

Editor's Report for 2006

William Martin, September 2006

Once again in 2005, manuscript submissions to *Molecular Biology and Evolution* were up and the acceptance rate was down. Prior to electronic publishing, *MBE* was typically receiving 350–450 manuscripts per year. We received 729 manuscripts in 2004 and 801 in 2005, and the current projection is ~900 for 2006 with a continued upward trend (fig. 1*a* and *b*). *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%, which has dropped further still through August of 2006. At present, over 100,000 *MBE* articles per month are downloaded from the journal's Web site (<http://mbe.oxfordjournals.org/>).

Standard institutional subscriptions declined slightly in 2005 over 2004, 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 Society for Molecular Biology and Evolution (SMBE) will continue to follow carefully in the coming years. With more institutes and libraries moving to online access, thereby increasing journal availability to readers, the number of personal subscriptions fell from 533 (2004) to 388 (2005). Through OUP's ar-

rangement with developing countries, 1,188 institutes in developing countries received *MBE* online free of charge in 2005, a marked increase over 914 free institutional sites in developing countries for 2004.

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 is maintaining its scientific standing at the forefront of the field. The most common way to assess a journal's standing is through a statistic called the impact factor. In 2005, *MBE*'s impact factor remained stably above that of all other journals in the field of molecular evolution (fig. 2).

Since the previous Editor's Report, 13 new Associate Editors (AEs) have joined the board and 3 stepped down. Incoming were Adriana Briscoe, Jody Hey, Hope Hollocher, Aoife McLysaght, Stephanie Monks, Connie Mulligan, Yoko Satta, Anne Stone, Naoko Takezaki, Koichiro Tamura, Sarah Tishkoff, Marcy Uyenoyama, and Ziheng Yang. I am grateful for their hard work thus far and look

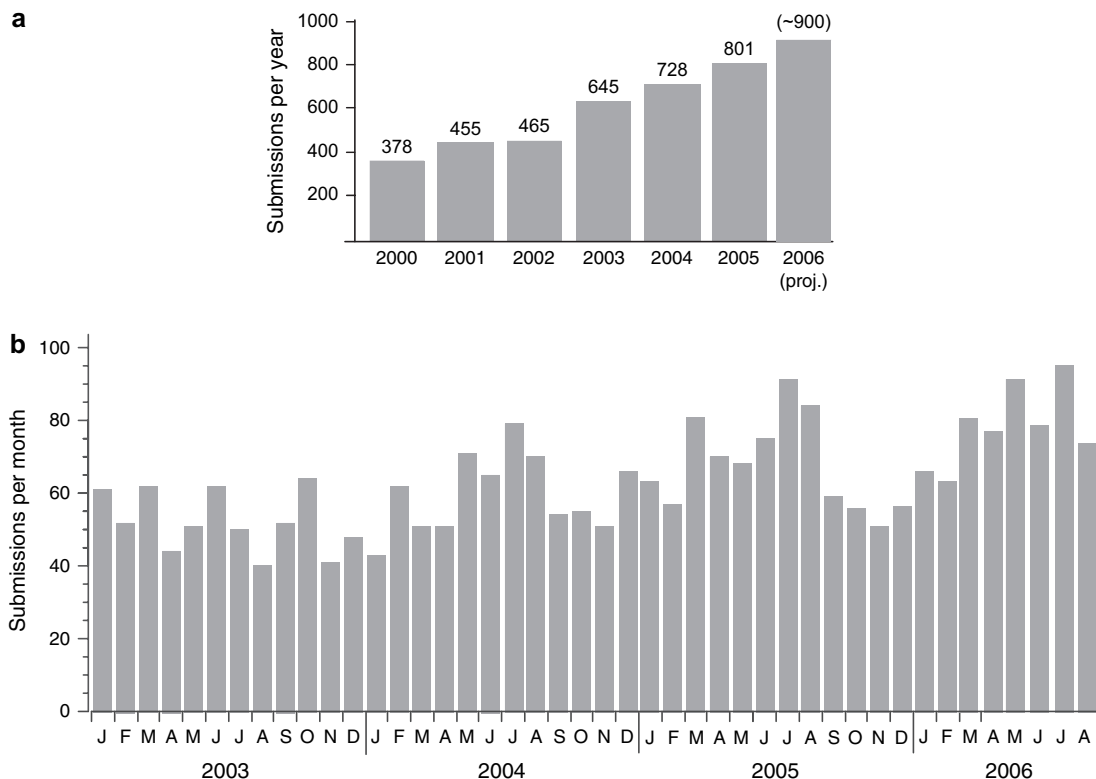


FIG. 1.—Submission and usage trends at *MBE*. (a) Submissions per year 2000–2006. (b) Submissions per month 2003–2006.

