MBE Emerging Classics 2021

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Molecular Biology and Evolution provides yearly recognition of recently published manuscripts that have made strong impressions on our research community since their publication. Below, we highlight ten discoveries, five methods, and five resources as "Emerging Classics" based on citations accrued per fractional year since print publication. Articles are listed alphabetically by the first author's family name. Total citation counts were obtained from Web of Science on November 6, 2020. We congratulate these authors on the significance of their contributions and look forward to seeing new classics emerge in the years to come.

Discoveries

Insights from the shell proteome: biomineralization to adaptation (**2017**) Arivalagan and colleagues in Volume 34(1) Pp. 66–77.

Deciphering the routes of invasion of Drosophila suzukii by means of ABC random forest (**2017**) Fraimout and colleagues in Volume 34(4) Pp. 980–996.

Shotgun mitogenomics provides a reference phylogenetic framework and timescale for living Xenarthrans (**2016**) Gibb and colleagues in Volume 33(3) Pp. 621–642.

Between a pod and a hard test: the deep evolution of amoebae (**2017**) Kang and colleagues in Volume 34(9) Pp. 2258–2270.

Adaptation of S. cerevisiae to fermented food environments reveals remarkable genome plasticity and the footprints of domestication (**2018**) Legras and colleagues in Volume 35(7) Pp. 1712–1727.

Comparative genomics of early-diverging mushroom-forming fungi provides insights into the origins of lignocellulose decay capabilities (**2016**) Nagy and colleagues in Volume 33(4) Pp. 959–970.

Survival and evolution of a large multidrug resistance plasmid in new clinical bacterial hosts (**2016**) Porse and colleagues in Volume 33(11) Pp. 2860–2873.

Phylogenomic data yield new and robust insights into the phylogeny and evolution of weevils (**2018**) Shin and colleagues in Volume 35(4) Pp. 823–836.

Whole-genome sequencing of native sheep provides insights into rapid adaptations to extreme environments (**2016**) Yang and colleagues in Volume 33(10) Pp. 2576–2592.

The diversification of plant NBS-LRR defense genes directs the evolution of microRNAs that target them (**2016**) Zhang and colleagues in Volume 33(10) Pp. 2692–2705.

Methods

Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks (**2017**) Didelot and colleagues in Volume 34(4) Pp. 997–1007.

Coevolutionary landscape inference and the context-dependence of mutations in beta-lactamase TEM-1 (**2016**) Figliuzzi and colleagues in Volume 33(1) Pp. 268–280.

The unreasonable effectiveness of convolutional neural networks in population genetic inference (**2019**) Flagel and colleagues in Volume 36(2) Pp. 220–238.

Bayesian inference of species networks from multilocus sequence data (**2018**) Zhang and colleagues in Volume 35(2) Pp. 504–517.

Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets (**2018**) Zhou and colleagues in Volume 35(2) Pp. 486–503.

Resources

ModelTest-NG: a new and scalable tool for the selection of DNA and protein evolutionary models (**2020**) Darriba and colleagues in Volume 37(1) Pp. 291–294.

MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger data sets (**2016**) Kumar and colleagues in Volume 33(7) Pp. 1870–1874.

SMS: smart model selection in PhyML (**2017**) Lefort and colleagues in Volume 34(9) Pp. 2422–2424.

DnaSP 6: DNA sequence polymorphism analysis of large data sets (**2017**) Rozas and colleagues in Volume 34(12) Pp. 3299–3302.

Molecular evolutionary genetics analysis (MEGA) for macOS (**2020**) Stecher and colleagues in Volume 37(4) Pp. 1237–1239.

Editorial

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