


Themed Issue on Ecology and Management of Snook *Centropomus* spp. in the Americas

Population structure of the Common Snook: Evidence of genetic isolation in the Gulf of Mexico and connectivity across the western Atlantic

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ABSTRACT

Objective: The Common Snook *Centropomus undecimalis* is a species widely distributed throughout the western Atlantic, playing a key ecological role in coastal and estuarine ecosystems. Despite its broad distribution from Florida to southeastern Brazil, little is known about the genetic patterns underlying its population connectivity. This study aimed to characterize the genetic structure of this species and to infer patterns of genetic diversity and connectivity across its range.

Methods: A total of 100 individuals collected from Florida to southeastern Brazil were genotyped at 11 microsatellite loci. Genetic structure was assessed using Bayesian clustering analysis, discriminant analysis of principal components, and analysis of molecular variance. Genetic differentiation among populations was estimated by pairwise F_{ST} , and recent gene flow was inferred from migration proportions among the identified genetic profiles.

Results: Three distinct genetic profiles were identified: one exclusive to the southern Gulf of Mexico (Gulf Profile) and two along the Atlantic coast (Northern and Southern profiles), both contributing to a central mixed zone in northern South America. Analysis of molecular variance revealed greater variation within populations (68.8%). When admixed individuals (<80% assignment) were excluded, the variation among groups increased to 27.2%, while within-group variation remained high (68.4%). The Gulf Profile showed strong differentiation from the others ($F_{ST} = 0.33-0.39$), whereas differentiation between the Northern and Southern profiles was lower but significant ($F_{ST} = 0.038$). Recent migration analysis indicated high genetic self-recruitment within each profile (68–99%) and limited gene flow among them, except for significant migration from the Southern Profile to the Northern Profile (migration rate = 0.301). Genetic diversity was high across all profiles, with greater allelic richness and heterozygosity in the Gulf Profile and lower values in the Southern Profile; 90 private alleles were identified, most of them in the Gulf Profile.

Conclusions: The Common Snook exhibits an isolated stock in the southern Gulf of Mexico, likely maintained by historical processes and local oceanographic dynamics, such as the Loop Current and cyclonic vortices. Along the Atlantic coast, two distinct genetic profiles (Northern and Southern) are connected by a transitional zone in northern South America characterized by extensive genetic admixture. Atlantic connectivity appears to be facilitated by ocean currents and the species' broad ecological plasticity, including tolerance to salinity variation and diadromous migrations. These findings provide valuable insights for conservation and fisheries management strategies throughout the distributional range of this species.

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RESUMO

Objetivo: O Robalo Flexa *Centropomus undecimalis* é uma espécie amplamente distribuída ao longo do Atlântico ocidental, desempenhando um papel ecológico fundamental nos ecossistemas costeiros e estuarinos. Apesar de sua ampla distribuição do estado da Flórida até o sudeste do Brasil, pouco se sabe sobre os padrões genéticos que sustentam a conectividade entre suas populações. Este estudo teve como objetivo caracterizar a estrutura genética desta espécie e inferir padrões de diversidade genética e conectividade ao longo de sua área de ocorrência.

Métodos: Um total de 100 indivíduos, coletados desde a Flórida até o sudeste do Brasil, foi genotipado para 11 loci microssatélites. A estrutura genética foi avaliada por meio de análise de agrupamento Bayesiana, análise discriminante de componentes principais e análise de variância molecular. A diferenciação genética entre populações foi estimada pelos valores de F_{ST} par a par, e o fluxo gênico recente foi inferido a partir das proporções de migração entre os perfis genéticos identificados.

Resultados: Três perfis genéticos distintos foram identificados: um exclusivo do sul do Golfo do México (Perfil Golfo) e dois ao longo da costa Atlântica (perfis Norte e Sul), ambos contribuindo para uma zona de mistura ao norte da América do Sul. A análise de variância molecular revelou maior variação dentro das populações (68.8%). Quando os indivíduos de contribuição genética misturada (<80% de atribuição) foram excluídos, a variação entre grupos aumentou para 27.2%, enquanto a variação dentro dos grupos permaneceu alta (68.4%). O Perfil Golfo apresentou forte diferenciação em relação aos demais ($F_{ST}=0.33-0.39$), enquanto a diferenciação entre os perfis Norte e Sul foi menor, mas significativa ($F_{ST}=0.038$). A análise de migração recente indicou elevado autorecruzamento genético dentro de cada perfil (68–99%) e fluxo gênico limitado entre eles, exceto por migração significativa do Perfil Sul para o Perfil Norte ($m=0.301$). A diversidade genética foi alta em todos os perfis, com maior riqueza alélica e heterozigiosidade no Perfil Golfo e valores menores no Perfil Sul; 90 alelos privados foram identificados, a maioria no Perfil Golfo.

Conclusões: O Robalo Flexa apresenta um estoque isolado no sul do Golfo do México, provavelmente mantido por processos históricos e dinâmicas oceanográficas locais, como a Corrente de Loop e vórtices ciclônicos. Ao longo da costa Atlântica, dois perfis genéticos distintos (Norte e Sul) estão conectados por uma zona de transição no norte da América do Sul, caracterizada por ampla mistura genética. A conectividade Atlântica parece ser facilitada pelas correntes oceânicas e pela ampla plasticidade ecológica da espécie, incluindo tolerância à variação de salinidade e migrações diádromas. Esses resultados fornecem informações valiosas para estratégias de conservação e manejo pesqueiro em toda a área de distribuição desta espécie.

KEYWORDS: Atlantic coast of the Americas, Centropomidae, gene flow, genetic diversity, marine connectivity, microsatellite markers, oceanographic barriers

LAY SUMMARY

We identified an isolated Common Snook stock in the Gulf of Mexico and two connected Atlantic lineages, revealing population structure, gene flow, and a genetic mixing zone. These findings may guide effective management.