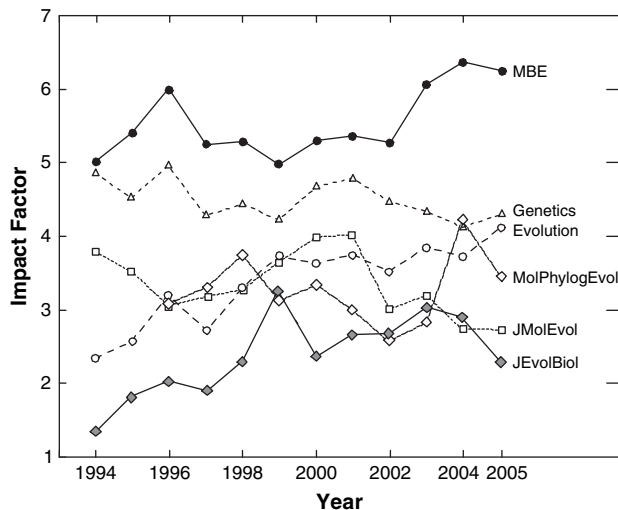


FIG. 2.—*MBE*'s impact factor in relation to other journals in the field since 1994.

forward to their continued service during the coming term. David Goldstein, Mark Springer, and Pierre Capy, 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 yet; but with a current 40:60 proportion, we are moving in the right direction.

MBE is committed to rapid handling of manuscripts. In 2005, the average manuscript handling time from submission to decision was stable at 28 days. Manuscripts accepted in *MBE* are now available via advance access on the Web site 2 days after acceptance.

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 August 2006. The titles provide an indication of what sorts of evolutionary topics have the attention of those who access our journal through the Web. Some of the journal's most highly

Table 1
Current Top-Accessed Papers at *MBE*

Top 10 Abstracts September 2005–August 2006

2369	Saitou and Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. <i>Mol Biol Evol.</i> 4:406.
2342	Nei. 2005. Selectionism and neutralism in molecular evolution. <i>Mol Biol Evol.</i> 22:2318.
2271	Lynch. 2006. The origins of eukaryotic gene structure. <i>Mol Biol Evol.</i> 23:450.
1333	Pericic et al. 2005. High-resolution phylogenetic analysis of southeastern Europe traces major episodes of paternal gene flow among slavic populations. <i>Mol Biol Evol.</i> 22:1964.
989	Huson and Bryant. 2006. Application of phylogenetic networks in evolutionary studies. <i>Mol Biol Evol.</i> 23:254.
969	Verginelli et al. 2005. Mitochondrial DNA from prehistoric canids highlights relationships between dogs and south-east European wolves. <i>Mol Biol Evol.</i> 22:2541.
952	Blair and Hedges. 2005. Molecular phylogeny and divergence times of deuterostome animals. <i>Mol Biol Evol.</i> 22:2275.
921	Rogers and Harpending. 1992. Population growth makes waves in the distribution of pairwise genetic differences. <i>Mol Biol Evol.</i> 9:552.
901	Wray et al. 2003. The evolution of transcriptional regulation in eukaryotes. <i>Mol Biol Evol.</i> 20:1377.
731	Fang et al. 2005. How essential are nonessential genes? <i>Mol Biol Evol.</i> 22:2147.

Top 10 Full-Text HTML Articles September 2005–August 2006

4721	Weale et al. 2002. Y-chromosome evidence for Anglo-Saxon mass migration. <i>Mol Biol Evol.</i> 19:1008.
3501	Lynch. 2006. The origins of eukaryotic gene structure. <i>Mol Biol Evol.</i> 23:450.
3010	Wray et al. 2003. The evolution of transcriptional regulation in eukaryotes. <i>Mol Biol Evol.</i> 20:1377.
2509	Hawks et al. 2000. Population bottlenecks and pleistocene human evolution. <i>Mol Biol Evol.</i> 17:2.
2123	Loogvälli et al. 2004. Disuniting uniformity: a pied cladistic canvas of mtDNA haplogroup H in Eurasia. <i>Mol Biol Evol.</i> 21:2012.
1887	Brooks et al. 2002. Evolution of amino acid frequencies in proteins over deep time: inferred order of introduction of amino acids into the genetic code. <i>Mol Biol Evol.</i> 19:1645.
1683	Pericic et al. 2005. High-resolution phylogenetic analysis of southeastern Europe traces major episodes of paternal gene flow among slavic populations. <i>Mol Biol Evol.</i> 22:1964.
1572	Li et al. 2004. Microsatellites within genes: structure, function, and evolution. <i>Mol Biol Evol.</i> 21:991.
1538	Gogarten et al. 2002. Prokaryotic evolution in light of gene transfer. <i>Mol Biol Evol.</i> 19:2226.
1518	Lerat and Moran. 2004. The evolutionary history of quorum-sensing systems in bacteria. <i>Mol Biol Evol.</i> 21:903.

