

# Genetic variability of Chilean and Peruvian surf clams (*Donax marincovichii* and *Donax obesulus*)

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## Introduction

Exposed intertidal sandy beaches are commonly dominated by surf clams of the genus *Donax* (Ansell 1983). In Peru and Chile these bivalves play an important role for artisanal fisheries. Within this genus, the taxonomic status of *Donax marincovichii* and *D. obesulus*, distributed along the Peruvian coastline, is controversially discussed (Coan 1983, Guzmán et al. 1998). As morphometric comparisons reveal no significant differences we possibly deal with a single, rather than with two species.

The aim of this study is twofold: First, we want to establish a molecular marker suitable for barcoding and providing evidence, based on sequence data, concerning this taxonomic controversy. Second, we want to estimate the genetic relatedness among geographically distant populations along the Peruvian coastline.



*D. marincovichii* (23 mm)

*D. obesulus* (17 mm)

## Material and Methods

Specimens of the two putative species *D. marincovichii* and *D. obesulus* were sampled at nine beaches along their distribution (S18°27'53.8"/W70°18'24.3" to S3°33'57"/W80°27'5"). Additionally, specimens of *D. asper* and *D. hanleyanus* were sampled from one beach each. Opened and closed shells were conserved in >80% ethanol. DNA was extracted with the Qiagen Dneasy kit according to the manufacturer's recommendations. 10-100 ng DNA were used for PCR-amplification of a fragment of the cytochrome oxidase I (COI) using the primers HCO (5'-TAAACTTCAGGTGACCAAAAAATCA-3') and LCO (5'-GGTCAACAAATCATAAAGATATTGG-3') (Folmer et al. 1994) in 25 µl reactions. PCR products were purified using the Qiagen DNA purification kit according to the manufacturer's recommendations. Sequencing was conducted on an ABI 3730xl automated sequencer. Sequence data were processed and aligned using the ClustalW algorithm. Phylogenetic analysis was performed using PAUP4beta10.



*D. hanleyanus* (30 mm)

*D. asper* (30 mm)

## Results and Discussion

Sequence data from the COI proved to be useful for species discrimination within the genus *Donax*: The taxonomic status of both species, *D. asper* and *D. hanleyanus* is well supported. However, there is no indication of reproductive isolation between *D. marincovichii* and *D. obesulus* in the COI data (Fig. 2a). With 0 – 1.2% sequence divergence, the divergence between *D. marincovichii* and *D. obesulus* is on the order of known intraspecific variability in the COI gene (Held 2000; and Fig. 2b). Therefore, the taxonomic status of the two species must be questioned.

No genetic differentiation between the geographically separated *D. marincovichii* populations could be observed from the sequence data. In the future, molecular markers with higher resolving power (e.g. AFLP, Microsatellites) must be analysed for these puposes.



Fig. 1: Geographical distribution (—) and sampling localities (1-11) of *D. marincovichii* and *D. obesulus* along the Chilean and Peruvian coast. Locality 12 shows the beach where *D. hanleyanus* was sampled.

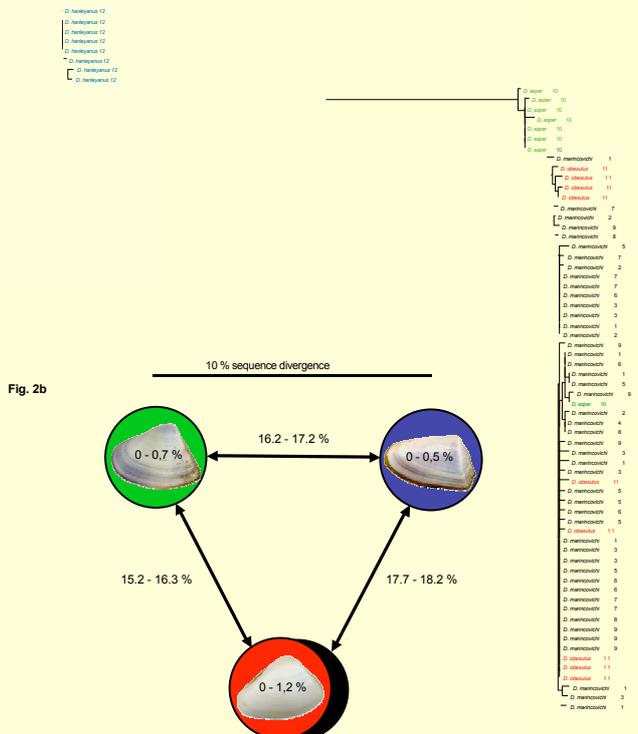
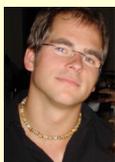


Fig. 2: (a) Relatedness between the *Donax* species investigated in this study based on the investigation of a 606 bp fragment of the mitochondrial cytochrome oxidase I. (b) interspecific and intraspecific (in circles) genetic distances between *D. asper*, *D. hanleyanus*, *D. obesulus*, and *D. marincovichii*. *D. obesulus* and *D. marincovichii* cannot be distinguished based on the COI data.



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