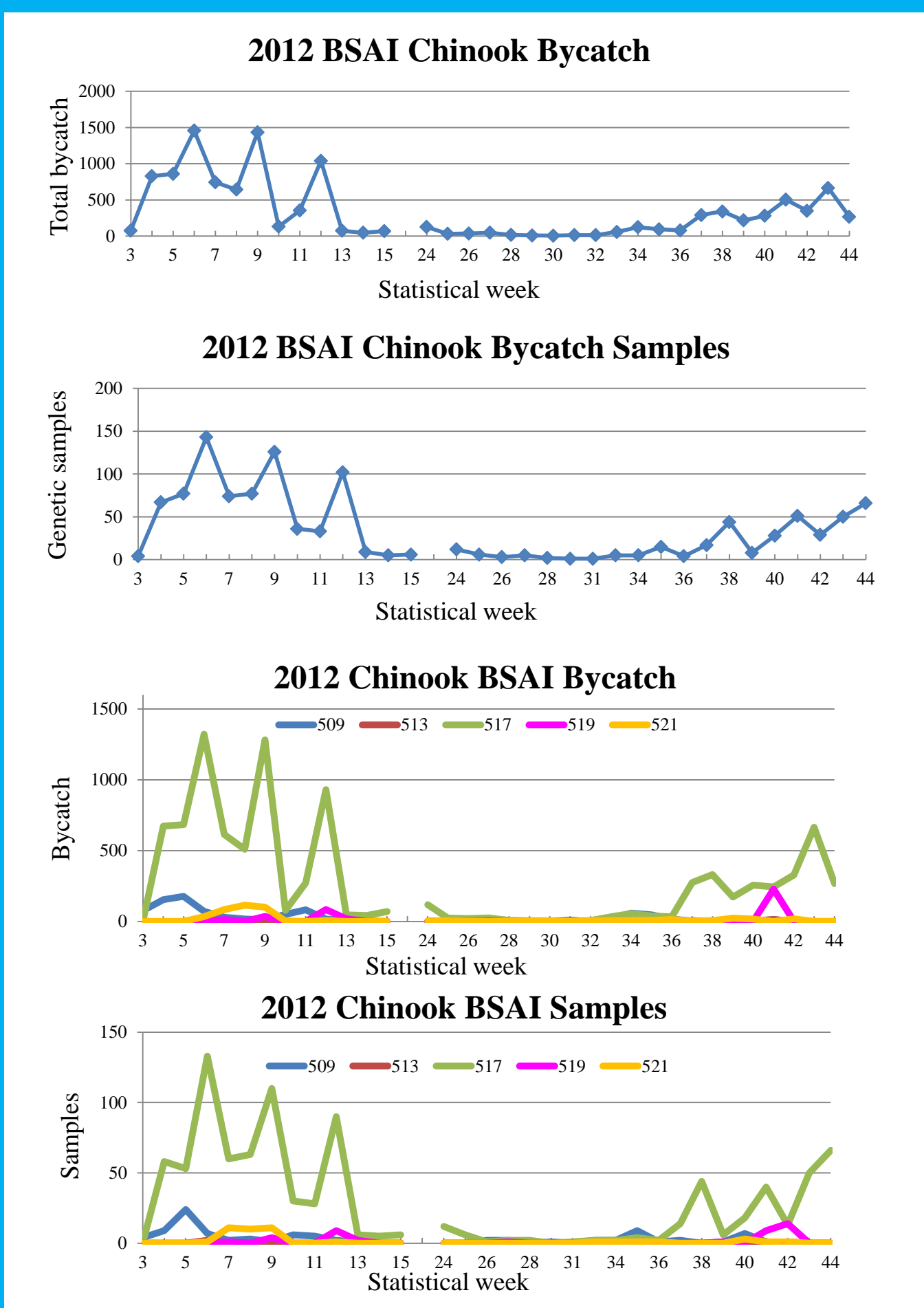


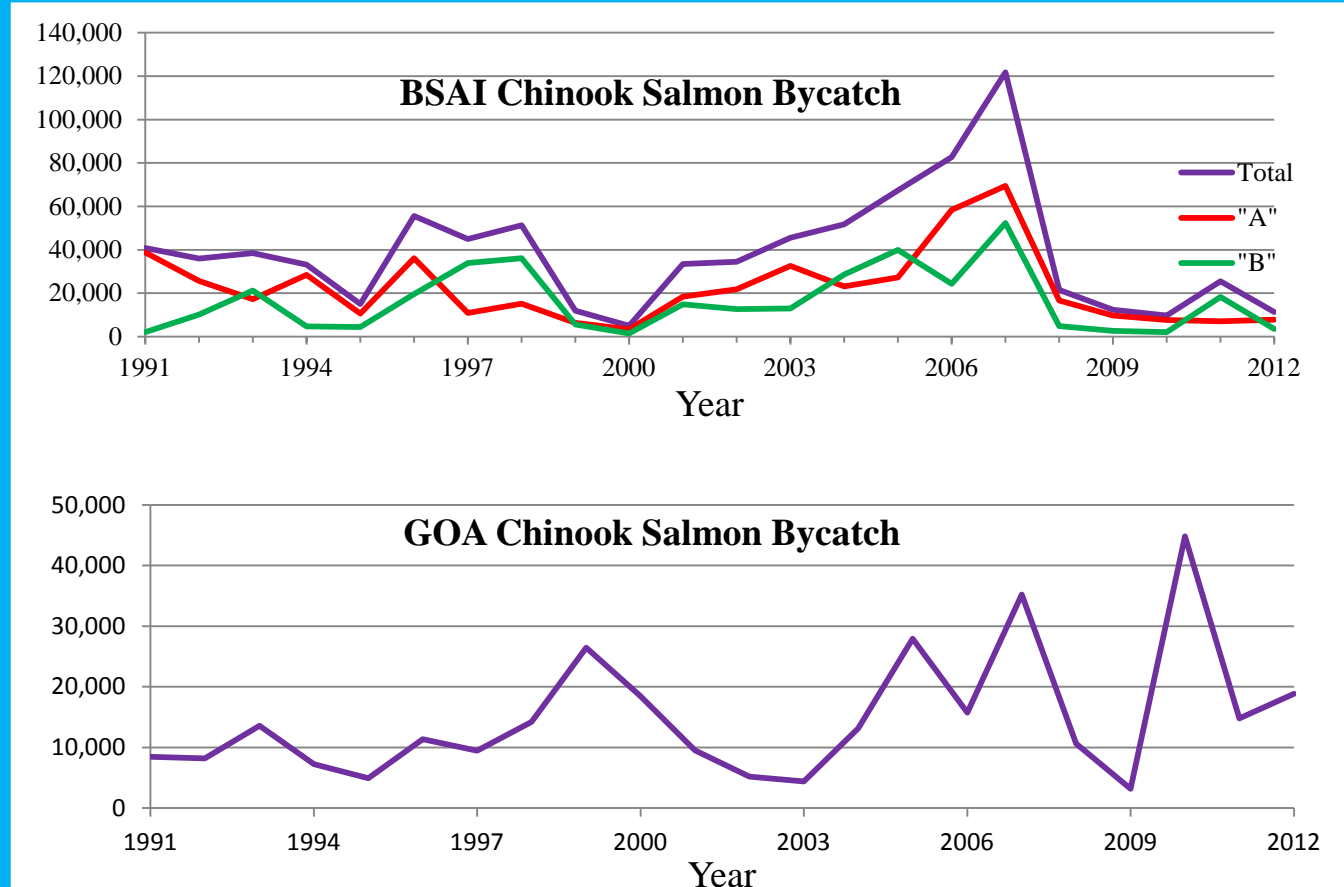
Genetic Stock composition estimates of Chinook salmon incidentally taken as bycatch in the 2012 Bering Sea and Gulf of Alaska Trawl Fisheries

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Number of BSAI Chinook salmon bycatch and genetic samples graphed by statistical week. Top two panels show totals, bottom two panels totals by NMFS statistical areas.



Yearly estimates of the Chinook salmon bycatch from the pollock trawl fisheries in the BSAI (total, “A” & “B” season) from the BSAI (top) and GOA (bottom).



