

Dispersal mechanisms of the *Halophila ovalis* population in Taiwanese waters



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● Abstract

In recent years, coastal development and marine pollution are causing dramatic decline of marine ecosystems, especially seagrass ecosystem which locates exclusively in subtidal zone. Understanding their dispersal mechanisms and connectivity are very important for restoration, conservation and management of seagrasses. *Halophila ovalis* (R. Br.) Hook. f. (Figure 1) is a widely distributed species in the Indo-Pacific. Around Taiwanese water, it can be found in Taiwan, Penghu Islands and Dongsha atoll. Previous literature indicated their fruits and seeds which digested by birds were have a much higher germination rate. Therefore, the biotic vector such as migratory birds may play an important role on their long distance dispersal. If the migratory shore birds are responsible for carrying new recruits from different geographic populations (countries), a temporal genetic structure shift could be expected.

● Materials and Methods :

616 species from 23 sites for consecutive years used in this study (Figure 2). ITS was used to barcode specimens from different sites. 10 microsatellite loci were used for genotyping, pairwise F_{st} values were estimated by MSA and GenAlEx was used to perform Principal coordinates analyses (PCoA). STRUCTURE was used to reveal population structure. Isolation by distance (IBD) test was carried out by Genepop version 4.2.

● Results :

The results of ITS analyses showed that all haplotypes were clustered with reference ITS sequences of *H. ovalis* downloaded from GenBank (Figure 3). The Structure Harvester showed $\Delta k=17$ has the highest Ln prob (Figure 5). The genetic structure under $K=17$ showed that local populations which separated only few kms were genetically different and temporal shift between 2017 and 2018 (Figure 4), and the PCoA showed that populations from different regions are close related to each other (Figure 6). The populations sampled also fit with an isolation by distance model based on a Mantel test ($P < 0.001$). (Figure 7).

Figure 3. Phylogenetic tree of *Halophila* species

(XJ13, 14, ZT20, 28, CLF15, 19, CLR18, 25, DGY17, 18, QW6, 10, QT3,8 are from Penghu Islands. DSN2,3 are form Dongsha atoll. QW10,21 are from Qigu)

