

References

- Abrams, P. A. 2000. The evolution of predator–prey interactions: theory and evidence. *Annual Review of Ecology and Systematics*, **31**, 79–105.
- Abrams, P. A. and Matsuda, H. 1994. The evolution of traits that determine ability in competitive contests. *Evolutionary Ecology*, **8**, 667–86.
- Acinas, S. G., Klepac-Ceraj, V., Hunt, D. E., et al. 2004. Fine-scale phylogenetic architecture of a complex bacterial community. *Nature*, **430**, 551–4.
- Ackerly, D. D., Schilck, D. W., and Webb, C. O. 2006. Niche evolution and adaptive radiation: testing the order of trait divergence. *Ecology*, **87**, S50–61.
- Adams, D. C. 2010. Parallel evolution of character displacement driven by competitive selection in terrestrial salamanders. *BMC Evolutionary Biology*, **10**, 72.
- Aguilée, R., Gascuel, F., Lambert, A., and Ferriere, R. 2018. Clade diversification dynamics and the biotic and abiotic controls of speciation and extinction rates. *Nature Communications*, **9**, 3013.
- Alberti, M., Marzluff, J., and Hunt, V. M. 2017. Urban driven phenotypic changes: empirical observations and theoretical implications for eco-evolutionary feedback. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **372**, 20160029.
- Al-Ghazzewi, F. H. and Tester, R. F. 2016. Biotherapeutic agents and vaginal health. *Journal of Applied Microbiology*, **121**, 18–27.
- Allmon, W. D. 1992. A causal analysis of stages in allopatric speciation. In: Futuyma, D. and Antonovics, J. (eds) *Oxford Surveys in Evolutionary Biology*. Oxford: Oxford University Press.
- Alroy, J. 2008. Dynamics of origination and extinction in the marine fossil record. *Proceedings of the National Academy of Sciences of the United States of America*, **105**, 11536–42.
- Alzate, A., Janzen, T., Bonte, D., Rosindell, J., and Etienne, R. S. 2017. A simple spatially explicit neutral model explains range size distribution of reef fishes. *bioRxiv*, doi: <https://doi.org/10.1101/238600>.
- Arnegard, M. E., McIntyre, P. B., Harmon, L. J., et al. 2010. Sexual signal evolution outpaces ecological divergence during electric fish species radiation. *The American Naturalist*, **176**, 335–56.
- Aze, T., Ezard, T. H., Purvis, A., Coxall, H. K., Stewart, D. R., Wade, B. S. and Pearson, P. N. 2011. A phylogeny of Cenozoic macroperforate planktonic foraminifera from fossil data. *Biological Reviews*, **86**, 900–927.
- Baack, E., Melo, M. C., Rieseberg, L. H., and Ortiz-Barrientos, D. 2015. The origins of reproductive isolation in plants. *New Phytologist*, **207**, 968–84.
- Balint, M., Pfenninger, M., Grossart, H. P., et al 2018. Environmental DNA time series in ecology. *Trends in Ecology & Evolution*, **33**, 945–57.
- Bantinaki, E., Kassen, R., Knight, C. G., Robinson, Z., Spiers, A. J., and Rainey, P. B. 2007. Adaptive divergence in experimental populations of *Pseudomonas fluorescens*. III. Mutational origins of wrinkly spreader diversity. *Genetics*, **176**, 441–53.

- Barley, A. J., Brown, J. M., and Thomson, R. C. 2018. Impact of model violations on the inference of species boundaries under the multispecies coalescent. *Systematic Biology*, **269**, 269–84.
- Barluenga, M., Stolting, K. N., Salzburger, W., Muschick, M., and Meyer, A. 2006. Sympatric speciation in Nicaraguan crater lake cichlid fish. *Nature*, **439**, 719–23.
- Barracough, T. G. 2006. What can phylogenetics tell us about speciation in the Cape flora? *Diversity and Distributions*, **12**, 21–6.
- Barracough, T. G. 2010. Evolving entities: towards a unified framework for understanding diversity at the species and higher levels. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **365**, 1801–13.
- Barracough, T. G. 2015. How do species interactions affect evolutionary dynamics across whole communities? *Annual Review of Ecology, Evolution, and Systematics*, **46**, 25–48.
- Barracough, T. G. 2019. Species matter for predicting the functioning of evolving microbial communities. Unpublished work.
- Barracough, T. G. and Herniou, E. 2003. Why do species exist? Insights from sexuals and asexuals. *Zoology*, **106**, 275–82.
- Barracough, T. G. and Humphreys, A. M. 2015. The evolutionary reality of species and higher taxa in plants: a survey of post-modern opinion and evidence. *New Phytologist*, **207**, 291–6.
- Barracough, T. G. and Nee, S. 2001. Phylogenetics and speciation. *Trends in Ecology & Evolution*, **16**, 391–9.
- Barracough, T. G. and Savolainen, V. 2001. Evolutionary rates and species diversity in flowering plants. *Evolution*, **55**, 677–83.
- Barracough, T. G. and Vogler, A. P. 2000. Detecting the geographical pattern of speciation from species-level phylogenies. *The American Naturalist*, **155**, 419–34.
- Barracough, T. G. and Vogler, A. P. 2002. Recent diversification rates in North American tiger beetles estimated from a dated mtDNA phylogenetic tree. *Molecular Biology and Evolution*, **19**, 1706–16.
- Barracough, T. G., Harvey, P. H., and Nee, S. 1995. Sexual selection and taxonomic diversity in passerine birds. *Proceedings of the Royal Society B: Biological Sciences*, **259**, 211–15.
- Barracough, T. G., Harvey, P. H., and Nee, S. 1996. Rate of rbcL gene sequence evolution and species diversification in flowering plants (angiosperms). *Proceedings of the Royal Society B: Biological Sciences*, **263**, 589–91.
- Barracough, T. G., Barclay, M. V. L., and Vogler, A. P. 1998a. Species richness: does flower power explain beetle-mania? *Current Biology*, **8**, R843–5.
- Barracough, T. G., Vogler, A. P., and Harvey, P. H. 1998b. Revealing the factors that promote speciation. *Philosophical Transactions of the Royal Society of London Series B: Biological Sciences*, **353**, 241–9.
- Barracough, T. G., Hogan, J. E., and Vogler, A. P. 1999. Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coleoptera: Cicindelidae). *Proceedings of the Royal Society B: Biological Sciences*, **266**, 1061–7.
- Barracough, T. G., Birky, C. W., and Burt, A. 2003. Diversification in sexual and asexual organisms. *Evolution*, **57**, 2166–72.
- Barracough, T. G., Fontaneto, D., Ricci, C., and Herniou, E. A. 2007. Evidence for inefficient selection against deleterious mutations in cytochrome oxidase I of asexual bdelloid rotifers. *Molecular Biology and Evolution*, **24**, 1952–62.
- Barracough, T. G., Fontaneto, D., Herniou, E. A., and Ricci, C. 2008. The evolutionary nature of diversification in sexuals and asexuals. In: Butlin, R., Bridle, J., and Schluter, D. (eds) *Speciation and Ecology*. Cambridge: Cambridge University Press.

- Barracough, T. G., Hughes, M., Ashford-Hodges, N., and Fujisawa, T. 2009. Inferring evolutionarily significant units of bacterial diversity from broad environmental surveys of single-locus data. *Biology Letters*, **5**, 425–8.
- Barracough, T. G., Balbi, K. J., and Ellis, R. J. 2012. Evolving concepts of bacterial species. *Evolutionary Biology*, **39**, 148–57.
- Barroso-Batista, J., Sousa, A., Lourenco, M., Bergman, M. L., Sobral, D., Demengeot, J., Xavier, K. B., and Gordo, I. 2014. The first steps of adaptation of *Escherichia coli* to the gut are dominated by soft sweeps. *PLoS Genetics*, **10**, e1004182.
- Barth, J. M. I., Berg, P. R., Jonsson, P. R., et al. 2017. Genome architecture enables local adaptation of Atlantic cod despite high connectivity. *Molecular Ecology*, **26**, 4452–66.
- Bazin, E., Glemin, S., and Galtier, N. 2006. Population size does not influence mitochondrial genetic diversity in animals. *Science*, **312**, 570–2.
- Behrouzi, P. and Wit, E. C. 2019. Detecting epistatic selection with partially observed genotype data by using copula graphical models. *Journal of the Royal Statistical Society Series C: Applied Statistics*, **68**, 141–60.
- Bell, G. 1982. *The Masterpiece of Nature*. Berkeley: University of California Press.
- Bell, G. 2007. The evolution of trophic structure. *Heredity*, **99**, 494–505.
- Bell, T. 2010. Experimental tests of the bacterial distance–decay relationship. *ISME Journal*, **4**, 1357–65.
- Bell, T., Newman, J. A., Silverman, B. W., Turner, S. L., and Lilley, A. K. 2005. The contribution of species richness and composition to bacterial services. *Nature*, **436**, 1157–60.
- Bendall, M. L., Stevens, S. L. R., Chan, L.-K., et al. 2016. Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. *ISME Journal*, **10**, 1589–1601.
- Bergsten, J., Bilton, D. T., Fujisawa, T., et al. 2012. The effect of geographical scale of sampling on DNA barcoding. *Systematic Biology*, **61**, 851–69.
- Bergstrom, C. T., Lipsitch, M., and Levin, B. R. 2000. Natural selection, infectious transfer and the existence conditions for bacterial plasmids. *Genetics*, **155**, 1505–19.
- Berkhout, J., Bosdriesz, E., Nikerel, E., et al. 2013. How biochemical constraints of cellular growth shape evolutionary adaptations in metabolism. *Genetics*, **194**, 505–12.
- Bestion, E., Garcia-Carreras, B., Schaum, C. E., Pawar, S., and Yvon-Durocher, G. 2018. Metabolic traits predict the effects of warming on phytoplankton competition. *Ecology Letters*, **21**, 655–64.
- Betts, A., Gray, C., Zelek, M., MacLean, R. C., King, K. C. 2018. High parasite diversity accelerates host adaptation and diversification. *Science*, **360**, 907–911.
- Billard, S., López-Villavicencio, M., Hood, M. E., Giraud, T. 2012. Sex, outcrossing and mating types: unsolved questions in fungi and beyond. *Biology*, **25**, 1020–1038.
- Bininda-Emonds, O. R. P., Cardillo, M., Jones, K. E., et al. 2007. The delayed rise of present-day mammals. *Nature*, **446**, 507–12.
- Birand, A., Vose, A., and Gavrillets, S. 2012. Patterns of species ranges, speciation, and extinction. *The American Naturalist*, **179**, 1–21.
- Birky, C. W. 2010. Positively negative evidence for asexuality. *Journal of Heredity*, **101**, S42–5.
- Birky, C. W., Wolf, C., Maughan, H., Herbertson, L., and Henry, E. 2005. Speciation and selection without sex. *Hydrobiologia*, **546**, 29–45.
- Birky, C. W., Adams, J., Gemmel, M., and Perry, J. 2010. Using population genetic theory and DNA sequences for species detection and identification in asexual organisms. *PLoS One*, **5**, e10609.
- Bishop, C. J., Adams, J., Aanensen, D. M., Jordan, G. E., Kilian, M., Hanage, W. P., and Spratt, B. G. 2009. Assigning strains to bacterial species via the internet. *BMC Biology*, **7**, 3.

