



DNA barcoding of fisheries catch to reveal composition and distribution of cutlassfishes along the Taiwan coast



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ARTICLE INFO

Article history:

Received 30 May 2016

Received in revised form

15 November 2016

Accepted 21 November 2016

Handled by Prof. George A. Rose

Keywords:

Cutlassfish

Species composition

Fisheries catch

DNA barcoding

16S rDNA

Pacific

ABSTRACT

Multiple cutlassfishes share similar morphological characteristics and habitats and together contribute to substantial fisheries catch in the northwestern Pacific coast. Because information on the composition and distribution for these cutlassfishes is currently lacking, they are being managed as one species. To fill this knowledge gap, we initiated a survey of species composition and distribution for cutlassfishes at several primary landing sites along Taiwan coast (longitudes: 120–122°E, latitudes: 22.5–25°N) during 2013–2014. We conducted sampling on multiple fisheries (total N = 1305): pair trawlers (at the NE and SW coasts), stick-held dip nets (northern coast), fyke nets (NW coast), and set nets (E coast). Using the DNA barcoding methods (with mitochondrial DNA genes 16S rDNA and Cytochrome C oxidase I (COI)), we confirmed presence of four cutlassfish species in the fisheries catch: *Trichiurus japonicus*, *T. nanhaiensis*, *T. lepturus*, and *Tentoriceps cristatus*. The *T. japonicus* is a dominant species that constitutes 40–100% of catch abundance of cutlassfish throughout Taiwan coasts, while the other three species are generally in lower abundance than *T. japonicus* and display relatively confined distributions. Our findings provided advanced knowledge on composition for cutlassfishes and highlighted a need to account for differences in abundance, distribution and life histories among various cutlassfish species for management of the multispecies fisheries in the NW Pacific.

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1. Introduction

Effective management of multispecies fisheries requires setting harvesting rules based on species composition and distribution. However, such information is often overlooked for some fishes, for which the catch is combined with that of other species with similar body forms or habitats. A manifest case, the cutlassfish of the family Trichiuridae, constitutes about 40 species that inhabit tropical to temperate oceans (Nakamura and Parin, 1993). These cutlassfishes contribute upwards of 1250 kilotons per year globally, with 85% of global capture located in the NW Pacific (FAO FishStat, 2016, available at: <http://www.fao.org/fishery/species/2468/en>). The catch of these cutlassfish species has been indistinguishably and inaccurately summarized as of one single species in fisheries statistics reports. Such misreporting can potentially lead to bias in assess-

ment of stock status for these cutlassfish species (e.g., see Branch et al., 2011).

The cutlassfish fisheries rank in the top 9 coastal fisheries in Taiwan, providing 7300 ± 1700 (mean $\pm$ sd) tons of annual catch (Taiwan Fisheries Yearbook 2003–2014, Fisheries Agency, Council of Agriculture, available at: <http://www.fao.gov.tw/en/PublicationsYearbook/>). Cutlassfishes are targeted by various fisheries; e.g., distant water trawlers and coastal trawlers jointly account for $\geq 60\%$ (range: 60–68%) of total annual cutlassfish catch (Taiwan Fisheries Yearbook 2003–2014, FA). To a lesser extent, gillnets, set nets, as well as recreational fishermen also harvest cutlassfishes. Most of the cutlassfish fisheries are seasonal, with some exceptions of coastal trawlers in northeastern Taiwan, where cutlassfish are caught year round (HYW, unpublished data). Overall cutlassfish landings however, have been decreasing over recent years (Chiou et al., 2006; also Taiwan Fisheries Yearbook 2003–2014, FA, Fig. 1). Consequently, it is imperative to understand the composition and distribution of the catch of cutlassfishes, providing baseline information to enhance effective management of cutlassfish fisheries.

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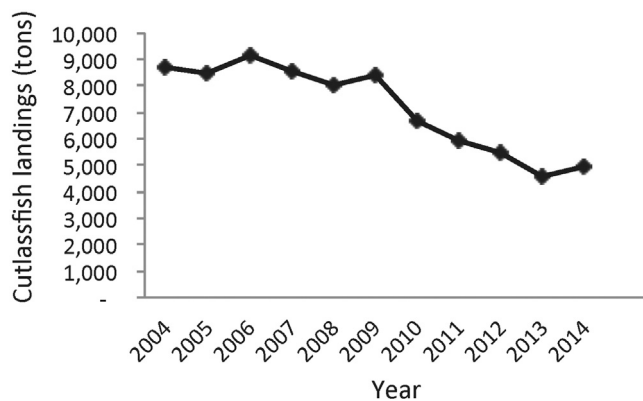


Fig. 1. Time series of landings of cutlassfish in Taiwan. Data.

Source: Taiwan Fisheries Yearbook 2003–2014, Fisheries Agency, Council of Agriculture.

Previous studies revealed presence of at least five *Trichiurus* cutlassfish species in the NW Pacific Ocean. These include two closely related species: *Trichiurus lepturus* Linnaeus, 1758, a globally-distributed species, and *T. lepturus japonicus*, first described as a subspecies of *T. lepturus* (Temminck and Schlegel, 1844), but later suggested to be independent of *T. lepturus* based on evidence from mitochondrial DNA markers Cytochrome C oxidase I, 16S rDNA, and Cytochrome B (Chakraborty and Iwatsuki, 2006; Tzeng et al., 2007; Tzeng and Chiu, 2012) and some osteological and morphometric characters (Lee et al., 1977; Tzeng et al., 2007). Nonetheless, differences in the morphometric traits between these two species are delicate and demand careful measurements and examinations (Tzeng et al., 2007). Furthermore, Wang et al. (1993) identified two new species of cutlassfishes: *T. nanhaiensis* and *T. brevis*, from the coast of China with evidence from allozyme markers. Yet another potential new species, *T. cf. nanhaiensis*, which resembles *T. nanhaiensis* in appearance, was suggested based on Cytochrome B and 16S rDNA evidence (Hsu et al., 2007). It is likely that these cutlassfishes coexist and together contribute to substantial fisheries catch in the NW Pacific.

