Spatial and temporal variation in Hawaiian green turtle somatic growth behavior

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The spatial and temporal somatic growth behaviour of green sea turtles resident in several Hawaiian foraging grounds was explored using a robust local regression modelling approach. The sampling design in this long-term mark-recapture program was mixed longitudinal and included growth records for turtles from the Hawaiian genetic stock ranging between 28 and 89 cm SCL. The expected size-specific growth rate function at all sampled foraging grounds was nonmonotonic rising from mean recruitment size (25-35 cm SCL) to maximum growth ca 52-55 cm SCL before declining to negligible growth at carapace sizes greater than 70 cm SCL that were foraging ground dependent. The expected age-specific growth functions derived by numerical differentiation showed that the juvenile growth spurt for immature greens resident in the various foraging grounds occurs from 7-15 years-at-large since recruitment with the immature developmental phase for the Hawaiian green turtle ranging from 25-50 years since recruitment from the pelagic developmental phase. Significant temporal variability in growth behaviour was also found at all sampled foraging grounds that probably reflects local population density-dependent effects and the fact that the nesting population of this stock has increased significantly since the 1980s. The juvenile growth spurt and slow size-, age- and foraging ground specific growth rates for immatures observed for the Hawaiian green sea turtle genetic stock are also growth characteristics for green sea turtles resident in southern Great Barrier Reef waters.

Hawksbill sea turtles: islands of marine biodiversity

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INTRODUCTION

As more sea turtles research is directed towards habitat utilization, we have been able to observe a variety of ecological interactions as they occur in nature. The meaning of these relationships may lead to a better understanding of the host, its habitat, and other aspects related to habitat interactions. Besides predator prey relations there are a variety of interactions within sea turtle habitat, which may include commensal, parasitic, or mutualistic relationships. The close interaction between sea turtles and epibenthic organisms may reveal a great deal about the Chelonian host and it's surroundings. Ecological information of epibiota, and their symbiosis with marine turtles may shed new light on the biogeographical and evolutionary theories of marine benthic organisms, particularly for those with short dispersal capabilities. Sea turtles may provide connectivity between epibiotic populations separated by oceanic currents or basins.

When sea turtles were numerous (Jackson et al. 2001) there was significantly more sea turtle surface area available for epibiota. This may have influenced the evolution of marine biodiversity and biogeographic patterns of epibiotic species. For example hard shelled barnacles (Family Balanidae), have been found in sea turtle fossils from the Eocene (Ross and Newman 1967). Therefore we can assume that co-evolution has been taking place for a long time and has resulted in varying degrees of symbioses among marine turtle epibiota. A few species of epibionts are reported only from sea turtles including a red alga (Hollenberg et al. 1977), an amphipod (Thomas 1992), and some barnacles (Monroe and Limpus 1979).

All species of marine turtles host a species rich epifaunal community and *Eretmochelys imbricata* (Linnaeus 1766) supports species rich aggregations due to its tropical distribution and benthic habitat utilization. The epibiota of nesting and stranded marine turtles has been used to identify the hosts' range assuming these must overlap for colonization to occur. Caine (1986) was able to differentiate two sub populations of *Caretta caretta* based on epibiotic community composition. These results are supported by mDNA findings of Bowen et al. (1996). Other analyses of epibiotic associations have revealed temporal colonization patterns of gravid *Dermochelys coriacea* related to their movements in tropical waters associated to nesting areas (Eckert and Eckert 1987, 1988). The epibionts of nesting marine turtles are the most commonly described (Senties et

al. 1999, Matsuura and Nakamura 1993, Frick et al. 1998) due to the accessibility of this stage of the host's life cycle. The organisms associated with pelagic marine turtles are as difficult to document as the 'lost years' they represent, yet some pelagic host epibionts have been described for *C. caretta* (Davenport 1994, Dellinger et al. 1997, Frick et al. 2000). Stranded and dead turtles also provide a situation for epibiont analysis which may shed light on the cause or time of death (Bugoni et al. 2001). Unfortunately it is difficult to describe the normal epibiotic community from stranded or nesting marine turtles as they may undergo desiccation or other alterations when emerged.

Epibiotic communities overgrowing adult turtles may differ from those of juvenile or non-nesting individuals and these differences probably reveal important ecological information about the host. It was my objective to describe the epibiotic community associated with non-nesting *E. imbricata* of known foraging areas of 2 different habitats. I collected samples of the epibiotic community from one hundred and five individuals captured for tagging studies (van Dam and Diez 1998) in coral reef and rocky wall habitats of Mona Island, Puerto Rico. I also include data from observations of samples collected from *E. imbricata* of Desecheo and Culebra Islands, Puerto Rico.

METHODS

Specimens of the epibiotic community growing on *E. imbricata* were classified to the lowest possible taxon. In order to minimize errors in species identification the major phylogenetic groups were pooled and the algae were classified into functional groups (filamentous, calcareous erect, calcareous encrusting, and foliose).

To depict habitat associations of epibiotic taxa I assumed that the host turtles remain within a $1\ km^2$ home range, and therefore occupy the same general habitat throughout their developmental life stage (van Dam and Diez 1998, León and Diez 1999). This may lead to an epibiotic community structure specific of each habitat, similar to the hypothesis that recruitment plates reflect habitat. In order to detect habitat association of epibiota, the presence and absence of each epibiotic taxon was compared among two habitats; coral reef and rocky wall, by Chi squared contingency tables.

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