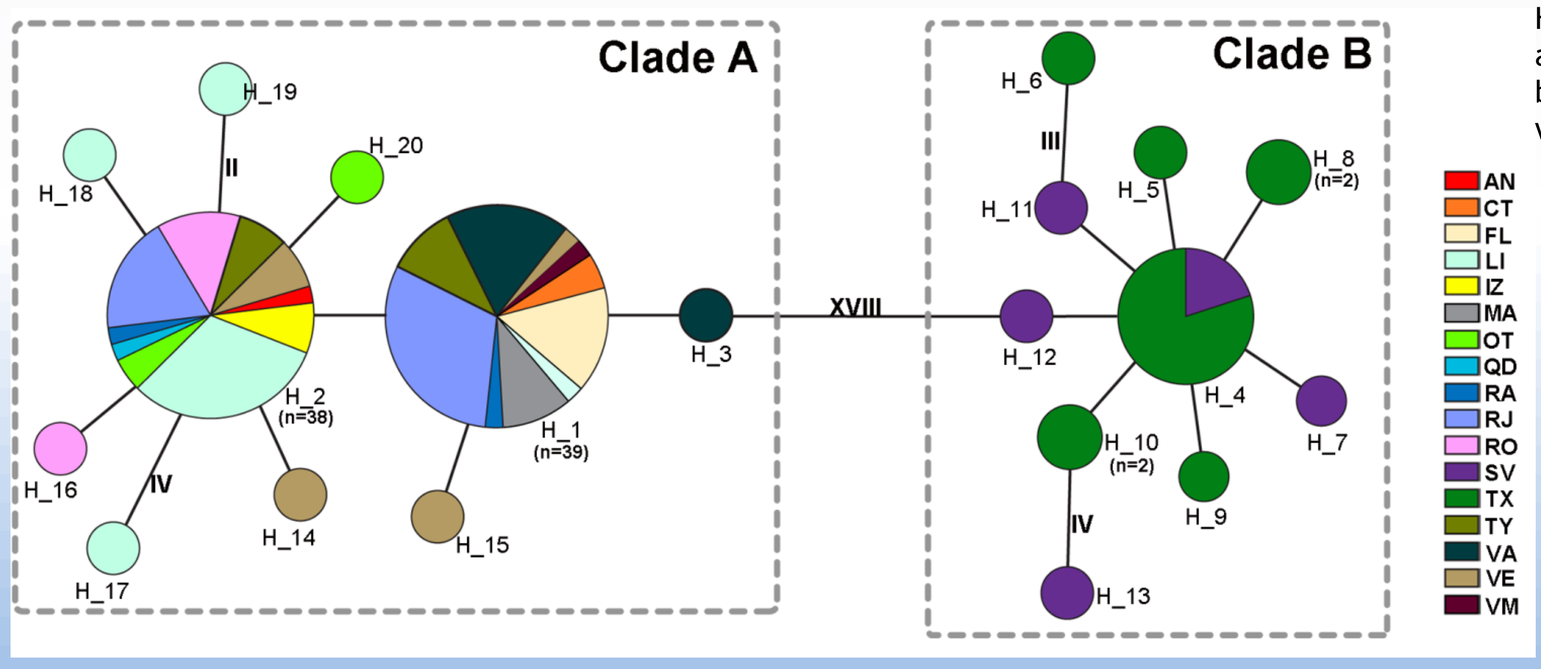

Fig. 3 Haplotype network for *Hydroides dianthus* from CO1 data. Haplotypes are marked as H_1 to H_20. Numbers of specimens are given for haplotypes with more than one specimen. Lines between circles represent one mutational step unless marked with roman numerals.

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