INTRODUCTION

The genus *Centropomus* comprises 13 species of neotropical fishes distributed along the Atlantic and Pacific coasts of the Americas (Carvalho-Filho et al., 2019). Of these, seven species occur in the western Atlantic, including the Common Snook *Centropomus undecimalis*. Due to its high commercial value (Ley & Allen, 2013), this species is intensively exploited by both artisanal and recreational fisheries (Lowerre-Barbieri et al., 2014). In addition, it exhibits zootechnical traits of considerable relevance for marine aquaculture (Costa Filho et al., 2013).

The Common Snook is a euryhaline and diadromous species (Rivas, 1986) capable of tolerating wide salinity fluctuations and migrating between marine and freshwater environments, both for feeding and reproduction (Pereira et al., 2020; Trotter et al., 2012). This species exhibits substantial ecological plasticity (Tringali et al., 1999), allowing it to utilize and colonize a broad range of coastal habitats (Trotter et al., 2021). However, its survival and reproductive success are severely impaired at temperatures below 12.5°C (Adams et al., 2012). Juvenile Common Snook typically inhabit shallow, slow-moving waters, such as brackish channels and saline lagoons that function as coastal nurseries (Stevens et al., 2021; Trotter et al., 2021), whereas adults predominantly occupy deeper coastal areas with higher salinity (Pereira et al., 2020).

The reproductive cycle of the Common Snook is closely tied to its seasonal migratory behavior (Lowerre-Barbieri et al., 2014; Trotter et al., 2021). Upon reaching sexual maturity, adults migrate to high-salinity coastal areas to spawn (Lowerre-Barbieri et al., 2014), as their gametes require elevated salinity levels for successful development and dispersal (Trotter et al., 2012). Fertilization is external, and both spawning activity and reproductive success are strongly influenced by the physicochemical properties of the water (Perera-García et al., 2011), particularly temperature and photoperiod, which vary throughout the species' geographic range.

The Common Snook is distributed from North Carolina, United States, through the Gulf of Mexico (hereafter, "Gulf") and the Antillean archipelago, extending south to Rio de Janeiro, Brazil (de Figueiredo-Filho et al., 2021), with occasional records as far south as the state of Rio Grande do Sul (Nascimento et al., 2022). Among western Atlantic centropomids, the Common Snook has the widest geographic range (Rivas, 1986) and is also the most extensively studied species within the genus.

Most genetic studies on the Common Snook have focused on populations in the Northern Hemisphere and have consistently reported high levels of genetic diversity in the sampled areas. Research conducted on the Florida peninsula (Tringali & Bert,

1996; Tringali et al., 2008) revealed pronounced population structure, with significant genetic differentiation between Gulf and Atlantic stocks. In the northwestern Gulf (Texas), Anderson et al. (2020) reported a single panmictic population. Hernández-Vidal et al. (2014) detected no evidence of population substructure in the southern Gulf, suggesting high gene flow between the Tabasco coast and the San Pedro River basin. However, a more recent study by Terán-Martínez et al. (2021) identified two distinct genetic clusters within the same region, specifically in the Usumacinta River basin of Mexico.

In the southwestern Atlantic, genetic studies of Common Snook remain limited and have been primarily focused on the Brazilian coastline. These studies revealed extensive gene flow spanning more than 3,800 km from Pará to Rio de Janeiro (Malcher et al., 2023). Mitochondrial DNA analyses further indicate transatlantic haplotype sharing between Brazil and Puerto Rico (de Oliveira et al., 2014). Historical demographic reconstructions suggest a population expansion during the Late Pleistocene, approximately 20,000 years ago, which temporally coincided with the regional proliferation of mangrove ecosystems (Malcher et al., 2023).

Despite these localized population assessments, no study has comprehensively examined the full geographic distribution of Common Snook. As a result, large-scale population structure and genetic diversity across the species' range remain poorly understood. Several major biogeographic barriers are present throughout its distribution, including the Amazon–Orinoco River freshwater plume (Araujo et al., 2022; Tosetto et al., 2022), contrasting oceanic current systems (Luiz et al., 2012; Rocha et al., 2005), and pronounced thermal and salinity gradients (Briggs & Bowen, 2013). These barriers have played a critical role in shaping the evolutionary history of *Centropomus* (Malcher et al., 2023) and are known to drive diversification and population structure in marine and estuarine fishes of the western Atlantic by limiting gene flow and promoting adaptive divergence (Piñeros & Gutiérrez-Rodríguez, 2017; Rocha et al., 2008; Rodrigues-Filho et al., 2023).

Accordingly, this study aimed to characterize the population genetic structure of the Common Snook across its distribution and to infer patterns of contemporary genetic connectivity and diversity.

METHODS

Study area and sample collection

This study analyzed biological material from 100 specimens of Common Snook collected across 13 locations throughout the western Atlantic. Sampling covered both the Atlantic and Gulf coasts of the Florida peninsula (United States); the coasts of Veracruz, Campeche, and Quintana Roo (Mexico); Limón (Costa Rica); Cartagena de Indias (Colombia); Miranda and Nueva Esparta (Venezuela); and the Brazilian states of Pará, Ceará, Rio Grande do Norte, Espírito Santo, and Rio de Janeiro. Specimens were obtained through field expeditions, from artisanal fisheries, and/or via scientific collections. Detailed information regarding sample provenance is provided in [Supplementary Table 1](#) (see online [Supplementary Material](#)).

