

# Editor's Report for 2006

William Martin, June 2007

Once again in 2006, manuscript submissions to *Molecular Biology and Evolution* (*MBE*) were up and the acceptance rate was down and that trend continued into 2007. Prior to electronic publishing, *MBE* was typically receiving 350–450 manuscripts per year. We received 729 manuscripts in 2004, 801 in 2005, and 880 in 2006 (fig. 1). *MBE* published 237 papers (2,376 pages) in 2004, corresponding to an acceptance rate of 33%. In 2005, we published 256 papers (2,552 pages) at an acceptance rate of 32%. In 2006, we published 246 papers (2,532 pages) at an acceptance rate of 28%. In 2006, over 1,100,000 *MBE* articles were downloaded from the journal's Web site (<http://mbe.oxfordjournals.org/>). In 2007, those positive trends appear to be staying stable.

Standard institutional subscriptions declined slightly in 2006 over 2005, but this was more than offset by a further substantial increase of institutional and corporate online-only access through consortial subscriptions at Oxford University Press (OUP). Increased access to *MBE* through consortial arrangements is an issue that the Society for Molecular Biology and Evolution (SMBE) will continue to follow carefully in the coming years. The number of personal subscriptions increased in 2006 to 482, and we hope that this trend will continue, sparked by new members at the annual SMBE meetings. Through OUP's arrangement with developing countries, 697 institutes in developing countries received *MBE* online free of charge in 2006.

Starting from January 2006, *MBE* implemented an Open Access policy through OUP. Many authors and institutes are actively taking advantage of this option. All *MBE* papers are freely available in electronic form 12 months after their appearance in print. Through OUP, *MBE* has also implemented a self-archiving policy for those authors who desire or require it.

*MBE* has held its ground in a rapidly growing field. The most common way to assess a journal's standing is through a statistic called the impact factor. In 2006, *MBE*'s impact factor reached 6.726, the best it had ever been (fig. 2), attesting to a job well done by the Associate Editors (AEs). Since the previous Editor's Report, 6 new AEs have joined the board and 4 have stepped down. Incoming were Patricia Beldade, Barbara Holland, Norihiro Okada, Andrew Roger, Beth Shapiro, and Jeff Thorne. I am grateful for their hard work so far. Brandon Gaut, Mark Ragan, Pekka Pamilo, and Ken Wolfe, who stepped down, made valuable contributions to the journal through many years of hard work, for which SMBE and I are deeply grateful. *MBE*'s success is directly attributable to the hard work of its AEs and the referees who advise them. We have not quite reached full gender equality on the *MBE* Editorial Board, which was a goal that I had set for my term, but at 23:32, we are close and steadily moving in the right direction.

*MBE* is committed to rapid handling of manuscripts. In 2006, the average manuscript handling time from submis-

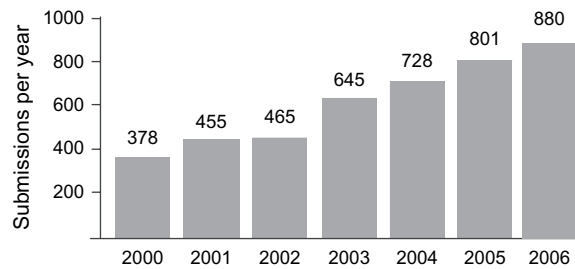


Fig. 1.—Submission per year at *MBE* 2000–2006.

sion to decision was 5 weeks. Manuscripts accepted in *MBE* appear in print 8 weeks after acceptance and are available via advance access on the Web site 2 days after acceptance. Those are good marks that attest to hard work by the AEs and our publisher, OUP.

What topics are currently hot at *MBE*? Table 1 lists the abstracts and full PDF articles that received the most hits at the Web site over the 12 months ending June 2007. The titles provide an indication of what sorts of evolutionary topics have the attention of those who access our journal through the web, which also underscore the broad scope of *MBE*, which I like to characterize as the world's leading specialist journal for science's broadest specific topic. Some of the journal's most highly accessed papers appeared 20 years ago, attesting to *MBE*'s tradition of publishing important advances. Table 2 provides an overview of those *MBE* titles from 2005 to 2006 that are currently receiving the most citations.

In 2004, we introduced a new category of papers at *MBE* called Letters. They have an abstract, short and to the point, and present results (not just debate). We have received over 300 submissions as Letters thus far, and I hope that readers are finding them to be an interesting addition to the journal.

