

Genetics for Managers:

Defining population structure and demographic connectivity



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Outline

- Genetics basics
- Choice of markers
- Management questions
- Marine turtle examples
- Possible applications for oystercatchers

Terminology

- Genome: the sum total of genetic sequence of an organism
- Locus: the location of a particular gene in the genome
- Allele: A variant of a particular gene
- City Analogy

Genetic/Demographic Processes

- How do we distinguish different populations genetically:
 - Mutation
 - Genetic Drift
 - Migration
 - Selection (in theory, not with neutral markers we would normally use)

Mutation

- The ultimate source of genetic variation
 - eg. C changes to T or (ACTA)₁₅ becomes (ACTA)₁₆
 - Mutation rates vary with different parts of the genome
 - Typically rare

Genetic Drift

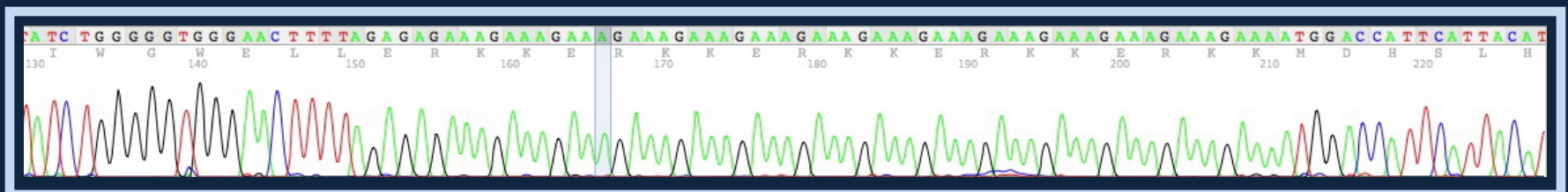
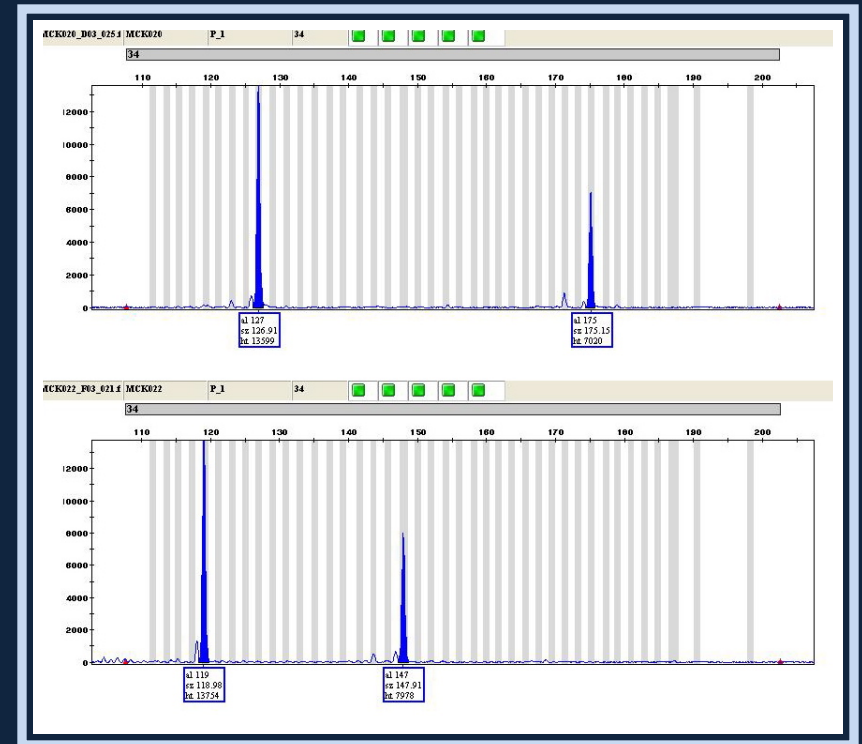
- Random sampling error that leads to population subdivision
 - Typically very slow process, especially in larger populations ($\sim 4N$ generations)
 - Typically a “weak” process, falls apart in the presence of even very limited gene flow

Nuclear Genome

- Contained within cellular nuclei
- Bi-parental inheritance
- Identify individuals, population structure, gene flow, relatedness, etc.
- Different marker types (Which question?)
 - AFLPs (amplified fragment length polymorphisms)
 - Microsatellites
 - SNPs (single nucleotide polymorphisms)

