

Genetic Stock Assessment of
Merluccius capensis and *Merluccius*
paradoxus

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Evolutionary History of Hake Species

- Analyses of mtDNA and allozyme data suggest that the two hake species have different evolutionary histories.
- *M. paradoxus*' origin along the SA coastline is old (approx 10-15 MYA) and they share a relationship with *M. polli* .
- *M. capensis* is recent species (2 MYA), and they share close evolutionary history with *M. merluccius*.

Life history of the species

- Temporal and spatial patterns in hake spawning are being resolved under a separate research.
- Spawning of *M. capensis* is geographically widely distributed, and *M. paradoxus* spawns mainly between Agulhas Bank and St. Helena Bay.
- Seems that most spawning takes place between mid July till mid September.
- Seems to be a general northward movement of *M. paradoxus* as they mature. Longshore movements of *M. capensis* are limited.

Importance for stock structure

- Begg et al. (1999) describes a stock as a *semi-discrete group of fish with some definable attributes which are of interest to fishery managers*
- For fishes, random mating throughout the range is rare.
- There is thus a tendency for large populations of fish to form a structured series of discrete populations .
- These population can separate in space, in time, or in both.

Preliminary investigations into the stock structure of SA Merluccius

- von der Heyden et al. (2007) sampled 311 *M. capensis* and 333 *M. paradoxus* between Luderitz and south of Cape Point and detected shallow but significant mtDNA population differentiation for adult *M. paradoxus* (older than 3-4 years).
- No mtDNA structure was evident for *M. capensis*.

mtDNA Temporal stability

- 1013 adult *M. paradoxus* (longer than 30cm), sampled over a period of three years (2005 - 2007).
- For 2005, fish from southern Namibia to the western Agulhas Bank.
- For 2006, fish were sampled from the most northern distribution on the border with Angola, but none from southern Namibia.
- For 2007, samples ranged from southern Namibia to the western Agulhas Bank.
- Analyses of population structure revealed a similar northern (Namibian) - southern (South African) differentiation but the boundaries were not as exact as in the first study.

Nuclear DNA?

Eight microsatellites were genotyped in 209 *M. paradoxus* (57 trawls) and 222 *M. capensis* (24 trawls)

Represented fish collected during 2005 and 2006.

Based on Bayesian STRUCTURE analyses the preliminary report indicated three likely stocks in *M. capensis* (map inset) and one in *M. paradoxus*.



Bloomer et al. 2009

Problems identified with the outcome of the genetic data up to 2011.

- Lack of comprehensive sampling throughout the range of the species (different years included samples from different sites).
- Lack of temporal stability throughout the range for both species (sampling at the same time).
- Lack of a comparative dataset from both mtDNA and nuclear DNA origin.

