CHAPTER 71-13

GENETIC DIVERSITY AND EVOLUTION OF BRACHYURA

BY

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INTRODUCTION

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Brachyura is widely acknowledged for its morphological and ecological versatility, but the underlying genetic diversity has not received much attention until recently. Genetic diversity determines phenotypes and also provides the raw material for natural selection and adaptation. The members of the taxon have thus the potential to evolve and adapt to the changing environment, which may ultimately result in speciation. A clear picture of both species diversity and genetic diversity is therefore useful to better understand the evolutionary past and to predict the adaptability of a taxon. This field of research is relatively new for Brachyura and Crustacea in general, as it is for most invertebrates other than insects. The classic work by Hessler et al. (1982) was based entirely on morphological analyses. With regard to the genetic diversity of Crustacea, the first studies based on polychromatism were focused on non-decapods (Bocquet et al., 1977;
Hedgecock et al., 1982). Only crayfishes among decapods have been studied to any extent (Black, 1975; Black & Huner, 1976). Studies on the genetic diversity of brachyurans only started about ten years after the introduction of *allozyme* analysis as a tool for determining genetic *polymorphism* in natural *populations* (Harris, 1966; Lewontin & Hubby, 1966). The earliest applications of this technique to Brachyura included its use in estimating intraspecific *genetic divergence* (Gooch, 1977; Nelson & Hedgecock, 1980; Redfield et al., 1980) and for discriminating between species of *Uca* (Ocypodidae) (Salmon et al., 1979). The use of *molecular techniques* in genetic and *evolutionary studies* of brachyurans has therefore a relatively short history of less than four decades. Because of the rapid advance in techniques for analysing *DNA* especially after the development of the polymerase chain reaction (*PCR*), however, the applications in genetic and evolutionary studies in Brachyura have emerged as one of the most thriving fields of research. The number of publications in this field of study on Brachyura has increased from less than 15 per year in the early 2000s to nearly 50 in 2014 (fig. 71-13.1). The utility of molecular tools is widely appreciated and has taken an increasingly important role in the *phylogenetic reconstruction* of Brachyura and other taxa. The *molecular approach* has also much contributed to our understanding on the genetic diversity, *systematics*, *ecology*, *biogeography*, and *evolution* of this morphologically and ecologically versatile group of decapods.

We first introduce the various molecular techniques that have been applied for studying genetic diversity and evolution of Brachyura. We will then review the three major research areas applying these molecular techniques, namely (1) *intraspecific genetic studies* including *phylogeography*, population genetic structure and genetic diversity of brachyuran crabs, (2) the use of molecular techniques for *identifying brachyuran species*,

![Fig. 71-13.1. Number of journal papers published between 1990 and 2014 (conference abstracts and book chapters not included) on genetic diversity and evolution of Brachyura based on molecular studies.](image)