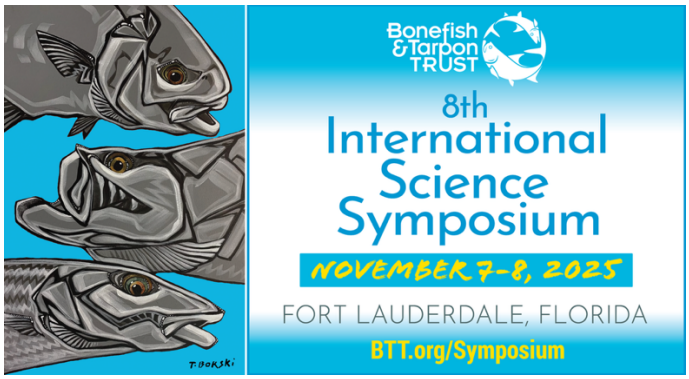


Assessing Genetic Connectivity of Permit (Trachinotus falcatus) Between South Florida and Belize

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Understanding population structure and connectivity is essential for effective fisheries management, particularly for wide-ranging marine species like Permit (*Trachinotus falcatus*). We investigated the genetic structure and diversity of Permit at ecologically important locations (e.g., nursery habitats and spawning sites) in South Florida and Southern Belize using mitochondrial DNA. A total of 401 Permit (n = 318 Florida, 83 Belize) revealed 18 unique DNA sequences (haplotypes), with one dominant haplotype (H1) present in over 80% of individuals across all sites. Genetic diversity was low, and AMOVA results indicated that >99% of genetic variation is described by variation among individuals of the same site groups, implying high population connectivity. Pairwise F_{ST} values showed no significant genetic differentiation among Florida locations, as well as no differentiation between South Florida and Belize. These results support high population connectivity in South Florida and between South Florida and Belize, suggesting extensive larval dispersal. Connectivity is likely facilitated by regional ocean currents, with Belize potentially serving as a larval source for Florida. While high population connectivity may buffer against localized demographic declines, low genetic diversity and ongoing threats (e.g., habitat degradation, shark depredation, and fishing pressure) underscore the need for continued monitoring and protection of critical spawning sites, such as the seasonally closed Western Dry Rocks Marine Protected Area, offshore of Key West, Florida.