Biological tissues were preserved in 95% ethanol and are currently housed in the collections of the Laboratory of Genetics

and Conservation at the Institute of Coastal Studies, Federal University of Pará, Bragança, Brazil; the Florida Museum of Natural History, Florida, United States; the Faculty of Biology at Universidad Michoacana de San Nicolás de Hidalgo, Morelia, Mexico; the Zoological Museum of the University of Costa Rica (UCR), San José, Costa Rica; the Institute of Biology at Universidad Nacional Autónoma de México, Mexico City, Mexico; and the Department of Biodiversity Conservation at El Colegio de la Frontera Sur, Chiapas, Mexico.

Laboratory procedures

Genomic DNA was extracted using the Wizard Genomic DNA Purification Kit (Promega) following the manufacturer's protocol. The DNA quality was assessed by 1% agarose gel electrophoresis, and concentrations were quantified using a NanoDrop 2000 spectrophotometer (Thermo Scientific). Eleven microsatellite loci (*Cun01*, *Cun03*, *Cun05B*, *Cun08*, *Cun09*, *Cun11*, *Cun14*, *Cun16*, *Cun18*, *Cun19*, and *Cun22*), which were previously developed by Seyoum et al. (2005), were amplified. Forward primers were labeled with an M13 tail following the protocol described by Schuelke (2000).

Polymerase chain reaction amplifications were performed in a final volume of 13 μ L, containing 2 μ L of dNTPs (1.25 mM); 1.3 μ L of 10 \times PCR buffer (200-mM tris-HCl, pH 8.4; 500-mM KCl); 1.5 μ L of MgCl₂ (50 mM); 0.1 μ L of *Taq* DNA polymerase (5 U/ μ L; Invitrogen); 0.5 μ L each of the forward primer, reverse primer, and M13 tail (200 ng/ μ L); and 1 μ L of genomic DNA (~50 ng/ μ L). The final volume was adjusted with nuclease-free water. Thermal cycling conditions consisted of an initial denaturation at 94°C for 5 min; 30 cycles of denaturation at 94°C for 30 s, annealing at 63°C for 45 s, and extension at 72°C for 45 s; eight additional cycles with an annealing temperature of 53°C; and a final extension at 72°C for 10 min. The PCR products were visualized by electrophoresis on 1.5% agarose gels and subsequently genotyped using an ABI 3500XL genetic analyzer (Applied Biosystems) with the ET-ROX-500 size standard (Applied Biosystems).

Data analyses

Alleles were scored using GeneMapper (Applied Biosystems) and exported to Microsoft Excel for further analyses. The program FreeNA (Chapuis & Estoup, 2007) was used to detect and estimate null allele frequencies (r). Deviations from Hardy–Weinberg equilibrium (HWE) and linkage disequilibrium were assessed using Arlequin version 3.5.2.2 (Excoffier & Lischer, 2010) and GENEPOP version 4.2 (Rousset, 2008) based on the Markov chain approach with 10,000 permutations and a significance level α of 0.05. A Bonferroni correction for multiple comparisons was subsequently applied.

The number of genetic clusters (K) across the species' range was estimated using STRUCTURE version 2.3.4 (Pritchard et al., 2000). We used an admixture model with correlated allele frequencies and a burn-in of 50,000 iterations followed by 1 million Markov chain–Monte Carlo (MCMC) iterations, without incorporating population location as a prior (LOCPRIOR model). We simulated population values from $K=1$ to $K=13$, with 10 independent runs for each value of K . To determine the most likely number of genetic clusters, we used the ΔK method described by Evanno et al. (2005),

as implemented in StructureSelector (Li & Liu, 2018). The alignment of membership coefficients across the 10 replicates for each K was performed using CLUMPP version 1.1.2 (Jakobsson & Rosenberg, 2007), with graphical visualizations generated using StructuRly (Criscuolo & Angelini, 2020). At the most likely value of K , membership coefficients were obtained from the STRUCTURE output matrices, representing the average probability of assigning individuals from each locality to one of the genetic clusters ($K=3$; Supplementary Table 2).

Population structure was assessed using discriminant analysis of principal components (DAPC), which was implemented in the adegenet package (Jombart et al., 2010) within the R statistical environment (R Core Team, 2015). This method combines an initial principal components analysis step, which ensures uncorrelated variables, with a subsequent discriminant analysis (Jombart & Collins, 2015), maximizing separation among groups. Prior to the DAPC, individuals were grouped using K -means clustering implemented in the “find.clusters” function of the adegenet package. The optimal number of clusters (K) was determined using the Bayesian information criterion (BIC), with the lowest BIC value selected as indicating the most likely structure. The number of retained principal components was defined through cross validation, ensuring robustness and consistency in the inference of genetic structure.

The distribution of genetic variability was assessed through analysis of molecular variance, performed with 1,000 permutations in Arlequin version 3.5.2.2 (Excoffier & Lischer, 2010), considering the groupings defined by STRUCTURE analysis and DAPC. Genetic differentiation among profiles was quantified using pairwise genetic differentiation index F_{ST} estimates between all genetic clusters.

Recent migration rates were estimated using a Bayesian framework implemented in BayesAss version 3.1 (Wilson & Rannala, 2003). Convergence was achieved after 3 million MCMC iterations, with delta values adjusted to 0.15 for allele frequencies (p), migration rates (m), and inbreeding coefficients (f), resulting in acceptance rates within the recommended range (40–60%). Final analyses were performed using 50 million MCMC iterations, with sampling every 1,000 iterations and a burn-in period of 10 million iterations.

Genetic diversity parameters were quantified for the identified genetic profiles. Allelic counts were obtained using Genepop version 4.2 (Rousset, 2008), observed heterozygosity (H_o) and expected heterozygosity (H_e) were calculated per locus in Arlequin version 3.5.2.2 (Excoffier & Lischer, 2010), and deviations from HWE were assessed using a Markov chain algorithm with 10,000 permutations ($\alpha=0.05$). Allelic richness (R_a) and private allelic richness ($P-R_a$) were estimated with HP-Rare (Kalinowski, 2005) using allele rarefaction and hierarchical resampling to correct for unequal sample sizes among populations.

