appear well-supported and whether names are available for them.

Several names in current use require revision. For example, *Cyclonaias* is an objective synonym of *Rotundaria*, which becomes the oldest available name for a major subgroup of *Quadrula*. *Anadontina*, usually buried in synonymy of the eastern North American *Alasmidonta*, is an overlooked senior synonym of *Lamellidens*, a major south Asian genus. *Potomida* is the oldest available genus for *Margaritifera auricularia*, if it is separated from *Margaritifera*, rather than for *Psilunio littoralis*. *Nodularia*, often treated as a synonym of *Unio*, appears genetically well-differentiated. Although current usage includes numeous independent clades in *Lampsilis* and *Villosa*, almost no names exist for dividing up these heterogeneous groups. True *Anodonta* probably does not exist in eastern North America, though the western North American *Anodonta* species are not far from *A. cygnea*. Revision of the classification of this diverse, imperiled group of bivalves will provide a better guide to their true relationships and thus of their biology than the current nomenclature, but it will require extensive effort.

GENETIC VARIABILITY OF CHILEAN AND PERUVIAN SURF CLAMS (*DONAX MARINCOVICHI* AND *DONAX OBESULUS*)

Carstensen, D., Herrmann, M., Laudien, J., Schiel, S., Arntz, W., Leese, F., and Held, C.

Alfred Wegener Institute for Polar and Marine Research Bremerhaven, Germany; (1) dcarstensen@awi-bremerhaven.de*

Exposed intertidal sandy beaches are commonly dominated by surf clams of the genus *Donax*. In Peru and Chile these bivalves play an important role for artisanal fisheries. Beside that, little is known about the taxonomy, biology, and the clam's susceptibility to climatically induced changes. The taxonomic status of the two "species" *Donax marincovichi* and *Donax obesulus*, distributed along the Peruvian coastline, is controversially discussed. As morphometric comparisons reveal no significant differences we possibly deal with a single rather than with two species. Furthermore, our knowledge on larval dispersal allowing gene flow among populations is scarce. Therefore, both putative *Donax* species were sampled at ten beaches along the coastline from northern Chile to northern Peru. Partial cytochrome oxidase I sequences were analysed in order to estimate the genetic distances between both putative species and to estimate the intraspecific gene flow along the coastline. Region specific patterns and the dependence on recruitment of local stocks are discussed.

MORPHOLOGICAL PHYLOGENETICS OF THE EARLY BIVALVIA

Carter, J.G., Campbell, D.C., and Campbell, M.R.

(1) Department of Geological Sciences, University of North Carolina at Chapel Hill, NC 27599-3315, USA; treatise@unc.edu.*
(2) Department of Biological Sciences, Biodiversity and Systematics, University of Alabama, Box 870345, Tuscaloosa, AL, 35847-0345, USA; amblema@bama.ua.edu.
(3) 2233 Mount Pleasant Road, Bloomington, IN, 47421, USA; ecphora@indiana.edu.

Fossil bivalves provide ample characters of shell morphology, hinge dentition, ligament structure, shell-muscle scars, and shell and ligament microstructure to provide a sound basis for phylogenetic studies independent of genetics and soft anatomy. Such studies have an advantage over neontological approaches because they permit the researcher to focus on older, more plesiomorphic members of a clade, thereby reducing convergence, and because they can identify ancestors as opposed to just close common ancestry. The present study of 296 predominantly Paleozoic and Mesozoic bivalves is based on 126 parsimony-informative characters for the Subclass Palaeotaxodonta, 183 for the Superorder Pteriomorphia, and 156 for the Superorder Heteroconchia.

The analysis of 40 Palaeotaxodonta resulted in 14 most parsimonious trees with 613 steps. The strict consensus tree showed the Solemyidae as a sister group to Early Ordovician *Afghanodesma* (Nuculoidea) and the paraphyletic family Praenuculidae (Nuculoidea). The Praenuculidae gave rise independently to the Nuculidae, and then, in no indicated order, to the Tironuculidae (Nuculoidea), Malletiidae (Nuculanoidea), Ctenodontidae, and a polyphyletic Cardiolariidae. The majority rule consensus tree provided a more definitive sequence, with the Praenuculidae giving rise to the Nuculidae, then the Ctenodontidae, Tironuculidae, and Malletiidae, with the Cardiolariidae being polyphyletic. These results are compatible with neontological evidence for very close affinity between the Solemyoidea and the Nuculoidea (1), but they contradict paleontological evidence that the Ctenodontidae gave rise to the Solemyidae (2). Secondary loss of hinge teeth