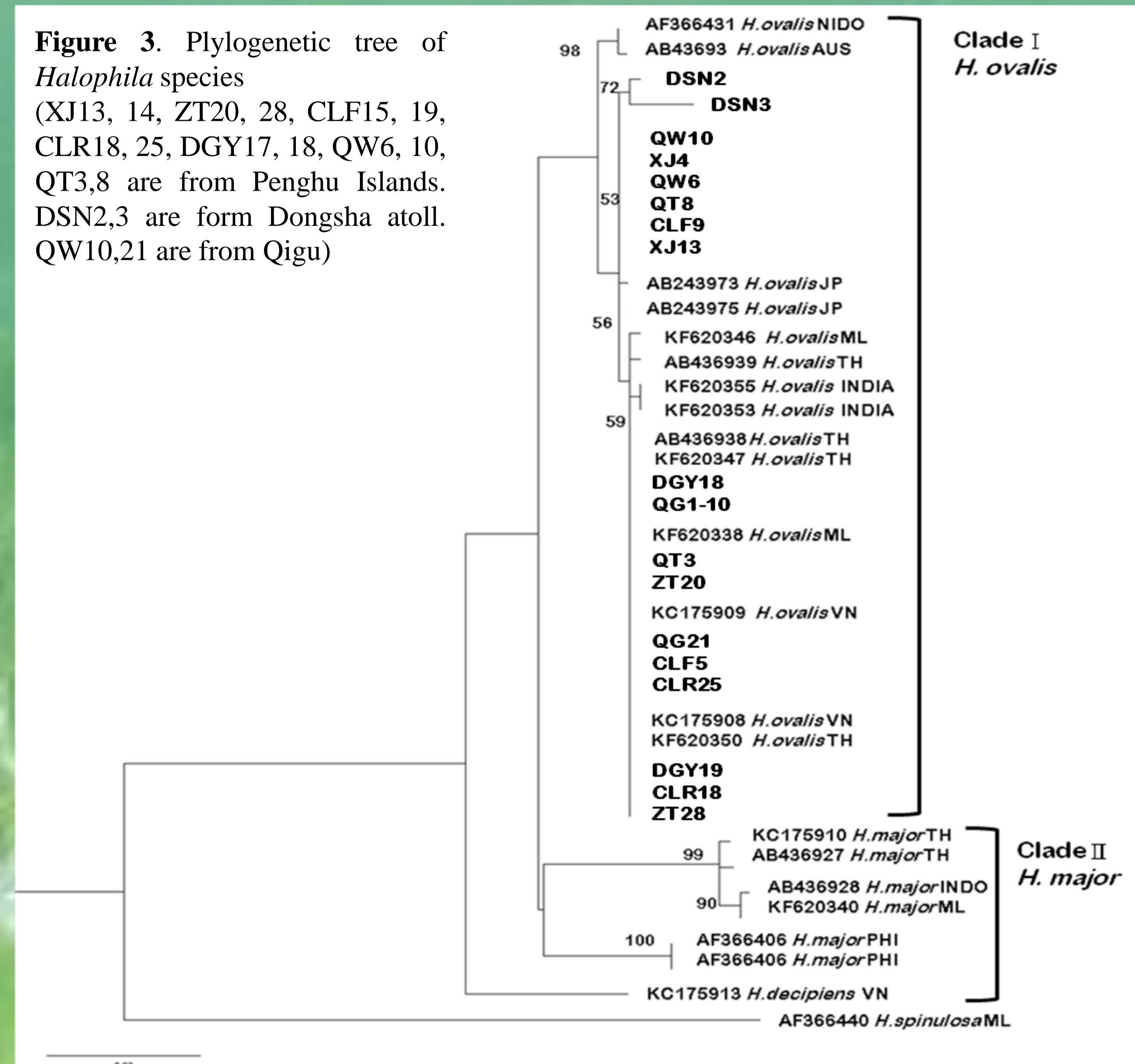


Figure 4. The result of assignment test based on 10 microsatellite loci under $K=17$ scenario