RESULTS

Estimates of null allele frequencies r , obtained with FreeNA, were consistently low ($r < 0.10$), providing no evidence for

the presence of null alleles. Considering all pairs of loci, most showed conformity with HWE across the analyzed populations, although four markers (*Cun01*, *Cun09*, *Cun18*, and *Cun22*) exhibited significant deviations. No evidence of linkage disequilibrium was found after Bonferroni correction. Since these deviations were neither extensive nor consistent among loci and populations, all markers were retained for subsequent analyses (detailed in Supplementary Table 1).

Genetic structure

Bayesian clustering analysis revealed three clusters ($K=3$) across the sampled range, as illustrated in Figure 1, defining three distinct genetic profiles (Supplementary Plot 1 [see online Supplementary Material]). One cluster (represented in green in Figure 1) is restricted to the Gulf and strongly characterizes all individuals from Veracruz and Campeche in the southern Gulf. The remaining two clusters (represented in blue and orange in Figure 1) occur along the Atlantic coast, each predominating at opposite extremes of the species' range (additional information on the composition of these profiles is provided in Supplementary Figure 1 [see online Supplementary Material]).

The average ancestry proportions per locality (Supplementary Table 2) delineate the population profiles of the Common Snook: the Gulf Profile, composed of the green cluster and exclusive to localities in the southern Gulf; the Northern Profile, dominated by the blue cluster (≥ 0.64) and extending from Florida to Colombia; and the Southern Profile, enriched in the orange cluster (≥ 0.54) and spanning from Venezuela to southeastern Brazil. Notably, although assigned to different profiles, samples from Cartagena de Indias (Colombia) and Miranda/Nueva Esparta (Venezuela) exhibited similar proportions of the blue and orange clusters, evidencing a transitional zone characterized by substantial genetic admixture (Figure 1). The DAPC, guided by the lowest BIC value, independently corroborated this tripartite genetic structure (Figure 2).

The analysis of molecular variance, considering all individuals within the three identified genetic profiles, showed that most of the variation occurred within populations (68.8% of the total variation; $\Phi_{ST}=0.31$), followed by variation among groups (24.7%; $\Phi_{CT}=0.24$) and among populations within groups (6.5%; $\Phi_{SC}=0.08$). When all admixed individuals were removed from the analysis, retaining only specimens with more than 80% assignment to a single profile (see Supplementary Table 1), the proportion of variation among groups increased to 27.2% ($\Phi_{CT}=0.27$), while variation within populations remained high (68.4%; $\Phi_{ST}=0.31$). All values were statistically significant ($P < 0.05$; Supplementary Table 3). Pairwise F_{ST} values indicated strong differentiation between the Gulf Profile and the other profiles, with F_{ST} of 0.33 relative to the Northern Profile and 0.39 relative to the Southern Profile, whereas differentiation between the Northern and Southern profiles was lower ($F_{ST}=0.038$) though still significant (Table 1).

Recent migration rates

Based on the identified genetic profiles, recent migration estimates revealed high levels of self-recruitment, particularly

