Editor's Report for 2003 and January to June, 2004

William Martin, June 2004

Molecular Biology and Evolution is the journal of the Society for Molecular Biology and Evolution, SMBE. The journal and the society were founded by Walter Fitch and Masatoshi Nei, both of whom decisively shaped the field of molecular evolution from its incipience. Their contributions to the society, the journal, and the field are now acknowledged in *MBE*: their names are printed in the masthead of every issue to honor the Founding Editors.

Simon Easteal's five-year term as editor ended in December 2003. He did a herculean job. When Simon took office, the handling of manuscripts at *MBE* involved shipping, stacking, and storing several tons of paper per year. At the end of his term, *MBE* had safely navigated the dramatic—but vital—transition into the age of electronic publishing. The move to electronic publishing was accompanied by the move to Oxford University Press as the journal's new publisher starting in January 2003. The journal is owned by SMBE, which arranges with the publisher to produce the journal. The journal's fate is thus in the hands of scientists—the members of SMBE—all of whom owe Simon Easteal enduring thanks for his service and for managing *MBE*'s stable transition into the era of electronic publishing.

Manuscript submissions to *MBE* are up and the acceptance rate is down. Prior to the move to electronic submission, *MBE* was typically receiving 350–450 manucripts per year (378 in the 12 months ending June 2000, 455 in the following 12 months, and 465 in the 12 months ending June 2002). In 2003 (January 1 to December 31) *MBE* received 645 manuscripts, an increase of roughly 50%. *MBE* published 239 papers (2361 pages) in 2003, corresponding to a rejection rate of 63%. This trend is continuing. As of June 16 we have received 319 manuscripts in 2004 and published 117 papers (1164 pages), including the June issue, pushing the acceptance rate below 35%.

The move to electronic publishing reflects a change in the way that scientists and libraries are approaching the publication process. Institutional subscriptions dipped in 2003 (536) over 2002 (593), accompanied by an increase of institutional online-only access through consortial subscriptions at OUP encompassing 882 additional institutional sites. This trend becomes all the more evident when one recalls that *MBE* had five online-only institutional subscriptions in 2001 and 15 in 2002 (see *Mol. Biol. Evol.* 19:2353–2354, 2002). Increased access to *MBE* through consortial arrangements is an issue that SMBE will need to follow carefully in the coming years. With more institutions and libraries moving to online access, thereby increasing the journal's availability to readers, the number of personal subscriptions fell sharply from 937 (2002) to 523 (2003). The decline in personal subscriptions is by no means specific to *MBE*; it is affecting other journals, too, yet the lack of Web-based subscription procedures in 2003 may have played a role as well. The decline seems to have leveled off with 468 personal subscriptions registered as of June 1, 2004. But SMBE will need to follow this matter closely and implement measures to increase the number of personal subscriptions. Through OUP's arrangement with developing countries, 256 institutions in such regions of the world received *MBE* online free of charge in 2003, with an increase to 361 as of June 2004, accompanied by 187 reduced-rate online subscriptions in developing countries thus far in 2004, dramatically up from 17 in 2003.

The trend towards increased online-only access is becoming an issue for all major journals. Many, including PNAS (PNAS 101:8509, 2004), are experimenting with a system called Open Access, which boils down to a pay-to-publish model in which authors assume increased publication charges for producing the journal, whereby free access to papers published in this mannner is available to everyone on the Web. Though SMBE has not formulated a policy on Open Access as yet, the SMBE Council is paying close attention to this development. These are turbulent times for the scientific publishing process, but *MBE* is well-positioned for the future.

