# Population genomic structure in Sardinops sagax

GGGGTOCGAGTTGTAATTTGTAGAGG GOTCAAATTTGAAATCTGGCTCCT CGTGTGCCTACTGAGTTCCCTGGAAC CGGGTGCCTACTGAGTTCCCTGGA GAGAGCCCCGTCTGGTAGGACACCC GGGTTCCTTCCGAGTTCCCTGGAACG OGGGTTCOTTCCGAGTTCCCTGGAACC GGTTCOTTCCGAGTTCCCTGGAACGGG TACATGGATAACCGTGGTA CGGGACGCCATAGAGGGTGAG GGTTCCTTCCGAGTTCCCTGGAA GGAACGGG<mark>ACGCCATAGA</mark>GGG TGGCTCCTTCGGGGCCCGAG GAGCCCCGTCTGGTCGGAAACCCA ATAGAGGGTGAGAGCCCCGTCTGG





Peter Teske





West coast

Similar to: Norway



**Southwest coast**Similar to: Irish Sea

One of the world's bestdefined thermal gradients



Northeast coast
Similar to: Red Sea



**East coast** 

Similar to: **Eastern Mediterranean** 

**South coast**Similar to: **Portugal** 



### Genetic structure often mirrors biogeography Each species may comprise up to four 'cryptic species'

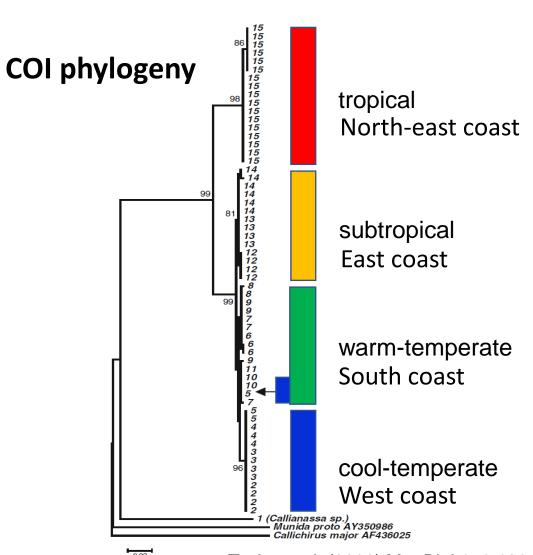


#### Kraussillichirus kraussi

(sandprawn)