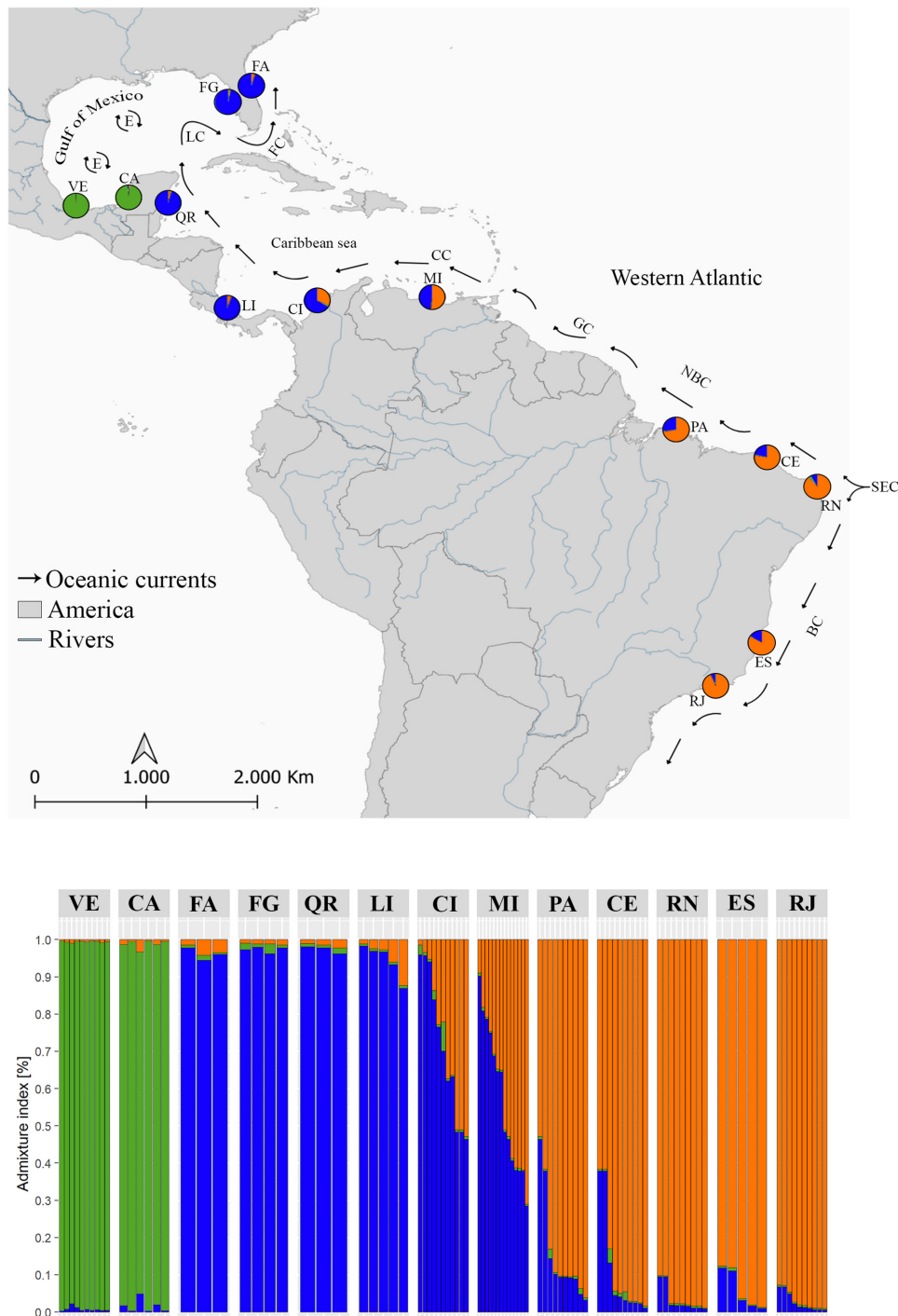


Figure 1. Geographic distribution of Common Snook samples analyzed, showing the proportions of the identified genetic profiles (top panel) and the composition of genetic clusters (bottom panel). Abbreviations are as follows: FC = Florida Current; LC = Loop Current; E = Cyclonic Eddy; CC = Caribbean Current; GC = Guiana Current; NBC = North Brazil Current; SEC = South Equatorial Current; BC = Brazil Current; FA = Florida Atlantic (United States); FG = Florida Gulf (United States); VE = Veracruz (Mexico); CA = Campeche (Mexico); QR = Quintana Roo (Mexico); LI = Limón (Costa Rica); CI = Cartagena de Indias (Colombia); MI = Miranda and Nueva Esparta (Venezuela); PA = Pará (Brazil); CE = Ceará (Brazil); RN = Rio Grande do Norte (Brazil); ES = Espírito Santo (Brazil); RJ = Rio de Janeiro (Brazil).

within the Gulf Profile (0.97) and the Southern Profile (0.99). Migration rates between these groups were generally very low, ranging from 0.003 to 0.017 (Table 2). An exception was observed for gene flow from the Southern Profile, primarily

along the Brazilian coast, to the Northern Profile, which includes the Caribbean and Florida. This migration pathway exhibited a rate of 0.301 (95% credible interval = 0.269–0.330), indicating a pronounced pattern of asymmetric gene flow.

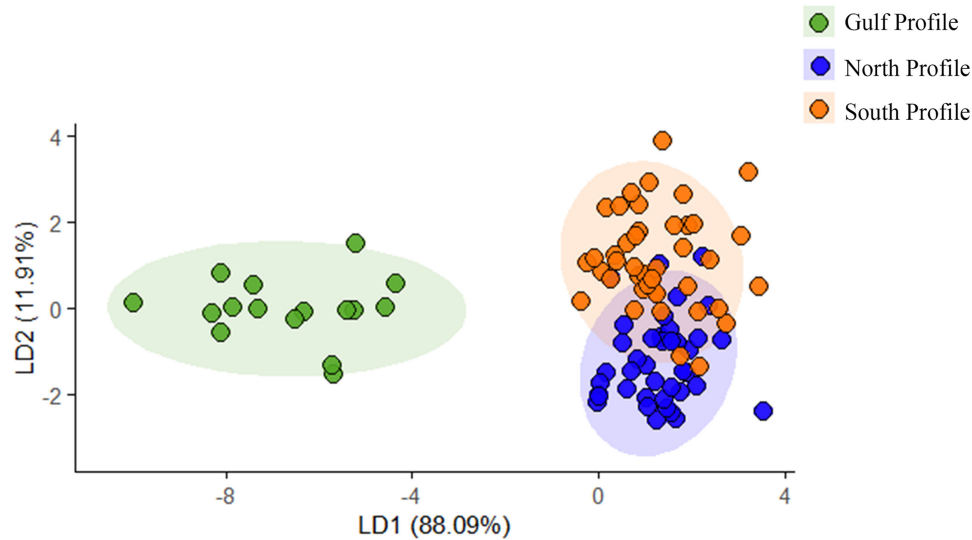


Figure 2. Results of the discriminant analysis of principal components (DAPC) showing the genetic clustering of Common Snook identified by the *find.clusters* algorithm. Each point represents an individual positioned along discriminant axes LD1 and LD2. Linear discriminant (LD) denotes the discriminant functions generated by the DAPC. Translucent ellipses indicate within-cluster dispersion, and colors represent the tree genetic profiles.

Table 1. Pairwise genetic differentiation index F_{ST} values between the genetic profiles of Common Snook in the tropical western Atlantic. Values below the diagonal correspond to analyses including all individuals, while values above the diagonal correspond to results after excluding individuals with admixed genetic composition (<80% assignment). All values were statistically significant ($P < 0.05$).

Genetic profile	Gulf Profile	Northern Profile	Southern Profile
Gulf Profile	–	0.30	0.39
Northern Profile	0.33	–	0.04
Southern Profile	0.39	0.03	–

Genetic diversity

All 11 microsatellite loci used in this study were polymorphic, yielding a total of 184 alleles. High levels of genetic diversity were observed across the three genetic profiles, with diversity indices consistently highest in the Gulf Profile and lowest in the Southern Profile. The number of alleles per locus (N_a) ranged from 11 to 24, with an average N_a of 16. Mean R_a ranged from 5.64 to 7.69, while $P-R_a$ ranged from 1.35 to 4.19.

