Assessing the effects of human selection through fishery on sea cucumber genetic structure and population dynamics

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Background

Sea cucumbers are important components in marine ecosystems and resources for coastal livelihoods. At least 66 species are fished from more than 40 countries and most of the harvests are processed, and then exported to Asian markets (Purcell et al. 2012). Sea cucumber stocks have been overfished in many countries as a result of ever-increasing market demand, uncontrolled exploitation and/or inadequate fisheries management. This situation has resulted in catch of new target species from Mediterranean Sea and Northeastern Atlantic Ocean whose fisheries are in the process of development (Aydin et al., 2011; González-Wangüemert et al. 2013a; b). Sea cucumber fishery in Turkish waters is focused mainly on *Holothuria polii, H. tubulosa* and *H. mammata* species, reaching important annual catches, around 600 000 kg in 2011.

Goals

We study the genetic and biological effects of the Turkish hookah diving fishery on these three sea cucumber target species. Our specific aims are: (i) to evaluate the status of the three species analysing the distribution of size classes of their populations from a traditional fishery area (Ayvalik) and a marine protected area (Kusadasi) and (ii) to look for genetic diversity features associated with the fishery selection.

Figure 2. a) Hookah diving vessels catching sea cucumbers; b) diver with the catches; c) Turkish women processing the sea cucumbers; d) drying sea cucumbers under sun; e) taking measures on *H. mammata*; e) *H. tubulosa*; f) *H. polii;* g) internal muscle bands; h) COI amplification.

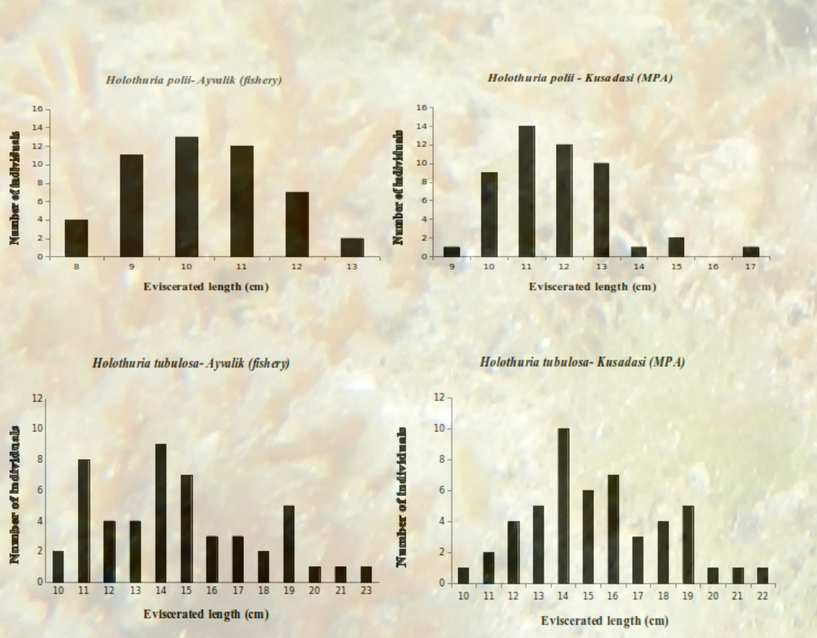


Figure 3. Length-frequency distribution of our target species (*Holothuria polii, H. tubulosa* and *H. mammata*) in Ayvalik and Kusadasi (Turkish coast).

Material and Methods

100 individuals per each species were sampled in Ayvalik and Kusadasi (Figure 1; 2a, b). The total length (EL) and gutted weight (EW) for each individual were registered (Fig 2e). For each specimen, a sample of the internal longitudinal muscle bands was taken and preserved in absolute ethanol (Fig 2h). Fragments of the mitochondrial genes cytochrome oxidase I (COI) and 16S rRNA were amplified (Fig 2i).

Results

H. polii individuals ranged in length from 8 to 13 cm in Ayvalik and from 9 to 17 cm in Kusadasi showing both localities an unimodal size-frequency distribution (Fig 3). *H. tubulosa* and *H. mammata* showed a multimodal distribution in protected and non-protected areas (Fig 3).

