

**Sponges and the Spatial Epidemiology of *Panulirus argus* Virus 1 (PaV1)
in Caribbean Spiny Lobsters Throughout the Florida Keys**

**Esponjas y La Epidemiología Espacial de *Panulirus argus* Virus 1 (PaV1)
en Langostas del Caribe a lo Largo de los Cayos de Florida**

**Éponges et L'épidémiologie Spatiale de Argus *Panulirus argus* Virus 1 (PAV1)
dans Langoustes des Caraïbes à travers les Keys de Floride**

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EXTENDED ABSTRACT

The Caribbean spiny lobster supports the highest valued marine fishery in the Caribbean where annual landings exceed \$1 billion. While spiny lobsters represent an important fishery, the effects of *Panulirus argus* Virus 1 (PaV1) on their populations and the fishery remain unknown. This pathogen is found throughout the Caribbean region and the Florida Keys (USA) where it is most lethal for juvenile lobsters in hard-bottom nursery habitats. However, PaV1 exhibits variability in prevalence across habitats of different type, community composition, and structural complexity. Prior work has shown that early benthic juvenile (EBJ) lobsters contract PaV1 in the hard-bottom areas of Florida Bay, but not in seagrass beds (Behringer and Butler, *unpub. data*). Sponges, organisms that oftentimes dominate hard-bottom habitat, provide shelter for sympatric lobsters. Since lobsters tend to shelter in and around sponges, sponges may play a role in the dispersal and transmission of PaV1.

The objective of the present study was to determine whether differences in PaV1 prevalence are correlated with habitat characteristics, specifically those associated with sponges. To identify the drivers of variability in PaV1 prevalence, we compared the abundance, diversity, and structural complexity of sponge communities with the prevalence of PaV1 throughout the Florida Keys. We hypothesized that areas with a relatively high density or diversity of sponges yield a greater prevalence of PaV1. To test this hypothesis, we performed a series of video belt transects in parallel with lobster population surveys to characterize the benthos at each sampling site and to measure the corresponding prevalence of PaV1. Videos were subsequently analyzed for describing sponge communities at each location. To determine disease prevalence, hemolymph or leg tissue samples from lobsters that had been previously collected by SCUBA divers were processed using a real-time quantitative polymerase chain reaction assay (Clark et al., in prep.). Using correlational and spatial statistics, we then compared PaV1 prevalence and the above sponge parameters.

Preliminary results indicate that there was no correlation between PaV1 prevalence, and sponge density or diversity. The mean density of newly-recruited sponges (< 20 cm in diameter) and larger, shelter-forming sponges (> 20 cm in diameter) were poorly associated with PaV1 prevalence at corresponding locations. Similar trends were observed when comparing the prevalence of PaV1 with the density of three common sponge species: loggerhead (*Spherospongia vesparium*), vase (*Ircinia campana*), and brown branching (*Ircinia* sp.). The density of these sponge species exhibited a weak relationship with the prevalence of this virus. While our initial findings did not support our hypothesis, we are currently investigating other habitat features (e.g., percentage of seagrass cover, abundance of corals, etc.) and how they may relate to PaV1 prevalence. Likewise, we will be employing additional tools for examining the spatial distribution of sponges. For example, methods described by Easson et al. (2013) will be implemented to identify clusters among and between sponge species using the following spatial statistics: Ripley's K function, Getis-Ord General G, and Moran's Index. Furthermore, we will examine the Florida Keys at the landscape level to determine oceanographic or geographic barriers potentially influencing the transmission of PaV1.

The spatial epidemiology of PaV1 across the Florida Keys has not been extensively researched thus making the present study an important and necessary one. While the mean prevalence of PaV1 in the Florida Keys was $63 \pm 0.25\%$ (standard error of the mean; $n = 20$), some areas had between 90 and 100% prevalence. Recent screening efforts revealed that many postlarval lobsters settled in the Florida Keys as healthy individuals (Clark and Behringer, *unpub. data*). It then stands to reason that lobsters are contracting the virus upon or after arrival into the Florida Keys, where PaV1 prevalence exceeded 40% in past years (Behringer et al., 2011). Therefore, habitat characteristics and complexity may facilitate the transmission of PaV1 on a local scale. Since sponges are not correlated with PaV1, we are currently examining other features of the habitat and environment that potentially drive variability in PaV1 prevalence. Determining a relationship between habitat heterogeneity and PaV1 prevalence would provide a powerful tool for predicting and ultimately managing disease "hotspots" in the marine environment.

KEYWORDS: Lobster, *Panulirus argus*, spatial epidemiology, disease, sponge

LITERATURE CITED

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