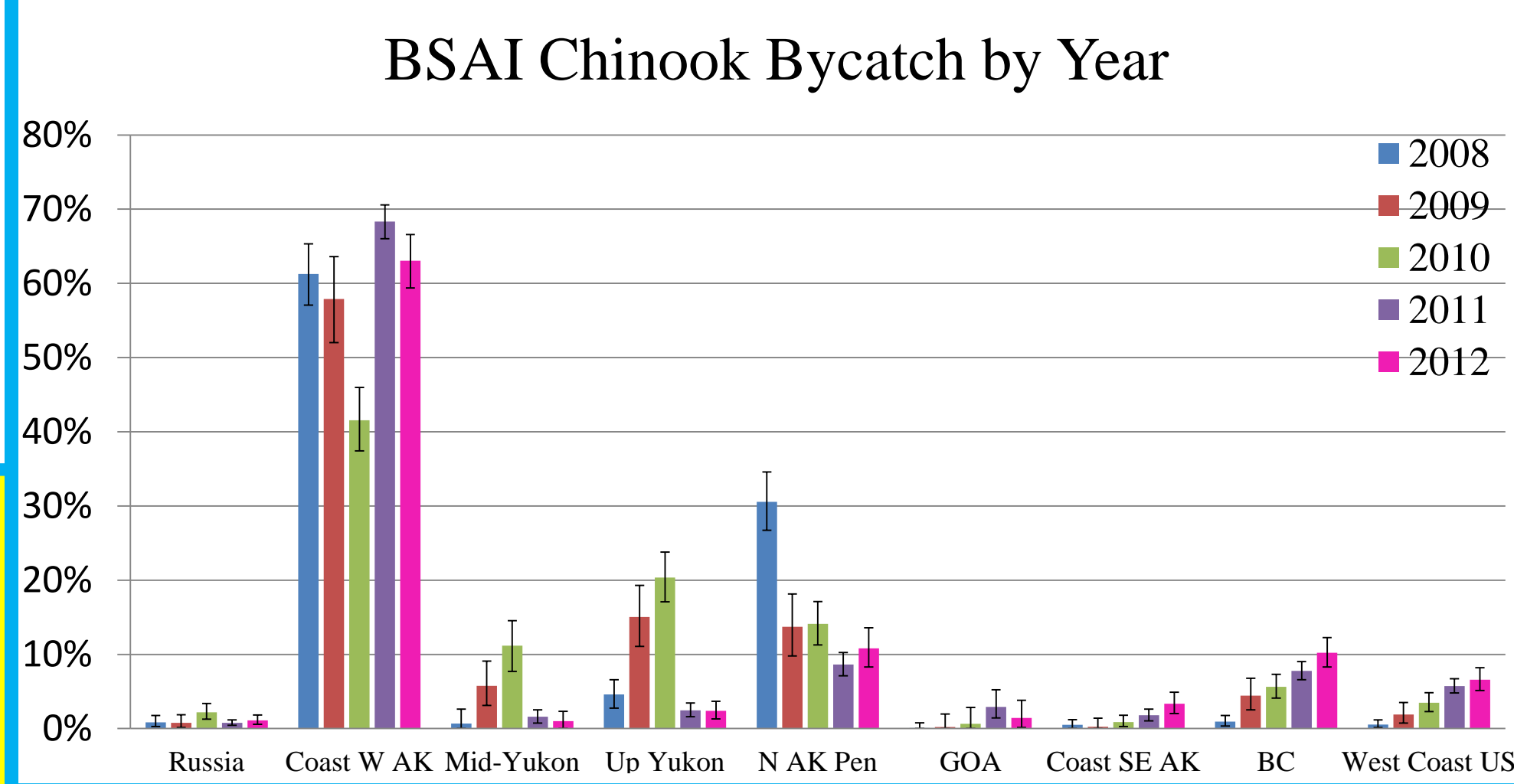
Bering Sea-Aleutian Islands

Results (BAYES) suggest that 88% of the 759 samples from the “A” season originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (68%), followed by the North Alaska Peninsula (16%), and Upper Yukon (3%). The other major contributor was British Columbia (7%). For the “B” season, over 53% of the 352 samples originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska region contributing the most (52%). This was followed by the West Coast U.S. stock (17%) and British Columbia (15%). For the entire year, an estimated 77% of the bycatch samples were estimated to be