

Editorial

Molecular tools are well established in marine microbiology and are increasingly being used with more complex marine taxa. Molecular data provide a complementary approach to discriminating species separated by subtle morphological characters. Recently, numerous studies have confirmed the usefulness of such data, in addition to morphology, as supplementary support for species identification. Until recently, larval and adult somatic morphology was the primary source of identification data, but over the past decade or so molecular data have become widely accessible, making it possible to use much larger datasets.

The estimated number of biological species that need to be described and the consequent difficulty of creating efficient tools is an important challenge to the taxonomy and ecology of the 21st century. In this context, the primary purpose of molecular data is usually not to produce new descriptions but to facilitate taxonomic expertise by developing a global standard for the identification of biological species. Furthermore, taxonomic expertise depends directly on the knowledge that evolves continually with the new data provided by traditional taxonomic research. The combination of both traditional approaches and molecular tools is a recipe for success.

In this volume of *Scientia Marina* we highlight the study of Guerao *et al.* (Guerao, G., K.B. Andree, C. Frogliá, C.G. Simeó and G. Rotllant., 2010. Identification of European species of *Maja* (Decapoda: Brachyura: Majidae): RFLP analyses of COI mtDNA and morphological considerations. *Sci. Mar.*, 75(1): 129-134) as our featured article. In the context of the integrative taxonomy advocated by many authors, this paper illustrates the different sides of taxonomic activities. First, it confirms the validity of subtle morphological characters that clearly differentiate the species of a large group of crabs. Second, it provides a useful tool for identifying the larvae and juveniles of these species of *Maja*, thus facilitating ecological studies on them.

E. Macpherson, Associate Editor
D. Vaqué, Editor-in-Chief