Red Snapper Preliminary Genetic Analysis Temporal Genetic Diversity Trends in the South Atlantic Bight

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Red Snapper Preliminary Data Analysis
Temporal Genetic Diversity Trends in the South Atlantic Bight

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Abstract: Analyses of red snapper collected in the South Atlantic Bight revealed only slight fluctuations in genetic diversity from 1975 to 2012. Estimates of effective population size suggest that red snapper experienced a genetic bottleneck that was not detected in genetic diversity estimates due to a lack of samples prior to 1975. Contemporary estimates of effective population size and inbreeding coefficients revealed the start of a genetic recovery of red snapper in the Atlantic.

Samples included:

Table 1. Summary of genotyped red snapper samples organized by year class and collection location.

Year Class	Collection Location					Total
	NC	SC	GA	FL	Unknown	
1975		1	3	109		113
1976				88		88
1980				20		20
1981				35		35
1982				23		23
1996		25	7	22	41	95
1997		8	6	25	48	87
2005		8	31	19	3	61
2006	4	19	9	27	11	70
2007	2	26	5	50	15	98
2008	3	14	4	51	20	92
2009		13	4	39	11	67
2010	18	11	6	56	7	98
2011	20	3	9	54		86
2012	1	1	8	36		46
Total	48	129	92	654	156	1079

Genetic Data: The source of genetic material from samples collected prior to 2012 was tissue on the surface of dried otoliths, while genetic material for samples collected in 2012-2013 was obtained from fin clips. DNA was isolated and 12 microsatellite loci were genotyped for further analyses.

Data Analyses: Red snapper were organized into year classes (fish spawned in the same year) using ages derived from sectioned otoliths. Potential spatial and temporal population divergences were tested using pairwise comparisons of F_{ST}, a measure of genetic distance, between year classes and were performed in Arlequin using 10,000 permutations. For each year class, basic genetic diversity indices including unbiased expected heterozygosity and inbreeding coefficients were calculated using Arlequin and mean rarified allelic richness (with year classes 1980-1982 removed due to small sample sizes) was calculated using the R package standArich. Significance levels for all simultaneous analyses were adjusted using a sequential Bonferroni correction.

The contemporary effective population size of Atlantic red snapper was estimated using the temporal method, which compares genetic drift that occurs between two cohorts and estimates effective population size based on an inverse relationship between effective population size and genetic drift. Estimates of long-term effective population size, which is measured on an evolutionary time scale, were calculated using a stepwise mutation model and a previously calculated mutation rate for the red snapper microsatellite markers (μ=2.71x10^{-4}).

Results:

- Red snapper from the South Atlantic Bight represented a homogenous population through space and time with no significant differences in F_{ST} occurring between states or year classes ($p \geq 0.207$).
- Expected heterozygosity, a measure of genetic diversity, showed little change over the time periods analyzed (range: 0.591 to 0.642). The relationship between estimates of red snapper abundance (SEDAR 24) and expected heterozygosity was significantly correlated in the most recent years (1996-2010; R^2=0.736, p=0.006; linear regression; Fig 1) but was not significant when all year classes were included (R^2=0.069, p=0.385; linear regression). Small sample sizes in some years (e.g., 1980-82, Table 1) may underlie the lack of significant relationships when considering all time-points.
- Allelic richness, a measure of allelic variation, showed a similar trend to expected heterozygosity (range: 7.40 to 8.11) with no significant correlation between abundance and allelic richness over all time points (R^2=0.149, p=0.271), but a significant relationship with only the most recent year classes (1997-2010; R^2=0.720, p=0.016; Fig 2).
- Inbreeding coefficient estimates were variable over time (range: -0.028 to 0.116) with many years in the 1970's and 1980's exhibiting substantially higher values, but have been decreasing (i.e., improving) since 2005 (Table 2).
- Contemporary estimates of effective population size have shown an increase in the 2000's relative to estimates in the prior decades. Long-term effective population size remained stable over time periods and was generally an order of magnitude greater than contemporary estimates (Table 3).