from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (63%), trailed by the North Alaska Peninsula (11%). Other contributors were British Columbia (10%) and West Coast U.S. (7%).

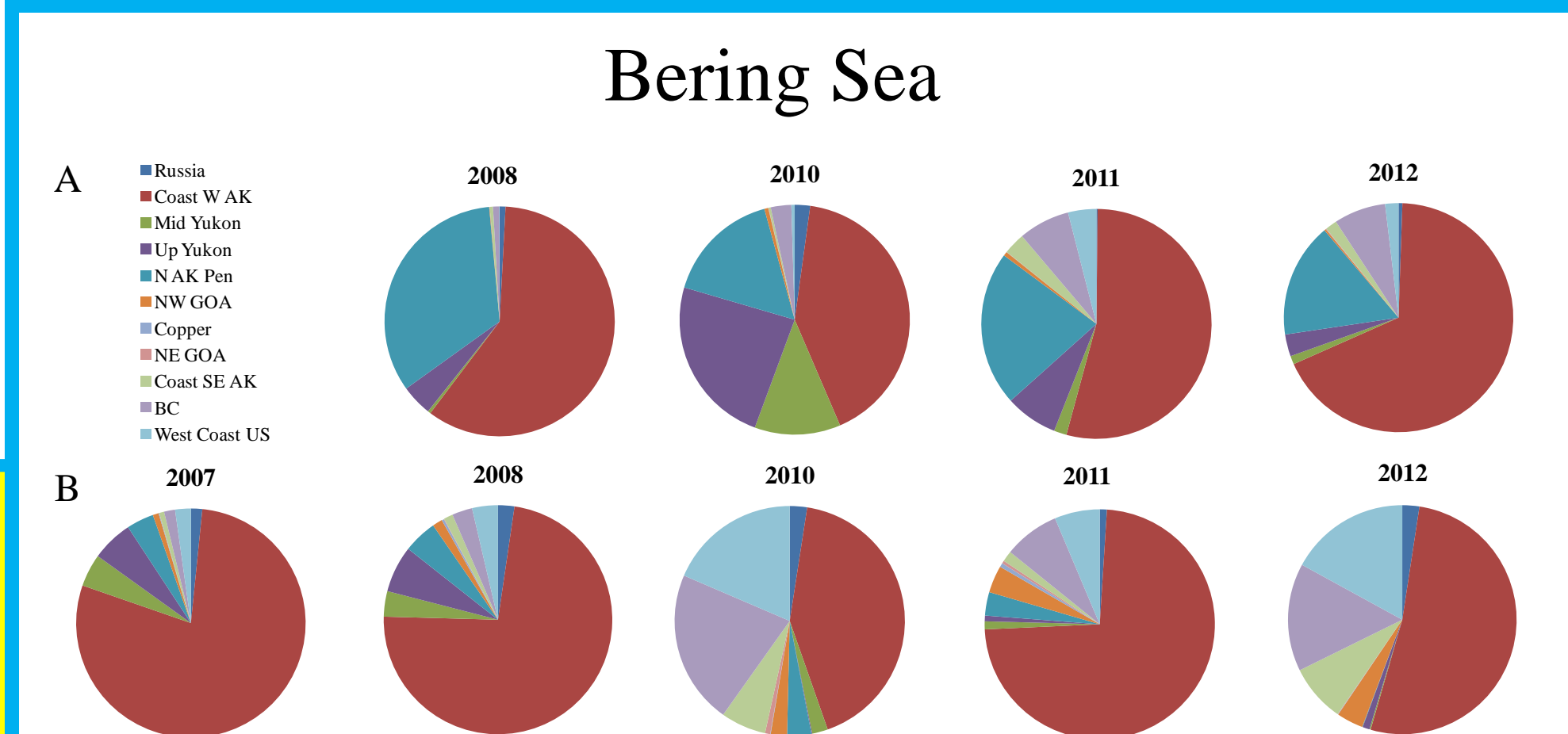
Acknowledgements: Genotyping for this analysis was funded partially by the North Pacific Fishey Research Foundation, and the Alaska Sustainable Salmon Fund. Thanks to ADF&G-Gene Conservation Lab for providing the SNP baseline and the group structures used in this study. Thanks to Ray Troll for the salmon picture. The findings and conclusions in this poster are those of the authors and do not necessarily represent the views of the National Marine Fisheries Service, NOAA