Top 10 Full-Text PDF Articles May 2005–April 2006

7631	Saitou and Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. <i>Mol Biol Evol.</i> 4:406.
3829	Lynch. 2006. The origins of eukaryotic gene structure. <i>Mol Biol Evol.</i> 23:450.
2869	Nei. 2005. Selectionism and neutralism in molecular evolution. <i>Mol Biol Evol.</i> 22:2318.
2460	Wray et al. 2003. The evolution of transcriptional regulation in eukaryotes. <i>Mol Biol Evol.</i> 20:1377.
2215	Huson and Bryant. 2006. Application of phylogenetic networks in evolutionary studies. <i>Mol Biol Evol.</i> 23:254.
1750	Li et al. 2004. Microsatellites within genes: structure, function, and evolution. <i>Mol Biol Evol.</i> 21:991.
1536	Excoffier and Slatkin. 1995. Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population. <i>Mol Biol Evol.</i> 12:921.
1434	Gojobori and Nei. 1986. Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. <i>Mol Biol Evol.</i> 4:418.
1376	Wright and Gaut. 2005. Molecular population genetics and the search for adaptive evolution in plants. <i>Mol Biol Evol.</i> 22:506.
1263	Blair and Hedges. 2005. Molecular phylogeny and divergence times of deuterostome animals. <i>Mol Biol Evol.</i> 22:2275.

Table 2
Current Top-Cited Papers from 2004 and 2005 at *MBE*

Top-Cited 2004 Papers

- 67 Simmons MP. How meaningful are Bayesian support values? *Mol Biol Evol.* 21:188.
 64 Christoffels A. Fugu genome analysis provides evidence for a whole-genome duplication early during the evolution of ray-finned fishes. *Mol Biol Evol.* 21:1146.
 47 Yoon HS. A molecular timeline for the origin of photosynthetic eukaryotes. *Mol Biol Evol.* 21:809.
 46 Siepel A. Phylogenetic estimation of context-dependent substitution rates by maximum likelihood. *Mol Biol Evol.* 21:468.
 44 Bryant D. Neighbor-Net: an agglomerative method for the construction of phylogenetic networks. *Mol Biol Evol.* 21:255.
 44 Suzuki Y. False-positive selection identified by ML-based methods: examples from the Sig1 gene of the diatom *Thalassiosira weissflogii* and the tax gene of a human T-cell lymphotropic virus. *Mol Biol Evol.* 21:914.
 43 Li YC. Microsatellites within genes: structure, function, and evolution. *Mol Biol Evol.* 21:991.
 41 Shagin DA. GFP-like proteins as ubiquitous metazoan superfamily: evolution of functional features and structural complexity. *Mol Biol Evol.* 21:841.
 39 Meunier J. Recombination drives the evolution of GC-content in the human genome. *Mol Biol Evol.* 21:984.
 37 Zhang JZ. Frequent false detection of positive selection by the likelihood method with branch-site models. *Mol Biol Evol.* 21:1332.

Top-Cited 2005 Papers

- 45 Philippe H. Multigene analyses of bilaterian animals corroborate the monophyly of Ecdysozoa, Lophotrochozoa, and Protostomia. *Mol Biol Evol.* 22:1246.
 35 Yang ZH. Bayes empirical Bayes inference of amino acid sites under positive selection. *Mol Biol Evol.* 22:1107.
 31 Ho SYW. Time dependency of molecular rate estimates and systematic overestimation of recent divergence times. *Mol Biol Evol.* 22:1561.
 28 Conticello SG. Evolution of the AID/APOBEC family of polynucleotide (deoxy)cytidine deaminases. *Mol Biol Evol.* 22:367.
 27 Pond SLK. Not so different after all: a comparison of methods for detecting amino acid sites under selection. *Mol Biol Evol.* 22:1208.
 23 Stajich JE. Disentangling the effects of demography and selection in human history. *Mol Biol Evol.* 22:63.
 19 Arisue N. Root of the eukaryota tree as inferred from combined maximum likelihood analyses of multiple molecular sequence data. *Mol Biol Evol.* 22:409.
 18 Wright SI. Molecular population genetics and the search for adaptive evolution in plants. *Mol Biol Evol.* 22:506.
 17 Philip GK. The Opisthokonta and the Ecdysozoa may not be clades: stronger support for the grouping of plant and animal than for animal and fungi and stronger support for the Coelomata than Ecdysozoa. *Mol Biol Evol.* 22:1175.
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accessed papers appeared 20 years ago, attesting to *MBE*'s tradition of seminal scientific advances. Table 2 provides an overview of those *MBE* titles from 2004 and 2005 that are currently receiving the most citations.

In 2004, we introduced a new category of papers at *MBE* called Letters. They have an abstract, are short and to the point, and present results (not just debate). We have

received over 200 submissions as Letters thus far, and I hope that readers are finding them to be an interesting addition to the journal.

The Editorial Office is running smoothly. The electronic manuscript handling system is running smoothly. The interactions with OUP are running smoothly. It was another good year for the journal.