Different cutlassfishes display variable life history patterns. For example, Shih et al. (2011) suggested that *T. japonicus* displayed higher growth rates and extended spawning seasons compared to *T. sp. 2* (which may be synonymous with *T. nanhaiensis* based on the yellowish-green dorsal fin color observed by Hsu et al., 2009) and *T. lepturus*. Differences in such life history patterns potentially indicate different sustainability under fisheries exploitation (Wang et al., 2014; Wright, 2014). Unfortunately, to date these cutlassfishes are still considered as a single-species fisheries resource, and information of among-species distributions and relative abundance is generally lacking (but see Shih et al., 2011).

DNA barcoding (Hebert et al., 2003) is a powerful method of assigning species identity based on a standardized fragment sequence of the mitochondrial gene Cytochrome C Oxidase I (COI). It has also been based on other genes and applied for situations that defy traditional morphologically-based identifications; e.g., species that share similar morphological characters (Krück et al., 2013), such as jellyfish (Prieto et al., 2013), or specimens of the larval stage (Neira and Keane, 2008; Ayala et al., 2016). DNA barcoding has proved a useful tool to ascertain species composition and diversity of wild fish populations as well as seafood products (Rach et al., 2008; Rasmussen and Morrissey, 2008; Janzen et al., 2009; Botti and Giuffra, 2010; Lin and Galland, 2010; Armani et al., 2015; Pappalardo and Ferrito, 2015; Tuuli et al., 2016). Therefore, applying such a method to identify species in fisheries catch can help provide critical information on composition and relative abundance among exploited fishes (e.g., Neira and Keane, 2008; Botti and Giuffra, 2010; Ardura et al., 2013; Tzeng and Chiu, 2012).

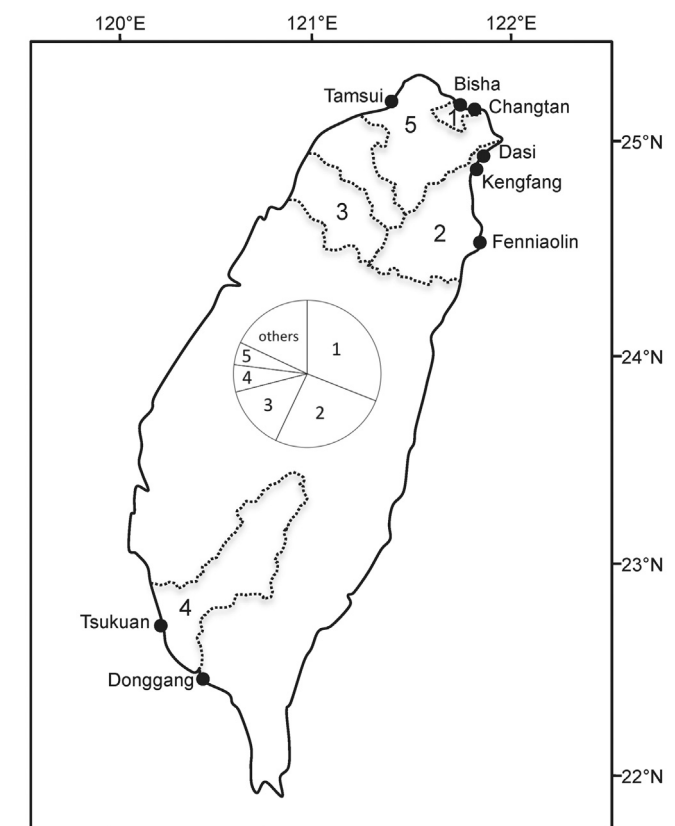


Fig. 2. Major fishing areas of cutlassfishes in Taiwan (dotted line, labelled from 1 to 5) and the sampling ports for this study as listed in Table 1. The pie chart shows the distribution of catch weight of the year from 1993 to 2014 among fishing areas.

Herein, we attempt to provide information on species distributions and relative abundance of cutlassfishes based on sampling of fisheries catch in Taiwan coasts. The objectives of our study were to explore spatial and temporal patterns in composition of cutlassfishes in the Taiwan coast based on species identity confirmed by DNA barcoding methods. Such information is critical to determining effective regulation policy for fisheries management.

2. Material and methods

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2.1. Sampling

Catch of cutlassfishes concentrated in the northern Taiwan, which comprise about 76% (range: 63–83%) of total annual cutlassfish catch in weight (Taiwan Fisheries Yearbook 2003–2014, FA, Fig. 2). According to this, we designed our sampling locations to focus on several major fishing ports in northern and southern Taiwan. In total, we collected cutlassfish specimens from eight fishing ports during 2013–2014 (Fig. 2, Table 1). These specimens represent catch by various cutlassfish fisheries during the major fishing seasons (Table 1). Landed fish were generally sorted into four size categories according to body depth: extra-large (>70 mm), large (45–70 mm), medium (25–45 mm), and small (20–25 mm). For each sampling at a port, we randomly selected 10 fish of large, medium, and small sizes, as well as some extra-large sized fish when available. Samples from Dasi and Kengfang prior to July 2013 were relatively scarce and were collected based on availability only. As these non-random samples comprise a relatively small portion

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