

Dispersal mechanisms of the *Halophila ovalis* population in the Northwestern Pacific: A preliminary study

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Abstract

In recent years, climate change, coastal development and marine pollution are causing dramatic decline of marine ecosystems, especially seagrass ecosystem which locates exclusively in subtidal zone. To understand their dispersal mechanisms and connectivity are very important for restoration, conservation and management of seagrasses. *Halophila ovalis* (R. Br.) Hook. f. 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. In present study, we performed the sampling for consecutive years in Penghu, Qigu and Dongsha atoll to reveal a possible temporal population structure shift to test the biotic dispersal hypothesis. ITS and hyper-variable microsatellite loci were used to barcode and reveal the population structure, respectively. The results of ITS analyses showed that all haplotypes were clustered with reference ITS sequences of *H. ovalis* downloaded from GenBank which excluded the possibility of mis-identification. Meanwhile, the genotyping is currently processing.

Keyword: seagrass, *Halophila ovalis*, population connectivity, dispersal mechanism