Cobia preliminary data analyses – US Atlantic and GOM genetic population structure

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Abstract: With available data (west FL and northern GOM have low sample sizes), GOM appears to be a genetically homogenous group continuing around the FL peninsula with a genetic break occurring around northern FL and GA. The Atlantic population segment appears to have a genetically homogenous offshore component and genetically unique inshore components.

Samples Included: all collected during the spring/summer (spawning period)
VA: inshore Chesapeake Bay aggregation (n=76), 2006-2008 (Jun-Aug)
NCoff: offshore northern NC (n=248), 2008-2010 (May-July)
SC: inshore Port Royal Sound aggregation (n=744), 2004-2011 (May-July)
SCoff: offshore southern SC (n=147), 2004-2011 (May-July)
FLEoff: offshore St. Lucie (n=154), 2011 (April-May)
FLSoff: offshore Key West (n=8), 2010 (April)
FLWoff: offshore Destin/Panama City (n=16), 2008 (April)
MSoff: offshore Ocean Spring (n=6), 2010 (May)
TXoff: offshore Port Aransas (n=62), 2010 (May-Aug)

Genetic Data: All fin clip samples were genotyped at 10 microsatellite loci (same as tested and used in our previous study; see manuscript for details on methodology, inshore/offshore definitions, etc.).

Data Analyses: All cultured fish were removed from the analyses as well as any wild recaptures. Based on previously detected lack of temporal comparisons within collection locations, samples were pooled across time. An exact G-test with Markov Chain permutations, as implemented in GENEPOP, was used to test for pairwise differences in genotypic distributions among collection locations. Markov chain parameters included 10,000 dememorizations, 100 batches and 5000 iterations per batch. Pairwise hierarchical R_{ST} statistics were calculated and an Analysis of Molecular Variance (AMOVA) was conducted as implemented in ARLEQUIN with 10,000 iterations to determine the degree of genetic structuring occurring among states. Significance levels for all simultaneous analyses were adjusted using a sequential Bonferroni correction.

Results: We have determined that
- Inshore VA and SC aggregations are distinct
    - Different from each other: G: p=0.000, R_{ST}: 0.022, p=0.000
    - Different from offshore groups: G: p=0.000-0.002, R_{ST}: 0.003-0.025, p=0.000-0.030
- SC and NC offshore collections are homogenous (G: p=0.029, R_{ST}: 0.001, p=0.136)
- TX through FL east coast offshore collections are homogenous (G: p=0.462-0.705, R_{ST}: 0.000, p=0.110-0.947)
- Two U.S. offshore groups are distinct: G: p=0.000-0.005, R_{ST}: 0.007, p=0.000
- AMOVA: R_{ST}: 0.008, p=0.000, variation among groups: 0.76%, p=0.004
- Although significant, low R_{ST} values indicate some gene flow occurs between groups

Recommendations: With available data (west FL and northern GOM have low sample sizes), GOM appears to be a genetically homogenous group continuing around the FL peninsula with a genetic break occurring around northern FL and GA. The Atlantic population segment appears to have a genetically homogenous offshore component and genetically unique inshore components.