Editor's Report for June, 2005

William Martin, June 2005

In 2004, manuscript submissions to *Molecular Biology and Evolution* were up, the impact factor was up, and the acceptance rate was down. Prior to electronic publishing, *MBE* was typically receiving 350–450 manucripts per year. We received 729 manuscripts in 2004 and the current projection is >800 for 2005 with a continued upward trend (fig. 1*a* and *b*). *MBE* published 239 papers (2,361 pages) in 2003, corresponding to an acceptance rate of 37%. In 2004, we published 238 papers (2,375 pages) at an acceptance rate of 33%, which has remained constant through June of 2005. During the period 2003–2005, electronic usage of the journal increased dramatically (fig. 1*c*). At present, over 100,000 *MBE* articles per month are downloaded from the journal's Web site (http://mbe.oxfordjournals.org/).

Electronic publishing continues to change the way that scientists and libraries approach the publication process. Institutional subscriptions dipped slightly in 2004 (513) over 2003 (536). Yet, this was accompanied by a further sharp increase of institutional and corporate online-only access through consortial subscriptions at Oxford University Press (OUP), encompassing 1,238 additional sites. Increased access to *MBE* through consortial arrangements is an issue that Society for Molecular Biology and Evolution (SMBE) has followed carefully in last 24 months and 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 very slightly from 523 (2003) to 509 (2004). Through OUP's arrangement with developing countries, 914 institutes in 57 developing countries received *MBE* online free of charge in 2004, a marked increase over 273 free institutional sites in developing countries for 2003.

Many journals continue to experiment with Open Access—a pay-to-publish model in which authors assume increased publication charges for producing the journal, whereby free access to papers published in this manner is available to everyone on the web. SMBE is following developments in the area of Open Access publishing carefully. At present, all *MBE* papers are freely available in electronic form 12 months after their appearance in print.

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. *MBE*'s impact factor rose to 6.4 this year and remained stably above that of other journals in the field of molecular evolution (fig. 2).

Starting in January 2005, six new Associate Editors (AEs) joined the board and two stepped down; incoming editors were Doug Crawford, Chuck Delwiche, John H. McDonald, Neelima Sinha, Marta Wayne, and George

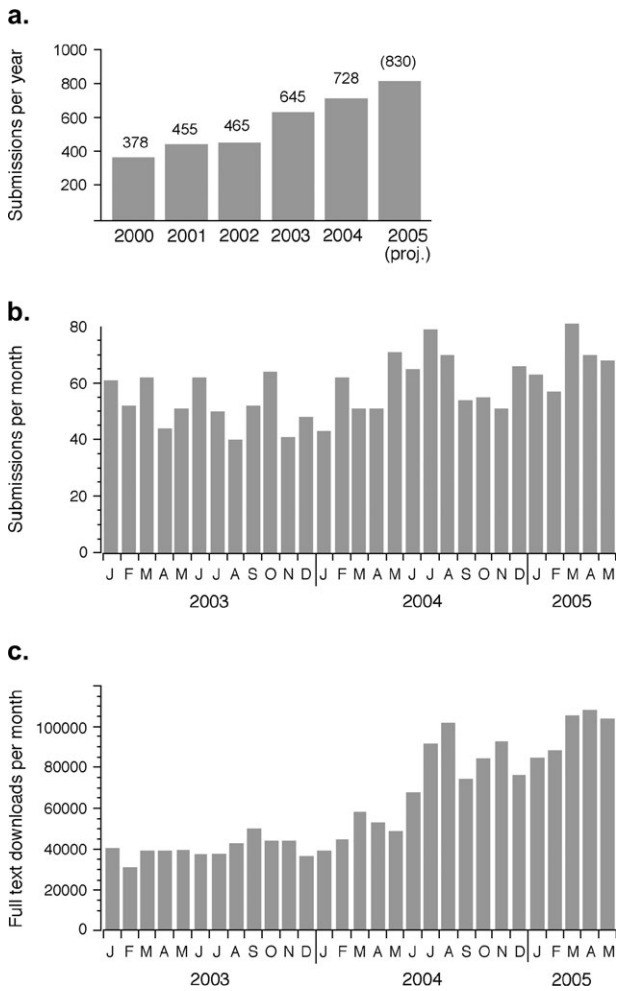

FIG. 1.—Submission and usage trends for *MBE*. (*a*) Submissions per year 2000–2005. (*b*) Submissions per month 2003–2005. (*c*) Number of downloads per month of *MBE* articles (hypertext markup language format and portable document format combined).