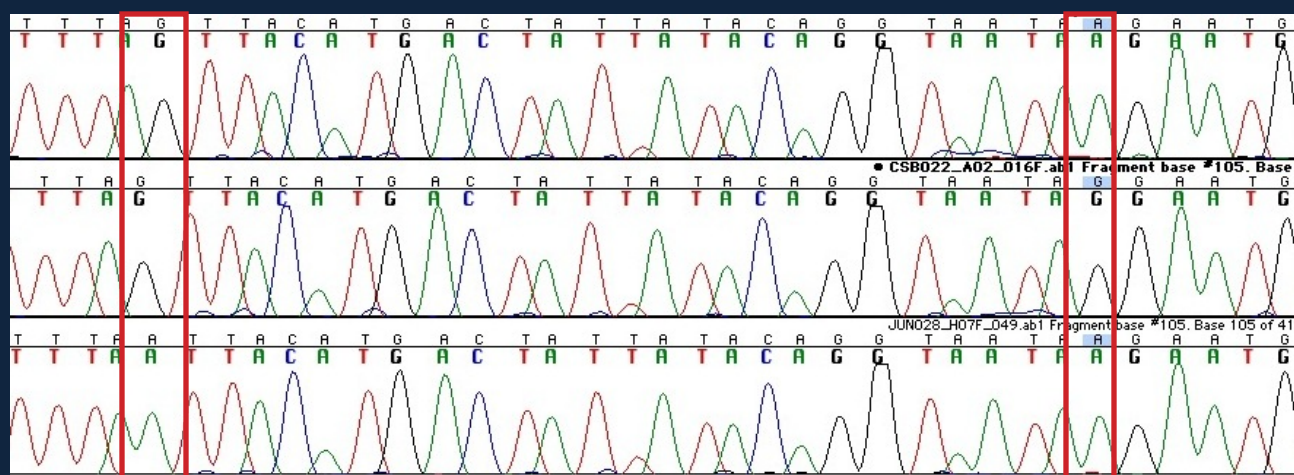
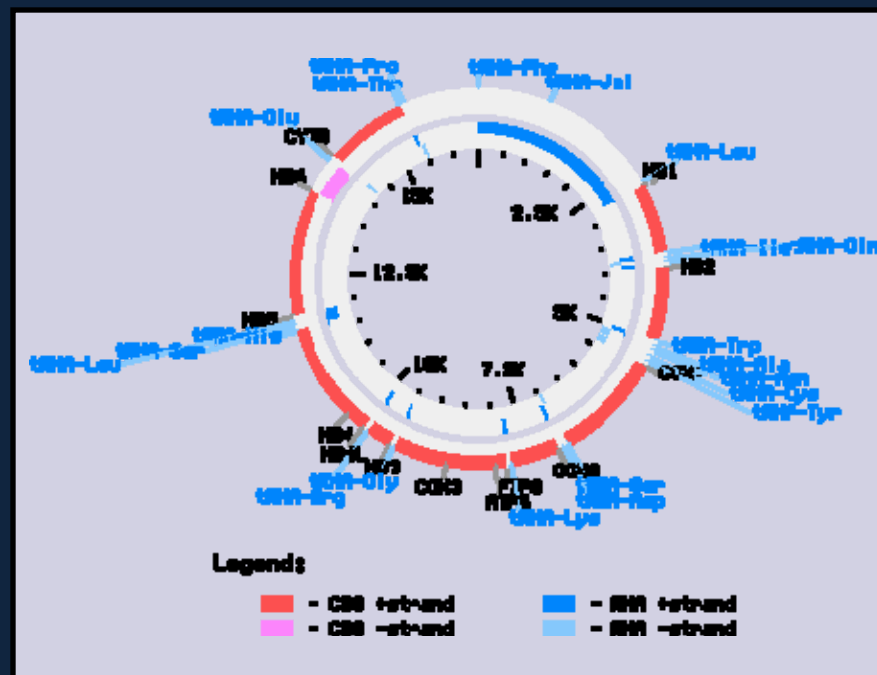
Microsatellites

- Simple tandem repeats (vary by repeat number)
- Eg. (GAAA)¹³
- High mutation rate
- Gene flow, relatedness, and individual identity

