

GENETIC CONNECTIVITY OF THE WIDESPREAD HYDROZOAN AGLANTHA DIGITALE FROM SUB-ARCTIC TO CENTRAL ARCTIC REGIONS

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Aglantha digitale is a very widespread species found in the northern seas and northern parts of the Atlantic and North Pacific oceans, ranging from about 35°N into the Arctic Ocean. *A. digitale* demography is tightly coupled with the distribution of warm Atlantic water, which could indicate that Atlantification can manifest of pushing the species poleward. The strengthening of the Atlantic water inflow into the Arctic may become very important for the polar pelagic ecosystems. The main objective of this study is to evaluate genetic connectivity of the widespread hydrozoan *Aglantha digitale* from sub-arctic to central arctic regions, to investigate the genetic structure and connectivity between populations from different geographical locations and detect different *A. digitale* lineages in various localities. *A. digitale* samples were collected at four separate localities: Svalbard, Southwest Greenland, the Chukchi Sea and the Central Arctic Ocean. These localities will help us understand whether genetic connectivity exists throughout the Arctic Ocean. The Qiagen and Chelex methods were used for the DNA extraction. DNA products were amplified using the Polymerase Chain Reaction using universal Folmer Primers and sequenced to obtain a 658 bp COI fragment. The analysis of sequences was done using the software CodonCode Aligner to edit and trim the sequences to 658bp length. The sequences were then aligned using ClustalW, in CodonCode Alligner. The genetic distance of each species was inferred using the Neighbour-Joining method, using the MEGA X software, with 2000 bootstrap replicates. A haplotype network was created using the PopART software to indicate the relationships between the identified haplotypes, using the Templeton, Crandall and Sing (TCS) method. The mtCOI sequenced data from 76 *A. digitale* specimens and *Nanomia cara*. The Neighbor-joining tree provided two clusters of *A. digitale*, one was influenced by the Atlantic and the other was influenced by the Pacific. Data showed that the Atlantic influence had high diversity and the Pacific influence with low diversity. These patterns of connectivity which impact population size are likely to be explained by glaciation events from the Last Glacial Maximum. The lack of haplotype diversity as presented in the Chukchi sea, could be due to the species being forced partially or completely out of high latitudes during the last glacial maximum, and later on to expand once more in the past 20Kyr. High genetic diversity could be due to the conditions from the Last Glacial Maximum, where large amounts of refugia has occurred for the species which has perhaps given the ability for *A. digitale* to thrive in various conditions and deeper waters and increased adaptive potential. These results therefore provide insight on any future studies dealing with genetic connectivity across the Arctic and Sub-Arctic.