Genetic Stock Composition

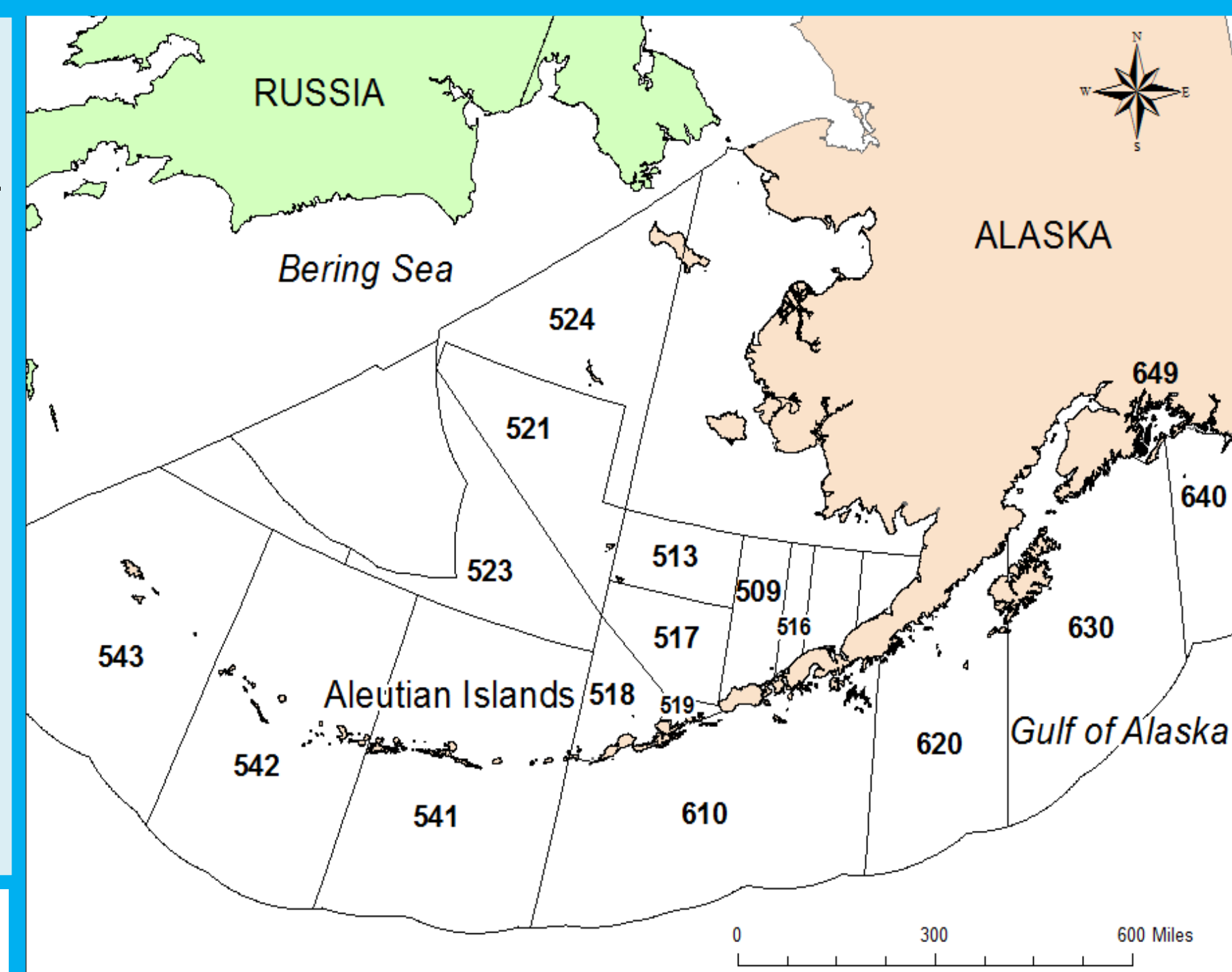
DNA was extracted from axillary process tissue and matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) genotyping was performed using a Sequenom MassARRAY iPLEX platform to genotype 43 SNP DNA markers represented in the ADF&G Chinook salmon baseline. From the 2012 Chinook salmon bycatch, a total of 2,126 samples were analyzed of which 2,059 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 96.8%. Stock composition estimates were derived using both BAYES (Bayesian analysis) and SPAM (maximum likelihood analysis) software and both methods yielded almost identical stock composition estimates.



