

A survey of the epibiota of *Eretmochelys imbricata* (Testudines: Cheloniidae) of Mona Island, Puerto Rico

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Abstract: Epibiotic organisms inhabiting non-nesting hawksbill sea turtles, *Eretmochelys imbricata* (Linnaeus, 1766), are described from Mona and Monito Islands, Puerto Rico. Epibiont samples from 105 turtles of shallow (< 40 m) water foraging habitats were collected and identified to the lowest possible taxon. This epibiotic assemblage consisting of at least 4 algal functional groups and 12 animal phyla represents the greatest phylogenetic diversity for marine turtle epibiota. Six groups are considered new reports for marine turtles. Most epibiont colonization was found on posterior marginal scutes and under overlapping scutes. Ecological attributes of epibiota and their symbiosis with *E. imbricata* provide a tool to understand basi and epibiont populations.

Key words: Epibiota, *Eretmochelys imbricata*, epibiont, ecology, Mona Island, Puerto Rico.

A variety of benthic organisms colonize the external surfaces of marine turtles of the Family Cheloniidae, including *Caretta caretta* (Linnaeus, 1758) (Caine 1986; Gramentz 1988; Frick *et al.* 1998), *Eretmochelys imbricata* (Dodd 1988), *Chelonia mydas* (Linnaeus, 1758) (Green 1998), *Lepidochelys olivacea* (Eschscholtz, 1829) (Díaz *et al.* 1992), and *L. kempfi* (Garman, 1880) (Márquez 1994). A diverse epibiotic community has been reported for nesting *C. caretta* (Frazier *et al.* 1985; Gramentz 1988; Frick *et al.* 1998, 2000), but few reports are available for immature and male turtles of all species. Although most epibionts seem to be commensal some turtle specific organisms such as a red alga (Senties *et al.* 1999), barnacles of the genus *Chelonibia* (Monroe & Limpus 1979), and an amphipod (Thomas 1992) have been described.

Epibiota have been proposed as a tool to understand the host's ecology (Frazier *et al.*

1992), range (Caine 1986), and movements (Eckert & Eckert 1988). Most surveys of marine turtle epibiota are conducted on nesting or stranded individuals, a situation that may bias the description of this community. Surveying non-nesting *E. imbricata* provides a better basis for understanding the epibiotic community. The objective of this survey is to describe the epibiota of non-nesting *E. imbricata*, since only one report of the algae is available (Cribb 1969).

Epibiota of *E. imbricata* captured in foraging habitats surrounding Mona and Monito Islands, Puerto Rico (18°05'N, 67°55'W) were sampled during July and August 1999. The study area is composed of coral reef and cliff wall habitats up to 40 m depths. Turtles were hand captured, measured straight carapace length (SCL), and tagged following procedures established by Van Dam and Diez (1998). Epibiota were carefully removed with a metal spatula from areas where colonization was

most developed (carapace, plastron, and skin) and were placed in separate sample vials half full of seawater. Organisms were sorted the same day they were collected with the aid of a dissection microscope. Algae were preserved directly in 10% formalin and classified into functional groups (filamentous, crustose, coralline, and foliose). Animals were placed in 70% ethyl alcohol and identified to the lowest possible taxon. The relative frequency for each taxon (functional group) was calculated by dividing the number of occurrences by the total number of turtles sampled.

One hundred and five turtles ranging between 20.0 and 85.0 cm SCL (mean 38.7 cm) were sampled. All turtles appeared to be in good health and none possessed external tumors, although two individuals were missing a hind flipper. The number of different epibiotic taxa per turtle ranged from zero to 20 (mean 9.25) and these were not damaging the hosts' tissue.

Epibiota were located most frequently on the post central scutes surrounding the posterior scute of the carapace and in spaces under overlapping scutes on the carapace. Only the caudal third of the plastron was overgrown by epibiota, mostly filamentous algae and harpacticoid copepods. Leathery surfaces (flippers, neck, tail, etc.) were colonized by filamentous algae and small cirripeds (*Platylepas* spp.). The location of the epibiotic community of *E. imbricata* at scute junctions differs from *C. caretta*, where carapace scutes are covered completely.