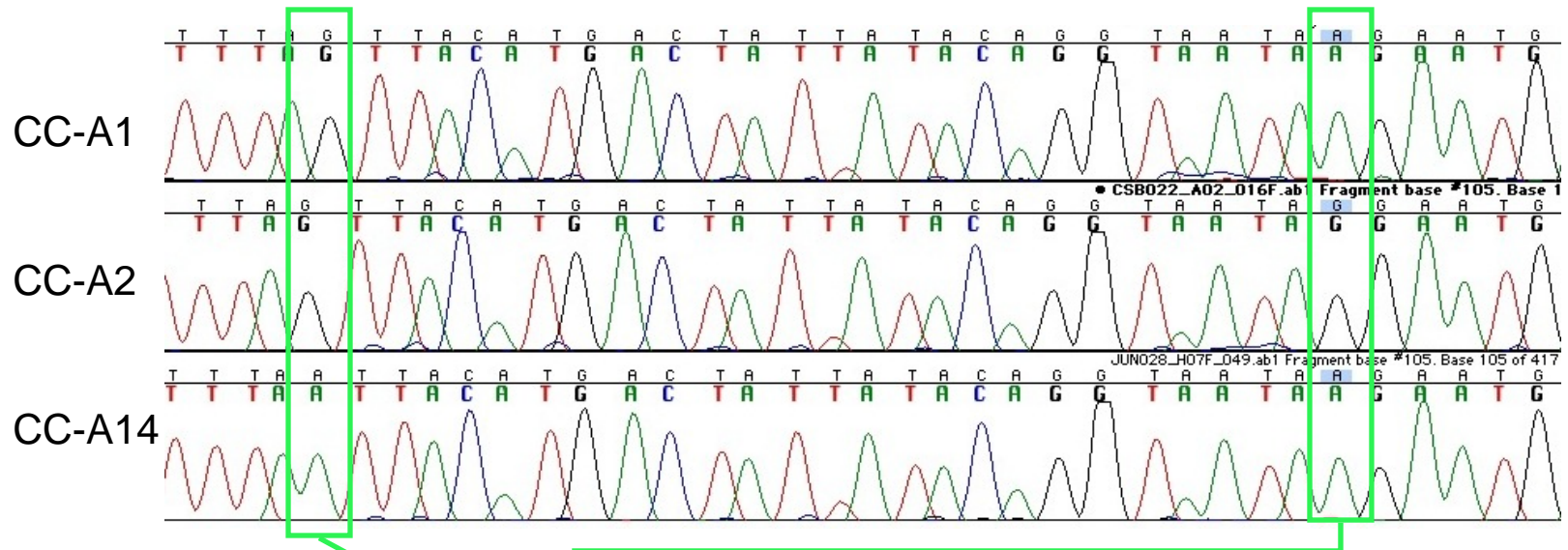


Mitochondrial Genome

- Maternally inherited
- Track distribution of matrilineal (rookery) lineages
- Variants known as “haplotypes”



Haplotype Variable Positions



		Variable Positions																															
		3	3	3	5	5	6	7	9	0	1	1	1	1	1	2	2	2	2	2	2	3	3	3	3	3	3	3	3	3	3	3	3
Haplotype		2	5	7	1	3	3	8	6	4	9	1	2	8	0	0	4	6	9	4	2	4	5	7	7	5	6	7	8	9	0		
★	CC-A1	T	G	T	T	T	A	G	A	A	C	G	G	C	C	G	C	A	-	A	A	T	A	C	-	-	-	-	-	-	-	-	
	CC-A14	T	G	T	T	T	A	A	A	A	C	A	G	C	C	A	C	A	-	A	A	T	A	C	-	-	-	-	-	-	-	-	
★	CC-A2	C	A	C	C	-	G	G	A	G	A	T	A	G	T	T	A	T	G	G	A	G	C	G	T	G	C	A	A	G	T		
	CC-A3	C	A	C	C	-	G	G	A	G	A	T	A	A	T	T	A	T	G	G	A	G	C	G	T	G	C	A	A	G	T		
	CC-A7	C	A	C	C	-	G	G	A	G	A	T	A	G	T	T	A	T	G	G	G	G	C	G	T	G	C	A	A	G	T		
	CC-A9	C	A	C	T	-	G	G	G	G	A	T	A	G	T	T	A	T	G	G	A	G	C	G	T	G	C	A	A	G	T		
	CC-A10	C	A	C	C	-	G	G	A	G	A	T	A	G	T	T	A	T	G	G	A	G	C	G	T	G	C	A	G	G	T		
	CC-A20	T	A	C	C	-	G	G	A	G	A	T	A	G	T	T	A	T	G	G	A	G	C	G	T	G	C	A	A	G	T		
	CC-A43	C	A	C	C	-	G	G	A	G	G	T	A	G	T	T	A	T	G	G	A	G	C	G	T	G	C	A	A	G	T		