Comparison of yearly stock composition estimates (2008-2012) based on genetic samples from the BSAI Chinook salmon bycatch. BAYES 95% credible intervals are plotted for yearly estimates



Comparison of “A” season genetic stock composition estimates for 2008, 2010-12 based on available genetic samples from the BSAI Chinook salmon bycatch. Comparison of “B” season genetic stock composition estimates for 2007, 2008, 2010-12 stock composition estimates based on available genetic samples from the BSAI “B” season Chinook salmon bycatch. The same genetic baseline and regional groupings were used in all analyses



NMFS statistical areas associated with the Bering Sea Aleutian Island (BSAI) and Gulf of Alaska (GOA) groundfish fisheries

Comparison with Previous Estimates

BSAI:

Comparisons among years are complicated due to different sampling strategies employed in different years, stock compositions from the analysis of the 2012 “A” season Chinook salmon bycatch samples were in general agreement with the 2008, 2010, and 2011 “A” season estimates. Most samples continued to be from stocks originating from river systems directly flowing into the Bering Sea, although differences were apparent between the 2010 and the other “A” season sample sets. The 2007, 2008, and 2011 “B” season stock composition estimates were similar with large amounts from Coastal Western Alaska. In contrast with the other “B” season estimates, the 2010 and 2012 “B” season estimates identified larger contributions from British Columbia, West Coast U.S. and Coastal Southeast Alaska stocks. When the stock compositions were analyzed for the entire year, Coastal Western Alaska stock compositions trended downward between 2008 and 2010 but increased in 2011, and remained at a similar level in 2012. North Alaska Peninsula stock compositions have remained consistent since 2009 reporting 11% of the bycatch in 2012. The upper and middle Yukon River contribution continued to be low in 2012, while Coastal Southeast Alaska, British Columbia and West Coast U.S. stock compositions continued their 5-year upward trend.

GOA:

The opportunistic sampling protocols employed between 2010 and 2012 limit the results to identifying only presence of individual stocks groups, however all years show an abundance of southern stock groups (British Columbia, West Coast U.S., and Coastal Southeast Alaska).

GOA:

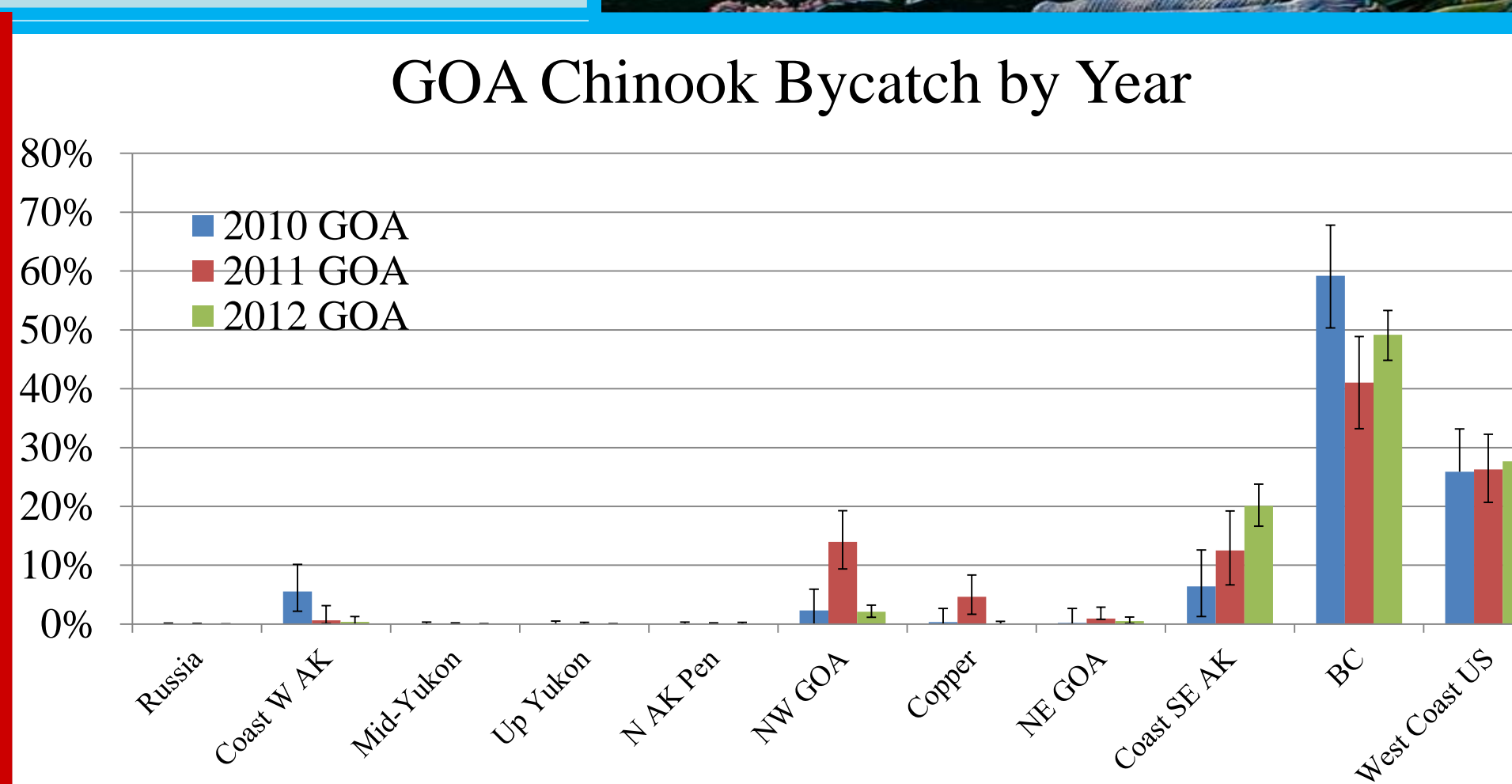
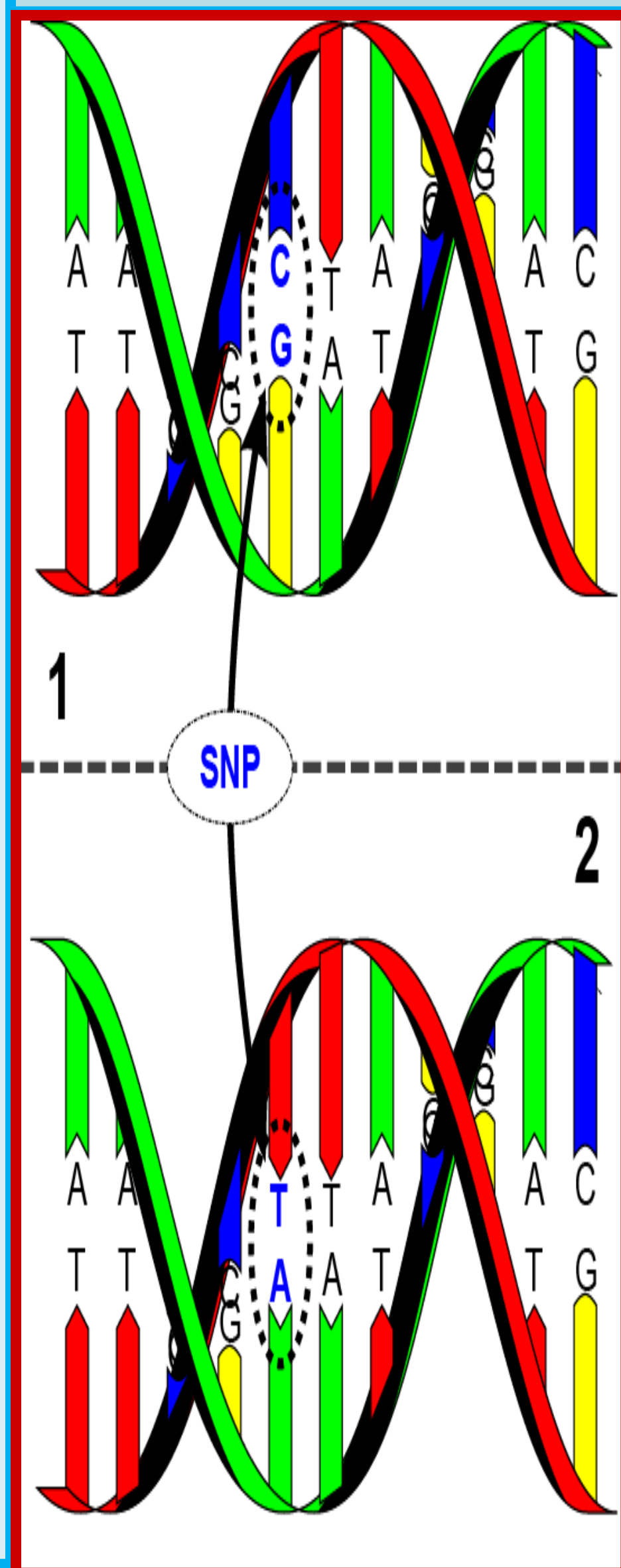
The opportunistic sampling protocols employed between 2010 and 2012 limit the results to identifying only presence of individual stocks groups, however all years show an abundance of southern stock groups (British Columbia, West Coast U.S., and Coastal Southeast Alaska).

