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Phylogeography and Population Genetics of Coastal Bivalves

Introduction

In coastal sediments, bivalves dominate biomass and are crucial to ecosystem functioning. Although local population extinctions are common, little is known on connectivity between coastal bivalve populations within and across regions.

Phylogeographic and population genetic analyses started at the Wadden Sea Station Sylt with studies on *Mya arenaria* which is widely distributed across the Northern Hemisphere but went extinct in Europe during glaciation. An ongoing study focuses on the Common cockle *Cerastoderma edule* which is abundant along European coasts. The sister species *C. glaucum* is topic of a third project, where individuals of the southern North Sea were analyzed using the RAPD method.

The Soft-shell clam *Mya arenaria*

The analysis of a partial sequence of Cytochrome B as mitochondrial marker and the internal transcribed spacer (ITS) of the nuclear rDNA suggest a recent recolonisation of Europe and the Pacific east coast originating from the West Atlantic (Fig. 1).

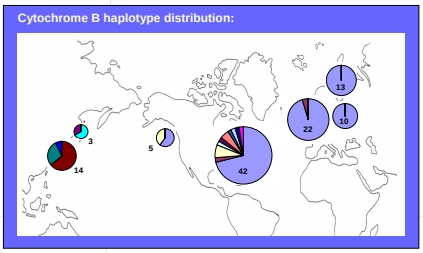

Figure 1: *Mya arenaria* unburied (left). Distribution of CytB haplotypes (colour of segments: proportion of different CytB haplotypes; Numbers: individuals analyzed)

⇒ Because of the distance and time of the first appearance in Europe, transport by early shipping is likely.

The Common cockle *Cerastoderma edule*

COI Analyses reveal slight geographic separation of *C. edule* - populations from Norway to Morocco with one dominant haplotype occuring at all sampling sites except in the Wadden Sea (Fig. 3) .

Figure 2: The Common cockle.

⇒ We assume extended larval drift across regions. The possibility of northern genotypes remains to be corroborated by AFLP analyses.

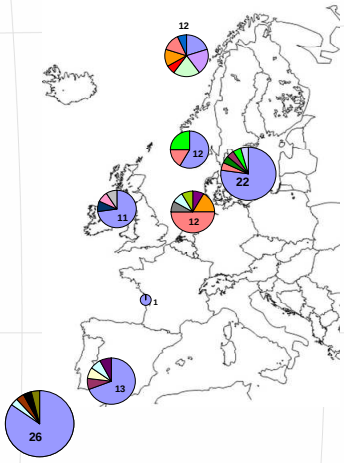

Figure 3: Distribution of haplotypes along the European shore (coloured segments: proportion of different COI haplotypes; numbers sum up individuals analyzed).

The Lagoon cockle *Cerastoderma glaucum*

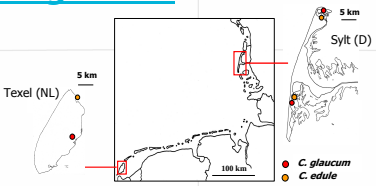

Figure 4: The Lagoon cockle (left) is mainly found in saltmarsh creeks and seagrass meadows. Sampling sites in the North Sea indicated rectangles and insets.

C. glaucum which is lacking plantonic larvae exhibited more genetic homogeneity within the locations sampled in the Wadden Sea than *C. edule* (Fig. 5). However, the apparently isolated populations (Fig. 4) also showed surprising similarity between the locations.

⇒ This may be explained either by a rather recent separation in this region or by frequent local extinction events and migrant birds serving as a vector of connectivity over wide distances between lagoonal populations of this cockle.

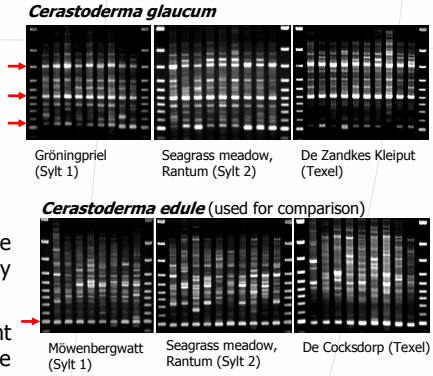

Figure 5: RAPD analysis shown with primer RA02

Summary and outlook

The shown examples of soft bottom bivalves suggest a high level of integration within European bivalve species.

Looking at population genetics may confirm hypotheses and generate new ideas of recent distribution and potential barriers. With this basal knowledge, experiments and well directed sampling will bring new impulses for the research on population connectivity.

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