- Blanchard, J. L., Jennings, S., Holmes, R., et al. 2012. Potential consequences of climate change for primary production and fish production in large marine ecosystems. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **367**, 2979–89.
- Bobay, L. M. and Ochman, H. 2017. Biological species are universal across life's domains. *Genome Biology and Evolution*, **9**, 491–501.
- Booker, T. R., Jackson, B. C., and Keightley, P. D. 2017. Detecting positive selection in the genome. *BMC Biology*, **15**, 98.
- Borgonie, G., Garcia-Moyano, A., Litthauer, D., et al. 2011. Nematoda from the terrestrial deep subsurface of South Africa. *Nature*, **474**, 79–82.
- Boschetti, C., Carr, A., Crisp, A., et al. 2012. Biochemical diversification through foreign gene expression in bdelloid rotifers. *PLoS Genetics*, **8**, e1003035.
- Brandt, L. J., Aroniadis, O. C., Mellow, M., et al. 2012. Long-term follow-up of colonoscopic fecal microbiota transplant for recurrent *Clostridium difficile* infection. *American Journal of Gastroenterology*, **107**, 1079–87.
- Brookfield, J. F. Y. 2016. Why are estimates of the strength and direction of natural selection from wild populations not congruent with observed rates of phenotypic change? *Bioessays*, **38**, 927–34.
- Browne, H. P., Forster, S. C., Anonye, B. O., et al. 2016. Culturing of 'unculturable' human microbiota reveals novel taxa and extensive sporulation. *Nature*, **533**, 543–6.
- Buckling, A., Maclean, R. C., Brockhurst, M. A., and Colegrave, N. 2009. *The Beagle* in a bottle. *Nature*, **457**, 824–9.
- Burger, R. and Lynch, M. 1995. Evolution and extinction in a changing environment—a quantitative-genetic analysis. *Evolution*, **49**, 151–63.
- Burgin, C. J., Colella, J. P., Kahn, P. L., and Upham, N. S. 2018. How many species of mammals are there? *Journal of Mammalogy*, **99**, 1–14.
- Burt, A. 2000. Perspective: sex, recombination, and the efficacy of selection—was Weismann right? *Evolution*, **54**, 337–51.
- Bush, R. M., Bender, C. A., Subbarao, K., Cox, N. J., and Fitch, W. M. 1999. Predicting the evolution of human influenza A. *Science*, **286**, 1921–5.
- Butlin, R., DeBelle, A., Kerth, C., et al. 2012. What do we need to know about speciation? *Trends in Ecology & Evolution*, **27**, 27–39.
- Cadillo-Quiroz, H., Didelot, X., Held, N. L., et al. 2012. Patterns of gene flow define species of thermophilic Archaea. *PLoS Biology*, **10**, e1001265.
- Cadotte, M. W., Livingstone, S. W., Yasui, S. L. E., et al. 2017. Explaining ecosystem multifunction with evolutionary models. *Ecology*, **98**, 3175–87.
- Carroll, A. C. and Wong, A. 2018. Plasmid persistence: costs, benefits, and the plasmid paradox. *Canadian Journal of Microbiology*, **64**, 293–304.
- Carrolo, M., Pinto, F. R., Melo-Cristino, J., and Ramirez, M. 2009. Pherotypes are driving genetic differentiation within *Streptococcus pneumoniae*. *BMC Microbiology*, **9**, 191.
- Carstens, B. C., Pelletier, T. A., Reid, N. M., and Satler, J. D. 2013. How to fail at species delimitation. *Molecular Ecology*, **22**, 4369–83.
- Case, T. J. and Taper, M. L. 2000. Interspecific competition, environmental gradients, gene flow, and the coevolution of species' borders. *The American Naturalist*, **155**, 583–605.
- Castiglia, R. 2014. Sympatric sister species in rodents are more chromosomally differentiated than allopatric ones: implications for the role of chromosomal rearrangements in speciation. *Mammal Review*, **44**, 1–4.
- Chan, K. O., Alexander, A. M., Grismer, L. L., et al. 2017. Species delimitation with gene flow: a methodological comparison and population genomics approach to elucidate cryptic species boundaries in Malaysian Torrent frogs. *Molecular Ecology*, **26**, 5435–50.

- Chesson, P. 2000. Mechanisms of maintenance of species diversity. *Annual Review of Ecology and Systematics*, **31**, 343–66.
- Chevin, L. M. 2016. Species selection and random drift in macroevolution. *Evolution*, **70**, 513–25.
- Chevin, L.-M., Lande, R., and Mace, G. M. 2010. Adaptation, plasticity, and extinction in a changing environment: towards a predictive theory. *PLoS Biology*, **8**, e1000357.
- Chira, A. M., Cooney, C. R., Bright, J. A., et al. 2018. Correlates of rate heterogeneity in avian ecomorphological traits. *Ecology Letters*, **21**, 1505–14.
- Chivian, D., Brodie, E. L., Alm, E. J., et al. 2008. Environmental genomics reveals a single-species ecosystem deep within earth. *Science*, **322**, 275–8.
- Claramunt, S., Derryberry, E. P., Remsen, J. V., and Brumfield, R. T. 2012. High dispersal ability inhibits speciation in a continental radiation of passerine birds. *Proceedings of the Royal Society B: Biological Sciences*, **279**, 1567–74.
- Clark, A. T. and Neuhauser, C. 2018. Harnessing uncertainty to approximate mechanistic models of interspecific interactions. *Theoretical Population Biology*, **123**, 35–44.
- Clarke, C. R., Karl, S. A., Horn, R. L., et al. 2015. Global mitochondrial DNA phylogeography and population structure of the silky shark, *Carcharhinus falciformis*. *Marine Biology*, **162**, 945–55.
- Clarkson, C. S., Weetman, D., Essandoh, J., et al. 2014. Adaptive introgression between *Anopheles* sibling species eliminates a major genomic island but not reproductive isolation. *Nature Communications*, **5**, 4248.
- Clatworthy, A. E., Pierson, E., and Hung, D. T. 2007. Targeting virulence: a new paradigm for antimicrobial therapy. *Nature Chemical Biology*, **3**, 541–8.
- Cohan, F. M. 2001. Bacterial species and speciation. *Systematic Biology*, **50**, 513–24.
- Cohan, F. M. and Perry, E. B. 2007. A systematics for discovering the fundamental units of bacterial diversity. *Current Biology*, **17**, R373–86.
- Collins, S. and Gardner, A. 2009. Integrating physiological, ecological and evolutionary change: a Price equation approach. *Ecology Letters*, **12**, 744–57.
- Condamine, F. L., Clapham, M. E., and Kergoat, G. J. 2016. Global patterns of insect diversification: towards a reconciliation of fossil and molecular evidence? *Scientific Reports*, **6**, 19208.
- Connallon, T. and Clark, A. G. 2014. Evolutionary inevitability of sexual antagonism. *Proceedings of the Royal Society B: Biological Sciences*, **281**, 20132123.
- Connell, J. H. 1983. On the prevalence and relative importance of interspecific competition—evidence from field experiments. *The American Naturalist*, **122**, 661–96.
- Cowling, R. M. and Holmes, P. M. 1992. Endemism and speciation in a lowland flora from the Cape floristic region. *Biological Journal of the Linnean Society*, **47**, 367–83.
- Coyne, J. A. and Orr, H. A. 1989. Patterns of speciation in *Drosophila*. *Evolution*, **43**, 362–81.
- Coyne, J. A. and Orr, H. A. 1997. 'Patterns of speciation in *Drosophila*' revisited. *Evolution*, **51**, 295–303.
- Coyne, J. A. and Orr, H. A. 1998. The evolutionary genetics of speciation. *Philosophical Transactions of the Royal Society of London Series B: Biological Sciences*, **353**, 287–305.
- Coyne, J. A. and Orr, H. A. 2004. *Speciation*. Sunderland, MA: Sinauer Associates.
- Coyne, J. A. and Price, T. D. 2000. Little evidence for sympatric speciation in island birds. *Evolution*, **54**, 2166–71.
- Crisp, M., Cook, L., and Steane, D. 2004. Radiation of the Australian flora: what can comparisons of molecular phylogenies across multiple taxa tell us about the evolution of diversity in present-day communities? *Philosophical Transactions of the Royal Society of London Series B: Biological Sciences*, **359**, 1551–71.
- Cruickshank, T. E. and Hahn, M. W. 2014. Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. *Molecular Ecology*, **23**, 3133–57.

- Dalquen, D. A., Zhu, T. Q., and Yang, Z. H. 2017. Maximum likelihood implementation of an isolation-with-migration model for three species. *Systematic Biology*, **66**, 379–98.
- Darwin, C. R. 1859. *On the Origin of Species*. London: John Murray.
- Darwin, C. 1871. *The Descent of Man and Selection in Relation to Sex*. London: John Murray.
- Dávalos, L. M. and Russell, A. L. 2014. Sex-biased dispersal produces high error rates in mitochondrial distance-based and tree-based species delimitation, *Journal of Mammalogy*, **95**, 781–91.
- Davies, T. J., Barraclough, T. G., Chase, M. W., Soltis, P. S., Soltis, D. E., and Savolainen, V. 2004a. Darwin's abominable mystery: insights from a supertree of the angiosperms. *Proceedings of the National Academy of Sciences of the United States of America*, **101**, 1904–9.
- Davies, T. J., Barraclough, T. G., Savolainen, V., and Chase, M. W. 2004b. Environmental causes for plant biodiversity gradients. *Philosophical Transactions of the Royal Society of London Series B: Biological Sciences*, **359**, 1645–56.
- Davies, T. J., Savolainen, V., Chase, M. W., Moat, J., and Barraclough, T. G. 2004c. Environmental energy and evolutionary rates in flowering plants. *Proceedings of the Royal Society B: Biological Sciences*, **271**, 2195–2200.
- Davies, T. J., Savolainen, V., Chase, M. W., Goldblatt, P., and Barraclough, T. G. 2005. Environment, area, and diversification in the species-rich flowering plant family Iridaceae. *The American Naturalist*, **166**, 418–25.
- Davies, T. J., Meiri, S., Barraclough, T. G., and Gittleman, J. L. 2007. Species co-existence and character divergence across carnivores. *Ecology Letters*, **10**, 146–52.
- Davis, J. I. and Nixon, K. C. 1992. Populations, genetic variation, and the delimitation of phylogenetic species. *Systematic Biology*, **41**, 421–35.
- Davis, M. P., Midford, P. E., and Maddison, W. 2013. Exploring power and parameter estimation of the BiSSE method for analyzing species diversification. *BMC Evolutionary Biology*, **13**, 38.
- De Mazancourt, C., Johnson, E., and Barraclough, T. G. 2008. Biodiversity inhibits species' evolutionary responses to changing environments. *Ecology Letters*, **11**, 380–8.
- De Paepe, M., Gaboriau-Routhiau, V., Rainteau, D., Rakotobe, S., Taddei, F., and Cerf-Bensussan, N. 2011. Trade-off between bile resistance and nutritional competence drives *Escherichia coli* diversification in the mouse gut. *PLoS Genetics*, **7**, e1002107.
- De Vos, J. M., Joppa, L. N., Gittleman, J. L., Stephens, P. R., and Pimm, S. L. 2015. Estimating the normal background rate of species extinction. *Conservation Biology*, **29**, 452–62.
- Debortoli, N., Li, X., Eyres, I., et al. 2016. Genetic exchange among bdelloid rotifers is more likely due to horizontal gene transfer than to meiotic sex. *Current Biology*, **26**, 723–32.
- Decaestecker, E., Gaba, S., Raeymaekers, J. a. M., et al. 2007. Host–parasite 'Red Queen' dynamics archived in pond sediment. *Nature*, **450**, 870–U16.
- Degnan, J. H. and Rosenberg, N. A. 2006. Discordance of species trees with their most likely gene trees. *PLoS Genetics*, **2**, 762–8.
- Dellicour, S. and Flot, J. F. 2015. Delimiting species-poor data sets using single molecular markers: a study of barcode gaps, haplowebs and GMYC. *Systematic Biology*, **64**, 900–908.
- Delzenne, N. M., Neyrinck, A. M., Backhed, F., and Cani, P. D. 2011. Targeting gut microbiota in obesity: effects of prebiotics and probiotics. *Nature Reviews Endocrinology*, **7**, 639–46.
- Desjardins-Proulx, P. and Gravel, D. 2012. How likely is speciation in neutral ecology? *American Naturalist*, **179**, 137–144.
- Dettman, J. R., Jacobson, D. J., and Taylor, J. W. 2003a. A multilocus genealogical approach to phylogenetic species recognition in the model eukaryote *Neurospora*. *Evolution*, **57**, 2703–20.
- Dettman, J. R., Jacobson, D. J., Turner, E., Pringle, A., and Taylor, J. W. 2003b. Reproductive isolation and phylogenetic divergence in *Neurospora*: comparing methods of species recognition in a model eukaryote. *Evolution*, **57**, 2721–41.

