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EDITORIAL

Editorial and Retrospective 2008

State of the Journal

We are pleased to report that *Molecular Ecology* continues to expand in size and impact. When we wrote this editorial, we were on track to publish 5300 pages in 2007, which represents a greater than 10% increase over the last year and a greater than 50% increase over the past 5 years. This increase in page numbers has been accompanied by an expansion in the number of issues from 12 to 24, as well as an increase in impact factor from 3.01 in 2002 to 4.83 in 2006 (Fig. 1). *Molecular Ecology* now ranks sixth in impact factor among the 114 journals listed in ISI's Ecology category in 2006, and second among ecology journals that publish primary research results.

Despite changes in our editorial and production staff, publication times at *Molecular Ecology* continue to be excellent. The time from manuscript receipt to an editorial decision averages 49 days. Our production staff moves accepted manuscripts to Online Early publication in 39–40 days, with the print version appearing approximately 20 days later. We thank journal secretaries, Elinor Smith and Simmoné Fellowes, and production editor, Gillian Carmichael, for their efforts in ensuring that manuscripts are efficiently processed, reviewed, and published.

Editorial Policy

We have implemented several editorial changes to increase the quality and visibility of science published in *Molecular Ecology* and *Molecular Ecology Resources* (formerly *Molecular Ecology Notes*), as well as to more effectively serve the molecular ecology community. We are now publishing a News and Views section edited by Nolan Kane (University of British Columbia). The section highlights papers we consider to be particularly newsworthy. Examples include Rod Peakall's perspective on the many challenges facing students of speciation in orchids, highlighting a recent paper on reproductive isolation between two closely related food-deceptive orchids (Moccia *et al*. 2007); Jim Moore's discussion of a recent study of inbreeding avoidance and mate choice in elephants (Archie *et al*. 2007); and Olson and Schaal's perspective on the evolution of vegetatively propagated crops, focusing on a study by (Deputie *et al*. 2007) that shows how traditional farming practices may promote sexual reproduction and gene flow between wild and cultivated cassava.

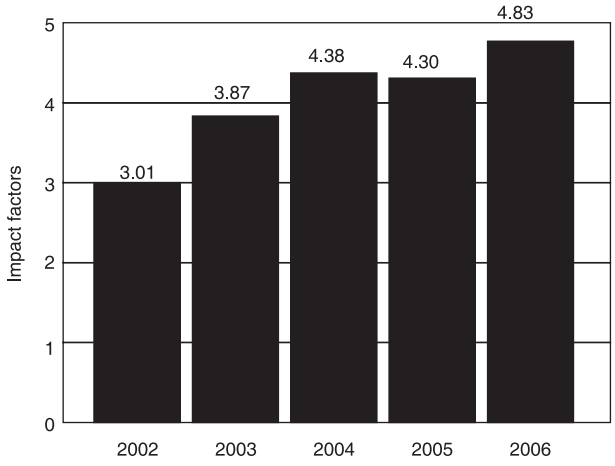

Fig. 1 Impact factors for *Molecular Ecology* over the past 5 years.

In addition to these Perspectives, the News and Views section reports on results from scientific meetings that are likely to be of interest to our readers. These include, for example, Landry and Aubin-Horth's discussion of the concept of ecological gene annotation, in the context of a symposium on Ecological Genomics in May 2007 in Toronto, Canada. We also are experimenting with podcasts of interviews with our authors and editors that can be downloaded for free. Podcasts available so far include an interview with Amy Bouck (Duke University), who discusses her article 'The molecular ecologist's guide to expressed sequence tags' (Bouck & Vision 2007), as well as an interview with chief editor L. Rieseberg, who describes a recent research article by his group (Lai *et al*. 2006) and provides advice on how to get published in *Molecular Ecology*.

Molecular Ecology continues to be closely linked to its sister journal, *Molecular Ecology Resources*, which focuses on tools and resources for molecular ecology. The journal's remit includes the development of (i) molecular markers and other genomic resources for nonmodel species; (ii) new molecular and computational methods; and (iii) DNA barcodes, DNA-based taxonomies, and other molecular diagnostic tools.

2007 Molecular Ecology Prize

The 2007 Molecular Ecology Prize was awarded to Pierre Taberlet, a pioneer of phylogeographical studies in plants,

particularly in the relation to alpine flora of Europe. He has developed and applied a variety of innovative methods to molecular ecology and added much needed rigour to the field, particularly with respect to data quality. Dr Taberlet also has served as an editor of *Molecular Ecology* for the past decade. A biography of Dr Taberlet and his contributions to molecular ecology can be found on page 514 of this issue.

