SUPPLEMENTARY MATERIAL S1

Collective exploitation of large prey by group foraging shapes aggregation and fitness of cnidarian polyps

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Molecular characterization of specimens, and phylogenetic and haplotype analyses of *Aurelia coerulea*

Methodology

Total genomic DNA of two different polyps (with vouchers G21_26 and G21_27) was extracted from a small piece of tissue and by using the 'salting out' procedure (Aljanabi and Martinez, 1997). The primer pair LCO1490 and HCO2198 (Folmer et al. 1994) was used for the amplification of the mitochondrial cytochrome oxidase subunit I (COI) gene, following cycling parameters: 5 min of initial DNA denaturation at 94°C; 35 cycles of 94°C/30 s (DNA denaturation), 48°C/60 s (annealing), 72°C/60 s (elongation); and 7 min of final extension at 72°C (Furfaro et al. 2016). The final volume of the PCR reaction was 20µl. The amplified products were sequenced at the European Division of Macrogen Inc. (Milan, Italy) and the resulted COI sequences were edited with Staden Package 2.0.0b9 (Staden et al., 2000). To exclude contaminations, BLASTN (Altschul et al., 1990) search was conducted in the GenBank database to confirm the

identity of the sequenced fragments. Consensus sequences were aligned together with sequences already available in GenBank using the Muscle algorithm implemented in MEGA 6.0 (Tamura et al., 2013). To evaluate the genetic distribution of the different haplotypes and to possibly investigate the origin of the samples object of the present study, we reconstructed the haplotypes network for the COI sequences by using the program PopArt (Population Analysis with Reticulate Trees) (available at: https://popart.maths.otago.ac.nz/) with the TCS as the network inference method (Clement et al., 2002).

OUTPUTS

Two COI sequences were obtained from the analysis of the two samples and identified as *Aurelia coerulea* according to BLAST analysis which resulted in 100% of homology with other sequences of *A. coerulea* already deposited in Genbank. Molecular comparison between the newly produced sequences and those retrieved from GenBank was carried out confirming the samples object of the present study belong to *A. coerulea* (Fig. S1). A reduced alignment (276 sequences and 642 bp) including only *A. coerulea* sequences and the out-group, was generated to investigate the intraspecific genetic variability. The haplotype network analysis was performed on this latter alignment and revealed the two investigated polyps belonging to two different haplotypes, one with western pacific origin and another simultaneously found in the Mediterranean Sea and Pacific Ocean (Fig. S2).

CONCLUSIONS

The haplotype network analysis revealed the two investigated polyps belonging to two different haplotypes, one with western pacific origin and another simultaneously found in the Mediterranean Sea and Pacific Ocean. This result is not surprising since it is known that among its congeners the jellyfish *A. coerulea* is the one with the broadest geographic range (Ki et al., 2008; Scorrano et al., 2017; Seo et al., 2021) and its haplotypes are widely distributed globally. Moreover, considering that this species was suggested to be native to the western Pacific (Japan, Korea and China) from where it dispersed globally by anthropogenic means (Dawson et al., 2005), the presence of a Pacific haplotype is almost expected and confirms this species originated from Indo-Pacific Ocean.