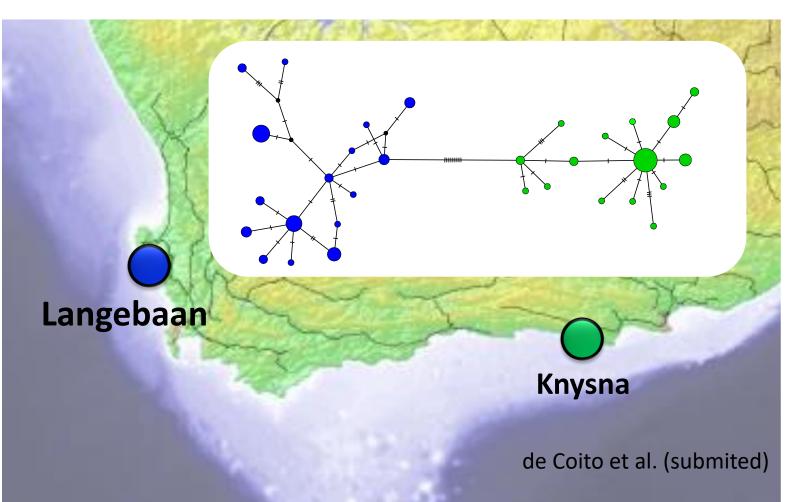


Pillay et al. 2017, Mar Ecol Prog Ser 347: 1-14

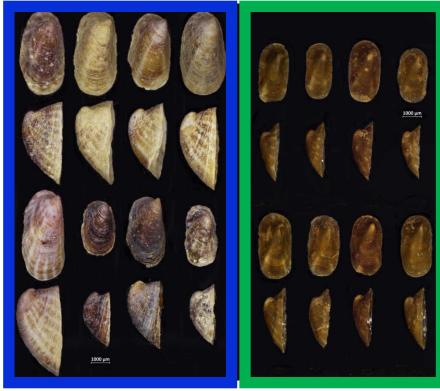


# Conservation applications

Translocations to increase genetic diversity must be prevented

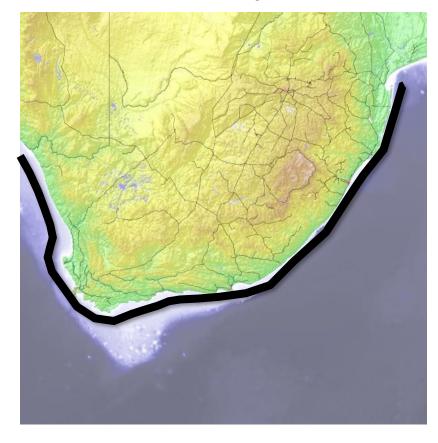


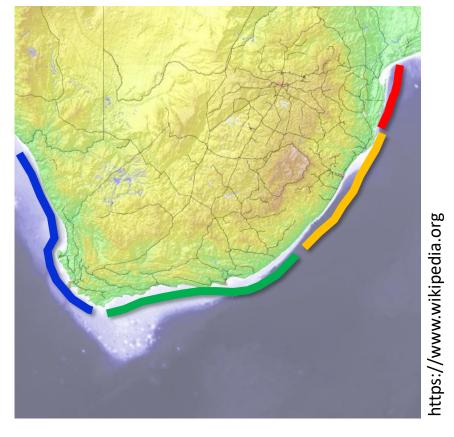
Siphonaria compressa (Critically Endangered)



## Not all species exhibit structure

Does this depend on dispersal ability?



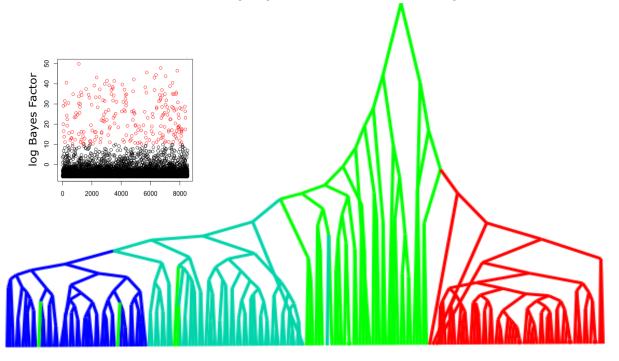


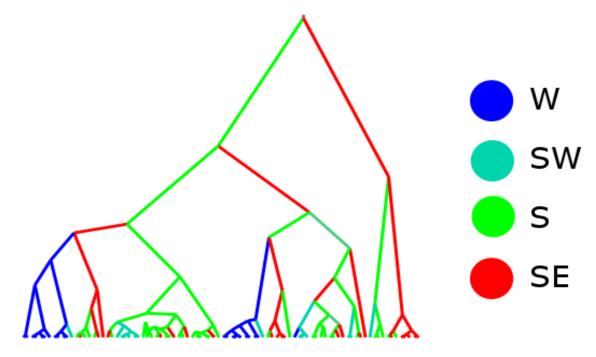
Active dispersers: **Genetic homogeneity?** 

Passive dispersers: **Genetic structure?** 

# Incipient ecological speciation?

Not supported by DNA barcoding





## ddRADseq SNPs

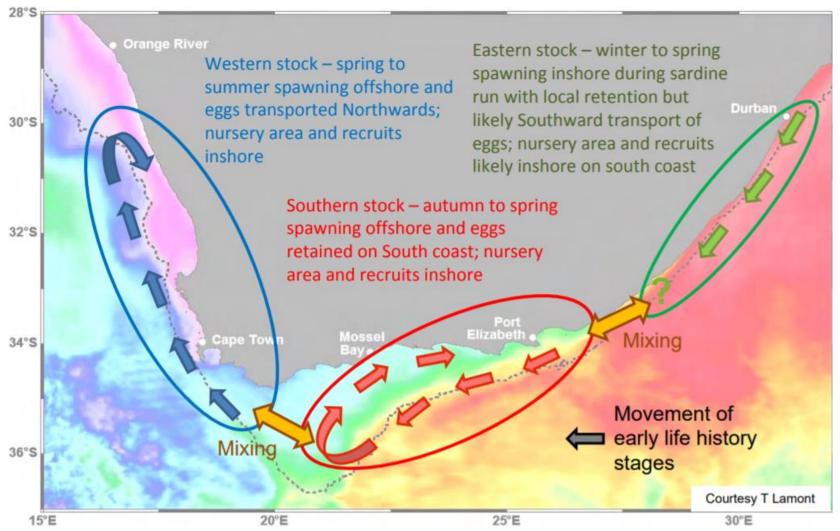
(under thermal selection)

COI

(incomplete lineage sorting)

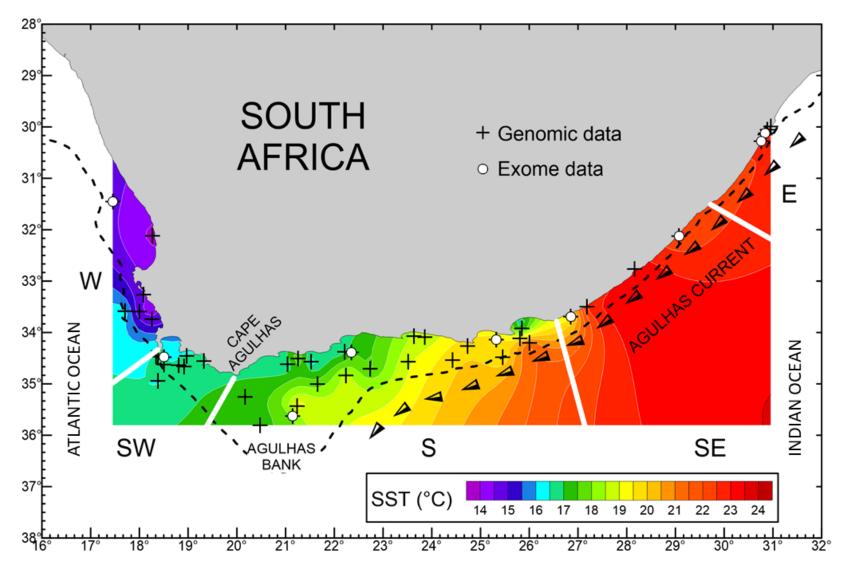
Drost et al. (2016) Mar Biodivers 46:465-471