While institutional subscription models and publication modes are changing, *MBE* has maintained its scientific standing at the forefront of the field. The most common way to assess a journal's success or standing is through a statistic called the impact factor. The impact factor of journal *Y* for a given year *X* is the average number of times that a paper appearing in journal *Y* is cited in any journal during the preceeding two-year period (the year that the

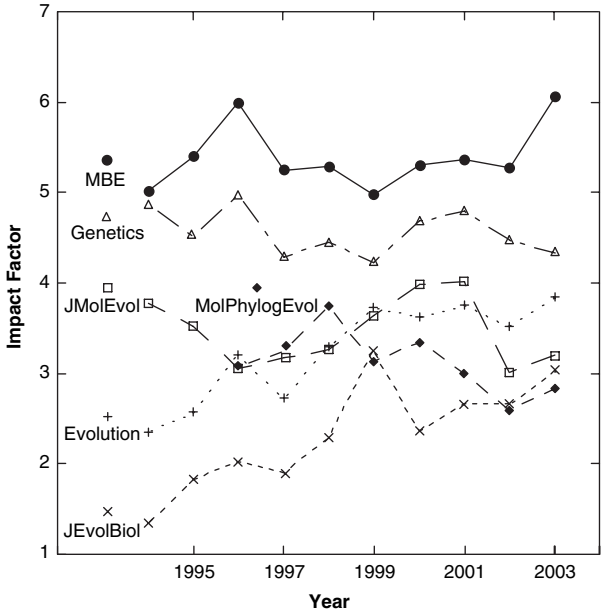

FIG. 1. *MBE*'s impact factor in relation to other journals in the field since 1994.

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Table 1
Current top-accessed papers at MBE

Current top 10 accessed abstracts at the MBE website (June 2003 to May 2004)

Number of Hits	Authors and Title
1,298	Gregory A. Wray, Matthew W. Hahn, Ehab Abouheif, James P. Balhoff, Margaret Pizer, Matthew V. Rockman, and Laura A. Romano. The Evolution of Transcriptional Regulation in Eukaryotes. (2003), Volume 20 Issue 9 1377–1419
567	Mark P. Simmons, Kurt M. Pickett, and Masaki Miya. How Meaningful Are Bayesian Support Values? (2004), Volume 21 Issue 1 188–199
518	Ravi Jain, Maria C. Rivera, and James A. Lake. Horizontal Gene Transfer Accelerates Genome Innovation and Evolution. (2003), Volume 20 Issue 10 1598–1602
497	N Saitou and M Nei. The neighbor-joining method: a new method for reconstructing phylogenetic trees (1987) Volume 4 Issue 4 406–425
436	You-Chun Li, Abraham B. Korol, Tzion Fahima, and Eviatar Nevo. Microsatellites Within Genes: Structure, Function, and Evolution (2004), Volume 21 Issue 6 991-1007
417	Jon P. Anderson, Gerald H. Learn, Allen G. Rodrigo, Xi He, Yang Wang, Hillard Weinstock, Marcia L. Kalish, Kenneth E. Robbins, Leroy Hood, and James I. Mullins. Predicting Demographic Group Structures Based on DNA Sequence Data (2003), Volume 20 Issue 7 1168–1180
405	Michael J. Sanderson, Amy C. Driskell, Richard H. Ree, Oliver Eulenstein, and Sasha Langley. Obtaining Maximal Concatenated Phylogenetic Data Sets from Large Sequence Databases (2003), Volume 20 Issue 7 1036–1042
392	Stephane Aris-Brosou and Ziheng Yang. Bayesian Models of Episodic Evolution Support a Late Precambrian Explosive Diversification of the Metazoa (2003), Volume 20 Issue 12 1947–1954
370	Yinglei Lai and Fengzhu Sun. The Relationship Between Microsatellite Slippage Mutation Rate and the Number of Repeat Units. (2003), Volume 20 Issue 12 2123–2131
368	Michael D. Sorenson, Elen Oneal, Jaime Garciáa-Moreno, and David P. Mindell. More Taxa, More Characters: The Hoatzin Problem Is Still Unresolved. (2003), Volume 20 Issue 9 1484–1498

Current top 10 downloaded PDF files at the MBE website (number of hits, June 2003 to May 2004)