A total of 90 private alleles were identified, the majority of which (48 alleles) were associated with the Gulf Profile. Values of H_o ranged from 0.25 to 0.77, while H_e ranged from 0.74 to 0.82. For all diversity metrics, the Gulf Profile consistently exhibited the highest values, whereas the Southern Profile showed the lowest. Detailed diversity statistics for each locus are provided in Table 3.

DISCUSSION

This study provides the first assessment of population structure in the Common Snook across a substantial portion of the species' geographic range. The results revealed significant population structuring, with the southern Gulf population being genetically isolated, whereas populations along the Atlantic

coast exhibited two predominant genetic profiles positioned at opposite ends of the distribution and some mixture in the middle part of the north–south distribution.

Previous studies conducted at local and regional scales have reported contrasting patterns of genetic structure for this species, particularly within the Gulf. Along the Florida peninsula, [Tringali and Bert \(1996\)](#) and [Tringali et al. \(2008\)](#) detected clear differentiation between Gulf and Atlantic stocks. Within the Gulf, population analyses identified genetic homogeneity in both the northwestern region (Texas; [Anderson et al., 2020](#)) and the southern Gulf (Tabasco; [Hernández-Vidal et al., 2014](#)). More recently, [Terán-Martínez et al. \(2021\)](#) identified two genetic clusters within the Usumacinta River basin, also located in the southern Gulf (Tabasco; [Terán-Martínez et al., 2021](#)). However, those findings may represent different spatial portions or sampling scale of a single, broadly connected population rather than entirely distinct genetic units. Along the South Atlantic coast, studies conducted in Brazil have reported a pattern of high gene flow across an extensive coastal region from Pará to Rio de Janeiro ([de Oliveira et al., 2014](#); [Malcher et al., 2023](#)). However, none of those studies simultaneously analyzed populations from both the southern Gulf and the Atlantic coast, thus previously limiting the ability to detect the genetic differentiation revealed in the present study. These findings highlight the importance of broad and geographically comprehensive sampling for robust large-scale phylogeographic inferences.

The isolated population in the Gulf of Mexico

Our results revealed the presence of a genetically isolated population of Common Snook in the southern Gulf, exhibiting extremely low rates of both immigrant influx and emigrant outflow relative to populations in the Atlantic and Caribbean. Both historical and contemporary hydrogeological processes, such as sea level fluctuations during the Pleistocene ([Malcher et al., 2023](#)) as well as past ([Arellano-Torres et al., 2023](#)) and present-day dynamics of ocean current systems in the Gulf

Table 2. Estimated recent migration and retention rates among Common Snook genetic profiles. Values in parentheses represent 95% credible intervals.

Source	Recipient		
	Gulf Profile	Northern Profile	Southern Profile
Gulf Profile	0.970 (0.909–0.998)	0.012 (0.000–0.043)	0.003 (0.000–0.013)
Northern Profile	0.013 (0.000–0.053)	0.679 (0.667–0.709)	0.003 (0.000–0.013)
Southern Profile	0.017 (0.000–0.062)	0.301 (0.269–0.330)	0.994 (0.979–0.999)

Table 3. Genetic diversity parameters for Common Snook across the western Atlantic based on 11 microsatellite loci. Parameters include the number of individuals analyzed per group (*n*), total number of alleles (*N*), number of alleles per locus within each group (*N_a*), number of private alleles (*P-N_a*), allelic richness (*R_a*), private allelic richness (*P-R_a*), observed heterozygosity (*H_o*), and expected heterozygosity (*H_e*). Bold italic values indicate significant differences (*P* < 0.05) between *H_o* and *H_e*.

Group	Diversity parameter	Locus											Percentage or mean
		<i>Cun01</i> (N=12)	<i>Cun03</i> (N=12)	<i>Cun05B</i> (N=11)	<i>Cun08</i> (N=20)	<i>Cun09</i> (N=24)	<i>Cun11</i> (N=17)	<i>Cun14</i> (N=21)	<i>Cun16</i> (N=15)	<i>Cun18</i> (N=14)	<i>Cun19</i> (N=19)	<i>Cun22</i> (N=19)	
Gulf Profile (n=16)	<i>N_a</i>	8	9	6	14	14	13	11	8	8	12	11	62%
	<i>P-N_a</i>	0	3	2	10	4	6	6	2	5	6	4	4.36
	<i>R_a</i>	5.20	7.04	4.90	9.84	10.15	9.25	7.80	6.38	5.98	9.01	9.02	7.69
	<i>P-R_a</i>	1.38	3.75	1.54	7.50	4.22	5.17	6.22	2.28	3.66	6.78	3.64	4.19
	<i>H_o</i>	0.37	0.75	0.75	0.75	0.56	0.56	0.75	0.81	0.43	0.68	0.25	0.77
	<i>H_e</i>	0.56	0.83	0.74	0.92	0.93	0.89	0.86	0.82	0.69	0.89	0.91	0.82
Northern Profile (n=40)	<i>N_a</i>	9	7	7	8	12	8	7	9	9	8	13	53%
	<i>P-N_a</i>	0	2	3	1	1	2	0	0	0	3	2	1.27
	<i>R_a</i>	6.50	4.35	4.08	5.67	8.58	5.23	5.16	6.00	7.30	4.82	8.68	6.03
	<i>P-R_a</i>	0.88	0.76	0.95	1.47	184	1.04	1.75	1.06	1.85	2.25	2.21	1.46
	<i>H_o</i>	0.73	0.73	0.46	0.69	0.50	0.76	0.57	0.73	0.57	0.61	0.65	0.70
	<i>H_e</i>	0.84	0.67	0.65	0.76	0.89	0.72	0.69	0.80	0.87	0.59	0.89	0.76
Southern Profile (n=44)	<i>N_a</i>	12	6	6	8	18	8	15	13	8	10	13	64%
	<i>P-N_a</i>	1	1	2	2	7	2	5	4	0	2	2	2.54
	<i>R_a</i>	6.64	2.89	3.64	4.38	8.08	4.40	7.01	7.35	5.31	4.97	7.39	5.64
	<i>P-R_a</i>	1.33	0.22	0.80	0.66	2.88	0.67	2.80	2.20	0.78	1.70	0.79	1.35
	<i>H_o</i>	0.67	0.51	0.51	0.62	0.44	0.51	0.77	0.68	0.63	0.53	0.57	0.51
	<i>H_e</i>	0.83	0.54	0.61	0.72	0.87	0.59	0.82	0.85	0.78	0.63	0.85	0.74