Questions

- Population structure and gene flow (eg. subpopulations?)
- Recruitment and relatedness-based questions (eg. natal site fidelity versus dispersal?)
- Mixed stock analyses and assignment tests (eg. migrants versus residents?)

F Statistics

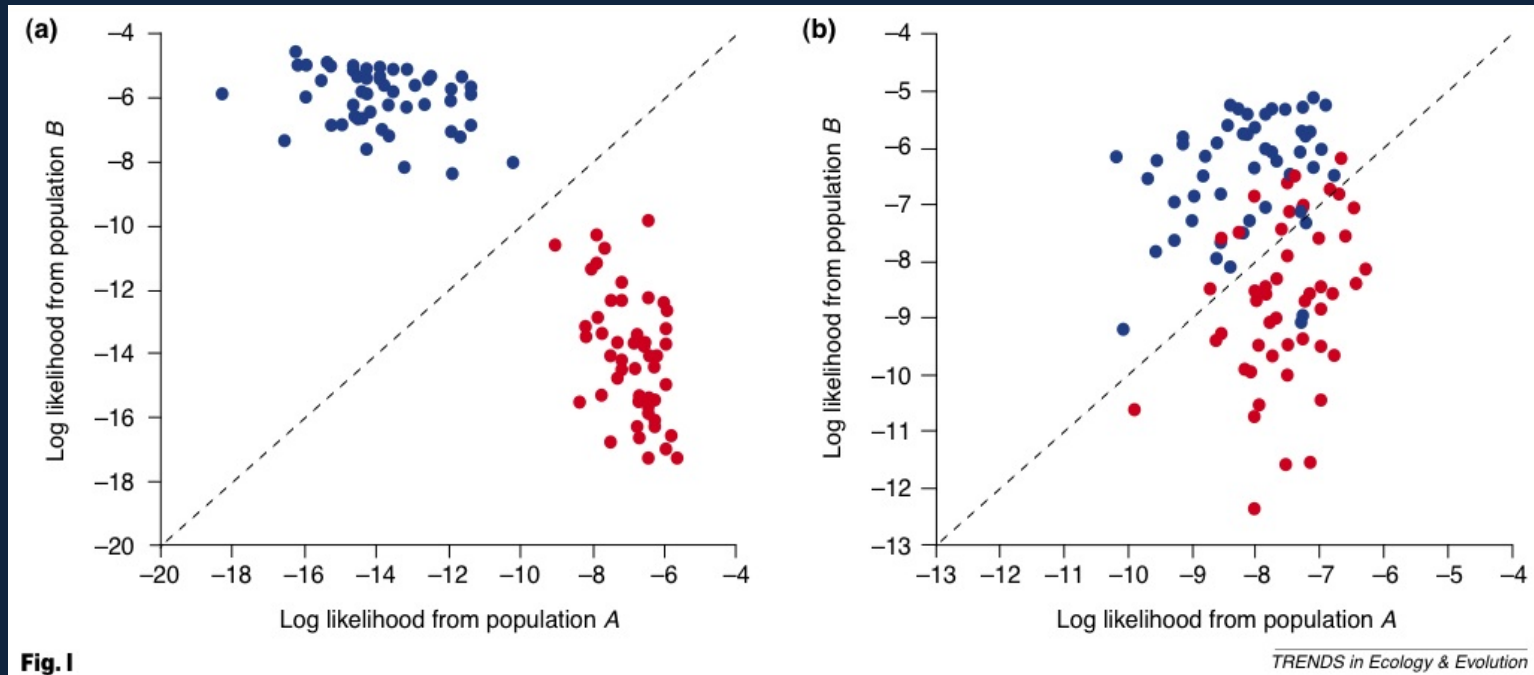
- Hierarchical measure of genetic variance
 - F_{ST} : measure of genetic variance AMONG populations
 - F_{ST} Values
 - <0.05 weak structure
 - $.05-.15$ moderate structure
 - $.15-.25$ strong structure
 - $>.25$ extremely strong structure