Sampling Issues

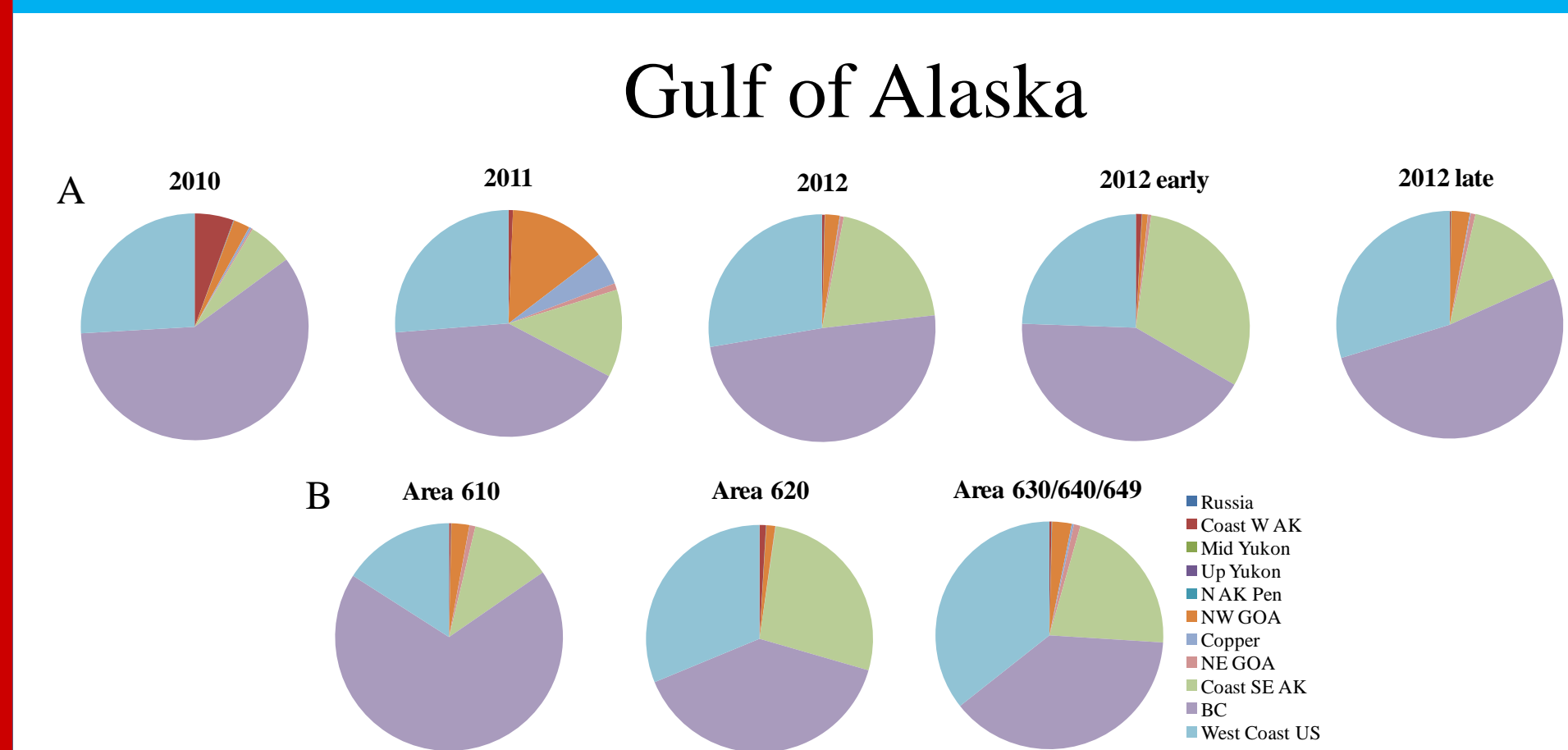
In 2011, systematic random sampling was implemented in the BSAI prohibited species catch. The observed genetic sampling rate in 2012 was 9.8%, close to the 10% goal. Opportunistic sampling was employed for the collection of the GOA Chinook salmon bycatch genetic samples. The sample set in 2012 is larger than the two previous years combined at 948, a 5% sampling rate. The lack of representative samples hinders calculating statistically reliable stock composition estimates.