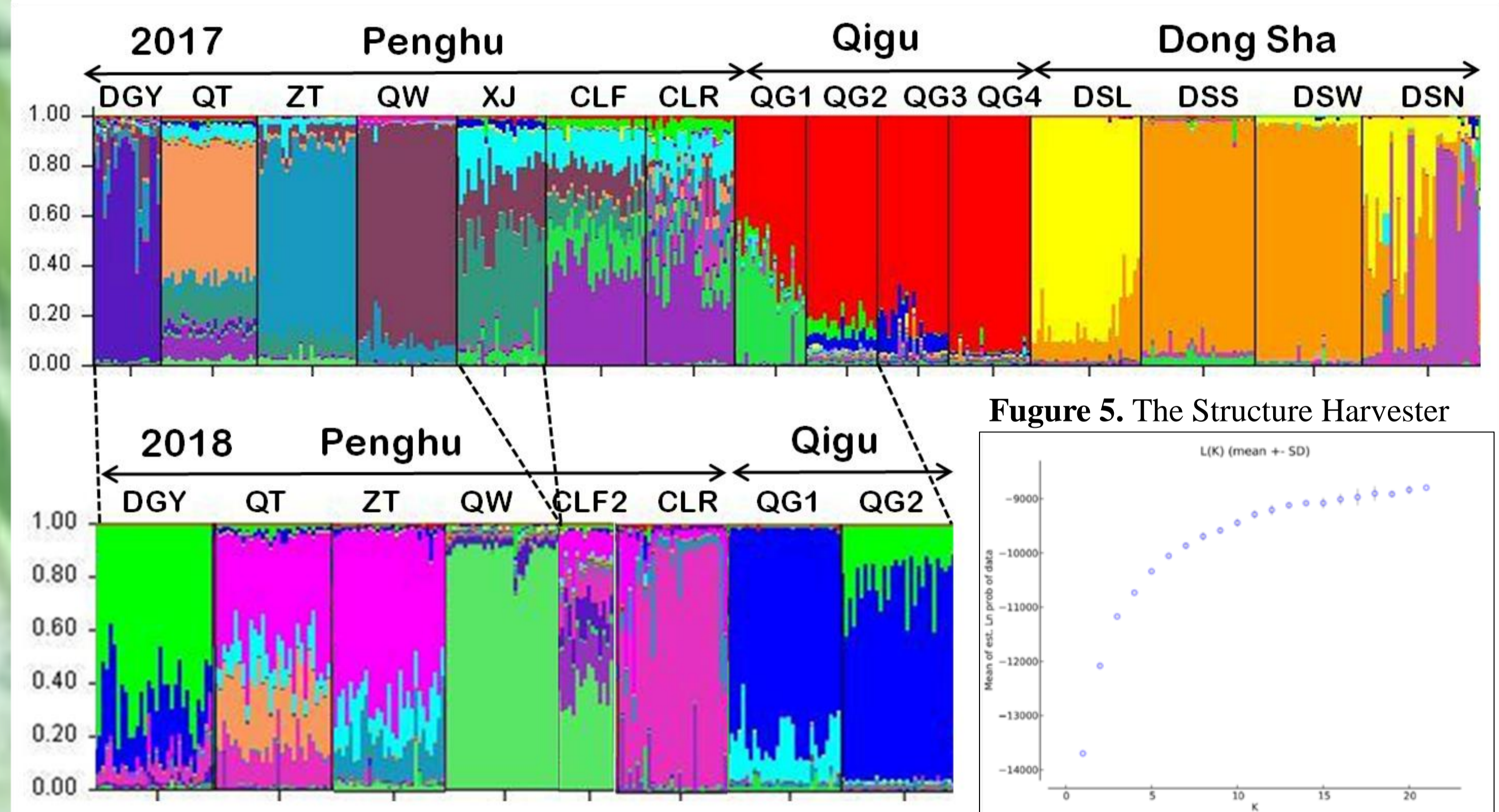
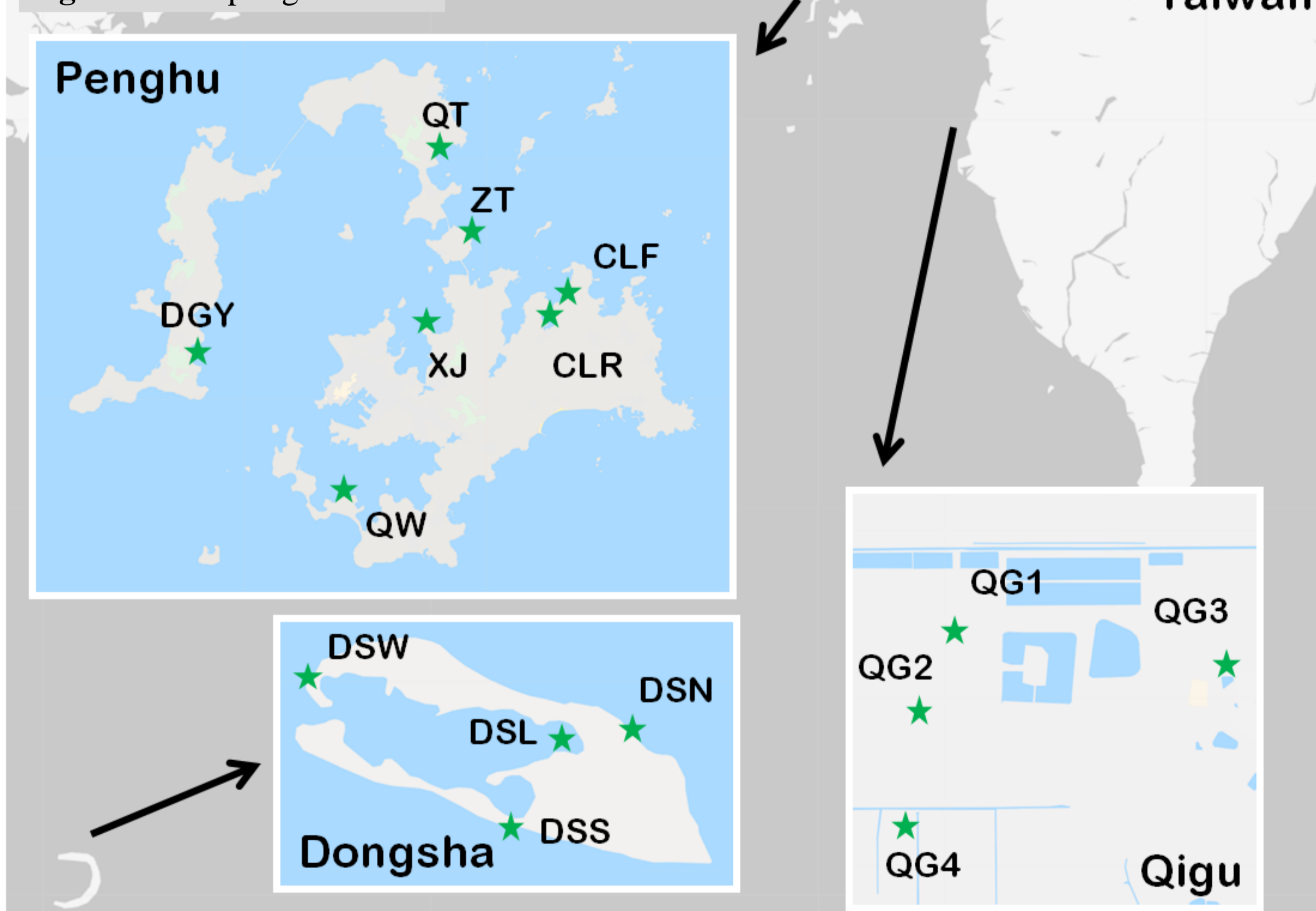