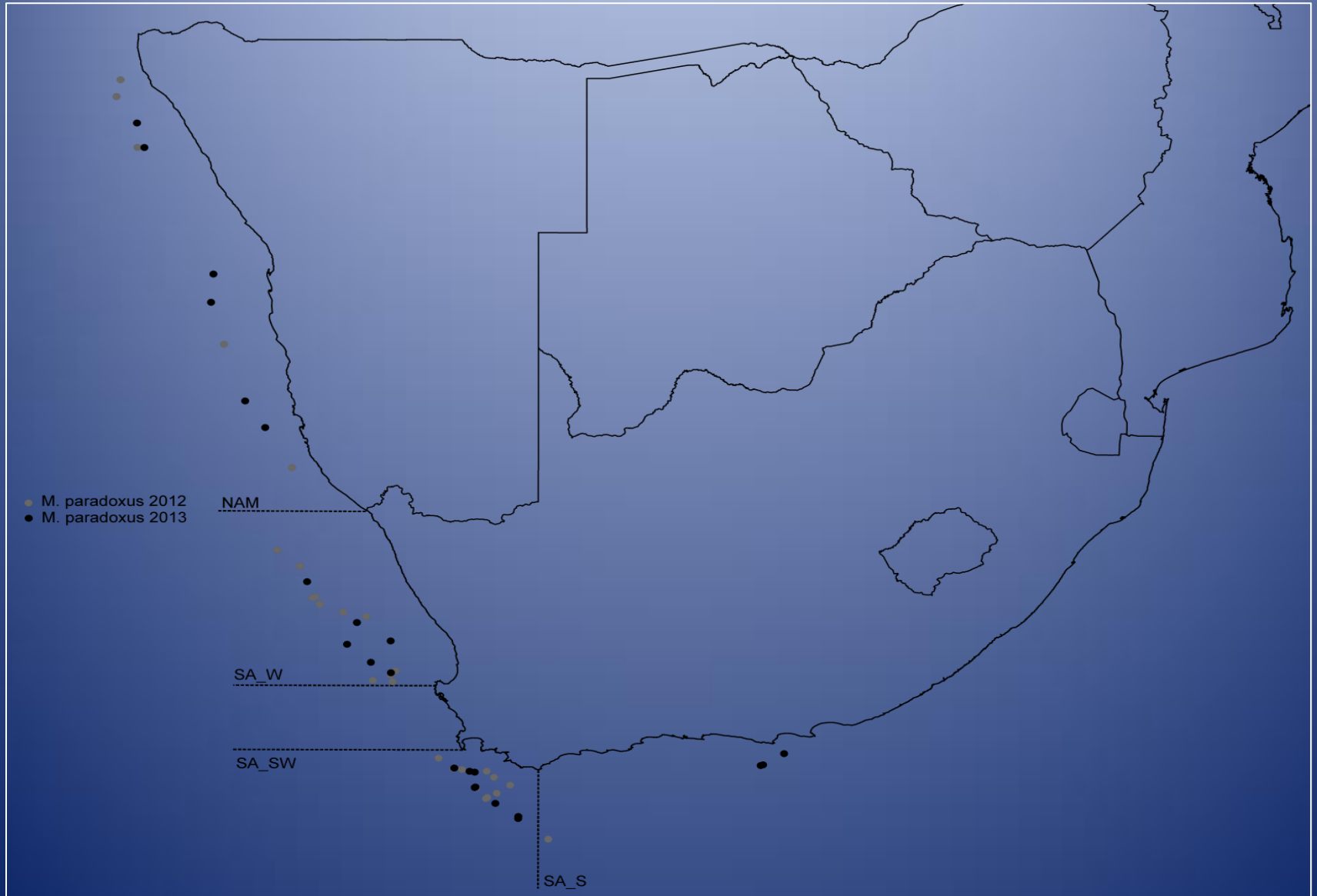
Planned research after 2011

- Obtain comprehensive sampling from throughout the range.
- Include temporal sampling for both species.
- Include microsatellite data on a large number of loci.