Special Issues and Reviews

Each year we identify topics that we think are of interest to our readers and/or that represent important future research directions that we would like to see included in *Molecular Ecology*. For example, in July 2007 we published a partial special issue on *The Genetics of Speciation* (see meeting review by Ortiz-Barrientos & Kane 2007). Highlights from the special issue include analyses of the history of divergence that contributed to a famous case of sympatric speciation, the apple maggot fly (Michel *et al*. 2007), as well as dissection of the genetics of reproductive isolation in rapidly speciating crickets from Hawaii (Shaw *et al*. 2007). In January 2008, a much larger special issue will be published that derives from a summit on *Microevolutionary Change in Human-Altered Environments (*see meeting report in Tseng 2007). The summit and special issue were organized by Tom Smith and Louis Bernatchez. Bernatchez also serves as our reviews editor, and he continues to do an excellent job in identifying timely topics for review and in recruiting able authors. Examples of reviews published in 2007 range from 'Pillars of Hercules: is the Atlantic–Mediterranean transition a phylogeographical break?' (Patarnello *et al*. 2007) to 'SINEs of progress: mobile element applications to molecular ecology' (Ray 2007) to 'Statistical analysis of amplified fragment length polymorphism data: a toolbox for molecular ecologists and evolutionists' (Bonin *et al*. 2007). We welcome suggestions from our authors and readers regarding subjects that are overdue for review or synthesis or that represent emerging subject areas or subfields that could be featured in special issues.

Fast Track papers

Fast Track papers report on discoveries of exceptional importance, similar to those published in the major weekly journals. As the name of this category suggests, the chief incentive for submitting these papers to *Molecular Ecology* is that Bob Wayne (our Fast Track Editor) provides a quick editorial decision regarding whether the papers will be reviewed, and then we do best to expedite review and publication if the decision is positive. Also, at our most recent editorial meeting, we decided that all Fast Track papers will be highlighted by perspectives in our News and Views section.

We have been very pleased with the quality of Fast Track papers. Impact factors are approximately twice that of regular articles, and several Fast Track papers have been featured by major weekly journals (e.g. Riley *et al*. 2006; Strasburg 2006). Major findings reported in from Fast Track papers in 2007 include discovery that the supposed successful recovery of an endangered subspecies of cutthroat trout in the USA has failed because of the systematic misidentification of endangered populations (Metcalf *et al*. 2007), the demonstration that the adaptive radiation of a freshwater fish genus from Indonesia was initiated by resource partitioning (Roy *et al*. 2007), and the calculation that — based on molecular marker assays of whale products – close to twice as many whales have been killed over a 5-year period than according to official reports (Baker *et al*. 2007; Clapham & Van Waerebeek 2007).

Reviewers

Lastly, we wish to express our gratitude to our many referees (listed in Table 1) for the donation of their time to the journal and to the discipline of molecular ecology.

Retrospective

As part of our drive to increase the visibility of the science published in *Molecular Ecology*, we have expanded our editorial to include a retrospective that highlights important discoveries in molecular ecology in the previous year.

Sympatric speciation

A longstanding debate in evolutionary biology is whether speciation often occurs in the absence of geographical barriers to gene flow (i.e. sympatry). Darwin (1859) viewed speciation as the outcome of competition for resources, which must necessarily occur in sympatry (or parapatry). However, convincing empirical examples are rare, and theoretical studies of the process indicate that the evolutionary conditions required for sympatric speciation are stringent.

In a novel approach to the problem, Gavrilets & Vose (2007) and Gavrilets *et al*. (2007) ask whether two putative examples of sympatric speciation — cichlids in Lake Apoyo in Nicaragua (Barluenga *et al*. 2006) and palms from Lord Howe Island (Savolainen *et al*. 2006) — are theoretically plausible. Gavrilets and coauthors show that fairly rapid sympatric speciation is possible in both cases, although under a restricted set of conditions. These include simple genetic control of the traits involved in habitat adaptation and assortative mating, as well as intermediate selection for local adaptation. Also, the fish speciation event requires that loci influencing assortative mating have strong effects, whereas in the palm example, speciation is aided by an

environmental effect on flowering time. The next step is to test these critical parameters empirically.

It is noteworthy that the majority of convincing examples of sympatric speciation involve fishes. Hubert *et al*. (2007a) provide yet another possible example, this time from the piranha genera *Serrasalmus.* Although this case is not as fully developed as the cichlid fish example discussed above, phylogeographical studies identified several pairs of sister species that have originated in the same river drainage and appear to represent examples of sympatric speciation.