- Dettman, J. R., Sirjusingh, C., Kohn, L. M., and Anderson, J. B. 2007. Incipient speciation by divergent adaptation and antagonistic epistasis in yeast. *Nature*, **447**, 585–8.
- Devaux, C. and Lande, R. 2008. Incipient allochronic speciation due to non-selective assortative mating by flowering time, mutation and genetic drift. *Proceedings of the Royal Society B: Biological Sciences*, **275**, 2723–32.
- Di Giuseppe, G., Dini, F., Vallesi, A., and Luporini, P. 2015. Genetic relationships in bipolar species of the protist ciliate, *Euplotes*. *Hydrobiologia*, **761**, 71–83.
- Diabate, A., Dao, A., Yaro, A. S., et al. 2009. Spatial swarm segregation and reproductive isolation between the molecular forms of *Anopheles gambiae*. *Proceedings of the Royal Society B: Biological Sciences*, **276**, 4215–22.
- Diehl, S. R. and Bush, G. L. 1989. The role of habitat preference in adaptation and speciation. In: Otte, D. and Endler, J. (eds) *Speciation and its Consequences*. Sunderland, MA: Sinauer Associates.
- Dimitriu, T., Misevic, D., Lotton, C., Brown, S. P., Lindner, A. B., and Taddei, F. 2016. Indirect fitness benefits enable the spread of host genes promoting costly transfer of beneficial plasmids. *PLoS Biology*, **14**, e1002478.
- Dittmar, E. L., Oakley, C. G., Conner, J. K., Gould, B. A., and Schemske, D. W. 2016. Factors influencing the effect size distribution of adaptive substitutions. *Proceedings of the Royal Society B: Biological Sciences*, **283**, 20153065.
- Dixit, P. D., Pang, T. Y., Studier, F. W., and Maslov, S. 2015. Recombinant transfer in the basic genome of *Escherichia coli*. *Proceedings of the National Academy of Sciences of the United States of America*, **112**, 9070–5.
- Dobzhansky, T. 1941. *Genetics and the Origin of Species*. New York: Columbia University Press.
- Dochtermann, N. A. and Matocq, M. D. 2016. Speciation along a shared evolutionary trajectory. *Current Zoology*, **62**, 507–11.
- Doerder, F. P. 2014. Abandoning sex: multiple origins of asexuality in the ciliate *Tetrahymena*. *BMC Evolutionary Biology*, **14**, 112.
- Domes, K., Norton, R. A., Maraun, M., and Scheu, S. 2007. Reeolution of sexuality breaks Dollo's law. *Proceedings of the National Academy of Sciences of the United States of America*, **104**, 7139–44.
- Doyle, J. J. 1995. The irrelevance of allele tree topologies for species delimitation, and a non-topological alternative. *Systematic Botany*, **20**, 574–88.
- Draghi, J. A. and Whitlock, M. C. 2012. Phenotypic plasticity facilitates mutational variance, genetic variance, and evolvability along the major axis of environmental variation. *Evolution*, **66**, 2891–902.
- Dunthorn, M. and Katz, L. A. 2010. Secretive ciliates and putative asexuality in microbial eukaryotes. *Trends in Microbiology*, **18**, 183–8.
- Dunthorn, M., Zufall, R. A., Chi, J. Y., Paszkiewicz, K., Moore, K., and Mahe, F. 2017. Meiotic genes in colpodean ciliates support secretive sexuality. *Genome Biology and Evolution*, **9**, 1781–7.
- Dupuis, J. R., Roe, A. D., and Sperling, F. a. H. 2012. Multi-locus species delimitation in closely related animals and fungi: one marker is not enough. *Molecular Ecology*, **21**, 4422–36.
- Dynesius, M. and Jansson, R. 2014. Persistence of within-species lineages: a neglected control of speciation rates. *Evolution*, **68**, 923–34.
- Eberle, J., Bazzato, E., Fabrizi, S., et al. 2019. Sex-biased dispersal obscures species boundaries in integrative species delimitation approaches. *Systematic Biology*, Early Online.
- Edwards, D. L. and Knowles, L. L. 2014. Species detection and individual assignment in species delimitation: can integrative data increase efficacy? *Proceedings of the Royal Society B: Biological Sciences*, **281**, 20132765.

- Edwards, S. V. and Beerli, P. 2000. Perspective: gene divergence, population divergence, and the variance in coalescence time in phylogeographic studies. *Evolution*, **54**, 1839–54.
- Ellegren, H. 2014. Genome sequencing and population genomics in non-model organisms. *Trends in Ecology & Evolution*, **29**, 51–63.
- Ellegren, H., Smeds, L., Burri, R., et al. 2012. The genomic landscape of species divergence in *Ficedula* flycatchers. *Nature*, **491**, 756–60.
- Enard, D., Cai, L., Gwennap, C., and Petrov, D. A. 2016. Viruses are a dominant driver of protein adaptation in mammals. *Elife*, **5**, e12469.
- Evans, M. R., Norris, K. J., and Benton, T. G. 2012. Predictive ecology: systems approaches. Introduction. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **367**, 163–9.
- Ewens, W. J. 1979. *Mathematical Population Genetics*. Berlin: Springer.
- Eyres, I., Boschetti, C., Crisp, A., et al. 2015. Horizontal gene transfer in bdelloid rotifers is ancient, ongoing and more frequent in species from desiccating habitats. *BMC Biology*, **13**, 90.
- Ezard, T. H. G., Pearson, P. N., and Purvis, A. 2010. Algorithmic approaches to aid species' delimitation in multidimensional morphospace. *BMC Evolutionary Biology*, **10**, 175.
- Ezard, T. H. G., Aze, T., Pearson, P. N., and Purvis, A. 2011. Interplay between changing climate and species' ecology drives macroevolutionary dynamics. *Science*, **332**, 349–51.
- Farrell, B. D. 1998. 'Inordinate fondness' explained: why are there so many beetles? *Science*, **281**, 555–9.
- Farrington, H. L., Lawson, L. P., Clark, C. M., and Petren, K. 2014. The evolutionary history of Darwin's finches: speciation, gene flow, and introgression in a fragmented landscape. *Evolution*, **68**, 2932–44.
- Felsenstein, J. 1981. Skepticism towards Santa Rosalia, or why are there so few kinds of animals? *Evolution*, **35**, 124–38.
- Felsenstein, J. 1985. Phylogenies and the comparative method. *The American Naturalist* **125**, 1–15.
- Fiegna, F., Moreno-Letelier, A., Bell, T., and Barraclough, T. G. 2015a. Evolution of species interactions determines microbial community productivity in new environments. *ISME Journal*, **9**, 1235–45.
- Fiegna, F., Scheuerl, T., Moreno-Letelier, A., Bell, T., and Barraclough, T. G. 2015b. Saturating effects of species diversity on life-history evolution in bacteria. *Proceedings of the Royal Society B: Biological Sciences*, **282**, 20151794.
- Fisher, R. A. 1930. *The Genetical Theory of Natural Selection*. Oxford: Oxford University Press.
- Fitzpatrick, B. M. and Turelli, M. 2006. The geography of mammalian speciation: mixed signals from phylogenies and range maps. *Evolution*, **60**, 601–15.
- Flint, H. J., Scott, K. P., Louis, P., and Duncan, S. H. 2012. The role of the gut microbiota in nutrition and health. *Nature Reviews Gastroenterology & Hepatology*, **9**, 577–89.
- Flot, J. F., Hespels, B., Li, X., et al. 2013. Genomic evidence for ameiotic evolution in the bdelloid rotifer *Adineta vaga*. *Nature*, **500**, 453–7.
- Foley, N. M., Springer, M. S., and Teeling, E. C. 2016. Mammal madness: is the mammal tree of life not yet resolved? *Philosophical Transactions of the Royal Society B: Biological Sciences*, **371**, 20150140.
- Fontaneto, D. and Barraclough, T. G. 2015. Do species exist in asexuals? Theory and evidence from bdelloid rotifers. *Integrative and Comparative Biology*, **55**, 253–63.
- Fontaneto, D., Herniou, E. A., Boschetti, C., et al. 2007. Independently evolving species in asexual bdelloid rotifers. *PLoS Biology*, **5**, 914–21.
- Foster, K. R. and Bell, T. 2012. Competition, not cooperation, dominates interactions among culturable microbial species. *Current Biology*, **22**, 1845–50.

- France, M. T., Mendes-Soares, H., and Forney, L. J. 2016. Genomic comparisons of *Lactobacillus crispatus* and *Lactobacillus iners* reveal potential ecological drivers of community composition in the vagina. *Applied and Environmental Microbiology*, **82**, 7063–73.
- Fraser, C., Hanage, W. P., and Spratt, B. G. 2007. Recombination and the nature of bacterial speciation. *Science*, **315**, 476–80.
- Friedman, J., Alm, E. J., and Shapiro, B. J. 2013. Sympatric speciation: when is it possible in bacteria? *PLoS One*, **8**, e53539.
- Friesen, V. L., Smith, A. L., Gomez-Diaz, E., et al. R. 2007. Sympatric speciation by allochrony in a seabird. *Proceedings of the National Academy of Sciences of the United States of America*, **104**, 18589–94.
- Frost, G. S., Walton, G. E., Swann, J. R., et al. 2014. Impacts of plant-based foods in ancestral hominin diets on the metabolism and function of gut microbiota in vitro. *MBio*, **5**, e00853-14.
- Fujisawa, T. and Barraclough, T. G. 2013. Delimiting species using single-locus data and the Generalized Mixed Yule Coalescent approach: a revised method and evaluation on simulated data sets. *Systematic Biology*, **62**, 707–24.
- Fujisawa, T., Vogler, A. P., and Barraclough, T. G. 2015. Ecology has contrasting effects on genetic variation within species versus rates of molecular evolution across species in water beetles. *Proceedings of the Royal Society B: Biological Sciences*, **282**, 20142476.
- Fujisawa, T., Aswad, A., and Barraclough, T. G. 2016. A rapid and scalable method for multilocus species delimitation using Bayesian model comparison and rooted triplets. *Systematic Biology*, **65**, 759–71.
- Fujita, M. K., Leache, A. D., Burbrink, F. T., McGuire, J. A., and Moritz, C. 2012. Coalescent-based species delimitation in an integrative taxonomy. *Trends in Ecology & Evolution*, **27**, 480–8.
- Funk, D. J. and Omland, K. E. 2003. Species-level paraphyly and polyphyly: frequency, causes, and consequences, with insights from animal mitochondrial DNA. *Annual Review of Ecology and Systematics*, **34**, 397–423.
- Funk, D. J., Nosil, P., and Etges, W. J. 2006. Ecological divergence exhibits consistently positive associations with reproductive isolation across disparate taxa. *Proceedings of the National Academy of Sciences of the United States of America*, **103**, 3209–13.
- Garud, N. R., Good, B. H., Hallatschek, O., and Pollard, K. S. 2017. Evolutionary dynamics of bacteria in the gut microbiome within and across hosts. *bioRxiv*, doi: <https://doi.org/10.1101/210955>.
- Gavrilets, S. 2003. Perspective: models of speciation: what have we learned in 40 years? *Evolution*, **57**, 2197–215.
- Gavrilets, S. 2004. *Fitness Landscapes and the Origin of Species*. Princeton, NJ: Princeton University Press.
- Gavrilets, S. and Losos, J. B. 2009. Adaptive radiation: contrasting theory with data. *Science*, **323**, 732–7.
- Ghoul, M. and Mitri, S. 2016. The ecology and evolution of microbial competition. *Trends in Microbiology*, **24**, 833–45.
- Gianoli, E. 2004. Evolution of a climbing habit promotes diversification in flowering plants. *Proceedings of the Royal Society B: Biological Sciences*, **271**, 2011–15.
- Gillespie, R. 2004. Community assembly through adaptive radiation in Hawaiian spiders. *Science*, **303**, 356–9.
- Gillooly, J. F., Allen, A. P., West, G. B., and Brown, J. H. 2005. The rate of DNA evolution: effects of body size and temperature on the molecular clock. *Proceedings of the National Academy of Sciences of the United States of America*, **102**, 140–5.
- Giraud, T. and Gourbiere, S. 2012. The tempo and modes of evolution of reproductive isolation in fungi. *Heredity*, **109**, 204–14.