# 3 stock hypothesis



& Moloney C (unpublished)  $\bigcirc$ der Lingen van

# Sampling and sequencing



#### **Genomic data (ddRADseq):**

284 sardines

40 locations

8 295 SNPs

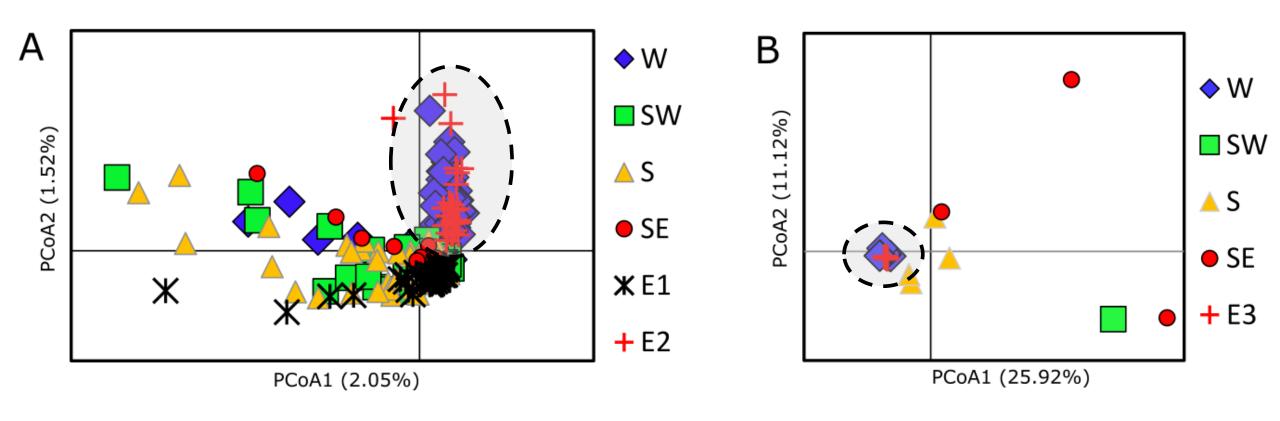
#### **Exome data (RNA-seq):**

14 sardines

7 locations

14 973 SNPs

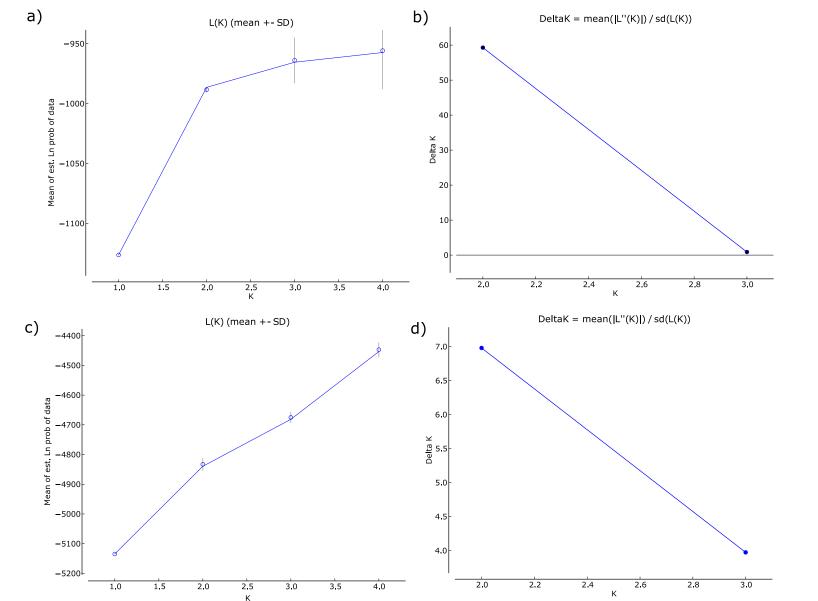
# Selectively neutral SNPs



**Genomic data** 

**Exome data** 

### Candidate SNPs: Identification of clusters



#### **Genomic data**

$$K = 2$$

#### **Exome data**

$$K = 2$$

STRUCTURE analyses followed by STRUCTURE HARVESTER

## Assignment to two stock components