Climate change

Changes in the earth's climate are predicted to dramatically impact the health and composition of ecological communities worldwide. Organisms may respond to environmental change through migration, plasticity, adaptation, or extinction. As discussed in a cogent review (Reusch & Wood 2007), the field of molecular ecology offers a synthetic approach that considers the interactions between the ecological (migration and plasticity) and evolutionary (adaptation) responses to climate change. This involves characterization of present day diversity of critical ecological communities (e.g. Apprill & Gates 2007; Pfenninger *et al*. 2007; Pommier *et al*. 2007; Van Oppen 2007), calculation of migration rates for all kinds of organisms (Byrne *et al*. 2007; Devaux *et al*. 2007; Fievet *et al*. 2007; Garcia *et al*. 2007; Giordano *et al*. 2007; Jones *et al*. 2007; Lukoschek *et al*. 2007; Richards *et al*. 2007; Underwood *et al*. 2007; Vignieri 2007; Watts *et al*. 2007; Werth *et al*. 2007), identification of traits that are likely to be under selection during climate change (Chapuis *et al*. 2007), determination of the genetic basis and heritability of these traits (Brock *et al*. 2007; Kassahn *et al*. 2007; Norry *et al*. 2007; Rako *et al*. 2007), and estimation of the effects of habitat fragmentation on the rate of adaptation (Ficetola *et al*. 2007; Johansson *et al*. 2007). Also, analyses of organismal responses to previous bouts of climate change (Brito 2007; Crottini *et al*. 2007; Hoarau *et al*. 2007; Naciri & Gaudeul 2007; Parisod & Besnard 2007) provide a means of predicting future responses.

Inbreeding vs. outbreeding depression

An important question in conservation biology is whether endangered populations have more to fear from inbreeding depression (the lost of fitness as a result of breeding among closely related individuals) than outbreeding depression (the loss of fitness due to breeding among distantly related individuals). In a review of this question (Edmands 2007) argues that while there is more evidence for the former, the loss of fitness from outbreeding depression may be comparable in magnitude to that resulting from inbreeding depression. However, there is a surprising paucity of data concerning outbreeding depression, particularly in later generation hybrids. Indeed, most studies of conservation-related consequences of hybridization have focused on the problem of genetic assimilation rather than outbreeding depression. Examples of rare taxa in danger of genetic assimilation include Spanish white-headed ducks (Munoz-Fuentes *et al*. 2007), red wolves (Adams *et al*. 2007), and golden-winged warblers (Vallender *et al*. 2007).

With respect to inbreeding depression, several studies published in *Molecular Ecology* in 2007 have analysed the effects of population bottlenecks on genetic variability. For example, an analysis of genetic variability in peregrine falcons (Brown *et al*. 2007) failed to find the signature of a genetic bottleneck, despite a devastating decline in population size during mid-20th century due to the bioaccumulation of organochlorine contaminants. Brown *et al*. attributed the lack of long-term genetic damage to rapid and effective recovery efforts. Likewise, researchers failed to detect molecular evidence of a bottleneck in kangaroo rats (Busch *et al*. 2007) and greater prairie-chickens (Johnson *et al*. 2007b), despite known reductions in population size. In contrast, genetic variation was found to be greatly reduced in the European bison and banteng cattle (Bradshaw *et al*. 2007; Radwan *et al*. 2007), both of which have experienced extreme bottlenecks: current populations derive from just a handful of founders. Finally, Hughes & Hughes (2007) attributed reductions in nucleotide sequence diversity at mitochondrial protein-coding loci in birds to population bottleneck effects during the most recent glaciations. The take home message from these studies is that population bottlenecks are unlikely to significantly affect genetic diversity unless they are severe or extend over very long time periods.

In the two studies that tested for correlations between heterozygosity and traits associated with fitness, inbreeding depression was found to be environment and trait dependent. For example, reduced heterozygosity was found to reduce clutch size, but not egg volume in a wild population of lesser kestrels (Ortego *et al*. 2007). Likewise, maternal, but not paternal, multilocus heterozygosity was positively associated with offspring survival in Seychelles warbler, but only in years with low survival probabilities (Brouwer *et al*. 2007).

