BACTERIAL VARIABILITY AMONG INDIVIDUAL PENAeid SHRIMP DIGESTIVE TRACTS

BY

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INTRODUCTION

Many herbivorous animals possess a host of internal bacteria. These bacteria often produce a complement of enzymes for digestion of plant foods and can synthesize compounds that are assimilated by the animal (reviewed by McBee, 1971; Hungate, 1975). An analogous type of symbiotic relationship has long been documented in ungulate herbivores (Hungate, 1975), and is also
present in many terrestrial invertebrates such as termites (e.g. Eutick et al., 1978; Schultz & Breznak, 1978).

Bacterial flora that assist in digestion and absorption of food in terrestrial invertebrates and vertebrates are now beginning to be characterized in marine invertebrates. This gut flora is believed to increase the digestive efficiency of invertebrates such as sea urchins, with a voluminous gut (Lasker & Giese, 1954; Fong & Mann, 1980). A similar symbiotic bacterial flora has been studied in crustaceans such as copepods, with a short, basically straight gut (Sochard et al., 1979). An analogous relationship could also be taking place in juvenile penaeid shrimp, which feed heavily on and assimilate plant material, especially epiphytic algae in seagrass meadows (Kitting et al., 1984). Large numbers of bacteria are capable of degrading many algal polysaccharides and other carbohydrates (Lasker & Giese, 1954; Prim & Lawrence, 1975; Dempsey & Kitting, 1987) and may play a significant role in digestion in the gut of shrimp (Dempsey & Kitting, 1987).

Previous papers on basic bacteriology of various shrimp deal with total heterotrophic bacteria pooled for the entire animal, or for “deheaded” animals (Green, 1949; Campbell & Williams, 1952; Cobb, 1973; Vanderzant et al., 1973; Alvarez, 1983). Few papers deal with the intestinal tract by itself (Williams et al., 1952b; Hood et al., 1977) and essentially no detailed quantitative data are available. These digestive tract bacteria may prove to be beneficial to common marine invertebrates such as penaeid shrimp, and are enumerated and identified in this paper. Variability from different individuals from different habitats is assessed in order to seek sources of such variable bacterial densities characteristic of these animals.

MATERIAL AND METHODS

Sampling procedures. — Brown shrimp (Penaeus aztecus Ives, 1891) and white shrimp (P. setiferus (L., 1767)) were collected from June to October, 1983, in seagrass meadows and open bays around Port Aransas, Texas, U.S.A. The open-bay shrimp were collected during 10-minute trawls. Individuals from seagrass meadows were collected with a push net or a seine. In both cases the animals were transported on ice to the laboratory, in individual sterile vials containing 0.45 μm filtered seawater, and were sampled within 2 h of capture. The 0.45 μm filtered seawater was used to reduce contamination to only the few “filterable bacteria” that would be sampled as colony-forming units on culture plates (Watson et al., 1977; Harvey & Young, 1980).

Sample preparation. — Only live animals were used to avoid a post-mortem bacterial shift. Wet weight and body length were recorded for each animal to detect relationships between bacterial number or composition and shrimp size. External bacteria were sampled within 2 hours of collection while the animals