- Gladyshev, E. A., Meselson, M., and Arkhipova, I. R. 2008. Massive horizontal gene transfer in bdelloid rotifers. *Science*, **320**, 1210–13.
- Goddard, M. R. and Burt, A. 1999. Recurrent invasion and extinction of a selfish gene. *Proceedings of the National Academy of Sciences of the United States of America*, **96**, 13880–5.
- Gomez, P. and Buckling, A. 2011. Bacteria–phage antagonistic coevolution in soil. *Science*, **332**, 106–9.
- Gonzalez-Voyer, A. and Kolm, N. 2011. Rates of phenotypic evolution of ecological characters and sexual traits during the Tanganyikan cichlid adaptive radiation. *Journal of Evolutionary Biology*, **24**, 2378–88.
- Gould, F., Brown, Z. S., and Kuzma, J. 2018. Wicked evolution: can we address the sociobiological dilemma of pesticide resistance? *Science*, **360**, 728–32.
- Gourbiere, S. and Mallet, J. 2010. Are species real? The shape of the species boundary with exponential failure, reinforcement, and the ‘missing snowball’. *Evolution*, **64**, 1–24.
- Grandcolas, P., Murienne, J., Robillard, T., et al. 2008. New Caledonia: a very old Darwinian island? *Philosophical Transactions of the Royal Society B: Biological Sciences*, **363**, 3309–17.
- Grant, P. R. and Grant, B. R. 2009. The secondary contact phase of allopatric speciation in Darwin’s finches. *Proceedings of the National Academy of Sciences of the United States of America*, **106**, 20141–8.
- Gray, J. C. and Goddard, M. R. 2012. Gene-flow between niches facilitates local adaptation in sexual populations. *Ecology Letters*, **15**, 955–62.
- Green, J. L. and Plotkin, J. B. 2007. A statistical theory for sampling species abundances. *Ecology Letters*, **10**, 1037–45.
- Grossenbacher, D. L. and Whittall, J. B. 2011. Increased floral divergence in sympatric monkey-flowers. *Evolution*, **65**, 2712–18.
- Guimarães, P. R., Jordano, P., and Thompson, J. N. 2011. Evolution and coevolution in mutualistic networks. *Ecology Letters*, **14**, 877–85.
- Gwynne, B. J., Gordon, T. R., and Davis, R. M. 1997. A new race of *Fusarium oxysporum* f. sp. *melonis* causing Fusarium wilt of muskmelon in the Central Valley of California. *Plant Disease*, **81**, 1095.
- Hanemaaijer, M. J., Collier, T. C., Change, A., et al. 2018. The fate of genes that cross species boundaries after a major hybridization event in a natural mosquito population. *Molecular Ecology*, **27**, 4978–4990.
- Hansen, T. F. 2006. The evolution of genetic architecture. *Annual Review of Ecology Evolution and Systematics*, **37**, 123–57.
- Hansen, T. F. and Houle, D. 2008. Measuring and comparing evolvability and constraint in multivariate characters. *Journal of Evolutionary Biology*, **21**, 1201–19.
- Hanson, S. J., Schurko, A. M., Hecox-Lea, B., Mark Welch, D. B., Stelzer, C.-P., Logsdon, J. M. 2013. Inventory and phylogenetic analysis of meiotic genes in monogonont rotifers, *Journal of Heredity*, **104**, 357–370.
- Harmon, L. J. 2018. *Phylogenetic Comparative Methods: Learning from Trees*. CreateSpace.
- Harmon, L. J. and Harrison, S. 2015. Species diversity is dynamic and unbounded at local and continental scales. *The American Naturalist*, **185**, 584–93.
- Harmon, L. J., Weir, J. T., Brock, C. D., Glor, R. E., and Challenger, W. 2008. GEIGER: investigating evolutionary radiations. *Bioinformatics*, **24**, 129–31.
- Harris, L. W. and Davies, T. J. 2016. A complete fossil-calibrated phylogeny of seed plant families as a tool for comparative analyses: testing the ‘Time for Speciation’ hypothesis. *PLoS One*, **11**, e0162907.
- Harrison, E. and Brockhurst, M. A. 2012. Plasmid-mediated horizontal gene transfer is a coevolutionary process. *Trends in Microbiology*, **20**, 262–7.

- Harrison, E., Guymer, D., Spiers, A. J., Paterson, S., and Brockhurst, M. A. 2015. Parallel compensatory evolution stabilizes plasmids across the parasitism–mutualism continuum. *Current Biology*, **25**, 2034–9.
- Harrison, R. G. and Larson, E. L. 2014. Hybridization, introgression, and the nature of species boundaries. *Journal of Heredity*, **105**, 795–809.
- Harvey, M. G., Seeholzer, G. F., Smith, B. T., Rabosky, D. L., Cuervo, A. M., and Brumfield, R. T. 2017. Positive association between population genetic differentiation and speciation rates in New World birds. *Proceedings of the National Academy of Sciences of the United States of America*, **114**, 6328–33.
- Hausdorf, B. and Hennig, C. 2010. Species delimitation using dominant and codominant multilocus markers. *Systematic Biology*, **59**, 491–503.
- Hausdorff, W. P. and Hanage, W. P. 2016. Interim results of an ecological experiment—conjugate vaccination against the pneumococcus and serotype replacement. *Human Vaccines & Immunotherapeutics*, **12**, 358–74.
- Hayward, A. D., Pemberton, J. M., Berenos, C., Wilson, A. J., Pilkington, J. G., and Kruuk, L. E. B. 2018. Evidence for selection-by-environment but not genotype-by-environment interactions for fitness-related traits in a wild mammal population. *Genetics*, **208**, 349–64.
- Hazzi, N. A., Moreno, J. S., Ortiz-Movliav, C., and Palacio, R. D. 2018. Biogeographic regions and events of isolation and diversification of the endemic biota of the tropical Andes. *Proceedings of the National Academy of Sciences of the United States of America*, **115**, 7985–90.
- Heard, S. B. 1992. Patterns in tree balance among cladistic, phenetic, and randomly generated phylogenetic trees. *Evolution*, **46**, 1818–26.
- Hebert, P. D. N., Cywinska, A., Ball, S. L., and Dewaard, J. R. 2003. Biological identifications through DNA barcodes. *Proceedings of the Royal Society B: Biological Sciences*, **270**, 313–21.
- Hein, J., Schierup, M. H., and Wiuf, C. 2005. *Gene Genealogies, Variation and Evolution: A Primer in Coalescent Theory*. Oxford: Oxford University Press.
- Hendry, A. P. 2017. *Eco-evolutionary Dynamics*. Princeton, NJ: Princeton University Press.
- Hendry, A. P., Huber, S. K., De Leon, L. F., Herrel, A., and Podos, J. 2009. Disruptive selection in a bimodal population of Darwin's finches. *Proceedings of the Royal Society B: Biological Sciences*, **276**, 753–9.
- Hennig, W. 1966. *Phylogenetic Systematics*. Urbana: University of Illinois Press.
- Herniou, E., Theze, J., Cory, J., and Vaamonde, C. L. 2015. Diversity, species delimitation, and evolution of insect viruses. *Genome*, **58**, 226.
- Herron, M. D. and Doebeli, M. 2013. Parallel evolutionary dynamics of adaptive diversification in *Escherichia coli*. *PLoS Biology*, **11**, e1001490.
- Hey, J. 1991. The structure of genealogies and the distribution of fixed differences between DNA sequence samples from natural populations. *Genetics*, **128**, 831–40.
- Hey, J. 2001. The mind of the species problem. *Trends in Ecology & Evolution*, **16**, 326–9.
- Higgs, P. G. and Derrida, B. 1992. Genetic distance and species formation in evolving populations. *Journal of Molecular Evolution*, **35**, 454–65.
- Hillis, D. M., Bull, J. J., White, M. E., Badgett, M. R., and Molineux, I. J. 1992. Experimental phylogenetics—generation of a known phylogeny. *Science*, **255**, 589–92.
- Holmes, E. C. 2013. What can we predict about viral evolution and emergence? *Current Opinion in Virology*, **3**, 180–4.
- Holmes, M. W., Hammond, T. T., Wogan, G. O. U., et al. 2016. Natural history collections as windows on evolutionary processes. *Molecular Ecology*, **25**, 864–81.
- Holt, B. G. and Jonsson, K. A. 2014. Reconciling hierarchical taxonomy with molecular phylogenies. *Systematic Biology*, **63**, 1010–17.

- Hooper, D. M. and Price, T. D. 2017. Chromosomal inversion differences correlate with range overlap in passerine birds. *Nature Ecology & Evolution*, **1**, 1526–34.
- Hopkins, R. 2013. Reinforcement in plants. *New Phytologist*, **197**, 1095–103.
- Hou, J., Friedrich, A., De Montigny, J., and Schacherer, J. 2014. Chromosomal rearrangements as a major mechanism in the onset of reproductive isolation in *Saccharomyces cerevisiae*. *Current Biology*, **24**, 1153–9.
- Huang, Y. J. and LiPuma, J. J. 2016. The microbiome in cystic fibrosis. *Clinics in Chest Medicine*, **37**, 59–67.
- Hubbell, S. P. 2001. *The Unified Neutral Theory of Biodiversity and Biogeography*. Princeton, NJ: Princeton University Press.
- Hudson, L. N., Blagoderov, V., Heaton, A., et al. 2015. Insect: automating the digitization of natural history collections. *PLoS One*, **10**, e0143402.
- Hudson, R. R. 1991. Gene genealogies and the coalescent process. *Oxford Surveys in Evolutionary Biology*, **7**, 1–44.
- Hudson, R. R. and Coyne, J. A. 2002. Mathematical consequences of the genealogical species concept. *Evolution*, **56**, 1557–65.
- Hufford, K. M. and Mazer, S. J. 2003. Plant ecotypes: genetic differentiation in the age of ecological restoration. *Trends in Ecology & Evolution*, **18**, 147–55.
- Hughes, C. and Eastwood, R. 2006. Island radiation on a continental scale: exceptional rates of plant diversification after uplift of the Andes. *Proceedings of the National Academy of Sciences of the United States of America*, **103**, 10334–9.
- Humphreys, A. M. and Barraclough, T. G. 2014. The evolutionary reality of higher taxa in mammals. *Proceedings of the Royal Society B: Biological Sciences*, **281**, 20132750.
- Humphreys, A. M., Rydin, C., Jonsson, K. A., Alsop, D., Callender-Crowe, L. M., and Barraclough, T. G. 2016. Detecting evolutionarily significant units above the species level using the Generalised Mixed Yule Coalescent method. *Methods in Ecology and Evolution*, **7**, 1366–75.
- Hunt, T., Bergsten, J., Levkanicova, Z., et al. 2007. A comprehensive phylogeny of beetles reveals the evolutionary origins of a superradiation. *Science*, **318**, 1913–16.
- Hunter, D. C., Pemberton, J. M., Pilkington, J. G., and Morrissey, M. B. 2018. Quantification and decomposition of environment–selection relationships. *Evolution*, **72**, 851–66.
- Hunter, J. P. 1998. Key innovations and the ecology of macroevolution. *Trends in Ecology & Evolution*, **13**, 31–6.
- Huttenhower, C., Gevers, D., Knight, R., et al. 2012. Structure, function and diversity of the healthy human microbiome. *Nature*, **486**, 207–14.
- Igea, J., Bogarin, D., Papadopoulos, A. S. T., and Savolainen, V. 2015. A comparative analysis of island floras challenges taxonomy-based biogeographical models of speciation. *Evolution*, **69**, 482–91.
- Ingram, T. 2011. Speciation along a depth gradient in a marine adaptive radiation. *Proceedings of the Royal Society B: Biological Sciences*, **278**, 613–18.
- Jackson, N. D., Carstens, B. C., Morales, A. E., and O'Meara, B. C. 2017. Species delimitation with gene flow. *Systematic Biology*, **66**, 799–812.
- James, J. E., Piganeau, G., and Eyre-Walker, A. 2016. The rate of adaptive evolution in animal mitochondria. *Molecular Ecology*, **25**, 67–78.
- Jansson, R. and Davies, T. J. 2008. Global variation in diversification rates of flowering plants: energy vs. climate change. *Ecology Letters*, **11**, 173–83.
- Jeltsch, A. 2003. Maintenance of species identity and controlling speciation of bacteria: a new function for restriction/modification systems? *Gene*, **317**, 13–16.