Invasive species

Invasive species pose a major burden on the world's economy. Invading nonindigenous species lower crop yield, cause human disease, destroy stored food, kill livestock and timber, reduce the quality of rangeland, aquatic, and forest environments, clog water intake pipes and water filtration systems, and lead to the expenditure of billions of dollars in chemical and biological control measures. Besides direct economic costs, invasive species threaten biodiversity and the functioning of ecosystems,

rivalling habitat loss in their destructive effect. Molecular ecological approaches provide information on the genetic identity of invasive populations (Drescher *et al*. 2007), where they came from (Kauserud *et al*. 2007b; Zhou *et al*. 2007), their evolutionary histories (Aketarawong *et al*. 2007; Herborg *et al*. 2007; Mock *et al*. 2007; Stone *et al*. 2007), patterns of hybridization with native species or other alien taxa (Gonthier *et al*. 2007; Kolbe *et al*. 2007), and even the genetic changes that underlie adaptation to disturbed habitats (Kane & Rieseberg in press). This basic information is required for effective management of invasive species. In addition, genomic studies conducted in ecological settings may provide information on how certain genetic changes contribute to invasiveness and the ecological contexts of these effects.

Cryptic species

Species inventories and assessment of species numbers play a crucial role in the conservation and management of biodiversity, as well as in studies of ecosystem function, community ecology, biogeography, phylogeny, and evolution. Molecular approaches, such as molecular phylogenetics, barcoding, DNA taxonomy, and molecular phylogeography, are playing an increasingly important role in quantifying organismal diversity, in part because of their ability to detect cryptic biological species. In 2007, new cryptic species were reported in rhodophyte seaweeds (Andreakis *et al*. 2007), trapdoor spiders (Stockman & Bond 2007), *Dioryctria* moths (Roe & Sperling 2007), cellar fungi (Kauserud *et al*. 2007a), mygalomorph spiders (Starrett & Hedin 2007), acanthocephalan parasites (Steinauer *et al*. 2007), freshwater crayfish (Apte *et al*. 2007), subterranean amphipods (Finston *et al*. 2007), and *Lycaena* butterflies (Oliver & Shapiro 2007).

Fig wasps

Figs and the wasps that pollinate them provide a high-profile example of an obligate insect–plant mutualism and possibly of strict-sense cospeciation. However, a comprehensive phylogenetic analysis of the five genera of fig wasps indicates that wasps not only switch between different host species, but that most host trees are pollinated by multiple wasp species (Marussich & Machado 2007). These results imply that previous assertions of strict codivergence are invalid.

Evolution and speciation in the Hawaiian silverword alliance

The Hawaiian silverword alliance consists of 28 species and three genera (*Dubautia, Argyroxiphium*, and *Wilksia*) endemic to Hawaii. Although all 28 species appear to have arisen from a single mainland ancestor, they exhibit spectacular morphological and ecological diversity. The group includes rosette plants, cushion plants, subshrubs, shrubs, trees, and vines. Moreover, they occur in nearly all of the island habitats, ranging from sea level to alpine habitats, and wet tropical to desert-like conditions. So impressive is the broad array of morphological, anatomical and eco-physiological traits required for success in these habitats, that Carlquist (1974) referred to the silversword alliance as 'undoubtedly the most outstanding example of adaptive radiation among Hawaiian angiosperms.

In the first issue of October 2007, three different kinds of molecular markers, each with different evolutionary rates, were employed to analyse the effects on gene flow on the differentiation of two sister species of *Dubautia* through time (Friar *et al*. 2007; Lawton-Rauh *et al*. 2007a, b; Remington & Robichaux 2007). While analyses of microsatellite data suggest that contemporary gene flow is minimal, analyses of AFLP markers, as well as sequence data from a structural gene, imply differential gene flow among loci going back to the earliest stages of differentiation. These results not only demonstrate the power of using multiple kinds of molecular markers for analyses of gene flow through time, but they also show that adaptive radiation can occur despite significant gene exchange between diverging populations.

Gene flow

A major question in molecular ecology concerns the relative importance of divergent natural selection vs. physical barriers or distance in limiting gene flow. In most studies that addressed this issue in 2007, genetic differentiation was found to be correlated with a physical barrier or with geographical distance (e.g. Barbara *et al*. 2007a; Brouat *et al*. 2007; Buschbom 2007; Calderon *et al*. 2007; Drummond & Hamilton 2007; Ekblom *et al*. 2007; Fievet *et al*. 2007; Friesen *et al*. 2007; Grundmann *et al*. 2007; Hubert *et al*. 2007b; Johnson *et al*. 2007a; Liu *et al*. 2007; Mitrovski *et al*. 2007; Mora *et al*. 2007; Perez-Losada *et al*. 2007; Price *et al*. 2007; Spellman *et al*. 2007; Werth *et al*. 2007). In contrast, in only a handful of cases did natural selection appeared to be a more likely cause of population structure than geography (Angelone *et al*. 2007; Hemmer-Hansen *et al*. 2007; Reyes *et al*. 2007).

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