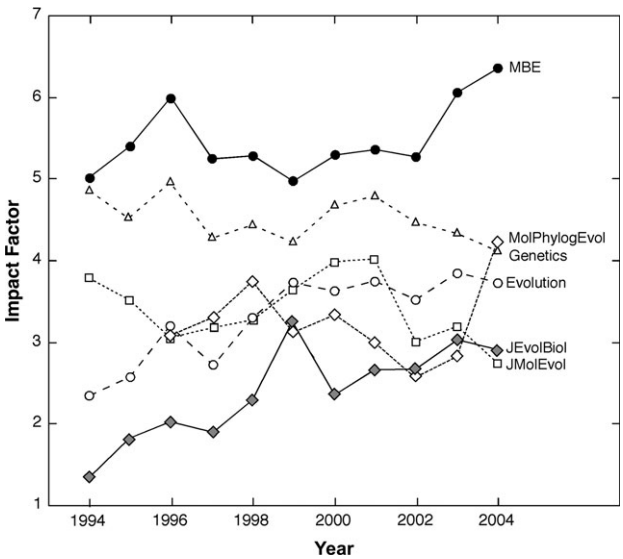

FIG. 2.—*MBE*'s impact factor in relation to other journals in the field since 1994.

Mol. Biol. Evol. 22(9):1940–1942. 2005
doi:10.1093/molbev/msi213

Table 1
Current Top-Accessed Papers in *MBE*

The Top-Downloaded Abstracts in the 12 Months from June 2004 to May 2005

1,103	Saitou, N., and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. **4**:406–425.
1,083	Li, Y.-C., A. B. Korol, T. Fahima, and E. Nevo. 2004. Microsatellites within genes: structure, function, and evolution. Mol. Biol. Evol. **21**:991–1007.
675	Wray, G. A., M. W. Hahn, E. Abouheif, J. P. Balhoff, M. Pizer, M. V. Rockman, and L. A. Romano. 2003. The evolution of transcriptional regulation in eukaryotes. Mol. Biol. Evol. **20**:1377–1419.
647	Aris-Brosou, S. 2005. Determinants of adaptive evolution at the molecular level: the extended complexity hypothesis. Mol. Biol. Evol. **22**:200–209.
645	Seo, T.-K., H. Kishino, and J. L. Thorne. 2004. Estimating absolute rates of synonymous and nonsynonymous nucleotide substitution in order to characterize natural selection and date species divergences. Mol. Biol. Evol. **21**:1201–1213.
634	Raymond, J., J. L. Siefert, C. R. Staples, and R. E. Blankenship. 2004. The natural history of nitrogen fixation. Mol. Biol. Evol. **21**:541–554.
628	Tang, H., G. J. Wyckoff, J. L., and C.-I. Wu. 2004. A universal evolutionary index for amino acid changes. Mol. Biol. Evol. **21**:1548–1556.
608	Philippe, H., E. A. Snell, E. Bapteste, P. Lopez, P. W. H. Holland, and D. Casane. 2004. Phylogenomics of eukaryotes: impact of missing data on large alignments. Mol. Biol. Evol. **21**:1740–1752.
604	Yoon, H. S., J. D. Hackett, C. Ciniglia, G. Pinto, and D. Bhattacharya. 2004. A molecular timeline for the origin of photosynthetic eukaryotes. Mol. Biol. Evol. **21**:809–818.
587	Inoue, J. G., M. Miya, K. Tsukamoto, and M. Nishida. 2003. Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels. Mol. Biol. Evol. **20**:1917–1924.

