

Assessing potential limitations when characterising the epibiota of marine megafauna: Effect of gender, sampling location, and inter-annual variation on the epibiont communities of olive ridley sea turtles



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ABSTRACT

The epibionts of marine megafauna can serve as valuable indicators of the host's health or behaviour; however, only a few studies have attempted to determine how and why epibiont communities vary between host individuals, populations, or even species. Further complicating efforts to compare epibiont communities of marine megafaunas is that measures of epibiont abundance and diversity may be influenced by the sampling methods and timing of the assessment. Here, we examined how host gender, geographic location, and sampling year affect measures of epibiont community structure in olive ridley sea turtles, *Lepidochelys olivacea*, in the East Pacific Ocean. To achieve this, we identified, enumerated, and then statistically compared the epibiont communities of (1) nesting female turtles sampled over different nesting seasons, (2) female turtles sampled on nesting beaches and at sea, and (3) female and male turtles, both sampled at sea. We did not discover statistically significant differences between the epibiont communities of nesting female turtles sampled on different years nor between females sampled on nesting beaches and at sea. However, we did observe a statistically significant difference between the epibiont communities of female and male turtles. Thus, we conclude that while sampling epibionts from nesting sea turtles may be an accurately and more logistically straight-forward method than sampling turtle at sea, it should not be assumed that epibiont communities of male and female hosts are identical. We also suggest that knowledge of the factors that drive intra-specific variation in the epibiont communities of marine megafauna, be it biological or methodological factors, is necessary before broader-scale meta-analyses are made to determine spatial and temporal patterns in the distribution of epibiont communities worldwide.

1. Introduction

The bodies of marine megafauna, including sea turtles, cetaceans, and sirenians, often serve as a colonisable substratum for epifaunal organisms or epibionts (Mignucci-Giannoni et al., 1998; Morales-Vela et al., 2008; Frick and Pfaller, 2013). Epibionts form a polyphyletic grouping, ranging from vertebrates to invertebrates (Caine, 1986; Guerrero-Ruiz and Urban, 2000) and from microscopic algae to bacteria (Aprill et al., 2014; Robinson et al., 2016a), with new epibiont species

frequently being described (Ogawa et al., 1997; Thurber et al., 2011; Majewska et al., 2015a). To characterise the diverse epibiota of marine megafauna, many studies have created annotated checklists of the epibiont taxa that have been identified from different hosts (Lazo-Wasem et al., 2011; Hayashi, 2013). However, few studies have attempted to determine how and why these epibiont communities vary between host individuals, populations, or even species (Domènech et al., 2015).

Epibiont communities tend to vary among hosts for three major

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reasons. Firstly, variation in the hosts' behaviour may expose them to different epibiont taxa. Indeed, for epibiosis to occur there must be spatial and temporal overlap between the epibiont and the basibiont at some point in their life cycles (Frick and Pfaller, 2013). In other words, the host must inhabit or traverse the specific habitat where the colonizing stage of the epibiont occurs. Animals with varying migratory strategies or foraging habitats may therefore host different epibiont communities (Casale et al., 2004; Reich et al., 2010). Similarly, some epibionts can only be transferred by direct physical contact between hosts, and so might be found only with highly social host species (Balbuena et al., 1995; Domènech et al., 2017).

Secondly, factors influencing episodic epibiont population growth and distribution alter the probability of encounter with hosts. For example, epibionts that thrive under specific oceanographic conditions, such as warmer waters, will be more prevalent when those conditions are present. In addition, many epibiont taxa, such as barnacles, have planktonic larval forms and thus depend on ocean current patterns to disperse them for a chance meeting with a suitable host. Shifts in current patterns, on short or long time scales, could also result in new host and epibiont combinations (Pascual et al., 2007).

Thirdly, hosts may differ in their suitability as a colonisable substratum. Indeed, variation in host morphology or physiology, such as the differences between adults and juveniles or between males and females, could alter the suitability for epibiont settlement and colonization. In turn, this could lead to intra-specific variation in epibiont communities. Indeed, mature male long-finned pilot whales, *Globicephala melas*, host greater abundances of the whale-louse, *Isocyamus delphini*, relative to females or juveniles of either sex (Balbuena and Raga, 1991), potentially due to differences in the morphology of the genital slit, where the epibionts tend to congregate. Differences in the texture of the skin or carapace between hosts could also lead to differential patterns of epibiont settlement, as seen in male and female horseshoe crabs *Tachypleus gigas* (Patil and Anil, 2000).