At least 93 different epibionts currently referred to as operational taxonomic units (OTU) were identified, including 12 animal phyla and at least four algae phyla. Frequent (> 20% occurrence) epibiota were filamentous algae, annelids, calcareous encrusting algae, barnacles, bryozoans, harpacticoid copepods, foraminiferans, coralline erect algae, sponges, amphipods, mollusks (bivalves, gastropods, and a polyplacophoran), nematodes and sipunculids. Less frequent taxa included dipterans (Family Chironomidae), tunicates, tanaids, hydrozoans, ostracods, decapods (alpheid shrimps and crabs), isopods, anthozoans (anemones and gorgonians), echinoderms (urchin and brittle stars), a fish larva (Family Atherinidae), and a flatworm.

Six taxa (foraminiferans, nematodes, sipunculids, ostracods, dipterans, and echinoderms) are new reports of marine turtle epibiota.

Algae were the most commonly occurring epibiota comprised of filamentous, calcareous encrusting, coralline erect and foliose functional groups. Filamentous algae formed short turfs under overlapping scutes and on the posterior scute of the carapace that entrapped particles forming a sandy micro-habitat suitable for meiofauna. This type of sand accumulation is rarely observed on *C. mydas* inhabiting the same foraging habitats. Smoother scutes of *C. mydas* may inhibit algae colonization and their constant swimming probably prevents sand accumulations.

This survey of *E. imbricata* reveals the most diverse epibiotic community reported for marine turtles, although this diversity is probably underestimated, due to lack of species level identifications. The host's range and habitat are probable reasons for this higher biodiversity, in contrast to *C. caretta* occupying less diverse habitats (Caine 1986; Frick *et al.* 1998). Differences in behavior among species may also influence the biodiversity of the epibiotic assemblage. For example, *E. imbricata*'s habit of wedging into crevices to feed and rest may promote the colonization of many organisms that would otherwise not be possible.

Barnacles have been reported as the most common epibiont for various cheloniids (Monroe & Limpus 1979; Gramentz 1988; Díaz *et al.* 1992; Márquez 1994). Both gooseneck and acorn forms were present on *E. imbricata*, the skin being mostly covered by *Platylepas* sp. and the carapace by *Chelonibia caretta* (Spengler, 1790). This contrasts with other reports (Caine 1986; Gramentz 1988; Frick *et al.* 1998) of carapace barnacles that identify *Ch. testudinaria* (Linnaeus, 1758) as the most common species. Additionally, *Chelonibia* spp. were rarely encountered on sub adult individuals (<65 cm SCL).

The epibiotic assemblage of small (< 25 cm SCL) turtles concurs with the known ontogenetic habitat shifts of *E. imbricata*. The lack of algae, the presence of gooseneck barnacles (*Lepas* spp.) and Columbus crabs (*Planes minutus* (Linnaeus, 1758) of three small turtles suggests that these individuals recently arrived

from a superficial pelagic habitat where *Lepas* spp. larvae are most abundant and *P. minutus* have been reported. The Sargasso Sea, which is believed to be a sea turtle nursery habitat, also hosts Columbus crabs that may be cleaning their hosts (Frick *et al.* 2000). Therefore, the analysis of epibiotic assemblages may be used as a tool for studying sea turtles if the community and its dynamics are well understood.

The relationship between epibiotic organisms and their host may seem casual, but the migrations completed by marine turtles may provide genetic or dispersion corridors for some invertebrate species such as crustaceans and tunicates that have short lived or directly developed larvae. Their dispersion ability may be enhanced by occupying the surface of a migrating turtle. This fact may warrant the revision of some marine biogeographical theories.

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RESUMEN

Los organismos epibióticos del carey de concha (*Eretmochelys imbricata*) de las islas de Mona y Monito, Puerto Rico, se describen por primera vez. Se tomaron muestras de los epibiontes de ciento cinco tortugas entre 20 y 85 cm (medida recta del caparazón). Se identificaron organismos de 12 filos animales, de los cuales seis taxones fueron nuevos hallazgos, y al menos 4 grupos funcionales de algas que representan la mayor biodiversidad filogenética de la comunidad epibiótica de cualquier especie de quelonio marino. La comunidad epibiótica se encontró más frecuentemente en la parte posterior dorsal y ventral de las tortugas y debajo de los escudos imbricados del caparazón.

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