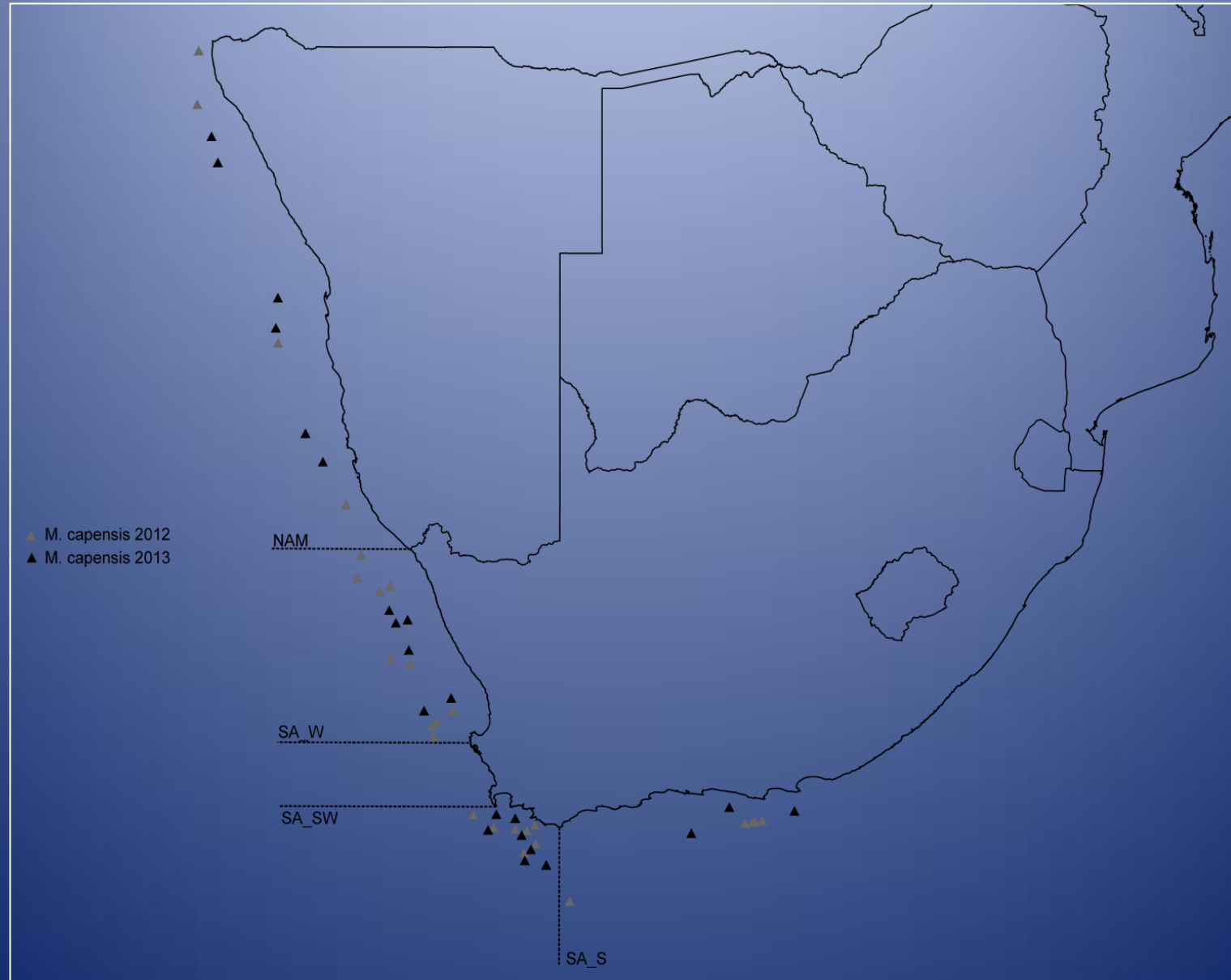
Individuals selected for DNA extraction:

- All four regions as defined in von der Heyden et al. included: 2012 + 2013; 2014 collection planned.
- *M. paradoxus* = 897 fish (2012 = 230 Namibia; 2013 = 154 Namibia).
- *M. capensis* = 974 fish (2012 = 209 Namibia; 2013 = 180 Namibia).

M. Paradoxus sampling (2012 + 2013)



M. capensis sampling (2012 + 2013)



Preliminary mtDNA results

- Nucleotide diversity (π), haplotype diversity (h) and results from analyses of molecular variance, *M. paradoxus* (n = 293) and *M. capensis* (n = 279).

	π	h	Φ_{ST}	p	% Variation	
					Among regions	Within regions
<i>M. paradoxus</i>	0.002	0.554	0.009	0.12	0.99	99.01
<i>M. capensis</i>	0.006	0.854	0.000	0.60	0.00	100.00

mtDNA AMOVA results

- Pairwise Φ_{ST} values indicating the differentiation among regions with *M. paradoxus* above and *M. capensis* below the diagonal. All Φ_{ST} values were non-significant ($p > 0.05$).

	NAM	SA_W	SA_SW	SA_S
NAM	-	0.032	0.001	0.000
SA_W	0.000	-	0.014	0.000
SA_SW	0.000	0.001	-	0.018
SA_S	0.002	0.007	0.000	-

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