(Candela et al., 2019), likely contributed to the origin and long-term persistence of this isolated population. Similar patterns of genetic isolation have been reported in other widely distributed marine and estuarine fish species, including the Smallscale Fat Snook *Centropomus parallelus* (Seyoum et al., 2022), Lane Snapper *Lutjanus synagris* (Karlsson et al., 2009), Finetooth Shark *Carcharhinus isodon* (Portnoy et al., 2016), Red Drum *Sciaenops ocellatus* (Hollenbeck et al., 2019), and Gafftopsail Catfish *Bagre marinus* (Portnoy et al., 2024).

Global geological events, such as the Last Glacial Maximum, likely played a direct role in the population isolation observed in the Common Snook. During the late Pleistocene, sea levels dropped by up to 120 m below present-day levels (Ludt & Rocha, 2015), leading to a significant retreat of coastlines and a drastic reduction in available coastal habitats in the Gulf (Donoghue, 2011). The combination of shallow-water habitat loss, surface water cooling, increased discharge from the Mississippi River, and the topography of the Yucatán Peninsula significantly altered ocean circulation patterns in the region, restricting the inflow of oceanic currents into the Gulf (Arellano-Torres et al., 2023). Instead, the flow was rerouted directly through the Florida and Cuba straits (Nürnberg et al., 2008).

These changes likely disrupted connectivity between biogeographic regions and limited gene flow between stocks inside and outside the Gulf (Clark et al., 2009). Consequently, reduced connectivity may have promoted genetic drift and driven population differentiation over time, resulting in the

genetic isolation patterns observed today. Similar patterns of genetic structuring associated with marine regressions and paleogeographic changes have been reported for other broadly distributed coastal species in the western Atlantic (Ludt & Rocha, 2015), highlighting the critical role of historical processes in shaping genetic diversity and population structure in marine communities.

On a more recent time scale, the isolation of the southern Gulf stock is likely maintained by a combination of ecological and oceanographic factors, including the absence of suitable habitats, particularly along the Yucatán Peninsula (McMahan et al., 2013), and the region's semi-enclosed and complex ocean current system (Figure 1). One of the main components of this system is the Loop Current, a warmwater flow that moves northward into the Gulf through the Yucatán Channel (Candela et al., 2019). As it progresses, portions of the current break off and form vortices (Loop Current eddies) that drift westward and southward, especially in the central Gulf (Centurioni & Niiler, 2003), while the main flow continues toward the Florida Straits and subsequently into the Atlantic (Candela et al., 2019). This movement generates an internal circulation system (Weisberg & Liu, 2017) that likely helps to maintain the genetic isolation of the southern Gulf stock, as evidenced by the low rates of immigration and emigration of Common Snook observed in this study. Additionally, the persistent cyclonic gyre in the deeper regions of the Bay of Campeche (Sturges et al., 2005) appears to further restrict the

dispersal of adult individuals—and, more importantly, larvae and juveniles—within the southern Gulf.

It is important to note that this genetic differentiation was confirmed for localities in the southern Gulf; however, this profile may extend to other regions of the Gulf that were not included in this study, in a manner similar to that reported by Seyoum et al. (2022) for Smallscale Fat Snook. Those authors also identified a distinct stock in the southern Gulf and signs of differentiation toward the north, a pattern similar to that observed for Common Snook in the present study. These similarities suggest that shared historical and oceanographic processes may have shaped population structure in both species and indicate that additional sampling in more northern regions, such as Texas, could reveal similar genetic discontinuities in Common Snook. In contrast, populations along the Gulf-facing coast of the Florida peninsula share the same genetic profile (the Northern Profile described in this study) as populations from the North Atlantic (Figure 1). The population structure observed within the Gulf may be consistent with the findings reported by Portnoy and Gold (2012), who identified a biogeographic break near Mobile Bay, Alabama. Similar patterns have also been described for other estuarine-dependent fishes, including the Blacknose Shark *Carcharhinus acronotus* (Portnoy et al., 2014), Finetooth Shark (Portnoy et al., 2016), Spotted Seatrout *Cynoscion nebulosus* (Seyoum et al., 2017), and Red Drum (Hollenbeck et al., 2019). Nevertheless, broader sampling throughout the Gulf is still required to test and further support this scenario for the Common Snook.

Our results for the Florida localities revealed a high degree of genetic similarity between populations from the Atlantic and Gulf coasts, contrasting with the patterns previously reported by Tringali et al. (2008). This divergence is likely attributable to differences in the number of loci analyzed. Furthermore, the limited sample size from these regions in the present study, together with the potential inclusion of hatchery-reared individuals or descendants of fish released through stock enhancement programs in Florida (Tringali et al., 2008), may also have contributed to the observed divergence.

