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.

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 con-
tributions 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 evolution-
ists’ (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 our 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 suc-
cessful 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
speciation is possible in both cases, although
under a restricted set of conditions. These include simple
biological 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. 2007), 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.
rivaling 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 (Kaiserud 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), Diorctria moths (Roe & Sperling 2007), cellar fungi (Kaiserud 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, 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; Ekbloom et al. 2007; Fievet et al. 2007; Frierson et al. 2007; Grundmann et al. 2007; Hubert et al. 2007b; Johnson et al. 2007a; Liu et al. 2007; Mitrovski et al. 2007; Morais 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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