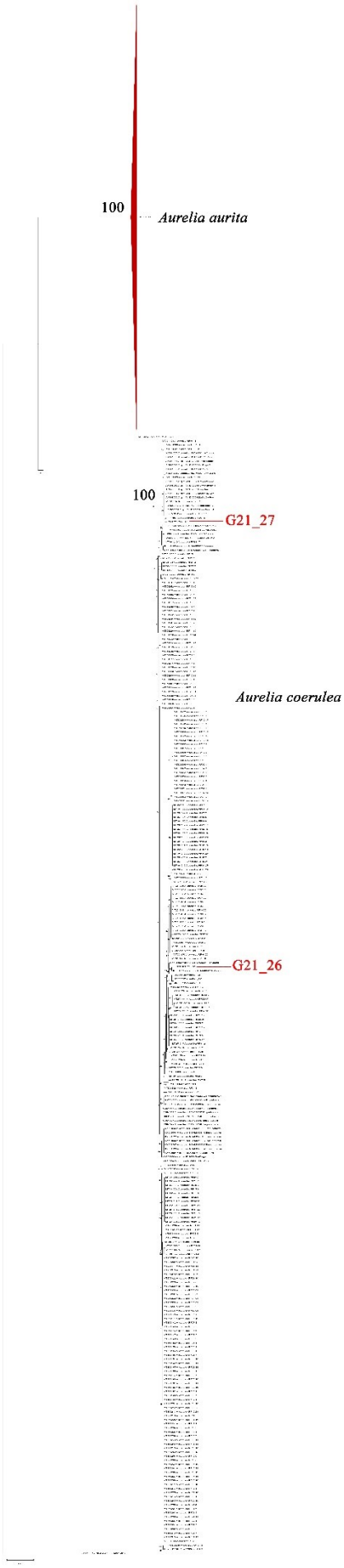
100
Aurelia aurita
100
G21_27
Aurelia coerulea
G21_26

Figure S1: COI Neighbour Joining topology based on uncorrected *p*-distances showing the two polyps here investigated belong to *Aurelia coerulea* monophyletic clade.

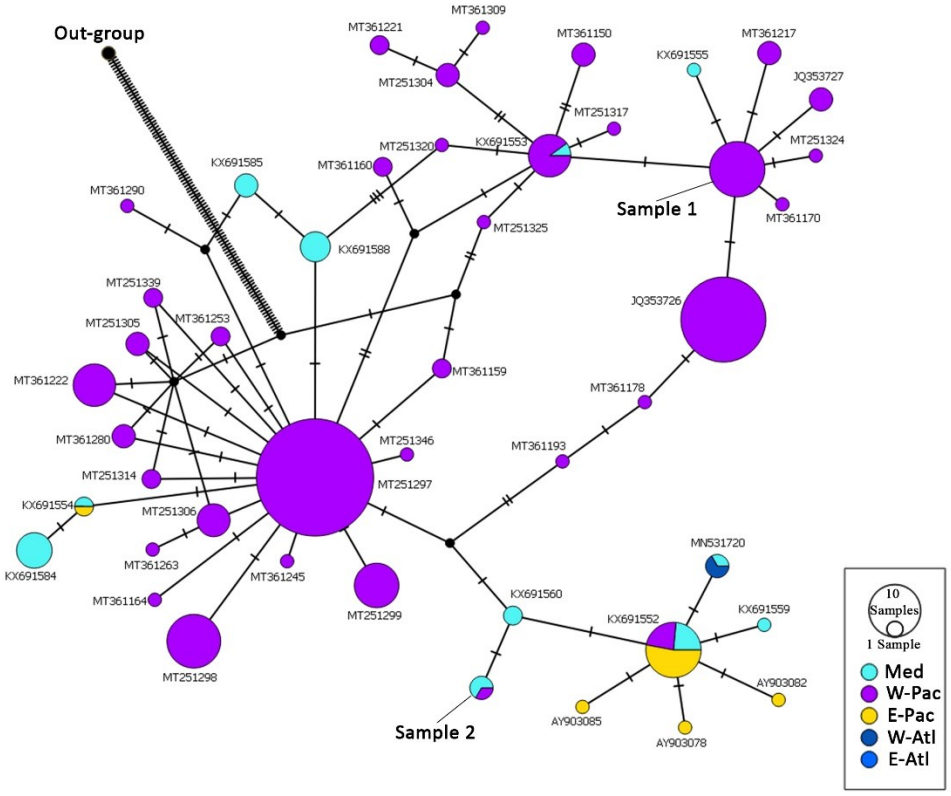

Figure S2: COI Haplotype (TCS) network showing the phylogeography of the different haplotypes of *Aurelia coerulea* collected worldwide. Each circle represents individual haplotypes. The size of each circle is directly proportional to the haplotype frequency while their colour indicates the geographic origin of the samples. Each perpendicular bar represents a 1-nucleotide mutational change. Small black dots indicate unsampled haplotypes.

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