It is also important to remember that a host's suitability as a colonisable substratum may also change temporally or with the behaviour of the host. A dead or stranded host may provide a much less hospitable habitat than a living host whereas a debilitated host may offer opportunity for greater than usual levels of colonization (Sloan et al., 2014). Moreover, many epibionts are mobile and can rapidly abandon their host if needed. It has thus been hypothesised that abundance of mobile epibionts on stranded animals or, in the case of sea turtles, nesting females, would be far fewer than those on free-swimming animals (Lazo-Wasem et al., 2011). This has been born out indirectly with epibiotic crabs on sea turtles. When olive ridley turtles *Lepidochelys olivacea* were sampled at sea in the East Pacific Ocean, 42% of 181 turtles hosted

crabs (Pfaller et al., 2014). In comparison, aggregating data from three separate studies, only 3% of nesting olive ridley turtles in the eastern Pacific hosted *Planes* spp. (Lazo-Wasem et al., 2011; Majewska et al., 2015b; Robinson et al., 2016b).

Sea turtles are an ideal model species to investigate the factors influencing intra-specific variation in epibiont community structure. This is because sea turtles are arguably the marine taxa with the most diverse epibiont communities (Caine, 1986; Pfaller et al., 2008; Corrêa et al., 2014), including many epibionts that are found on a variety of other marine megafauna (Suarez-Morales et al., 2010; Zardus et al., 2014). Sea turtles are also highly mobile, with large variation between individuals both in terms of movement patterns and foraging preferences (Vander Zanden et al., 2010; Robinson et al., 2017). Thus, they are suited for examining how variation in individual behaviour can influence epibiont communities. Lastly, female sea turtles routinely nest on tropical beaches around the world. Thus, they provide a unique opportunity to examine how mobile epibionts respond to hosts that leave the water. This may not only provide insights into whether epibiont communities sampled on sea turtles in-water or on nesting beaches are comparable, but also whether the epibiont communities of stranded animals are comparable to their free-swimming counterparts.

Here, we assessed whether the epibiont communities of olive ridley sea turtles in the East Pacific differed between genders, sampling years, and geographic location. We achieved this by sampling and comparing the epibiont communities of (1) nesting female turtles sampled over different nesting seasons, (2) female turtles sampled on nesting beaches and at sea, and (3) female and male turtles, both sampled at sea. Understanding the impact of each of these factors helps assess whether short-term sampling (e.g. during a single nesting season) of epibionts from nesting sea turtles is representative of long-term epibiont communities for the entire population. More importantly, this information can also provide information about how and why epibiont communities may vary between hosts. In turn, this information can help us to understand spatial and temporal variation in epibiont communities, may reveal interesting insights into the evolutionary history of both epibiont and host, and facilitate the use of epibionts as ecological indicators.

2. Methodology

To collect epibionts, we sampled olive ridley turtles on the Pacific coast of the Guanacaste Province of Costa Rica between 2015 and 2016. Turtles were sampled from two locations: male and female turtles encountered at-sea between Playas Del Coco and Cabuyal (within 3 km of the shore) and female turtles nesting on the beaches of Parque Nacional Marino Las Baulas (Fig. 1).

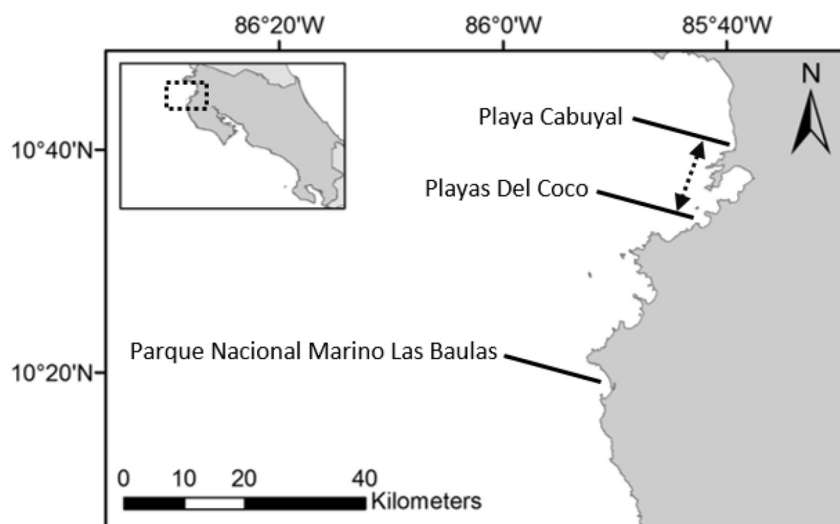


Fig. 1. Map indicating the study sites along the Pacific coast of Costa Rica, Central America. At-sea sampling of olive ridley turtles for epibionts was conducted in the waters between Playas Del Coco and Cabuyal as indicated by the dotted arrowed line. Sampling of nesting female olive ridley turtles was conducted on Cabuyal and the beaches within Parque Nacional Marino Las Baulas.

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