The Top-Downloaded PDF Articles in the 12 Months from June 2004 to May 2005

5,960	Saitou, N., and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. **4**:406–425.
2,803	Wray, G. A., M. W. Hahn, E. Abouheif, J. P. Balhoff, M. Pizer, M. V. Rockman, and L. A. Romano. 2003. The evolution of transcriptional regulation in eukaryotes. Mol. Biol. Evol. **20**:1377–1419.
1,843	Li, Y.-C., A. B. Korol, T. Fahima, and E. Nevo. 2004. Microsatellites within genes: structure, function, and evolution. Mol. Biol. Evol. **21**:991–1007.
1,656	Tang, H., G. J. Wyckoff, J. L., and C.-I. Wu. 2004. A universal evolutionary index for amino acid changes. Mol. Biol. Evol. **21**:1548–1556.
1,251	Goldman, N., and Z. Yang. 1994. A codon-based model of nucleotide substitution for protein-coding DNA sequences. Mol. Biol. Evol. **11**:725–736.
1,222	Excoffier, L., and M. Slatkin. 1995. Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population. Mol. Biol. Evol. **12**:921–927.
1,220	Ikemura, T. 1985. Codon usage and tRNA content in unicellular and multicellular organisms. Mol. Biol. Evol. **2**:13–34.
1,190	Nei, N., and T Gojobori. 1986. Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. Mol. Biol. Evol. **3**:418–426.
1,116	Levinson, G., and G. A. Gutman. 1987. Slipped-strand mispairing: a major mechanism for DNA sequence evolution. Mol. Biol. Evol. **4**:203–221.
1,105	Philippe, H., E. A. Snell, E. Bapteste, P. Lopez, P. W. H. Holland, and D. Casane. 2004. Phylogenomics of eukaryotes: impact of missing data on large alignments. Mol. Biol. Evol. **21**:1740–1752.

Zhang. I am grateful for their hard work thus far and look forward to their continued service during the coming term. Nick Goldman and Peer Bork, 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 current success is directly attributable to the hard work of its AEs and the referess who advise them.

MBE is committed to rapid handling of manuscripts. In 2004, the average manuscript handling time from submission to decision was 28 days. Manuscripts accepted in *MBE* are available via advance access on the Web site 5 days after acceptance. The time from acceptance to appearance in print averaged less than 8 weeks in 2004. That mark is two-third of its 2003 value and is stable in 2005. The May and April 2005 issues were larger to reduce backlog and maintain rapid publication.

What topics are currently hot in *MBE*? Table 1 lists the abstracts and full portable document format articles that received the most hits at the Web site over the 12 months ending June 2005. 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 accessed papers appeared 20 years ago, attesting to *MBE*'s tradition of long-lasting scientific advances. Table 2 provides an overview of those *MBE* papers from 2003 and 2004 that are currently receiving the most citations.

In 2004, we introduced a new category of papers in *MBE* called Letters. They have an abstract, are short and to the point, and present results (not just debate). We have received 109 submissions as Letters thus far, 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. It was a good year for the journal.

Table 2
Current Top-Cited Papers from 2003 and 2004 in *MBE*

The Top-Cited 2003 Papers Ranked by Number of Citations from Appearance to June 2005