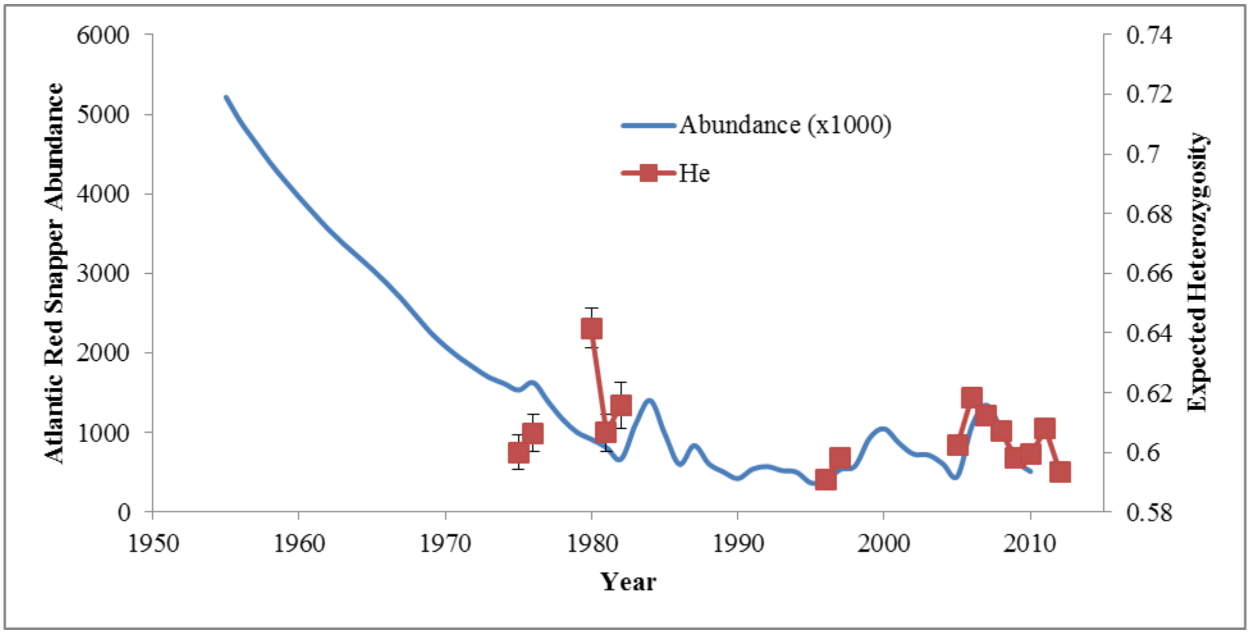

Figure 1. Atlantic red snapper abundance as estimated by SEDAR (2010) and expected heterozygosity estimates with standard error for each year class analyzed.

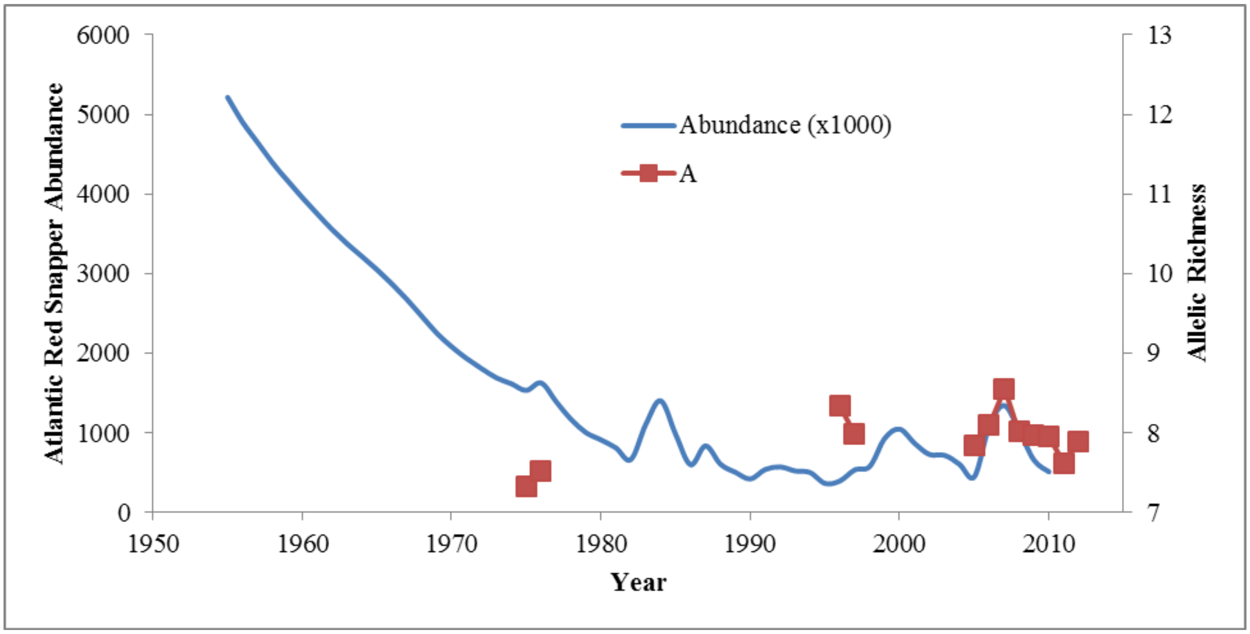

Figure 2. Atlantic red snapper abundance as estimated by SEDAR (2010) and allelic richness estimates with standard error for each year class analyzed.

Table 2. Inbreeding coefficient estimates for Atlantic red snapper at each year class analyzed.

Year Class	Fis
1975	0.028
1976	0.069
1980	0.116
1981	0.004
1982	0.094
1996	0.023
1997	0.026
2005	0.111
2006	0.021
2007	0.035
2008	0.026
2009	0.019
2010	0.005
2011	-0.008
2012	-0.028

Table 3. Contemporary (left) and long-term (right) effective population size estimates for Atlantic red snapper with 95% confidence intervals listed for estimates produced by GONe. The contemporary estimate of effective population size from 2005-2011 represents a mean of several calculations so no confidence interval is reported.

Year Class	Ne	-95%CI	+95%CI	Collection Year	Long-term Ne
1977-1978	209.07	159.54	265.19	**1977-1978**	2,440.65
1981-1982	20.42	14.75	27.01	**1983-1984**	2,747.00
1996-1997	253.41	194.06	320.55	**1999-2000**	2,454.53
2005-2011	505.35	-	-	**2007, 2008, 2009**	2,850.98
				2012-2013	2,446.78

Conclusions: No substantial decrease in red snapper genetic diversity was detected in the time periods analyzed, likely because all available samples were collected after the largest reduction in population abundance, but strong correlations in recent years between genetic diversity and population abundance showed that small changes in abundance can cause similar fluctuations in genetic diversity. The large discrepancy between long-term and contemporary effective population size estimates suggests that a genetic bottleneck did occur, but was not efficiently detected in genetic diversity metrics due to a lack of genetic samples prior to overfishing. The recent increase in contemporary effective population size and decreasing inbreeding coefficient, however, suggest a recent demographic increase in the Atlantic red snapper population.