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.
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.
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. Paradoxus sampling (2012 + 2013)
M. capensis sampling (2012 + 2013)
Preliminary mtDNA results

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

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<tr>
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<th>$\pi$</th>
<th>$h$</th>
<th>$\Phi$ST</th>
<th>$p$</th>
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<td>Among regions</td>
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<tr>
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<td>0.554</td>
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<td><em>M. capensis</em></td>
<td>0.006</td>
<td>0.854</td>
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mtDNA AMOVA results

• Pairwise ΦST values indicting the differentiation among regions with *M. paradoxus* above and *M. capensis* below the diagonal. All ΦST values were non-significant (*p > 0.05*).

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Discussion

• The highest level of differentiation was detected among the Namibian and West – Coast SA samples for *M. paradoxus*.

• However, pairwise ΦST values were not significant between any of the sampling sites.
Acknowledgements

• Kay Welsch.
• SA and Namibian teams on board of Dr Fridtjof Nansen.
• Paul Kainge for Namibian logistics and support.
• Tore Stromme and Oddgeir Alvheim for logistics and back-up on Nansen.
• Dr Rob Leslie and his team for Africana sampling.
• Capfish and particularly Mel Smith for commercial sampling.