Loggerhead turtles- microsatellite F_{ST} values 0-0.0096 (North Carolina vs. Florida panhandle)

Assignment Tests

- Bayesian clustering or maximum likelihood
- Often more sensitive than traditional F-statistics in delimiting subpopulation numbers and boundaries
- No a priori knowledge or constraints
- Success depends on how differentiated populations are

Assignment Tests



$F_{ST}=0.14$; 99.9% confident

$F_{ST}=0.04$; 90.2% confident

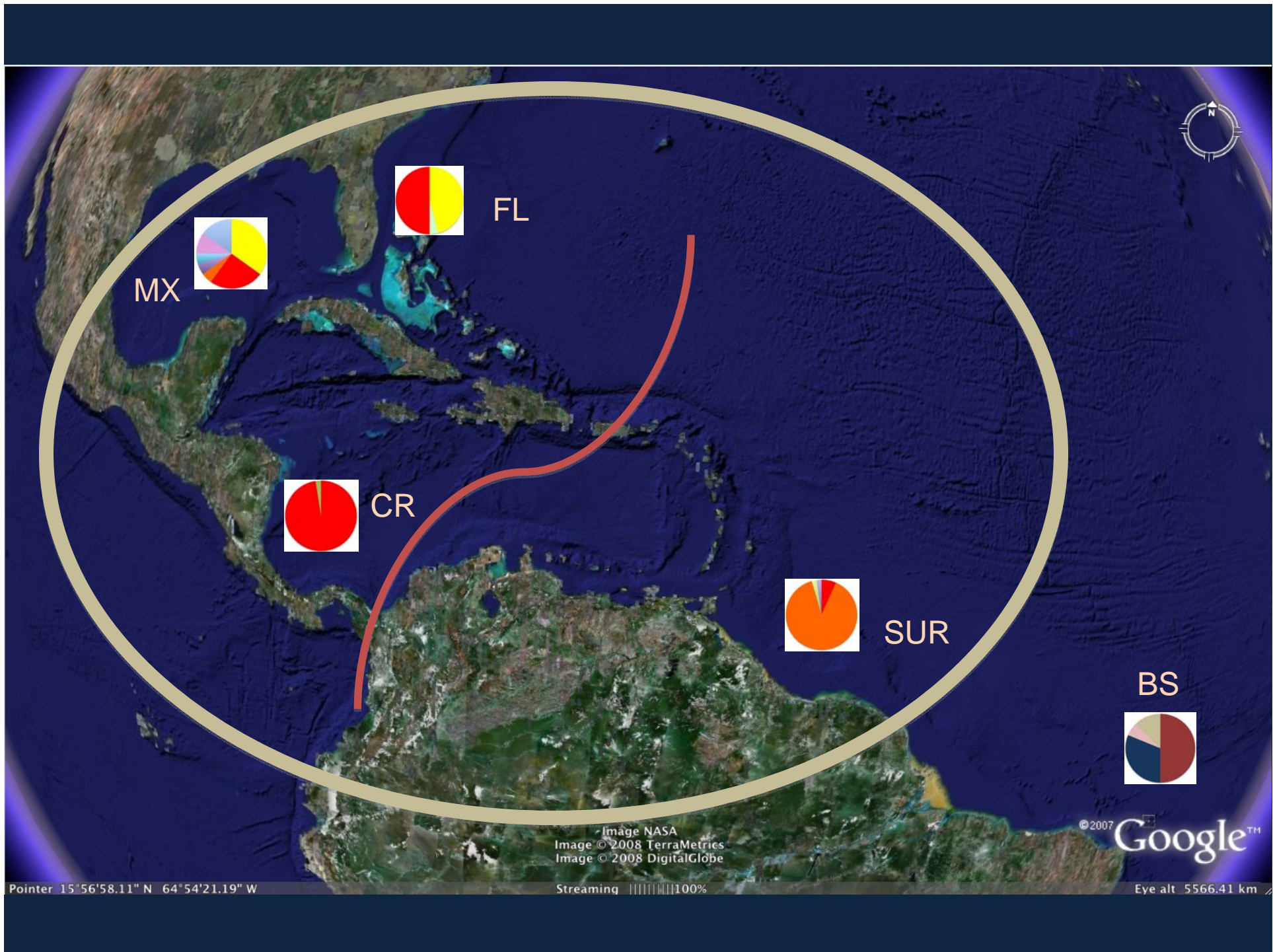
Webster et al. 2002

Mixed Stock Analysis

- Marine and anadromous fisheries
 - Very strong structure among breeding populations “stocks”
 - Oceanic life history stages (winter flocks) often represent mixtures of many breeding populations
 - Use baseline data from breeding areas to predict contributions of breeding populations to mixed foraging groups

