Genetic structure and dispersal capabilities of dolphinfish (Coryphaena hippurus) in the western central Atlantic

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The combination of tagging and genetic approaches (e.g., DNA sequencing and microsatellite analyses) has led to significant improvements in characterizing the stock and population structure of marine pelagic fishes, in interpreting biomass dynamic models, in generating stock-recruitment curves, and in conducting cohort analyses (Graves, 1998; Reiss et al., 2009). Specifically, tag and genetic data can be used to estimate regional biomass exchange and define stocks demographically; this information is useful in the stock assessment process (Waples et al., 2008). Alternatively, tag or genetic data have allowed scientists to refine assessment models and facilitate a more precise allocation of management effort. Therefore, this combination of approaches provides more realistic estimates of immigration, emigration, mortality (natural and anthropogenic), and the extent of population mixing, all of which are informative in assessment models (Hilborn and Walters, 1992).

The results of these models provide fishery managers with information necessary to adjust fishing effort, set size limits and quotas, identify seasonal hot spots and essential fish habitat (e.g., Sargassum), and protect spawning stocks to safeguard recruitment and future landings (Alldendorf et al., 1987), although the applicability of management measures can vary depending on effective population size (i.e., small versus large). Nevertheless, tag and genetic data are increasingly used to manage highly migratory fish stocks because they provide better estimates of spatiotemporal population differentiation and effective population sizes (Hauser and Carvalho, 2008).