Number of Hits	Authors and Title
4,891	N Saitou and M Nei. The neighbor-joining method: a new method for reconstructing phylogenetic trees (1987) Volume 4 Issue 4 page 406
3,174	Gregory A. Wray, Matthew W. Hahn, Ehab Abouheif, James P. Balhoff, Margaret Pizer, Matthew V. Rockman, and Laura A. Romano. The Evolution of Transcriptional Regulation in Eukaryotes. (2003), Volume 20 Issue 9 1377–1419
1,390	L Excoffier and M Slatkin. Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population. (1995) Volume 12 Issue 5 page 921
1,269	N Goldman and Z Yang. A codon-based model of nucleotide substitution for protein-coding DNA sequences. (1994) Volume 11 Issue 5 page 725
1,156	John S. Mattick and Michael J. Gagen. The Evolution of Controlled Multitasked Gene Networks: The Role of Introns and Other Noncoding RNAs in the Development of Complex Organisms. (2001) Volume 18 Issue 9 page 1611
1,106	M Nei and T Gojobori. Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. (1986) Volume 3 Issue 5 page 418
1,053	J. Peter Gogarten, W. Ford Doolittle, and Jeffrey G. Lawrence. Prokaryotic Evolution in Light of Gene Transfer. (2002) Volume 19 Issue 12 page 2226
1,025	G Levinson and GA Gutman. Slipped-strand mispairing: a major mechanism for DNA sequence evolution. (1987) Volume 4 Issue 3 page/article 203
919	Marc A. Heim, Marc Jakoby, Martin Werber, Cathie Martin, Bernd Weisshaar, and Paul C. Bailey. The Basic Helix-Loop-Helix Transcription Factor Family in Plants: A Genome-Wide Study of Protein Structure and Functional Diversity. (2003), Volume 20 Issue 5 page 735
918	AG Clark. Inference of haplotypes from PCR-amplified samples of diploid populations. (1990) Volume 7 Issue 2 page 111

paper appeared, $X - 2$, plus the subsequent year, $X - 1$). As with all statistics, some caution is warranted in the interpretation of impact factors, but they are widely used by publishers, societies, editors, librarians, and authors to compare the influence that journals are having on scientific progress. During the ten years of editorship under Barry Hall and Simon Easteal, *MBE*'s impact factor remained stably above that of all other journals in the field of molecular evolution (Fig. 1).

With the increased rejection rate, there has been an increase in the number of decisions that have been lamented or contested at *MBE*. There may be cases in which authors may recognize well-justified and strongly substantiated scientific grounds to request an appeal of the decision that has been handed down on a manuscript. In that event, authors are entitled to submit such an appeal to the editor, in which issues or arguments of a scientific nature—and scientific nature only—are tersely brought to the fore that might warrant the reconsideration of a decision. In any case, the chances of a successful appeal are extremely slight. During his five years of service to the journal, Simon Easteal reversed only one decision, attesting to the outstanding quality of work delivered by the associate editors at *MBE*.

Starting in January 2004, ten new associate editors joined the board and seven stepped down. Incoming were Robin Bush, T. Martin Embley, Takashi Gojobori, Laura Katz, Peter Lockhart, Lisa Matisoo-Smith, Lauren McIntyre, Billie Swalla, Arndt von Haeseler, and Jennifer Wernegreen. I am grateful for their hard work thus far and look forward to their continued service during the coming term. Keith Crandall, Tony Dean, Adam Eyre-Walker, Axel Meyer, Stephen Palumbi, David Rand, and Wolfgang Stephan, who stepped down, made valuable contributions to the journal through many years of hard work, for which Simon, SMBE, and I are deeply grateful.

Table 2
Current top-cited papers from 2002 and 2003 at MBE

Top cited 2002 papers (all from Volume 19, appearance to June 2004)