Genetics versus Demography

- Demographic connectivity inferred from genetic data inherently limited
 - 1 effective migrant per generation prevents genetic divergence (probably more like 5-10 realistically)
 - Time lags



Caribbean Foraging Areas

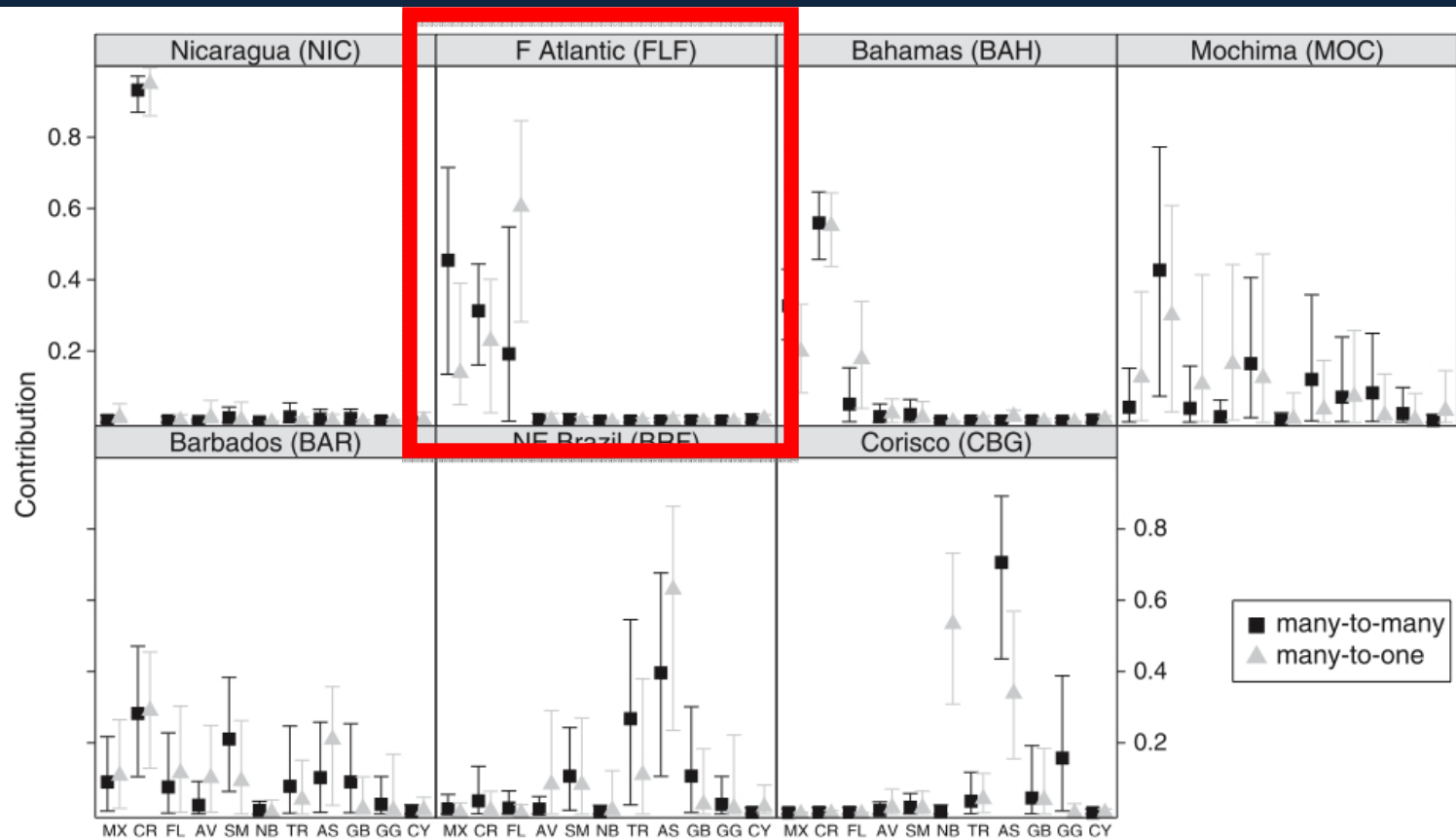


Fig. 2 Foraging-ground-centric results from many-to-many and many-rookery-to-one-foraging ground analyses. Black squares, many-rookery-to-one-foraging ground; grey triangles, many-to-many. Bars represent 95% confidence limits. MX (Mexico), CR (Costa Rica), FL (Florida), AV (Aves Island), SM (Surinam), BR (NE Brazil), TR (Trindade), AS (Ascension), GB (Guinea Bissau), GG (Gulf of Guinea), CY (Cyprus).

Bolker et al. 2007

Loggerhead turtles in the southeastern US

- Demographic parameters:
 - Intra-seasonal clutch frequency
 - Remigration intervals
 - Natal philopatry versus natal dispersal
 - Recruitment
 - Lifetime fecundity and fitness
 - Reproductive longevity
 - Connectivity of various nesting beaches (scale of management units)

Traditional Approaches

- Flipper-tagging
 - Logistically difficult
 - Scale of site fidelity versus tagging effort
- Satellite telemetry
 - Attach transmitter to first females to nest
 - Biased towards “experienced” nesters?

A New Approach

- Genetic-mark recapture
 - Non-invasive to nesting female
 - Logistically practical across the entire state
 - Individual identification and relatedness
- Preliminary results
 - At least 452 individual turtles nested in 08
 - Generational overlap
 - Early nesting females may be a biased sample
 - Sister pairs hint at strong fitness differentials