Figure 2. Sampling localities



Principal Coordinates (PCoA)

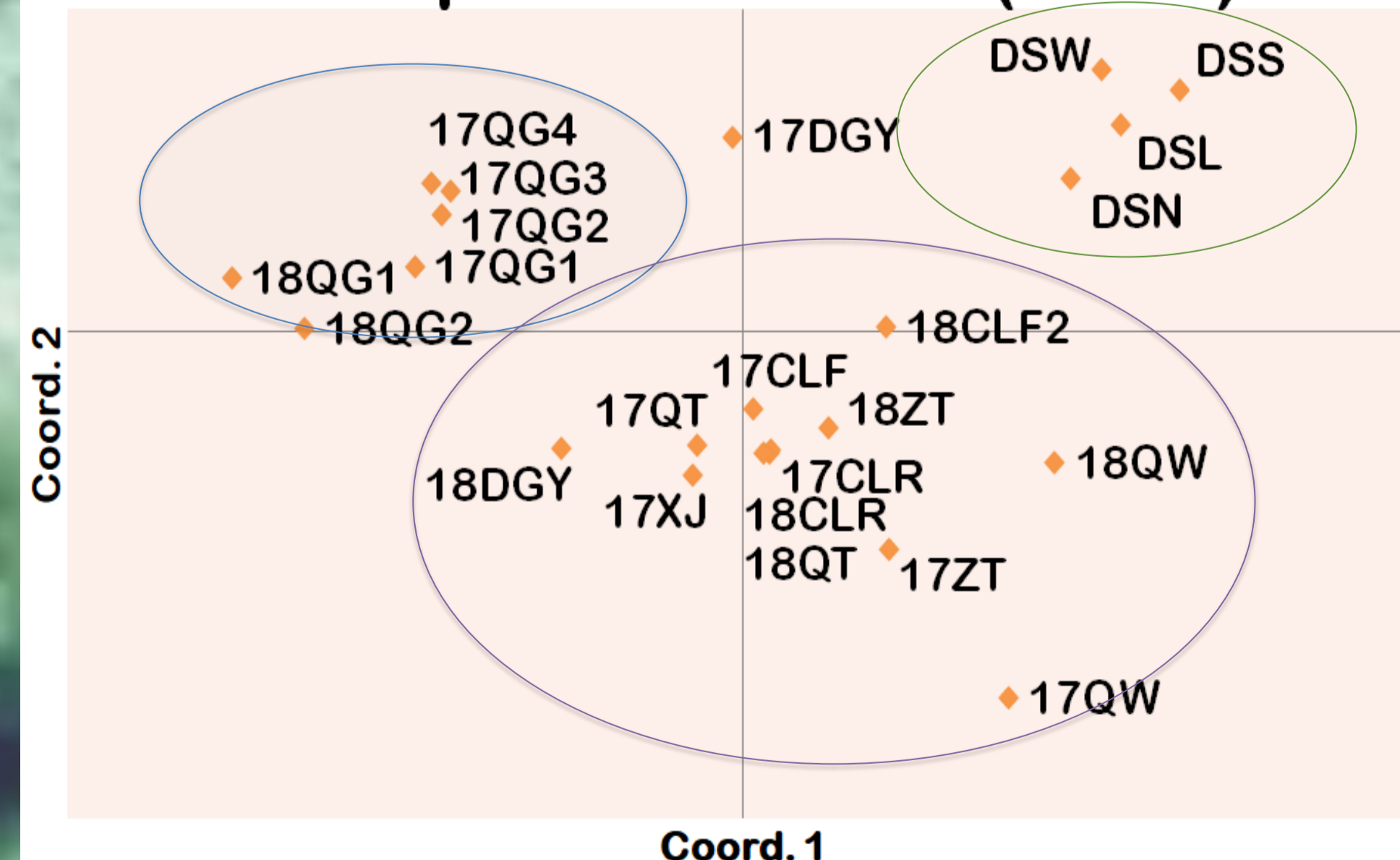


Figure 6.