Number of Citations	Authors and Title
61	Michael J. Sanderson. Estimating Absolute Rates of Molecular Evolution and Divergence Times: A Penalized Likelihood Approach.
39	Thorsten Burmester, Bettina Ebner, Bettina Weich, and Thomas Hankeln. Cytoglobin: A Novel Globin Type Ubiquitously Expressed in Vertebrate Tissues.
37	Michael W. Gaunt and Michael A. Miles. An Insect Molecular Clock Dates the Origin of the Insects and Accords with Palaeontological and Biogeographic Landmarks.
35	J. Peter Gogarten, W. Ford Doolittle, and Jeffrey G. Lawrence. Prokaryotic Evolution in Light of Gene Transfer.
31	Jon Mallatt and Christopher J. Winchell. Testing the New Animal Phylogeny: First Use of Combined Large-Subunit and Small-Subunit rRNA Gene Sequences to Classify the Protostomes.
30	Carlos A. Machado, Richard M. Kliman, Jeffrey A. Markert, and Jody Hey. Inferring the History of Speciation from Multilocus DNA Sequence Data: The Case of Drosophila pseudoobscura and Close Relatives.
29	Ziheng Yang and Rasmus Nielsen. Codon-Substitution Models for Detecting Molecular Adaptation at Individual Sites Along Specific Lineages.
29	Oriane Matte-Tailliez, Céline Brochier, Patrick Forterre, and Hervé Philippe. Archaeal Phylogeny Based on Ribosomal Proteins.
29	Dorothée Huchon, Ole Madsen, Mark J. J. B. Sibbald, Kai Ament, Michael J. Stanhope, François Catzeflis, Wilfried W. de Jong, and Emmanuel J. P. Douzery. Rodent Phylogeny and a Timescale for the Evolution of Glires: Evidence from an Extensive Taxon Sampling Using Three Nuclear Genes.
27	Matthew V. Rockman and Gregory A. Wray. Abundant Raw Material for Cis-Regulatory Evolution in Humans.
27	Pierre Darlu and Guillaume Lecointre. When Does the Incongruence Length Difference Test Fail?
24	Emmanouil T. Dermitzakis and Andrew G. Clark. Evolution of Transcription Factor Binding Sites in Mammalian Gene Regulatory Regions: Conservation and Turnover.
22	Jeffrey D. Silberman, Alastair G. B. Simpson, Jaroslav Kulda, Ivan Cepicka, Vladimir Hampl, Patricia J. Johnson, and Andrew J. Roger. Retortamonad Flagellates are Closely Related to Diplomonads—Implications for the History of Mitochondrial Function in Eukaryote Evolution.
22	Toomas Kivisild, Helle-Viivi Tolk, Jüri Parik, Yiming Wang, Surinder S. Papiha, Hans-Jürgen Bandelt, and Richard Villems. The Emerging Limbs and Twigs of the East Asian mtDNA Tree.
22	Zhenglong Gu, Andre Cavalcanti, Feng-Chi Chen, Peter Bouman, and Wen-Hsiung Li. Extent of Gene Duplication in the Genomes of Drosophila, Nematode, and Yeast.
21	Erik Richly, Joachim Kurth, and Dario Leister. Mode of Amplification and Reorganization of Resistance Genes During Recent Arabidopsis thaliana Evolution.
21	P. Lopez, D. Casane, and H. Philippe. Heterotachy, an Important Process of Protein Evolution.

Top cited 2003 papers (all from Volume 20, number of citations from appearance to June 2004)

Number of Citations	Authors and Title
32	Michael E. Alfaro, Stefan Zoller, and François Lutzoni. Bayes or Bootstrap? A Simulation Study Comparing the Performance of Bayesian Markov Chain Monte Carlo Sampling and Bootstrapping in Assessing Phylogenetic Confidence.
31	Christophe J. Douady, Frédéric Delsuc, Yan Boucher, W. Ford Doolittle, and Emmanuel J. P. Douzery. Comparison of Bayesian and Maximum Likelihood Bootstrap Measures of Phylogenetic Reliability.
15	John M. Archibald, David Longet, Jan Pawlowski, and Patrick J. Keeling. A Novel Polyubiquitin Structure in Cercozoa and Foraminifera: Evidence for a New Eukaryotic Supergroup.
10	Robert Friedman and Austin L. Hughes. The Temporal Distribution of Gene Duplication Events in a Set of Highly Conserved Human Gene Families.
10	Galina V. Glazko and Masatoshi Nei. Estimation of Divergence Times for Major Lineages of Primate Species.
10	David S. Senchina, Ines Alvarez, Richard C. Cronn, Bao Liu, Junkang Rong, Richard D. Noyes, Andrew H. Paterson, Rod A. Wing, Thea A. Wilkins, and Jonathan F. Wendel. Rate Variation Among Nuclear Genes and the Age of Polyploidy in Gossypium.
9	Marc A. Heim, Marc Jakoby, Martin Werber, Cathie Martin, Bernd Weisshaar, and Paul C. Bailey. The Basic Helix–Loop–Helix Transcription Factor Family in Plants: A Genome-Wide Study of Protein Structure and Functional Diversity.
9	Nicolas Ray, Mathias Currat, and Laurent Excoffier. Intra-Deme Molecular Diversity in Spatially Expanding Populations.
8	James T. Harper and Patrick J. Keeling. Nucleus-Encoded, Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH) Indicates a Single Origin for Chromalveolate Plastids.
8	Teun van Rheede, Marcel M. W. Smolenaars, Ole Madsen, and Wilfried W. de Jong. Molecular Evolution of the Mammalian Prion Protein.