- Jerison, E. R. and Desai, M. M. 2015. Genomic investigations of evolutionary dynamics and epistasis in microbial evolution experiments. *Current Opinion in Genetics & Development*, **35**, 33–9.
- Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K., and Mooers, A. O. 2012. The global diversity of birds in space and time. *Nature*, **491**, 444–8.
- Jiggins, C. D., Mallarino, R., Willmott, K. R., and Bermingham, E. 2006. The phylogenetic pattern of speciation and wing pattern change in neotropical *Ithomia* butterflies (Lepidoptera: Nymphalidae). *Evolution*, **60**, 1454–66.
- Johansson, J. 2008. Evolutionary responses to environmental changes: how does competition affect adaptation? *Evolution*, **62**, 421–35.
- Johnson, L. P., Walton, G. E., Swann, J. R., Frost, G., Gibson, G. R., and Barraclough, T. G. 2019. Ecological and evolutionary dynamics of human faecal communities in vitro in response to inulin provision as a sole carbon source. Unpublished work.
- Jones, G., Aydin, Z., and Oxelman, B. 2015. DISSECT: an assignment-free Bayesian discovery method for species delimitation under the multispecies coalescent. *Bioinformatics*, **31**, 991–8.
- Jonsson, H., Schubert, M., Seguin-Orlando, A., et al. 2014. Speciation with gene flow in equids despite extensive chromosomal plasticity. *Proceedings of the National Academy of Sciences of the United States of America*, **111**, 18655–60.
- Jordan, D. S. 1905. The origin of species through isolation. *Science*, **22**, 545–62.
- Jörger, K. M. and Schrödl, M. 2013. How to describe a cryptic species? Practical challenges of molecular taxonomy. *Frontiers in Zoology*, **10**, 59.
- Keller, I., Wagner, C. E., Greuter, L., et al. 2013. Population genomic signatures of divergent adaptation, gene flow and hybrid speciation in the rapid radiation of Lake Victoria cichlid fishes. *Molecular Ecology*, **22**, 2848–63.
- Kerr, K. C. R. 2011. Searching for evidence of selection in avian DNA barcodes. *Molecular Ecology Resources*, **11**, 1045–55.
- Kerr, K. C. R., Stoeckle, M. Y., Dove, C. J., Weigt, L. A., Francis, C. M., and Hebert, P. D. N. 2007. Comprehensive DNA barcode coverage of North American birds. *Molecular Ecology Notes*, **7**, 535–43.
- Kettle, H., Louis, P., Holtrop, G., Duncan, S. H., and Flint, H. J. 2015. Modelling the emergent dynamics and major metabolites of the human colonic microbiota. *Environmental Microbiology*, **17**, 1615–30.
- Kingsolver, J. G., Diamond, S. E., Siepielski, A. M., and Carlson, S. M. 2012. Synthetic analyses of phenotypic selection in natural populations: lessons, limitations and future directions. *Evolutionary Ecology*, **26**, 1101–18.
- Kinnison, M. T. and Hendry, A. P. 2001. The pace of modern life. II: From rates of contemporary microevolution to pattern and process. *Genetica*, **112**, 145–64.
- Kisel, Y. and Barraclough, T. G. 2010. Speciation has a spatial scale that depends on levels of gene flow. *The American Naturalist*, **175**, 316–34.
- Kisel, Y., Moreno-Letelier, A. C., Bogarin, D., Powell, M. P., Chase, M. W., and Barraclough, T. G. 2012. Testing the link between population genetic differentiation and clade diversification in Costa Rican orchids. *Evolution*, **66**, 3035–52.
- Kleindorfer, S., O'Connor, J. A., Dudaniec, R. Y., Myers, S. A., Robertson, J., and Sulloway, F. J. 2014. Species collapse via hybridization in Darwin's tree finches. *The American Naturalist*, **183**, 325–41.
- Knowles, L. L. and Carstens, B. C. 2007. Delimiting species without monophyletic gene trees. *Systematic Biology*, **56**, 887–95.
- Koch, C., Konieczka, J., Delorey, T., et al. 2017. Inference and evolutionary analysis of genome-scale regulatory networks in large phylogenies. *Cell Systems*, **4**, 543–58.

- Koeppel, A., Perry, E. B., Sikorski, J., et al. 2008. Identifying the fundamental units of bacterial diversity: a paradigm shift to incorporate ecology into bacterial systematics. *Proceedings of the National Academy of Sciences of the United States of America*, **105**, 2504–9.
- Kopp, M. and Gavrillets, S. 2006. Multilocus genetics and the coevolution of quantitative traits. *Evolution*, **60**, 1321–36.
- Koraimann, G. and Wagner, M. A. 2014. Social behavior and decision making in bacterial conjugation. *Frontiers in Cellular and Infection Microbiology*, **4**, 54.
- Koskella, B. and Brockhurst, M. A. 2014. Bacteria-phage coevolution as a driver of ecological and evolutionary processes in microbial communities. *FEMS Microbiology Reviews*, **38**, 916–31.
- Koufopanou, V., Burt, A., and Taylor, J. W. 1997. Concordance of gene genealogies reveals reproductive isolation in the pathogenic fungus *Coccidioides immitis*. *Proceedings of the National Academy of Sciences of the United States of America*, **94**, 5478–82.
- Kovatcheva-Datchary, P., Egert, M., Maathuis, A., et al. 2009. Linking phylogenetic identities of bacteria to starch fermentation in an in vitro model of the large intestine by RNA-based stable isotope probing. *Environmental Microbiology*, **11**, 914–26.
- Kozak, K. H. and Wiens, J. J. 2006. Does niche conservatism promote speciation? A case study in North American salamanders. *Evolution*, **60**, 2604–21.
- Kraus, R. H. S., Kerstens, H. H. D., Van Hooft, P., et al. 2012. Widespread horizontal genomic exchange does not erode species barriers among sympatric ducks. *BMC Evolutionary Biology*, **12**, 45.
- Krausmann, F., Erb, K. H., Gingrich, S., et al. 2013. Global human appropriation of net primary production doubled in the 20th century. *Proceedings of the National Academy of Sciences of the United States of America*, **110**, 10324–9.
- Kubatko, L. S., Gibbs, H. L., and Bloomquist, E. W. 2011. Inferring species-level phylogenies and taxonomic distinctiveness using multilocus data in *Sistrurus* rattlesnakes. *Systematic Biology*, **60**, 393–409.
- Kuehne, H. A., Murphy, H. A., Francis, C. A., and Sniegowski, P. D. 2007. Allopatric divergence, secondary contact and genetic isolation in wild yeast populations. *Current Biology*, **17**, 407–11.
- Lackey, A. C. R. and Boughman, J. W. 2017. Evolution of reproductive isolation in stickleback fish. *Evolution*, **71**, 357–72.
- Lahaye, R., Van Der Bank, M., Bogarin, D., et al. 2008. DNA barcoding the floras of biodiversity hotspots. *Proceedings of the National Academy of Sciences of the United States of America*, **105**, 2923–8.
- Lahr, D. J. G., Parfrey, L. W., Mitchell, E. a. D., Katz, L. A., and Lara, E. 2011. The chastity of amoebae: re-evaluating evidence for sex in amoeboid organisms. *Proceedings of the Royal Society B: Biological Sciences*, **278**, 2081–90.
- Lamanna, F., Kirschbaum, F., Ernst, A. R. R., Feulner, P. G. D., Mamonekene, V., Paul, C., and Tiedemann, R. 2016. Species delimitation and phylogenetic relationships in a genus of African weakly-electric fishes (Osteoglossiformes, Mormyridae, *Campylomormyrus*). *Molecular Phylogenetics and Evolution*, **101**, 8–18.
- Lamsdell, J. C. 2016. Horseshoe crab phylogeny and independent colonizations of fresh water: ecological invasion as a driver for morphological innovation. *Palaeontology*, **59**, 181–94.
- Lande, R. 1976. Natural selection and random genetic drift in phenotypic evolution. *Evolution*, **30**, 314–34.
- Lande, R. 1979. Quantitative genetic-analysis of multivariate evolution, applied to brain-body size allometry. *Evolution*, **33**, 402–16.

- Lande, R. 1981. Models of speciation by sexual selection on polygenic characters. *Proceedings of the National Academy of Sciences of the United States of America*, **78**, 3721–5.
- Lande, R. 2014. Evolution of phenotypic plasticity and environmental tolerance of a labile quantitative character in a fluctuating environment. *Journal of Evolutionary Biology*, **27**, 866–75.
- Lässig, M., Mustonen, V., and Walczak, A. M. 2017. Predicting evolution. *Nature Ecology & Evolution*, **1**, 0077.
- Lavin, M., Schrire, B. P., Lewis, G., et al. 2004. Metacommunity process rather than continental tectonic history better explains geographically structured phylogenies in legumes. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **359**, 1509–22.
- Lawrence, D. and Barraclough, T. G. 2016. Evolution of resource use along a gradient of stress leads to increased facilitation. *Oikos*, **125**, 1284–95.
- Lawrence, D., Fiegna, F., Behrends, V., et al. 2012. Species interactions alter evolutionary responses to a novel environment. *PLoS Biology*, **10**, e1001330.
- Lawrence, D., Bell, T., and Barraclough, T. G. 2016. The effect of immigration on the adaptation of microbial communities to warming. *The American Naturalist*, **187**, 236–48.
- Le Corre, V. and Kremer, A. 2012. The genetic differentiation at quantitative trait loci under local adaptation. *Molecular Ecology*, **21**, 1548–66.
- Leache, A. D., Koo, M. S., Spencer, C. L., Papenfuss, T. J., Fisher, R. N., and McGuire, J. A. 2009. Quantifying ecological, morphological, and genetic variation to delimit species in the coast horned lizard species complex (*Phrynosoma*). *Proceedings of the National Academy of Sciences of the United States of America*, **106**, 12418–23.
- Leinonen, T., O'Hara, R. B., Cano, J. M., and Merila, J. 2008. Comparative studies of quantitative trait and neutral marker divergence: a meta-analysis. *Journal of Evolutionary Biology*, **21**, 1–17.
- Lessios, H. A. 1998. The first stage of speciation as seen in organisms separated by the Isthmus of Panama. In: Howard, D. J. and Berlocher, S. H. (eds) *Endless Forms: Species and Speciation*. New York: Oxford University Press.
- Li, W., Ortiz, G., Fournier, P.-E., et al. 2010. Genotyping of human lice suggests multiple emergences of body lice from local head louse populations. *PLoS Neglected Tropical Diseases*, **4**, e641.
- Lieberman, E., Hauert, C., and Nowak, M. A. 2005. Evolutionary dynamics on graphs. *Nature*, **433**, 312–16.
- Linder, H. P. 2003. The radiation of the Cape flora, southern Africa. *Biological Reviews*, **78**, 597–638.
- Linder, H. P. 2005. Evolution of diversity: the Cape flora. *Trends in Plant Science*, **10**, 536–41.
- Liti, G., Barton, D. B. H., and Louis, E. J. 2006. Sequence diversity, reproductive isolation and species concepts in *Saccharomyces*. *Genetics*, **174**, 839–50.
- Liu, L. and Yu, L. L. 2010. Phybase: an R package for species tree analysis. *Bioinformatics*, **26**, 962–3.
- Lobato, E., Geraldes, M., Melo, M., Doutrelant, C., and Covas, R. 2017. Diversity and composition of cultivable gut bacteria in an endemic island bird and its mainland sister species. *Symbiosis*, **71**, 155–64.
- Loeuille, N. and Loreau, M. 2005. Evolutionary emergence of size-structured food webs. *Proceedings of the National Academy of Sciences of the United States of America*, **102**, 5761–6.
- Lohse, K. 2009. Can mtDNA barcodes be used to delimit species? A response to Pons et al. (2006). *Systematic Biology*, **58**, 439–42; discussion 442–4.
- Losos, J. B. and Schluter, D. 2000. Analysis of an evolutionary species–area relationship. *Nature*, **408**, 847–50.