Gulf of Alaska

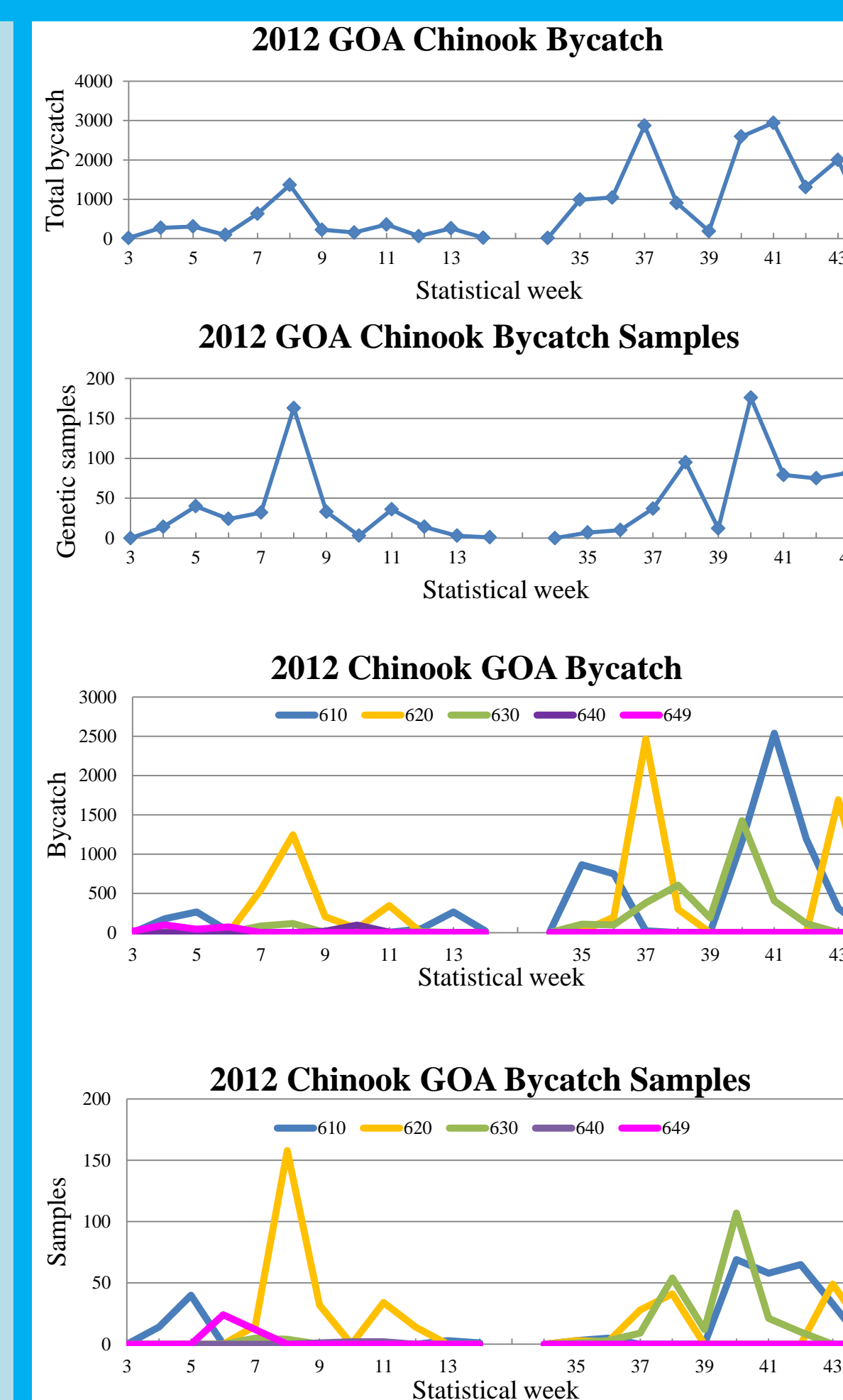
The BAYES results estimate that 99.6% of the 948 samples from the GOA originated from GOA/Pacific coastal regions, with the British Columbia contributing the most (49%), followed by the West Coast U.S. (28%) and Coastal Southeast Alaska (20%). The BAYES estimates for the early season (statistical weeks 3-14) showed British Columbia contributed the most (42%), followed by Coastal Southeast Alaska (31%) and the West Coast U.S. (24%). For the late season (statistical weeks 34-44), British Columbia (52%) predominated, higher than the West Coast U.S. (30%), and Coastal Southeast Alaska (15%). The westernmost area, 610, had the largest BAYES estimates from British Columbia (69%) with smaller components from the West Coast U.S. (16%), and Coastal Southeast Alaska (12%). Moving east into NMFS area 620, the British Columbia composition dropped (39%) while those from the West Coast U.S. (31%), and Coastal Southeast Alaska (27%) increased almost two-fold (Table 9). The samples from the three easternmost areas (630, 640, and 649) were combined due to sample size, although most were from area 630 (226). British Columbia had the highest BAYES composition (38%), the West Coast U.S. increasing (36%), and Coastal Southeast Alaska (22%) dropping.



Comparison of yearly stock composition estimates (2010-2012) based on available genetic samples from the GOA Chinook salmon bycatch. BAYES 95% credible intervals are plotted for yearly estimates.



Comparison of genetic stock composition estimates for 2010-12 based on available genetic samples from the GOA Chinook salmon bycatch. Panel A shows comparisons across time. Panel B shows comparisons between NMFS Statistical Areas in 2012. The same genetic baseline and regional groupings were used in all analyses



Number of GOA Chinook salmon bycatch and genetic samples graphed by statistical week. Top two panels show totals, bottom two panels totals by NMFS statistical areas



