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Population genetic differentiation of the black rockfish *Sebastes schlegelii* revealed by microsatellites

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ABSTRACTS

Sebastes schlegelii is one of the fishes that aggregate around drifting seaweed during their early development. To examine the population genetic structure of *S. schlegelii*, eight microsatellite DNA loci were used to interpret their life history characteristics and larval dispersal strategy. Two hundred and ten individuals from nine sites across the entire range of *S. schlegelii* in China and Japan were analyzed. The results indicated that the polymorphism information content, observed heterozygosity, and gene diversity of *S. schlegelii* were high. The results of analysis of molecular variance, pairwise F_{ST} values, and exact-P tests showed no genetic divergence among the different geographical populations and indicted the existence of high gene flow. There was no IBD pattern among populations. The results of the STRUCTURE analysis showed all the populations of *S. schlegelii* shared one gene pool. We concluded that larval dispersal with drifting seaweed and the environmental factors of the currents might play important roles in shaping the contemporary phylogeographical pattern and genetic homogeneity of *S. schlegelii*. The results of the microsatellite analysis were in accordance with the results revealed by mitochondrial DNA sequences and amplified fragment length polymorphism markers.

1. Introduction

The planktonic larval stage is important in the life history of many marine fishes. How far, and to what extent, larvae disperse from their natal sites remains a pressing question in conservation and fisheries biology (e.g., Christie et al., 2010). In addition, understanding the patterns of dispersal in marine environments is fundamental to the identification of fishery stocks and for the design of effective management strategies, such as marine-protected areas (Botsford et al., 2009). Larval dispersal is usually the focus of most investigations of connectivity in marine systems (Jones et al., 2009; Shanks, 2009). Many fish species, particularly large species with high economical and ecological value, are long lived and pass through several life stages (e.g., larvae, juvenile, maturing adults, and spawning adults) with different capacities for dispersal, different

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environmental preferences, and occupying entirely different trophic roles (Nakazawa et al., 2010; Berry et al., 2012). However, many marine species have restricted adult movement; therefore, their pelagic juvenile stages represent their most important dispersal mechanism (Cowen et al., 2006). Movements of pelagic stages are influenced by oceanographic processes in the marine environment, such as upwelling systems, fronts, moving convergences, eddies, and counter currents, which can lead to dispersal over hundreds of kilometers (Sponaugle et al., 2002; Palumbi, 2004). However, evidence shows that pelagic stages sometimes fail to fully achieve their dispersal potential (e.g., Liu et al., 2007), which suggests that the relationship between dispersal potential and realized gene flow among locations is complex. Assessing the influences of oceanographic factors and early life history traits in determining gene flow remains a major theme for marine research.

Sebastes schlegelii is a commercially valuable and ecologically important rockfish species found in the coastal areas of the Northwestern Pacific Ocean, especially in the Bohai Sea, Yellow Sea, and the coastal areas of Japan and the South Sea of Korea (Nakabo, 2000; Jin, 2006). Adults and the early life history stages of *S. schlegelii* constitute an important link in the transfer of energy and matter within the pelagic and benthic trophic webs, as well as in the benthopelagic coupling of the region (Rocha-Olivares and Vetter, 1999). *Sebastes schlegelii* is also important to the commercial fishing industry and to sport fishery; as a result, it is being fully exploited or even overexploited. A preliminary mitochondrial DNA (mtDNA) study (Zhang et al., 2014) and an amplified fragment length polymorphism (AFLP) study (Zhang et al., 2015) suggested that the *S. schlegelii* populations collected from Chinese and Japanese waters belonged to a single gene pool. The purpose of the present study was to estimate the levels of genetic diversity and to test for genetic structure in the northwest Pacific range of *S. schlegelii*, based on microsatellites.

2. Materials and methods

2.1. Sampling

The sample size consists of 210 individuals from 9 sites across its natural distribution, from Bohai Sea, Yellow Sea and Sea of Japan. Sampling information and sites are listed in Table 1 and Fig. 1, respectively.

2.2. Genotyping

All the individuals were screened for genetic variation at 8 microsatellite markers (Table 2). PCR products were genotyped on an AB3730 Genetic Analyzer (Applied Biosystems), with alleles scored against an internal size marker (LIZ-500) as PCR product size in base pairs, using GeneMapper v.4.0 (ABI Prism). In order to ensure accurate allele size scoring between runs, individuals with known allele sizes were used in each run as positive controls. Allelic and genotypic frequencies within samples were tested for deviations from Hardy-Weinberg outcrossing expectation within loci and for linkage equilibrium between loci using Genepop v.3.4 (Raymond and Rousset, 1995). Sequential Bonferroni corrections were used for multiple tests with $p < 0.05$ (Rice, 1989). Amplification errors, such as large allele drop out and stuttering were assessed in MICRO-CHECKER v.2.2.3 (van Oosterhout et al., 2006), while null allele frequencies were estimated in FreeNA (Chapuis and Estoup, 2007).

2.3. Statistical power

Although only microsatellite markers were scored, the number of primer combines, their frequency distributions, and the sample sizes used provide a statistical power that appeared sufficient for the primary goal of revealing population structuring. Using Powsim (Ryman and Palm, 2006), we assessed the power for detecting population differentiation for the present marker. We focused on the probability of obtaining a significant result ($P < 0.05$) in contingency tests when sampling 9 populations employing sample sizes corresponding to those from our sampling regions. The results indicate that the power of microsatellite marker is fairly high also at quite small levels of true differentiation (F_{ST}). For example, a true F_{ST} of 0.0099

Table 1
Sampling information of *Sebastes schlegelii* in the present study.

Population	Sample size	Collection date	Longitude(E)	Latitude(N)
Dalian (DL)	24	2009.03	121°38′45.94″	38°50′43.19″
Dandong (DD)	24	2009.04	124°18′24.50″	39°49′25.47″
Jiaonan (JN)	20	2009.04	120°04′38.91″	35°50′49.00″
Lianyungang (LYG)	24	2009.01	119°36′16.00″	34°42′23.06″
Qingdao (QD)	22	2009.04	120°22′48.55″	36°02′36.77″
Aomori (AM)	24	2008.06	140°46′14.20″	40°53′36.82″
Rizhao (RZ)	24	2008.12	119°35′16.12″	35°24′30.86″
Weihai (WH)	24	2009.03	122°12′17.88″	37°31′34.80″
Yantai (YT)	24	2007.01	121°29′33.44″	37°28′59.37″