Molecular Phylogeny of the Family Pomacentridae (Actinopterygii, Perciformes) Inferred from Mitochondrial 16S rDNA Sequences

Jeong Rack Koh1, 2, Ji Don Kum1 and Ui Wook Hwang1*

1Department of Biology, Teachers College, Kyungpook National University, Taegu 702-701, Korea
2Distant Water Fisheries Resources Team, National Fisheries Research and Development Institute

Received October 16, 2006; accepted November 22, 2006

ABSTRACT

Damselfish (Actinopterygii, Perciformes, Pomacentridae) are a diverse and widespread family consisting primarily of marine fish found throughout tropical oceans, and they are major members of coral reef communities. The phylogenetic relationships among the pomacentrids are highly controversial due to their dramatic and complicated morphological variations, and there are striking differences between the traditional phylogeny, which is based on morphologies, and the molecular phylogeny, which is based on DNA sequences. In the present study, the phylogenetic relationships among the pomacentrids were investigated using partial mitochondrial 16S rDNA sequences from 40 species, 19 genera, and 3 subfamilies. The partial 16S rDNAs from the four pomacentrid species (Pomacentrus coelestis, Pomacentrus bankaensis, Chromis fumea and Abudefaduf vaigiensis) were newly sequenced in this study. Bayesian analysis based on the 16S rDNA sequences reveals that the family Pomacentridae (BPP 74%) and the subfamily Amphiprioninae (99%), Dascyllus (90%), Stegastes (100%) and Abudefaduf (100%) are monophyletic groups. However, this study also shows that the subfamily Pomacentrinae may be divided into a primitive Assemblage I and an advanced Assemblage II. Pomacentrinae Assemblage II and the subfamily Amphiprioninae are grouped together (96%), and Assemblage II appears to be paraphyletic to the subfamily Amphiprioninae. Mecaenichthys immaculatus and Acanthochromis polyacanthus, which have traditionally been considered putative chromine members, appear with Chromis cyanea within Assemblage I and within Pomacentrinae Assemblage II, respectively. This study also reveals that Chromis, Amphiprion and Chrysiptera may not be monophyletic groups. These results are generally coincident with previous molecular findings. It is very likely that the traditional pomacentrid classification scheme needs to be thoroughly re-examined.

Key words: Damselfish, Pomacentridae, 16S rDNA, molecular phylogeny, Bayesian inference.
INTRODUCTION

There are only a few groups of coral reef fish that have been reported and studied to date. Damselfish (Actinopterygii, Perciformes, Pomacentridae) are one of the most famous families of coral reef fish because of their many members and wide distribution throughout the tropical oceans of the world. Most types of damselfish, which have invaded nearly every inshore habitat in tropical seas, are extremely successful from an evolutionary standpoint. While most damselfish inhabit tropical oceans, a few species permeate into freshwater. Damselfish have various colors and morphological patterns along their inhabitable areas (Allen, 1991; Baik, 1977). It is known that the family Pomacentridae consists of 340 species, at least 29 genera, and 4 subfamilies (Amphiprioninae, Chrominae, Lepidozyginae and Pomacentrinae) (Allen, 1991; Nelson, 1994). However, only 91 species in 19 genera were recorded (Masuda et al., 1984; Nakabo, 1993) in Japan, and only 13 species in 6 genera were recorded in Korea (Chyung, 1977; Kim et al., 1994a, 1994b; Koh et al., 1997; Lee and Kim, 1996).

The pomacentrid species exhibit complicated color patterns and morphological variations of the body, which vary among individuals as well as among populations within a species (Jordan and Tanaka, 1927; Kamohara, 1960; Moyer and Ida, 1976; Randall et al., 1981). Such dramatic and complicated morphological variations make it difficult to elucidate the pomacentrid phylogenetic relationships and to construct a reliable classification scheme (Allen, 1975, 1991; Jang-Liaw et al., 2002). The phylogenetic relationships among the pomacentrid members are highly controversial because striking differences exist between the traditional phylogenetic relationships, which are based on their morphologies and recently published molecular phylogenies, which are based on mitochondrial 16S rDNA and 12S rDNA sequences. Mitochondrial genes have often been used for researches to explore uncertain relationships in lower categorical levels, such as family, genus, species and even population (e.g. Ahn et al., 2006; Jung et al., 2006).

Few molecular phylogenetic studies have been conducted on the pomacentrid phylogeny thus far. For example, Tang (2001) reported 23 pomacentrid species (14 genera, 3 subfamilies) suggested the following criteria: 1) monophylies of the Pomacentridae family and subfamily Amphiprionae, and 2) the polyphyly of the Chrominae subfamily caused by the unexpected phylogenetic positioning of a member of Chrominae, Mecaenichthys and 3) the polyphyletic assemblage of the subfamily Pomacentrinae. Jang-Liaw et al. (2002) reported 48 pomacentrid species (19 genera, 3 subfamilies) and generally supported the result described by Tang (2001). More recently, Quenouille et al. (2004), with 103 pomacentrid species (18 genera, 3 subfamilies), presented big Bayesian inference trees inferred from three mitochondrial genes (ATPase8, ATPase6, cytochrome b) and from a nuclear gene (RAG1). All of the Bayesian trees inferred from the three mitochondrial genes, from RAG1, or from a combination of the data from the two showed that all three pomacentrid subfamilies should be rejected, and that the three genera, Amphiprion, Chromis and Chrysiptera, should also rejected as natural groups.

In the present study, we analyze the partial 16S rDNA sequences (ca. 500 bp) of 40 pomacentrid species (19 genera, 3 subfamilies) using Bayesian inferences to re-examine the enigmatic phylogenetic relationships of damselfish. Then we discuss the results of our study and compare them to other recent reports related to pomacentrid phylogeny.

MATERIALS AND METHODS

Sample Collection and Preservation

Among the 40 damselfish examined (Table 1), four species were newly collected from Pusan (Pomacentrus coelestis, Pomacentrus bankaensis and Abudefduf vaigiensis) and Cheju-Island (Chromis fumea), Korea in June 2003. The samples were stored in a -70°C deep freezer until the total cellular DNA was extracted. The species collected were identified according to the method described by Allen (1975, 1991), Nakabo (1993) and Nelson (1994). The measurements and counting of the samples were performed according to the method described by Randall and McCarthy (1988) and by Allen (1991).

Total Cellular DNA Extraction

The total cellular DNA was isolated from the four newly collected damselfish species. The frozen samples