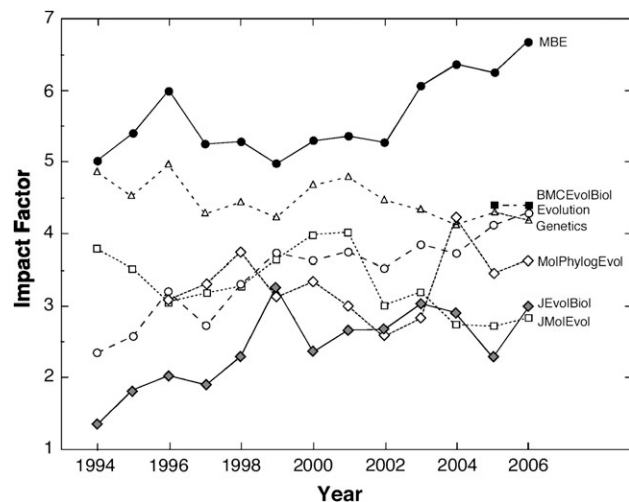


Fig. 2.—*MBE*'s impact factor in relation to other journals in the field since 1994.

**Table 1**  
**Current Top-Accessed Papers at *MBE***

Top 10 Abstracts June 2006–May 2007

3168	Saitou N, Nei M. 1987. The Neighbor-Joining method: a new method for reconstructing phylogenetic trees. 4:406.
2910	Inoue JG, et al. 2003. Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels. 20:1917.
2280	Lynch M. 2006. The origins of eukaryotic gene structure. 23:450.
1338	Ferry JG, House CH. 2006. The stepwise evolution of early life driven by energy conservation. 23:1286.
1312	Benton MJ, Donoghue PCJ. 2007. Paleontological evidence to date the tree of life. 24:26.
1217	Sorenson MD, et al. 2003. More taxa, more characters: the hoatzin problem is still unresolved. 20:1484.
1211	Gogarten JP, et al. 2002. Prokaryotic evolution in light of gene transfer. 19:2226.
1102	Rogers AR, Harpending H. 1992. Population growth makes waves in the distribution of pairwise genetic differences. 9:552.
1074	Pericic M, et al. 2005. High-resolution phylogenetic analysis of southeastern Europe traces major episodes of paternal gene flow among Slavic populations. 22:1964–1975.
1066	Weale ME, et al. 2002. Y chromosome evidence for Anglo-Saxon mass migration. 19:1008.

Top 10 Full-Text HTML Articles June 2006–May 2007

7046	Weale ME, et al. 2002. Y Chromosome evidence for Anglo-Saxon mass migration. 19:1008.
3486	Hawks J, et al. 2000. Population bottlenecks and Pleistocene human evolution. 17:2.
2739	Loogväli EL, et al. 2004. Disuniting uniformity: a pied cladistic canvas of mtDNA haplogroup H in Eurasia. 21:2012.
2597	Wray GA, et al. 2003. The evolution of transcriptional regulation in eukaryotes. 20:1377.
2147	Brooks DJ, et al. 2002. Evolution of amino acid frequencies in proteins over deep time: inferred order of introduction of amino acids into the genetic code. 19:1645.
2019	Pericic M, et al. 2005. High-Resolution phylogenetic analysis of Southeastern Europe traces major episodes of paternal gene flow among Slavic populations. 22:1964.
1935	Dupanloup I, et al. 2004. Estimating the impact of prehistoric admixture on the genome of Europeans. 21:1361
1864	Galián J, et al. 2002. The origin of multiple sex chromosomes in tiger beetles. 19:1792.
1843	Lerat E, Moran NA. 2004. The evolutionary history of quorum-sensing systems in bacteria. 21:903.
1540	Boyer SL, et al. 2001. Is the 16S–23S rRNA internal transcribed spacer region a good tool for use in molecular systematics and population genetics? A case study in cyanobacteria. 18:1057.

Top 10 Full-Text PDF Articles June 2006–May 2007

21480	Bush RM, et al. 1999. Positive selection on the H3 hemagglutinin gene of human influenza virus A. 16:1457.
15248	Clark AG. 1990. Inference of haplotypes from PCR-amplified samples of diploid populations. 7:111.
9416	Saitou N, Nei M. 1987. The Neighbor-Joining method: a new method for reconstructing phylogenetic trees. 4:406.
3519	Gibbs PE, et al. 1989. Evolution of legume seed storage proteins—a domain common to legumins and vicilins is duplicated in vicilins. 6:614.
2564	Gallin WJ. 1998. Evolution of the “classical” cadherin family of cell adhesion molecules in vertebrates. 15:1099.
2223	Wray GA, et al. 2003. The Evolution of transcriptional regulation in eukaryotes. 20:1377.
2063	Huson DH, Bryant D. 2006. Application of phylogenetic networks in evolutionary studies. 23:254–267.
1870	Weale ME, et al. 2002. Y chromosome evidence for Anglo-Saxon mass migration. 19:1008.
1815	Nei M, Gojobori T. 1986. Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. 3:418.
1797	Excoffier L, Slatkin M. 1995. Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population. 12:921.