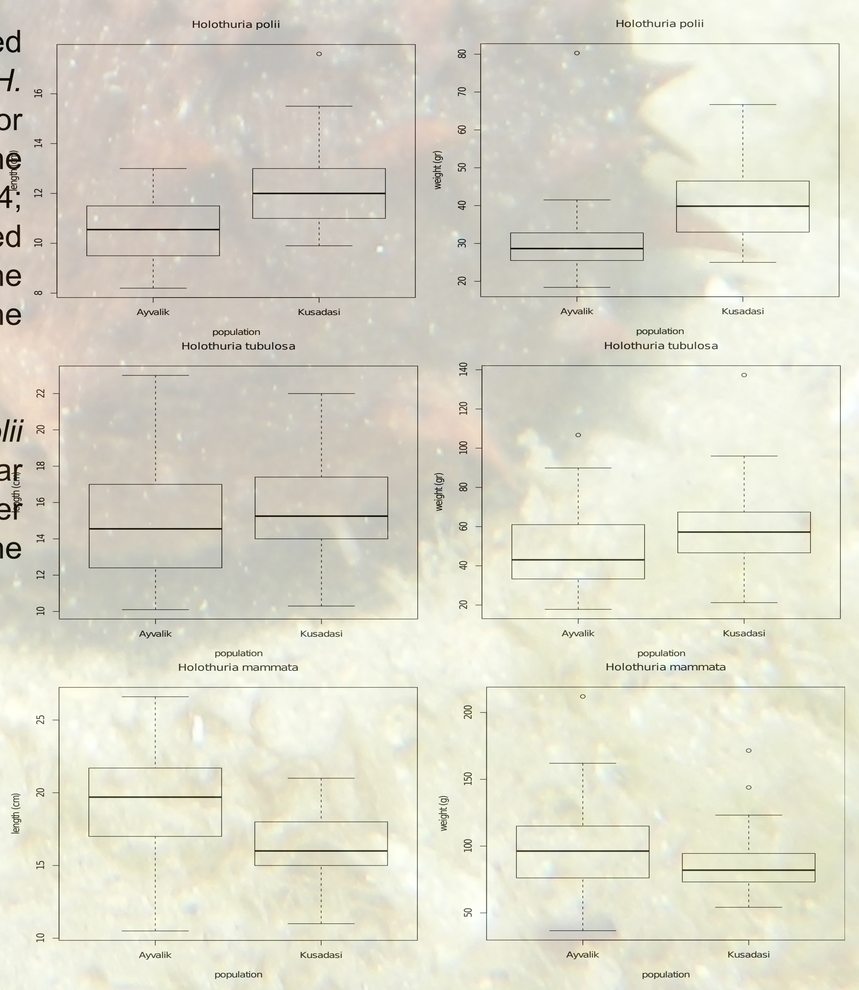
ANOVA performed on the protected and non-protected localities found significant differences for the length in *H. polii* and *H. mammata* showing the largest individuals for the first species in Kusadasi (protected area) and for the second one in Ayvalik (the non-protected area) (Fig 4; Table 1). Considering the gutted weight, ANOVA showed significant differences for the three species, being the individuals of *H. polii* and *H. tubulosa* from Kusadasi the heaviest ones.

Higher genetic diversity was observed in *H.polii* population from Kusadasi considering both molecular markers (Table 2). *H. tubulosa* also showed higher haplotype (COI) and nucleotide (16S) diversities in the protected population.

Figure 1. Sampling sites of *Holothuria polii, H. tubulosa* and *H. mammata* in Turkey. Ayvalik: fishery area; Kusadasi: protected area.

Region/Species	Localities	N	Nh (exc)	S	H	π
COI						
H. polii	Ayvalik	20	13 (6)	19	0.9105	0.0050
	Kusadasi	22	17 (10)	25	0.9697	0.0060
H. tubulosa	Ayvalik	19	13 (11)	31	0.8772	0.0151
	Kusadasi	16	12 (10)	28	0.9167	0.0104
H. mammata	Ayvalik	15	15 (14)	22	1.0000	0.0096
	Kusadasi	12	11 (10)	15	0.9848	0.0078
16S						
H. polii	Ayvalik	20	10 (6)	10	0.7105	0.0020
	Kusadasi	22	10 (6)	14	0.7489	0.0030
H. tubulosa	Ayvalik	21	10 (5)	32	0.8619	0.0095
	Kusadasi	24	8 (4)	28	0.7428	0.0103
H. mammata	Ayvalik	11	7 (5)	11	0.8909	0.0073
	Kusadasi	13	5 (3)	4	0.5385	0.0022

Table 2. Molecular diversity measures for populations of *Holothuria polii, H. tubulosa* and *H. mamata*. N, Number of individual; Nh, Number of haplotypes (exclusive); S, Polymorphic sites; H, Haplotype diversity; π, Nucleotide diversity.



Variable	Sum-of-squares	df	F- ratio	p
Length				
H. polii	60.996	1	32.182	**1.423e-07 *****
H. tubulosa	11.63	1	1.412	0.2376
H. mammata	282.83	1	30.475	**2.821e-07 *****
Weight				
H. polii	2777.3	1	31.552	**1.819e-07 *****
H. tubulosa	2737	1	7.2988	**0.008132 ****
H. mammata	2634	1	4.4293	**0.03791 ***

Table 1. ANOVA table for the variables length and weight considered in the study of the three target species.

Figure 4. Mean length and weight in the different sampled populations per each target species.

Discussion

Ayvalik is usually a target site for Turkish sea cucumber fisheries; this fact can be influencing the length and weight of its individuals because one of the main fishery effects is the frequency decreasing of the highest size classes (Purcell et al. 2012; Cariglia et al. 2013). Most of the total sea cucumbers catches in Turkey are focused on *H. polii* (80%), therefore the fishery effects could be more marked on this species. In fact, the heaviest and biggest individuals belong to the non-fishery area (Kusadasi). Some papers (Perez-Ruzafa et al., 2006; Teske et al., 2010) have described the existence of higher genetic diversity in protected populations, decreasing this in populations under heavy fishery pressure. Our results show in both genes, a higher genetic diversity in Kusadasi than Ayvalik for *H. polii*.

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