- Lynch, J. D. 1989. The gauge of speciation: on the frequencies of modes of speciation. In: Otte, D. and Endler, J. A. (eds) *Speciation and its Consequences*. Sunderland, MA: Sinauer Associates.
- Lynch, M. 1990. The rate of morphological evolution in mammals from the standpoint of the neutral expectation. *The American Naturalist*, **136**, 727–41.
- Lynch, M. and Hill, W. G. 1986. Phenotypic evolution by neutral mutation. *Evolution*, **40**, 915–35.
- Lynch, M. and Marinov, G. K. 2015. The bioenergetic costs of a gene. *Proceedings of the National Academy of Sciences of the United States of America*, **112**, 15690–5.
- Ma, L. J., Van Der Does, H. C., Borkovich, K. A., et al. 2010. Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. *Nature*, **464**, 367–73.
- Maclean, R. C., Dickson, A., and Bell, G. 2005. Resource competition and adaptive radiation in a microbial microcosm. *Ecology Letters*, **8**, 38–46.
- Maclean, R. C., Hall, A. R., Perron, G. G., and Buckling, A. 2010. The population genetics of antibiotic resistance: integrating molecular mechanisms and treatment contexts. *Nature Reviews Genetics*, **11**, 405–14.
- Maddison, W. P., Midford, P. E., and Otto, S. P. 2007. Estimating a binary character's effect on speciation and extinction. *Systematic Biology*, **56**, 701–10.
- Magallon, S. and Sanderson, M. J. 2001. Absolute diversification rates in angiosperm clades. *Evolution*, **55**, 1762–80.
- Magnuson-Ford, K. and Otto, S. P. 2012. Linking the investigations of character evolution and species diversification. *The American Naturalist*, **180**, 225–45.
- Maheshwari, S. and Barbash, D. A. 2011. The genetics of hybrid incompatibilities. *Annual Review of Genetics*, **45**, 331–55.
- Majewski, J. and Cohan, F. M. 1999. Adapt globally, act locally: the effect of selective sweeps on bacterial sequence diversity. *Genetics*, **152**, 1459–74.
- Mallet, J. 2008. Hybridization, ecological races and the nature of species: empirical evidence for the ease of speciation. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **363**, 2971–86.
- Mallet, J., Besansky, N., and Hahn, M. W. 2016. How reticulated are species? *Bioessays*, **38**, 140–9.
- Martin, C. H., Cutler, J. S., Friel, J. P., Toukpong, C. D., Coop, G., and Wainwright, P. C. 2015. Complex histories of repeated gene flow in Cameroon Crater Lake cichlids cast doubt on one of the clearest examples of sympatric speciation. *Evolution*, **69**, 1406–22.
- Martin, S. H., Dasmahapatra, K. K., Nadeau, N. J., et al. 2013. Genome-wide evidence for speciation with gene flow in *Heliconius* butterflies. *Genome Research*, **23**, 1817–28.
- Martin, S. H., Davey, J. W., Salazar, C., and Jiggins, C. D. 2019. Recombination rate variation shapes barriers to introgression across butterfly genomes. *PLoS Biology*, **17**, e2006288.
- Marvig, R. L., Sommer, L. M., Molin, S., and Johansen, H. K. 2015. Convergent evolution and adaptation of *Pseudomonas aeruginosa* within patients with cystic fibrosis. *Nature Genetics*, **47**, 57–64.
- Maynard Smith, J. and Szathmary, E. 1995. *The Major Transitions in Evolution*. New York: W.H. Freeman.
- Mayr, E. 1963. *Animal Species and Evolution*. Cambridge, MA: Harvard University Press.
- McGinty, S. E., Lehmann, L., Brown, S. P., and Rankin, D. J. 2013. The interplay between relatedness and horizontal gene transfer drives the evolution of plasmid-carried public goods. *Proceedings of the Royal Society B: Biological Sciences*, **280**, 20130400.
- McDaniel, S. F. and Shaw, A. J. 2005. Selective sweeps and intercontinental migration in the cosmopolitan moss *Ceratodon purpureus* (Hedw.) Brid. *Molecular Ecology*, **14**, 1121–32.
- McDonald, J. H. and Kreitman, M. 1991. Adaptive protein evolution at the *adh* locus in *Drosophila*. *Nature*, **351**, 652–4.

- Melendrez, M. C., Becraft, E. D., Wood, J. M., et al. 2016. Recombination does not hinder formation or detection of ecological species of *Synechococcus* inhabiting a hot spring cyanobacterial mat. *Frontiers in Microbiology*, **6**, 1540.
- Melian, C. J., Vilas, C., Baldo, F., Gonzalez-Ortegon, E., Drake, P., and Williams, R. J. 2011. Eco-evolutionary dynamics of individual-based food webs. *Advances in Ecological Research: The Role of Body Size in Multispecies Systems*, **45**, 225–68.
- Merila, J. and Hendry, A. P. 2014. Climate change, adaptation, and phenotypic plasticity: the problem and the evidence. *Evolutionary Applications*, **7**, 1–14.
- Messer, P. W., Ellner, S. P., and Hairston, N. G. 2016. Can population genetics adapt to rapid evolution? *Trends in Genetics*, **32**, 408–18.
- Meyer, C. P. and Paulay, G. 2005. DNA barcoding: error rates based on comprehensive sampling. *PLoS Biology*, **3**, 2229–38.
- Meyer, J. R., Dobias, D. T., Medina, S. J., Servilio, L., Gupta, A., and Lenski, R. E. 2016. Ecological speciation of bacteriophage lambda in allopatry and sympatry. *Science*, **354**, 1301–4.
- Millanes, A. M., Truong, C., Westberg, M., Diederich, P., and Wedin, M. 2014. Host switching promotes diversity in host-specialized mycoparasitic fungi: uncoupled evolution in the biatoropsis–usnea system. *Evolution*, **68**, 1576–93.
- Miller, E. A., Beasley, D. E., Dunn, R. R., and Archie, E. A. 2016. Lactobacilli dominance and vaginal pH: why is the human vaginal microbiome unique? *Frontiers in Microbiology*, **7**, 1936.
- Mindell, D. P. 2013. The tree of life: metaphor, model, and heuristic device. *Systematic Biology*, **62**, 479–89.
- Minot, S., Bryson, A., Chehoud, C., Wu, G. D., Lewis, J. D., and Bushman, F. D. 2013. Rapid evolution of the human gut virome. *Proceedings of the National Academy of Sciences of the United States of America*, **110**, 12450–5.
- Mirarab, S., Reaz, R., Bayzid, M. S., Zimmermann, T., Swenson, M. S., and Warnow, T. 2014. ASTRAL: genome-scale coalescent-based species tree estimation. *Bioinformatics*, **30**, i541–8.
- Mitter, C., Farrell, B., and Wiegmann, B. 1988. The phylogenetic study of adaptive zones: has phytophagy promoted insect diversification? *The American Naturalist*, **132**, 107–28.
- Monaghan, M. T., Wild, R., Elliot, M., et al. 2009. Accelerated species inventory on Madagascar using coalescent-based models of species delineation. *Systematic Biology*, **58**, 298–311.
- Moritz, C. C., Pratt, R. C., Bank, S., et al. 2018. Cryptic lineage diversity, body size divergence, and sympatry in a species complex of Australian lizards (*Gehyra*). *Evolution*, **72**, 54–66.
- Morjan, C. L. and Rieseberg, L. H. 2004. How species evolve collectively: implications of gene flow and selection for the spread of advantageous alleles. *Molecular Ecology*, **13**, 1341–56.
- Morlon, H. 2014. Phylogenetic approaches for studying diversification. *Ecology Letters*, **17**, 508–25.
- Moya-Larano, J., Verdeny-Vilalta, O., Rowntree, J., Melguizo-Ruiz, N., Montserrat, M., and Laiolo, P. 2012. Climate change and eco-evolutionary dynamics in food webs. *Advances in Ecological Research: Global Change in Multispecies Systems*, **47**, 1–80.
- Nachman, M. W. and Payseur, B. A. 2012. Recombination rate variation and speciation: theoretical predictions and empirical results from rabbits and mice. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **367**, 409–21.
- Nee, S. 2005. The neutral theory of biodiversity: do the numbers add up? *Functional Ecology*, **19**, 173–6.
- Nee, S., Mooers, A. O., and Harvey, P. H. 1992. Tempo and mode of evolution revealed from molecular phylogenies. *Proceedings of the National Academy of Sciences of the United States of America*, **89**, 8322–6.
- Nee, S., May, R. M., and Harvey, P. H. 1994. The reconstructed evolutionary process. *Philosophical Transactions of the Royal Society of London Series B: Biological Sciences*, **344**, 305–11.

- Neher, R. A., Bedford, T., Daniels, R. S., Russell, C. A., and Shraiman, B. I. 2016. Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. *Proceedings of the National Academy of Sciences of the United States of America*, **113**, E1701–9.
- Nicholson, J. K., Holmes, E., Kinross, J., Burcelin, R., Gibson, G., Jia, W. and Petttersen, S. 2012. Host-gut microbiota metabolic interactions. *Science*, **336**, 1262–1267.
- Niehus, R., Mitri, S., Fletcher, A. G., and Foster, K. R. 2015. Migration and horizontal gene transfer divide microbial genomes into multiple niches. *Nature Communications*, **6**, 8924.
- Nijman, V. and Aliabadian, M. 2013. DNA barcoding as a tool for elucidating species delineation in wide-ranging species as illustrated by owls (Tytonidae and Strigidae). *Zoological Science*, **30**, 1005–9.
- Northfield, T. D. and Ives, A. R. 2013. Coevolution and the effects of climate change on interacting species. *PLoS Biology*, **11**, e1001685.
- Nosil, P. 2012. *Ecological Speciation*. Oxford: Oxford University Press.
- Nosil, P., Funk, D. J., and Ortiz-Barrientos, D. 2009. Divergent selection and heterogeneous genomic divergence. *Molecular Ecology*, **18**, 375–402.
- Nowell, R. W., Almeida, P., Wilson, C. G., et al. 2018. Comparative genomics of bdelloid rotifers: insights from desiccating and nondesiccating species. *PLoS Biology*, **16**, e2004830.
- Nowell, R. W., Green, S., Laue, B. E. & Sharp, P. M., 2014. The extent of genome flux and its role in the differentiation of bacterial lineages. *Genome Biology and Evolution* **6**, 1514–1529.
- Obst, M., Faurby, S., Bussarawit, S., and Funch, P. 2012. Molecular phylogeny of extant horseshoe crabs (Xiphosura, Limulidae) indicates Paleogene diversification of Asian species. *Molecular Phylogenetics and Evolution*, **62**, 21–6.
- O'Brien, S., and Fothergill, J.L. 2017. The role of multispecies social interactions in shaping *Pseudomonas aeruginosa* pathogenicity in the cystic fibrosis lung. *FEMS Microbiology Letters*, **364**, fnx128
- O'Connor, M. I., Piehler, M. F., Leech, D. M., Anton, A., and Bruno, J. F. 2009. Warming and resource availability shift food web structure and metabolism. *PLoS Biology*, **7**, e1000178.
- O'Donnell, K., Kistler, H. C., Cigelnik, E., and Ploetz, R. C. 1998. Multiple evolutionary origins of the fungus causing Panama disease of banana: concordant evidence from nuclear and mitochondrial gene genealogies. *Proceedings of the National Academy of Sciences of the United States of America*, **95**, 2044–9.
- Omelchenko, M. V., Makarova, K. S., Wolf, Y. I., Rogozin, I. B., and Koonin, E. V. 2003. Evolution of mosaic operons by horizontal gene transfer and gene displacement in situ. *Genome Biology*, **4**, R55.
- Osmond, M. M. and De Mazancourt, C. 2013. How competition affects evolutionary rescue. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **368**, 20120085.
- Ostevik, K. L., Andrew, R. L., Otto, S. P., and Rieseberg, L. H. 2016. Multiple reproductive barriers separate recently diverged sunflower ecotypes. *Evolution*, **70**, 2322–35.
- Otto, S. P., and Michalakis, Y. 1998. The evolution of recombination in changing environments. *Trends in Ecology and Evolution*, **13**, 145–151.
- Otwinowski, J., McCandlish, D. M., and Plotkin, J. B. 2018. Inferring the shape of global epistasis. *Proceedings of the National Academy of Sciences of the United States of America*, **115**, E7550–8.
- Ozkilinc, H., Rotondo, F., Pryor, B. M., and Peever, T. L. 2018. Contrasting species boundaries between sections *Alternaria* and *Porri* of the genus *Alternaria*. *Plant Pathology*, **67**, 303–14.
- Papadopolou, A., Bergsten, J., Fujisawa, T., Monaghan, M. T., Barraclough, T. G., and Vogler, A. P. 2008. Speciation and DNA barcodes: testing the effects of dispersal on the formation of discrete sequence clusters. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **363**, 2987–96.