Genetic connectivity in the Atlantic

Along the western Atlantic, two distinct genetic profiles of the Common Snook were identified, each closely aligned with its respective geographic distribution (Figure 1). The Northern Profile comprises individuals distributed throughout North America and Central America, whereas the Southern Profile includes populations along the Brazilian coastline. A clear gradient in genetic contribution is observed from the distributional extremes toward the central region. Populations from northern South America (Colombia and Venezuela) exhibit a mixed genetic composition, reflecting contributions from both the Northern and Southern profiles. These findings suggest that the freshwater plume formed by the Amazon and Orinoco rivers, although traditionally considered a barrier to some species (Araujo et al., 2022; Tosetto et al., 2022), does not represent an effective genetic barrier for the Common Snook. This large-bodied, strong-swimming species appears capable of traversing this transitional zone and maintaining gene flow between populations located north and south of the plume. Furthermore, rivers located near this region may function as

nursery areas, concentrating juveniles from multiple spawning events along the plume and thereby potentially enhancing gene flow between populations distributed north and south of this transitional zone.

Similar to the pattern observed in the southern Gulf, migration rates indicated high levels of self-recruitment within Atlantic stocks. Estimates among regions revealed a greater proportion of migrants moving from the Brazilian coast toward the Caribbean, a pattern likely driven by the prevailing ocean current systems in the region (Araujo et al., 2022).

The most influential current facilitating this movement is the North Brazil Current, a branch of the South Equatorial Current, which flows northwestward and transitions into the Guiana Current. The Guiana Current transports low-salinity, nutrient-rich, and sediment-laden waters originating from the Amazon River toward the Caribbean Sea (Martins et al., 2022; Miloslavich et al., 2011). This oceanographic system is likely the one of the main factors responsible for genetic connectivity in Common Snook, facilitating long-distance dispersal of eggs and larvae and linking Brazilian coastal populations with those in the Caribbean (Cowen & Sponaugle, 2009; Selkoe et al., 2016). Similar patterns of gene flow mediated by ocean currents have been reported in other species with comparable ecological traits, including the Caribbean Red Snapper *Lutjanus purpureus* (Gomes et al., 2012), Yellowtail Snapper *Ocyurus chrysurus* (Da Silva et al., 2015), and Blackfin Tuna *Thunnus atlanticus* (Saillant et al., 2022).

In addition, bioecological traits, such as high plasticity and broad habitat use, likely contribute to the genetic homogenization observed among Atlantic stocks. Common Snook exhibit high tolerance to salinity fluctuations (euryhaline) and undertake migrations between freshwater, estuarine, and marine environments (diadromous). Throughout its life cycle, the Common Snook occupies a wide range of habitats, including streams, tidal creeks, saltwater lagoons, estuaries, mangroves, and coastal marine zones (Trotter et al., 2021).

In general, fish species that exploit a broader range of habitats tend to exhibit less pronounced genetic structure compared to species with more specialized habitat requirements (Luiz et al., 2012; Tosetto et al., 2022). The viability and dispersal of fertilized eggs also appear to be closely linked to these migratory behaviors (Lowerre-Barbieri et al., 2014). Adult individuals utilize freshwater habitats as thermal refuges during winter and migrate to higher-salinity coastal areas during warmer months, where elevated salinity enhances egg buoyancy and supports the formation of spawning aggregations throughout their range (Lowerre-Barbieri et al., 2014). Collectively, these factors likely facilitate the availability of multiple habitats functioning as ecological “stepping stones” between populations, promoting an effective mechanism of connectivity between the Brazilian coast and the Caribbean biogeographic region, as demonstrated in our study.

Limitations and future directions

This study has significantly advanced the understanding of population structure and genetic diversity in Common Snook, although some limitations should be acknowledged. The main limitation concerns the reduced number of samples in certain localities, which may underestimate their genetic representativeness and

influence differentiation estimates among the identified groups. Future studies should more thoroughly investigate the geographic limits of the genetic profile in the Gulf by including a broader range of samples across this region and should deepen our understanding of the genetic patterns of populations from both coasts of the Florida peninsula. Another aspect that deserves attention is the contact zone between the two Atlantic profiles, particularly in the northern portion of South America, where a potential transition area with intense genetic admixture appears to occur. Although microsatellites are highly informative markers due to their elevated allelic variability, genomic approaches based on next-generation sequencing have greater potential to reveal finer-scale patterns of molecular ecology, demography, adaptation, and evolutionary history, and such approaches should be incorporated into future studies on these fish.

SUPPLEMENTARY MATERIAL

Supplementary material is available at *Marine and Coastal Fisheries* online.

DATA AVAILABILITY

Data are available from the authors upon reasonable request.

ETHICS STATEMENT

All necessary permits were obtained for the execution of this study, which fully complied with all relevant regulations, and none of the samples included threatened or protected species. The collection of specimens and access to genetic material strictly followed the legislation in force in each of the countries involved. In Brazil, authorization was granted by Instituto Chico Mendes de Conservação da Biodiversidade (SISGENAEE8621); authorization in other countries was granted as follows: Mexico (Dirección General de Ordenamiento Pesquero y Acuícola [DGOPA]; Comisión Nacional de Acuicultura y Pesca [CONAPESCA]; Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación [SAGARPA]; PPF/DGOPA-035/15, CONAPESCA-PPF/DGOPA-262/17, PPF/DGOPA-065/21, PPF/DGOPA-07/23, PPF/DGOPA-025/23, and SAGARPA-CONAPESCA PPF/DGOPA-249/14) and Costa Rica (Sistema Nacional de Áreas de Conservación [SINAC]; Comisión Institucional de Biodiversidad [CBio]; R-SINAC-SE-DT-PI-029-2023, R-SINAC-ACG-PI-045-2023, and CBio-UCR-R-359).

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CONFLICTS OF INTEREST

The authors declare that there is no conflict of interest related to the publication of this manuscript.

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