PCoA plot Of *Halophila ovalis* collected from Penghu, Qigu and Dongsha for consecutive years.

Figure 1. *Halophila ovalis* in Dongsha atoll (2018. 01. 28)

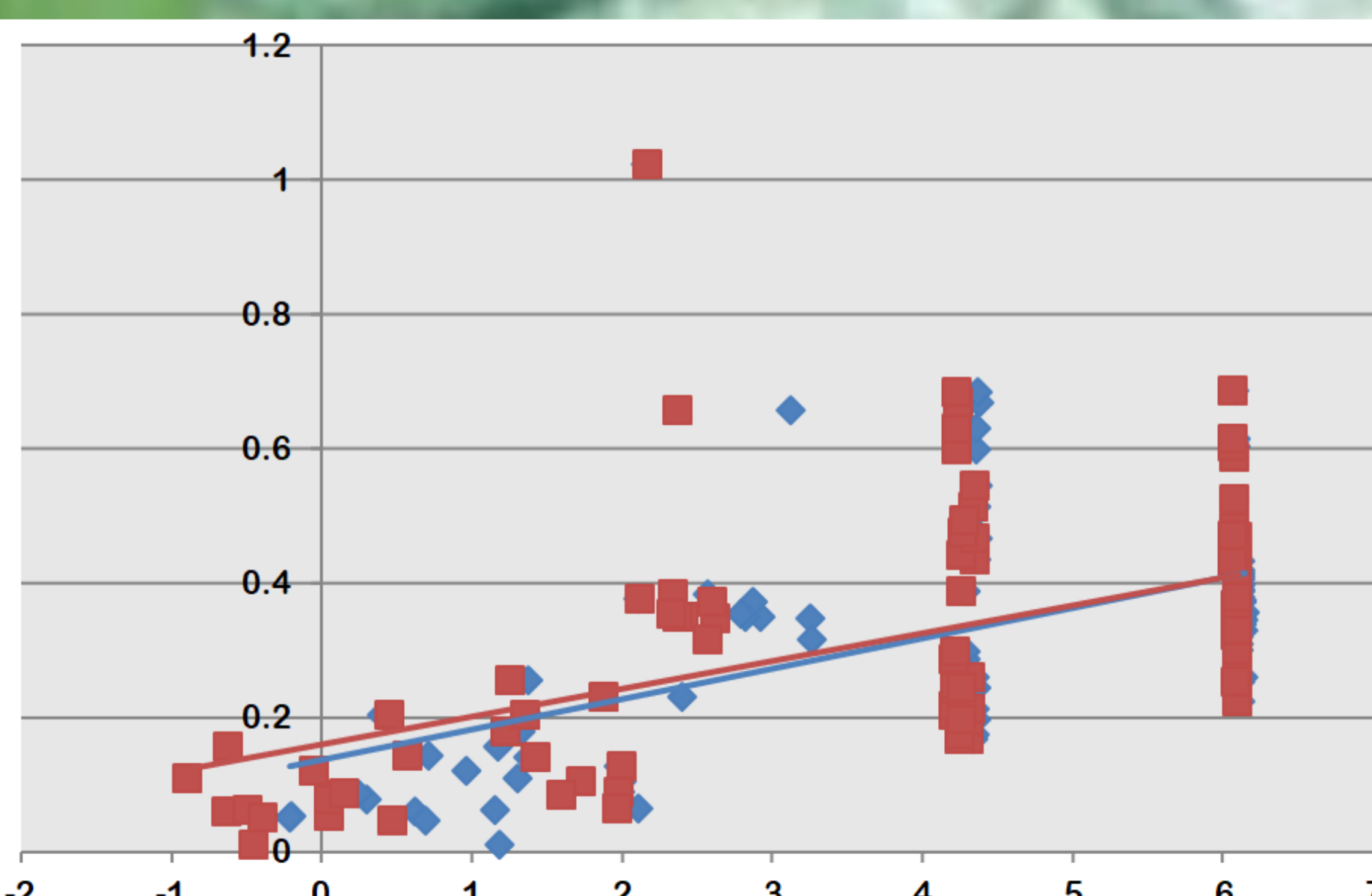


Figure 7.

IBD of *H. ovalis* populations within Taiwanese waters based on ship and geographic distance.

● Conclusions :

A temporal genetic structure shift between 2017 and 2018 was observed. This indicates either migratory birds or local adaptation may play an important role on shaping the genetic structure of *H. ovalis* in a small scale.

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