- Papadopoulou, A., Monaghan, M. T., Barraclough, T. G., and Vogler, A. P. 2009. Sampling error does not invalidate the Yule-Coalescent model for species delimitation. A response to Lohse (2009). *Systematic Biology*, **58**, 442–4.
- Papadopoulos, A. S. T., Baker, W. J., Crayn, D., et al. 2011. Speciation with gene flow on Lord Howe Island. *Proceedings of the National Academy of Sciences of the United States of America*, **108**, 13188–93.
- Papadopoulos, A. S. T., Price, Z., Devaux, C., et al. 2013. A comparative analysis of the mechanisms underlying speciation on Lord Howe Island. *Journal of Evolutionary Biology*, **26**, 733–45.
- Papke, R. T., Ramsing, N. B., Bateson, M. M., and Ward, D. M. 2003. Geographical isolation in hot spring cyanobacteria. *Environmental Microbiology*, **5**, 650–9.
- Paradis, E., Claude, J., and Strimmer, K. 2004. APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289–90.
- Paun, O., Turner, B., Trucchi, E., Munzinger, J., Chase, M. W., and Samuel, R. 2016. Processes driving the adaptive radiation of a tropical tree (*Diospyros*, Ebenaceae) in New Caledonia, a biodiversity hotspot. *Systematic Biology*, **65**, 212–27.
- Payseur, B. A., Presgraves, D. C., and Filatov, D. A. 2018. Introduction: sex chromosomes and speciation. *Molecular Ecology*, **27**, 3745–8.
- Peccoud, J., Ollivier, A., Plantegenest, M., and Simon, J.-C. 2009. A continuum of genetic divergence from sympatric host races to species in the pea aphid complex. *Proceedings of the National Academy of Sciences of the United States of America*, **106**, 7495–500.
- Pentinsaari, M., Salmela, H., Mutanen, M., and Roslin, T. 2016. Molecular evolution of a widely-adopted taxonomic marker (COI) across the animal tree of life. *Scientific Reports*, **6**, 35275.
- Perret, M., Chautems, A., Spichiger, R., Barraclough, T. G., and Savolainen, V. 2007. The geographical pattern of speciation and floral diversification in the neotropics: the tribe Sinningieae (Gesneriaceae) as a case study. *Evolution*, **61**, 1641–60.
- Perron, G. G., Gonzalez, A., and Buckling, A. 2007. Source-sink dynamics shape the evolution of antibiotic resistance and its pleiotropic fitness cost. *Proceedings of the Royal Society B: Biological Sciences*, **274**, 2351–6.
- Petchey, O. L., Pontarp, M., Massie, T. M., et al. 2015. The ecological forecast horizon, and examples of its uses and determinants. *Ecology Letters*, **18**, 597–611.
- Phillimore, A. B. and Price, T. D. 2008. Density-dependent cladogenesis in birds. *PLoS Biology*, **6**, 483–9.
- Phillimore, A. B., Freckleton, R. P., Orme, C. D. L., and Owens, I. P. F. 2006. Ecology predicts large-scale patterns of phylogenetic diversification in birds. *The American Naturalist*, **168**, 220–9.
- Phillimore, A. B., Orme, C. D. L., Thomas, G. H., et al. 2008. Sympatric speciation in birds is rare: insights from range data and simulations. *The American Naturalist*, **171**, 646–57.
- Phillimore, A. B., Hadfield, J. D., Jones, O. R., and Smithers, R. J. 2010. Differences in spawning date between populations of common frog reveal local adaptation. *Proceedings of the National Academy of Sciences of the United States of America*, **107**, 8292–7.
- Pigot, A. L. and Tobias, J. A. 2013. Species interactions constrain geographic range expansion over evolutionary time. *Ecology Letters*, **16**, 330–8.
- Pigot, A. L., Phillimore, A. B., Owens, I. P. F., and Orme, C. D. L. 2010. The shape and temporal dynamics of phylogenetic trees arising from geographic speciation. *Systematic Biology*, **59**, 660–73.
- Pinsky, M. L., Saenz-Agudelo, P., Salles, O. C., et al. 2017. Marine dispersal scales are congruent over evolutionary and ecological time. *Current Biology*, **27**, 149–54.
- Pitchers, W., Wolf, J. B., Tregenza, T., Hunt, J., and Dworkin, I. 2014. Evolutionary rates for multivariate traits: the role of selection and genetic variation. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **369**, 1–13.

- Polz, M. F., Alm, E. J., and Hanage, W. P. 2013. Horizontal gene transfer and the evolution of bacterial and archaeal population structure. *Trends in Genetics*, **29**, 170–5.
- Pons, J., Barraclough, T. G., Gomez-Zurita, J., et al. 2006. Sequence-based species delimitation for the DNA taxonomy of undescribed insects. *Systematic Biology*, **55**, 595–609.
- Popa, O., Landan, G., and Dagan, T. 2017. Phylogenomic networks reveal limited phylogenetic range of lateral gene transfer by transduction. *ISME Journal*, **11**, 543–54.
- Popp, J., Peto, K., and Nagy, J. 2013. Pesticide productivity and food security. A review. *Agronomy for Sustainable Development*, **33**, 243–55.
- Price, T. 2008. *Speciation in Birds*. Greenwood Village, CO: Roberts & Company.
- Price, T. D., Hooper, D. M., Buchanan, C. D., et al. 2014. Niche filling slows the diversification of Himalayan songbirds. *Nature*, **509**, 222–5.
- Proulx, S. R., Promislow, D. E. L., and Phillips, P. C. 2005. Network thinking in ecology and evolution. *Trends in Ecology & Evolution*, **20**, 345–53.
- Puillandre, N., Lambert, A., Brouillet, S., and Achaz, G. 2012. ABGD, automatic barcode gap discovery for primary species delimitation. *Molecular Ecology*, **21**, 1864–77.
- Qin, J., Li, R., Raes, J., et al. 2010. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **464**, 59–65.
- R Core Team 2018. R: A Language and Environment for Statistical Computing. Vienna: R Foundation for Statistical Computing. URL <https://www.R-project.org/>.
- Rabosky, D. L. 2010. Extinction rates should not be estimated from molecular phylogenies. *Evolution*, **64**, 1816–24.
- Rabosky, D. L. 2013. Diversity-dependence, ecological speciation, and the role of competition in macroevolution. *Annual Review of Ecology, Evolution, and Systematics*, **44**, 481–502.
- Rabosky, D. L. and Goldberg, E. E. 2015. Model inadequacy and mistaken inferences of trait-dependent speciation. *Systematic Biology*, **64**, 340–55.
- Rabosky, D. L. and Matute, D. R. 2013. Macroevolutionary speciation rates are decoupled from the evolution of intrinsic reproductive isolation in *Drosophila* and birds. *Proceedings of the National Academy of Sciences of the United States of America*, **110**, 15354–9.
- Rabosky, D. L., Chang, J., Title, P. O., et al. 2018. An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, **559**, 392–5.
- Rainey, P. B. and Travisano, M. 1998. Adaptive radiation in a heterogeneous environment. *Nature*, **394**, 69–72.
- Ravel, J., Gajer, P., Abdo, Z., et al. 2011. Vaginal microbiome of reproductive-age women. *Proceedings of the National Academy of Sciences of the United States of America*, **108**, 4680–7.
- Renaut, S., Grassa, C. J., Yeaman, S., et al. 2013. Genomic islands of divergence are not affected by geography of speciation in sunflowers. *Nature Communications*, **4**, 1827.
- Renner, S. S. and Zohner, C. M. 2018. Climate change and phenological mismatch in trophic interactions among plants, insects, and vertebrates. *Annual Review of Ecology, Evolution, and Systematics*, **49**, 165–82.
- Revell, L. J. 2012. Phytools: an R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution*, **3**, 217–23.
- Ribas, C. C., Aleixo, A., Nogueira, A. C. R., Miyaki, C. Y., and Cracraft, J. 2012. A palaeobiogeographic model for biotic diversification within Amazonia over the past three million years. *Proceedings of the Royal Society B: Biological Sciences*, **279**, 681–9.
- Ricci, C., Melone, G., Santo, N., Caprioli, M. 2003. Morphological response of a bdelloid rotifer to desiccation. *Journal of Morphology*, **257**, 246–253.
- Rice, W. R. and Hostert, E. E. 1993. Laboratory experiments on speciation: what have we learned in the last forty years? *Evolution*, **47**, 1637–53.

- Richards, E. J., Poelstra, J. W., and Martin, C. H. 2018. Don't throw out the sympatric speciation with the crater lake water: fine-scale investigation of introgression provides equivocal support for causal role of secondary gene flow in one of the clearest examples of sympatric speciation. *Evolution Letters*, **2**, 524–40.
- Ricklefs, R. E. 2003. Global diversification rates of passerine birds. *Proceedings of the Royal Society of London Series B: Biological Sciences*, **270**, 2285–91.
- Ricklefs, R. E. 2006. The unified neutral theory of biodiversity: do the numbers add up? *Ecology*, **87**, 1424–31.
- Ricklefs, R. E. 2007. Estimating diversification rates from phylogenetic information. *Trends in Ecology & Evolution*, **22**, 601–10.
- Rieseberg, L. H. 2001. Chromosomal rearrangements and speciation. *Trends in Ecology & Evolution*, **16**, 351–8.
- Rieseberg, L. H., Wood, T. E., and Baack, E. J. 2006. The nature of plant species. *Nature*, **440**, 524–7.
- Ritchie, M. G. 2007. Sexual selection and speciation. *Annual Review of Ecology Evolution and Systematics*, **38**, 79–102.
- Rivett, D. W., Scheuerl, T., Culbert, C. T., Mombrikotb, S. B., Johnstone, E., Barraclough, T. G., and Bell, T. 2016. Diversity-dependent attenuation of species interactions during bacterial succession. *ISME Journal*, **10**, 2259–2268.
- Robinson, C. J., Bohannan, B. J. M., and Young, V. B. 2010. From structure to function: the ecology of host-associated microbial communities. *Microbiology and Molecular Biology Reviews*, **74**, 453–76.
- Roderick, G. K., Hufbauer, R., and Navajas, M. 2012. Evolution and biological control. *Evolutionary Applications*, **5**, 419–23.
- Roemhild, R., Barbosa, C., Beardmore, R. E., Jansen, G., and Schulenburg, H. 2015. Temporal variation in antibiotic environments slows down resistance evolution in pathogenic *Pseudomonas aeruginosa*. *Evolutionary Applications*, **8**, 945–55.
- Romiguier, J., Gayral, P., Ballenghien, M., et al. 2014. Comparative population genomics in animals uncovers the determinants of genetic diversity. *Nature*, **515**, 261–3.
- Rosenberg, N. A. 2003. The shapes of neutral gene genealogies in two species: probabilities of monophyly, paraphyly, and polyphyly in a coalescent model. *Evolution*, **57**, 1465–77.
- Rosenberg, N. A. and Nordborg, M. 2002. Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. *Nature Reviews Genetics*, **3**, 380–90.
- Rosindell, J. and Cornell, S. J. 2007. Species–area relationships from a spatially explicit neutral model in an infinite landscape. *Ecology Letters*, **10**, 586–95.
- Rosindell, J., Harmon, L. J., and Etienne, R. S. 2015. Unifying ecology and macroevolution with individual-based theory. *Ecology Letters*, **18**, 472–82.
- Rosser, N., Kozak, K. M., Phillimore, A. B., and Mallet, J. 2015. Extensive range overlap between heliconiine sister species: evidence for sympatric speciation in butterflies? *BMC Evolutionary Biology*, **15**, 125.
- Roughgarden, J. 1976. Resource partitioning among competing species—a coevolutionary approach. *Theoretical Population Biology*, **9**, 388–424.
- Ryan, P. G., Bloomer, P., Moloney, C. L., Grant, T. J., and Delpont, W. 2007. Ecological speciation in South Atlantic Island finches. *Science*, **315**, 1420–3.
- Samuk, K., Owens, G. L., Delmore, K. E., Miller, S. E., Rennison, D. J., and Schluter, D. 2017. Gene flow and selection interact to promote adaptive divergence in regions of low recombination. *Molecular Ecology*, **26**, 4378–90.