The Editorial Office is running smoothly, as are the interactions with OUP, thanks to the continuous support that *MBE* receives from Cathy Kennedy in Oxford and Caitlyn Haase in the OUP production department. It was another good year for the journal. A word is due with regard to the timing of the Editor’s report, which always seems to appear a year late. That has to do with Article 5 of the SMBE by-laws (<http://www.smbe.org/bylaws.php>); SMBE meetings usually occur in June, at which time the Editor’s report is due, but by tradition they appear in the December issue.

This is my last Editor’s report for *MBE*. At the SMBE meeting in Auckland, 2005, I asked the SMBE Council, with Jeff Powell kindly presiding, to allow me to step down from this office 1 year early for reasons of workload. They

agreed, and at the SMBE meeting in Tempe, 2006, Marcy Uyenoyama was appointed as my successor to take office when Volume 24 Issue 12 fills up. I wish her good luck, a steady helm, and smooth sailing; most of all I wish her full support from her SMBE Council at all times. I want to thank once more Liz Raffaele in the Editorial Office and all AEs, whose rigor and enduring work have taken the journal safely from Simon Eastal’s hands into Marcy’s. My special thanks go to Dan Graur, whose original artwork has brightened the cover of *MBE* since 2003. Finally, I express sincere gratitude to those dedicated individuals who served the society with double duty on both the SMBE Council and the *MBE* Editorial Board during my term: Brian Golding, Jody Hey, Laura Katz, Sudhir Kumar, Marta Wayne, and George Zhang.

**Table 2**  
**Current Top-Cited Papers from 2005 to 2006 at MBE**

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Top-Cited 2006 Papers

- 81 Huson DH, Bryant D. Application of phylogenetic networks in evolutionary studies. 23:254.  
 30 Drummond DA, et al. A single determinant dominates the rate of yeast protein evolution. 23:327.  
 25 Parmley JL, et al. Evidence for purifying selection against synonymous mutations in mammalian exonic splicing enhancers. 23:301.  
 23 Steenkamp ET, et al. The protistan origins of animals and fungi. 23:93.  
 21 Lynch M. The origins of eukaryotic gene structure. 23:450.  
 20 Simpson AGB, et al. Comprehensive multigene phylogenies of excavate protists reveal the evolutionary positions of "primitive" eukaryotes. 23:615.  
 18 Baldo L, et al. Widespread recombination throughout *Wolbachia* genomes. 23:437.  
 15 Turmel M, et al. The chloroplast genome sequence of *Chara vulgaris* sheds new light into the closest green algal relatives of land plants. 23:1324.  
 15 Duarte JM, et al. Expression pattern shifts following duplication indicative of subfunctionalization and neofunctionalization in regulatory genes of *Arabidopsis*. 23:469.  
 15 Chang CC, et al. The chloroplast genome of *Phalaenopsis aphrodite* (Orchidaceae). 23:279.

Top-Cited 2005 Papers

- 97 Philippe H, et al. Multigene analyses of bilaterian animals corroborate the monophyly of Ecdysozoa, Lophotrochozoa, and Protostomia. 22:1246.  
 93 Yang ZH, et al. Bayes empirical Bayes inference of amino acid sites under positive selection. 22:1107.  
 73 Ho SYW, et al. Time dependency of molecular rate estimates and systematic overestimation of recent divergence times. 22:1561.  
 47 Conticello SG, et al. Evolution of the AID/APOBEC family of polynucleotide (deoxy) cytidine deaminases. 22:367.  
 48 Pond SLK, et al. Not so different after all: a comparison of methods for detecting amino acid sites under selection. 22:1208.  
 41 Stajich JE, et al. Disentangling the effects of demography and selection in human history. 22:63.  
 40 Leebens-Mack J, et al. Identifying the basal angiosperm node in chloroplast genome phylogenies: sampling one's way out of the felsenstein zone. 22:1948.  
 40 Blair JE, Hedges SB. Molecular phylogeny and divergence times of deuterostome animals. 22:2275.  
 37 Wright SI, Gaut GB. Molecular population genetics and the search for adaptive evolution in plants. 22:506.  
 37 Zhang J, et al. Evaluation of an improved branch-site likelihood method for detecting positive selection at the molecular level. 22:2472.
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