Timeliness of handling and publication is increasingly important to authors. *MBE* is committed to rapid handling of manuscripts. In 2003, the average manuscript handling time from submission to decision was 36 days, which has decreased to 28 days for the first 6 months of 2004. Manuscripts to appear in *MBE* are available on the journal's Advance Access Web site on average within 1.5 weeks of acceptance. The time from acceptance to publication in print averaged 12 weeks in 2003, partly due to the unavoidable delays incurred during the change of publisher. That time has now been reduced to less ten weeks in the first half of 2004, and with the publication of a larger July issue to reduce backlog we should reach the desired value of eight weeks from acceptance to print by the end of the year. The transition from Version 1 to Version 3 of ScholarOne's Manuscript Central, the journal's Web-based manuscript sumbission and handling system, occurred during the spring of 2004. It was a time that all of us on the editorial board will remember. Thanks to the persistence, expertise, and overtime duty of Liz

Raffaele at the editorial office, the transition was a success and went very smoothly for authors.

It is of interest to know what scientific topics are hot at *MBE*. In Table 1, I have listed the abstracts that received the most hits at the Web site and the papers that were most often downloaded as PDFs over the 12 months ending July 2004. The titles provide an indication of what sorts of evolutionary topics have the attention of those who access our journal through the Web. Table 2 provides a summary of those *MBE* papers from 2002 and 2003 that are receiving the highest number of citations. These are the ones that are having immediate impact; their titles provide an impression of some of the hot topics in the field. It should be gratifying to members of SMBE to see that the scientific content of the journal covers the full breadth of molecular evolution: methods, markers, molecules, and biology. Note that some of the journal's most highly accessed papers appeared almost 20 years ago. The journal's committment to the publication of new methods should be a mainstay for the future as well.

Starting in 2004, *MBE* has a new category of papers called Letters. These must have an abstract, are to be short and to the point, and must present results. The first criterion is important for our electronic readership. The last criterion allows for hefty debate of controversial topics, while ensuring that the pages of *MBE* are not devoted to arguments alone. Letters are being received regularly, I hope that readers will find them to be an interesting addition to the journal, as they present an opportunity to air issues of importance to all evolutionary biologists.

MBE works because of the effort invested by its associate editors and its referees. Finding suitable referees, keeping them on time, getting good reviews, and making clear-cut recommendations and decisions is not as easy as it might sound. Referees thus play a major role in forging the quality of papers that appear in *MBE*. In the words of a gray eminence with good advice: The review process is not an opportunity, it is a responsibility. As a quantitative guideline, for every paper that one publishes as communicating author, one should be preparing two referee reports for the scientific system. As a qualitative guideline, referee reports should address the written word, mention strengths as well as weaknesses, arrive at a clear recommendation to the associate editor, and be worded in such a manner that—regardless of verdict—they could be read aloud to the authors face to face, were it needed. The job of referees is to advise the associate editor fairly; the job of the associate editor is to decide.

Many things have changed at *MBE* in the last 18 months, but one constant has ensured our survival: Liz Raffaele at the editorial office. Liz ran the office during Simon Easteal's full term and—fortunately for us all—has stayed on. Alongside the scientific quality of papers that appear in the journal, Liz's experience, efficiency, and initiative are *MBE*'s steadiest keel.