

# New Evidence from Linguistic Phylogenetics Identifies Limits to Punctuational Change

Holman E., Wichmann S.

Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

---

## Abstract

© 2017 The Author(s) 2017. Published by Oxford University Press, on behalf of the Society of Systematic Biologists. All rights reserved. Since the early 1970s, biologists have debated whether evolution is punctuated by speciation events with bursts of cladogenetic changes, or whether evolution tends to be of a more gradual, anagenetic nature. A similar discussion among linguists has barely begun, but the present results suggest that there is also room for controversy over this issue in linguistics. The only previous study correlated the number of nodes in linguistic phylogenies with branch lengths and found support for punctuated equilibrium. We replicate this result for branch lengths, but find no support for punctuated equilibrium using a different, automated measure of linguistic divergence and a much larger data set. With the automated measure, segments of trees containing more nodes show no greater divergence from an outgroup than segments containing fewer nodes.

<http://dx.doi.org/10.1093/sysbio/syw106>

---

## Keywords

Historical linguistics, language evolution, lexical similarity, phyletic gradualism

## References

- [1] Atkinson Q.D., Gray R.D. 2005. Curious parallels and curious connections-phylogenetic thinking in biology and historical linguistics. *Syst. Biol.* 54:513-526.
- [2] Atkinson Q.D., Meade A., Venditti C., Greenhill S.J., Pagel M. 2008. Languages evolve in punctuational bursts. *Science*. 319:588.
- [3] Barraclough T.G., Harvey P.H., Nee S. 1996. Rate of rbcL gene sequence evolution and species diversification in flowering plants (angiosperms). *Proc. R. Soc. B.* 263:589-591.
- [4] Bochkarev V., Solovyev V., Wichmann S. 2014. Universals versus historical contingencies in lexical evolution. *J. R. Soc. Interface.* 11:20140841. Available from: URL <http://dx.doi.org/10.1098/rsif.2014.0841>.
- [5] Bokma F. 2002. Detection of punctuated equilibrium from molecular phylogenies. *J. Evol. Biol.* 15:1048-1056.
- [6] Brown J.M., Hedtke S.M., Lemmon A.R., Lemmon E.M. 2010. When trees grow too long: investigating the causes of highly inaccurate Bayesian branch-length estimates. *Syst. Biol.* 59:145-161.
- [7] Eldredge N., Gould S.J. 1972. Punctuated equilibria: an alternative to phyletic gradualism. In: Schopf T.J.M., editor. *Models in paleobiology*. San Francisco: Freeman Cooper. p. 82-115.
- [8] Hammarström H., Forkel R., Haspelmath M., Nordhoff S. 2014. *Glottolog 2.3*. Leipzig: Max Planck Institute for Evolutionary Anthropology. Available from: URL <http://glottolog.org>.
- [9] Holman E.W., Brown C.H., Wichmann S., Müller A., Velupillai V., Hammarström H., Sauppe S., Jung H., Bakker D., Brown P., Belyaev O., Urban M., Mailhammer R., List J.M., Egorov D. 2011. Automated dating of the world's language families based on lexical similarity. *Curr. Anthropol.* 52:841-875.

- [10] Lewis M.P., Simons G.F., Fennig C.D., editors. 2014. *Ethnologue: languages of the world*, 17th ed. Dallas: SIL International. Available from: URL <http://www.ethnologue.com>.
- [11] Mattila T.M., Bokma F. 2008. Extant mammal body masses suggest punctuated equilibrium. *Proc. R. Soc. B.* 275:2195-2199.
- [12] Mindell D.P., Sites J.W. Jr., Graur D. 1989. Speciation evolution: a phylogenetic test with allozymes in *Sceloporus* (Reptilia). *Cladistics.* 5:49-61.
- [13] Mooers A.Ø., Schluter D. 1998. Fitting macroevolutionary models to phylogenies: an example using vertebrate body sizes. *Contrib. Zool.* 68:3-18.
- [14] Nelson B.J., Andersen J.J., Brown J.M. 2015. Deflating trees: improving Bayesian branch-length estimates using informed priors. *Syst. Biol.* 64:441-447.
- [15] Pagel M., Venditti C., Meade A. 2006. Large punctuational contribution of speciation to evolutionary divergence at the molecular level. *Science.* 314:119-121.
- [16] Pennell M.W., Harmon L.J., Uyeda J.C. 2014. Is there room for punctuated equilibrium in macroevolution *Trends Ecol. Evol.* 29:23-32.
- [17] Rabosky D.L. 2012. Positive correlation between diversification rates and phenotypic evolvability can mimic punctuated equilibrium on molecular phylogenies. *Evolution.* 66: 2622-2627.
- [18] Rannala B., Zhu T., Yang Z. 2012. Tail paradox, partial identifiability, and influential priors in Bayesian branch length inference. *Mol. Biol. Evol.* 29:325-335.
- [19] Swadesh M. 1952. Lexico-statistic dating of prehistoric ethnic contacts with special reference to North American Indians and Eskimos. *Proc. Am. Philos. Soc.* 96:452-463.
- [20] Swadesh M. 1955. Towards greater accuracy in lexicostatistic dating. *Int. J. Am. Linguist.* 21:121-137.
- [21] Venditti C., Meade A., Pagel M. 2006. Detecting the node-density artifact in phylogeny reconstruction. *Syst. Biol.* 55:637-643.
- [22] Watrous L.E., Wheeler Q.D. 1981. The out-group comparison method of character analysis. *Syst. Zool.* 30:1-11.
- [23] Wichmann S., Holman E.W. 2009. Population size and rates of language change. *Hum. Biol.* 81:259-274.
- [24] Wichmann S., Holman E.W., Bakker D., Brown C.H. 2010. Evaluating linguistic distance measures. *Physica A.* 389:3632-3639.
- [25] Wichmann S., Müller A., Wett A., Velupillai V., Bischoffberger J., Brown C.H., Holman E.W., Sauppe S., Molocheva Z., Brown P., Hammarström H., Belyaev O., List J.M., Bakker D., Egorov D., Urban M., Mailhammer R., Carrizo A., Dryer M.S., Korovina E., Beck D., Geyer H., Epps P., Grant A., Valenzuela P. 2013. The ASJP Database (version 16). Available from: URL <http://asjp.cild.org>.