88	Alfaro, M. E., S. Zoller, and F. Lutzoni. 2003. Bayes or bootstrap? A simulation study comparing the performance of Bayesian Markov chain Monte Carlo sampling and bootstrapping in assessing phylogenetic confidence. Mol. Biol. Evol. **20**:255–266.
77	Douady, C. J., F. Delsuc, Y. Boucher, W. F. Doolittle, and E. J. P. Douzery. 2003. Comparison of Bayesian and maximum likelihood bootstrap measures of phylogenetic reliability. Mol. Biol. Evol. **20**:248–254.
63	Wray, G. A., M. W. Hahn, E. Abouheif, J. P. Balhoff, M. Pizer, M. V. Rockman, and L. A. Romano. 2003. The evolution of transcriptional regulation in eukaryotes. Mol. Biol. Evol. **20**:1377–1419.
39	Glazko, G. V., and M. Nei. 2003. Estimation of divergence times for major lineages of primate species. Mol. Biol. Evol. **20**:424–434.
33	Harper, J. T., and P. J. Keeling. 2003. Nucleus-encoded, plastid-targeted glyceraldehyde-3-phosphate dehydrogenase (GAPDH) indicates a single origin for chromalveolate plastids. Mol. Biol. Evol. **20**:1730–1735.
28	Heim, M. A., M. Jakoby, M. Werber, C. Martin, B. Weisshaar, and P. C. Bailey. 2003. The basic helix-loop-helix transcription factor family in plants: a genome-wide study of protein structure and functional diversity. Mol. Biol. Evol. **20**:735–747.
24	Nair, S., J. T. Williams, A. Brockman et al. (12 co-authors). 2003. A selective sweep driven by pyrimethamine treatment in southeast Asian malaria parasites. Mol. Biol. Evol. **20**:1526–1536.
24	Goremykin, V. V., K. I. Hirsch-Ernst, S. Wolfl, and F. H. Hellwig. 2003. Analysis of the *Amborella trichopoda* chloroplast genome sequence suggests that *Amborella* is not a basal angiosperm. Mol. Biol. Evol. **20**:1499–1505.
23	Townsend, J. P., D. Cavalieri, and D. L. Hartl. 2003. Population genetic variation in genome-wide gene expression. Mol. Biol. Evol. **20**:955–963.
23	Archibald, J. M., D. Longet, J. Pawlowski, and P. J. Keeling. 2003. A novel polyubiquitin structure in Cercozoa and Foraminifera: evidence for a new eukaryotic supergroup. Mol. Biol. Evol. **20**:62–66.

The Top-Cited 2004 Papers Ranked by Number of Citations from Appearance to June 2005

25	Simmons, M. P., K. M. Pickett, and M. Miya. 2004. How meaningful are Bayesian support values? Mol. Biol. Evol. **21**:188–199.
21	Yoon, H. S., J. D. Hackett, C. Ciniglia, G. Pinto, and D. Bhattacharya. 2004. Molecular timeline for the origin of photosynthetic eukaryotes. Mol. Biol. Evol. **21**:809–818.
19	Christoffels, A., E. G. L. Koh, J. M. Chia, S. Brenner, S. Aparicio, and B. Venkatesh. 2004. Fugu genome analysis provides evidence for a whole-genome duplication early during the evolution of ray-finned fishes. Mol. Biol. Evol. **21**:1146–1151.
17	Suzuki, Y., and M. Nei. 2004. 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**:914–921.
16	Siepel, A., and D. Haussler. 2004. Phylogenetic estimation of context-dependent substitution rates by maximum likelihood. Mol. Biol. Evol. **21**:468–488.
14	Qiu, W. G., N. Schisler, and A. Stoltzfus. 2004. The evolutionary gain of spliceosomal introns: sequence and phase preferences. Mol. Biol. Evol. **21**:1252–1263.
13	Zhang, L. Q., and W.-H. Li. 2004. Mammalian housekeeping genes evolve more slowly than tissue-specific genes. Mol. Biol. Evol. **21**:236–239.
14	Meunier, J., and L. Duret. 2004. Recombination drives the evolution of GC-content in the human genome. Mol. Biol. Evol. **21**:984–990.
13	Bryant, D., and V. Moulton. 2004. Neighbor-Net: an agglomerative method for the construction of phylogenetic networks. Mol. Biol. Evol. **21**:255–265.
13	Fischer, A., V. Wiebe, S. Pääbo, and M. Przeworski. 2004. Evidence for a complex demographic history of chimpanzees. Mol. Biol. Evol. **21**:799–808.