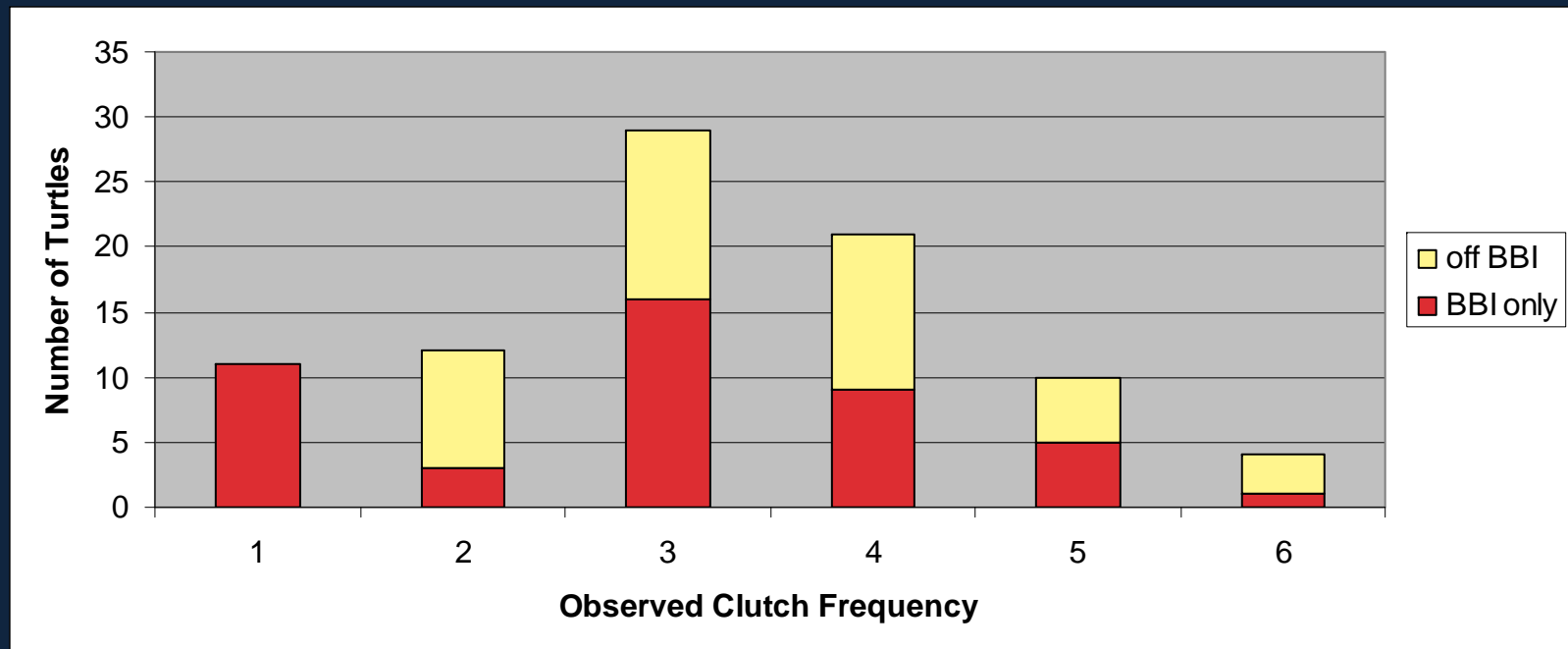
Satellite tagged females

	2005	2008
Sapelo Queen*	4 nests; all SAP	1 nest; SAP
Zapala	4 nests; SAP, OSS, SCI, WAS	4 nests; SAP
Georgia	4 nests; SAP	4 nests; SAP
Maureen	4 nests; CMB, OSS	3 nests; SAP
Pearl	6 nests; SAP	2 nests; SAP
Gypsy	4 nests; BBI, SAP	6 nests; BBI, SAP

Confirmed dead 6/7/08

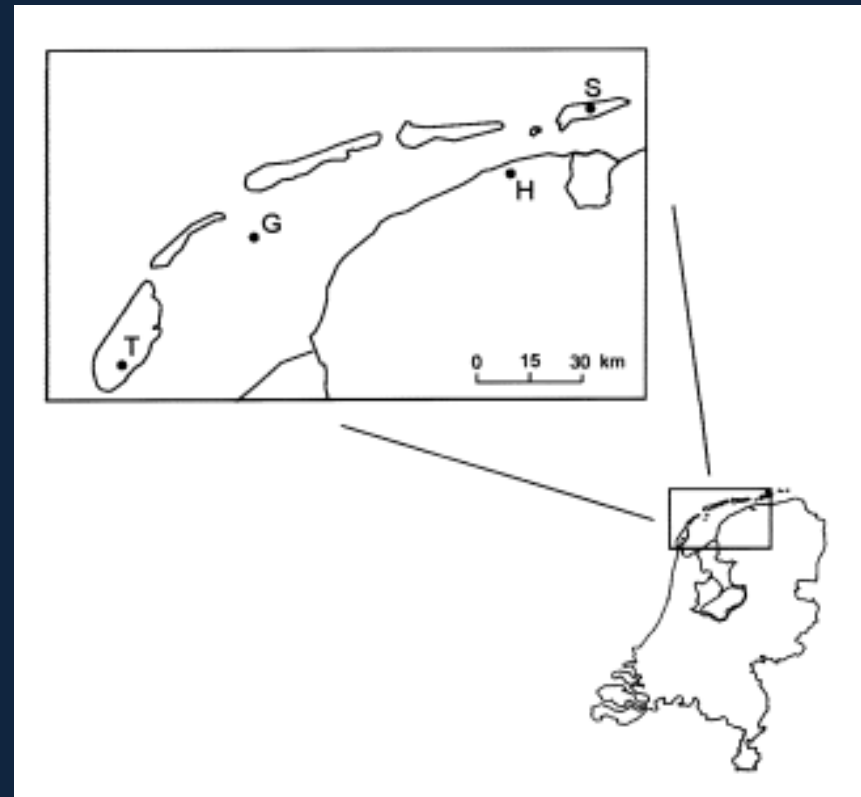
Blackbeard Island, GA

- 87% complete data
- 91 individuals laid 223 nests
- ~50% of turtles also nested off Blackbeard



Eurasian Oystercatchers

- Van Treuren et al. 1999
 - Similar life history characteristics to *palliatus*
 - No difference between leapfrogs and residents
 - No significant population structure ($F_{ST} = 0.0005$)
 - Lack of structure likely attributable to juvenile natal dispersal



Oystercatcher Potential

- Population structure
 - Mitochondrial screening
 - AFLP and/or microsatellite testing
- Demographic inferences based on relatedness:
 - Saturation sampling of breeding birds/chicks
 - Use individual ID and first order relative data to
 - Estimate reproductive longevity based on relatedness chains
 - Estimate scale of natal philopatry or dispersal

Questions ?