- San Millan, A. S., Pena-Miller, R., Toll-Riera, M., et al. 2014. Positive selection and compensatory adaptation interact to stabilize non-transmissible plasmids. *Nature Communications*, **5**, 5208.
- Sanderson, M. J. and Donoghue, M. J. 1994. Shifts in diversification rate with the origin of angiosperms. *Science*, **264**, 1590–3.
- Sasaki, A. and Godfray, H. C. J. 1999. A model for the coevolution of resistance and virulence in coupled host–parasitoid interactions. *Proceedings of the Royal Society B: Biological Sciences*, **266**, 455–63.
- Savolainen, V., Anstett, M. C., Lexer, C., et al. 2006. Sympatric speciation in palms on an oceanic island. *Nature*, **441**, 210–13.
- Scheuerl, T., Hopkins, M., Nowell, R. W., Rivett, D. W., Barraclough, T. G., and Bell, T. 2019. Bacterial adaptation is constrained in complex communities. In prep.
- Schiffman, J. S. and Ralph, P. L. 2018. System drift and speciation. *bioRxiv*, doi: <https://doi.org/10.1101/231209>.
- Schliep, K. P. 2011. phangorn: phylogenetic analysis in R. *Bioinformatics*, **27**, 592–3.
- Schliewen, U. K., Tautz, D., and Paabo, S. 1994. Sympatric speciation suggested by monophyly of Crater Lake cichlids. *Nature*, **368**, 629–32.
- Schluter, D. 1996. Adaptive radiation along genetic lines of least resistance. *Evolution*, **50**, 1766–74.
- Schluter, D. 2000. *The Ecology of Adaptive Radiation*. Oxford: Oxford University Press.
- Schluter, D. 2001. Ecology and the origin of species. *Trends in Ecology & Evolution*, **16**, 372–80.
- Schluter, D. 2009. Evidence for ecological speciation and its alternative. *Science*, **323**, 737–41.
- Schluter, D. 2016. Speciation, ecological opportunity, and latitude. *American Naturalist*, **187**, 1–18.
- Schluter, D. and Conte, G. L. 2009. Genetics and ecological speciation. *Proceedings of the National Academy of Sciences of the United States of America*, **106**, 9955–62.
- Schluter, D. and Pennell, M. W. 2017. Speciation gradients and the distribution of biodiversity. *Nature*, **546**, 48–55.
- Schmutzer, M. and Barraclough, T. G. 2019. The role of recombination, niche-specific gene pools and flexible genomes in the ecological speciation of bacteria. *Ecology and Evolution*, **9**, 4544–4556.
- Schnitzler, J., Barraclough, T. G., Boatwright, J. S., et al. 2011. Causes of plant diversification in the Cape biodiversity hotspot of South Africa. *Systematic Biology*, **60**, 343–57.
- Schoch, C. L., Seifert, K. A., Huhndorf, S., et al. 2012. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for fungi. *Proceedings of the National Academy of Sciences of the United States of America*, **109**, 6241–6.
- Scopece, G., Cozzolino, S., and Bateman, R. M. 2010. Just what is a genus? Comparing levels of postzygotic isolation to test alternative taxonomic hypotheses in Orchidaceae subtribe Orchidinae. *Taxon*, **59**, 1367–74.
- Seehausen, O., Vanalphen, J. J. M., and Witte, F. 1997. Cichlid fish diversity threatened by eutrophication that curbs sexual selection. *Science*, **277**, 1808–11.
- Seehausen, O., Van Alphen, J. J. M., and Lande, R. 1999. Color polymorphism and sex ratio distortion in a cichlid fish as an incipient stage in sympatric speciation by sexual selection. *Ecology Letters*, **2**, 367–78.
- Seehausen, O., Butlin, R. K., Keller, I., et al. 2014. Genomics and the origin of species. *Nature Reviews Genetics*, **15**, 176–92.
- Sepp, S. and Paal, J. 1998. Taxonomic continuum of *Alchemilla* (Rosaceae) in Estonia. *Nordic Journal of Botany*, **18**, 519–35.
- Shapiro, B. J. and Polz, M. F. 2014. Ordering microbial diversity into ecologically and genetically cohesive units. *Trends in Microbiology*, **22**, 235–47.
- Shapiro, B. J., Friedman, J., Cordero, O. X., et al. 2012. Population genomics of early events in the ecological differentiation of bacteria. *Science*, **336**, 48–51.

- Sheppard, R., Barraclough, T. G., and Jansen, V. A. 2019. The coevolution and control of conjugative plasmid transfer rate. Unpublished work.
- Shoae, S., Karlsson, F., Mardinoglu, A., Nookaew, I., Bordel, S., and Nielsen, J. 2013. Understanding the interactions between bacteria in the human gut through metabolic modeling. *Scientific Report*, **3**, 2532.
- Signorovitch, A., Hur, J., Gladyshev, E., and Meselson, M. 2015. Allele sharing and evidence for sexuality in a mitochondrial clade of bdelloid rotifers. *Genetics*, **200**, 581–90.
- Simpson, G. G. 1961. *Principles of Animal Taxonomy*. New York: Columbia University Press.
- Singhal, S., Huang, H. T., Grundler, M. R., et al. 2018. Does population structure predict the rate of speciation? A comparative test across Australia's most diverse vertebrate radiation. *The American Naturalist*, **192**, 432–47.
- Siren, J., Ovaskainen, O., and Merila, J. 2017. Structure and stability of genetic variance–covariance matrices: a Bayesian sparse factor analysis of transcriptional variation in the three-spined stickleback. *Molecular Ecology*, **26**, 5099–113.
- Sites, J. W. and Marshall, J. C. 2003. Delimiting species: a Renaissance issue in systematic biology. *Trends in Ecology & Evolution*, **18**, 462–70.
- Skeels, A. and Cardillo, M. 2019. Reconstructing the geography of speciation from contemporary biodiversity data. *The American Naturalist*, **193**, 240–255.
- Skulason, S. and Smith, T. B. 1995. Resource polymorphisms in vertebrates. *Trends in Ecology & Evolution*, **10**, 366–70.
- Slatkin, M. 1984. Ecological causes of sexual dimorphism. *Evolution*, **38**, 622–30.
- Slatkin, M. 1985. Gene flow in natural populations. *Annual Review of Ecology and Systematics*, **16**, 393–430.
- Slatkin, M. 1991. Inbreeding coefficients and coalescence times. *Genetical Research*, **58**, 167–75.
- Slatkin, M. and Smith, J. M. 1979. Models of coevolution. *Quarterly Review of Biology*, **54**, 233–63.
- Sleeth, M. L., Thompson, E. L., Ford, H. E., Zac-Varghese, S. E. K., and Frost, G. 2010. Free fatty acid receptor 2 and nutrient sensing: a proposed role for fibre, fermentable carbohydrates and short-chain fatty acids in appetite regulation. *Nutrition Research Reviews*, **23**, 135–45.
- Smillie, C., Garcillan-Barcia, M. P., Francia, M. V., Rocha, E. P. C., and De La Cruz, F. 2010. Mobility of plasmids. *Microbiology and Molecular Biology Reviews*, **74**, 434–52.
- Smillie, C. S., Smith, M. B., Friedman, J., Cordero, O. X., David, L. A., and Alm, E. J. 2011. Ecology drives a global network of gene exchange connecting the human microbiome. *Nature*, **480**, 241–4.
- Sobel, J. M., Chen, G. F., Watt, L. R., and Schemske, D. W. 2010. The biology of speciation. *Evolution*, **64**, 295–315.
- Solis-Lemus, C., Knowles, L. L., and Ane, C. 2015. Bayesian species delimitation combining multiple genes and traits in a unified framework. *Evolution*, **69**, 492–507.
- Soria-Carrasco, V., Gompert, Z., Comeault, A. A., et al. 2014. Stick insect genomes reveal natural selection's role in parallel speciation. *Science*, **344**, 738–42.
- Speirs, D. C., Greenstreet, S. P. R., and Heath, M. R. 2016. Modelling the effects of fishing on the North Sea fish community size composition. *Ecological Modelling*, **321**, 35–45.
- Stadler, T., Rabosky, D. L., Ricklefs, R. E., and Bokma, F. 2014. On age and species richness of higher taxa. *The American Naturalist*, **184**, 447–55.
- Stanley, S. M. 1979. *Macroevolution: Pattern and Process*. San Francisco: W.H. Freeman.
- Steiner, C. F. 2012. Environmental noise, genetic diversity and the evolution of evolvability and robustness in model gene networks. *PLoS One*, **7**, e52204.
- Stewart, F. M. and Levin, B. R. 1973. Partitioning of resources and the outcome of interspecific competition: a model and some general considerations. *The American Naturalist*, **107**, 171–98.

- Stewart, F. M. and Levin, B. R. 1977. Population biology of bacterial plasmids—a priori conditions for existence of conjugationally transmitted factors. *Genetics*, **87**, 209–28.
- Stoelting, K. N., Nipper, R., Lindtke, D., et al. 2013. Genomic scan for single nucleotide polymorphisms reveals patterns of divergence and gene flow between ecologically divergent species. *Molecular Ecology*, **22**, 842–55.
- Strauss, S. Y., Sahli, H., and Conner, J. K. 2005. Toward a more trait-centered approach to diffuse (co)evolution. *New Phytologist*, **165**, 81–9.
- Strayer, D. L. 2012. Eight questions about invasions and ecosystem functioning. *Ecology Letters*, **15**, 1199–210.
- Sukumaran, J. and Knowles, L. L. 2017. Multispecies coalescent delimits structure, not species. *Proceedings of the National Academy of Sciences of the United States of America*, **114**, 1607–12.
- Sun, J. M., Ni, X. J., Bi, S. D., et al. 2014. Synchronous turnover of flora, fauna, and climate at the Eocene–Oligocene boundary in Asia. *Scientific Reports*, **4**, 7463.
- Surette, M. G. 2014. The cystic fibrosis lung microbiome. *Annals of the American Thoracic Society*, **11**, S61–5.
- Swain, D. P., Sinclair, A. F., and Hanson, J. M. 2007. Evolutionary response to size-selective mortality in an exploited fish population. *Proceedings of the Royal Society B: Biological Sciences*, **274**, 1015–22.
- Tamminen, M., Virta, M., Fani, R., and Fondi, M. 2012. Large-scale analysis of plasmid relationships through gene-sharing networks. *Molecular Biology and Evolution*, **29**, 1225–40.
- Tang, C. Q., Humphreys, A. M., Fontaneto, D., and Barraclough, T. G. 2014a. Effects of phylogenetic reconstruction method on the robustness of species delimitation using single-locus data. *Methods in Ecology and Evolution*, **5**, 1086–94.
- Tang, C. Q., Obertegger, U., Fontaneto, D., and Barraclough, T. G. 2014b. Sexual species are separated by larger genetic gaps than asexual species in rotifers. *Evolution*, **68**, 2901–16.
- Tautz, D., Arctander, P., Minelli, A., Thomas, R. H., and Vogler, A. P. 2003. A plea for DNA taxonomy. *Trends in Ecology & Evolution*, **18**, 70–4.
- Taylor, J. W., Jacobson, D. J., Kroken, S., et al. 2000. Phylogenetic species recognition and species concepts in fungi. *Fungal Genetics and Biology*, **31**, 21–32.
- Templeton, A. 1989. The meaning of species and speciation: a population genetics approach. In: Otte, D. and Endler, J. (eds) *Speciation and its Consequences*. Sunderland, MA: Sinauer Associates.
- TerHorst, C. P., Zee, P. C., Heath, K. D., et al. 2018. Evolution in a community context: trait responses to multiple species interactions. *The American Naturalist*, **191**, 368–80.
- Thompson, L. R., Sanders, J. G., McDonald, D., et al. 2017. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, **551**, 457–63.
- Thorpe, R. B., Dolder, P. J., Reeves, S., Robinson, P., and Jennings, S. 2016. Assessing fishery and ecological consequences of alternate management options for multispecies fisheries. *ICES Journal of Marine Science*, **73**, 1503–12.
- Tilman, D. 1982. *Resource Competition and Community Structure*. Princeton, NJ: Princeton University Press.
- Tilman, D. and Lehman, C. 2001. Human-caused environmental change: impacts on plant diversity and evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **98**, 5433–40.
- Tobias, J. A., Seddon, N., Spottiswoode, C. N., Pilgrim, J. D., Fishpool, L. D. C., and Collar, N. J. 2010. Quantitative criteria for species delimitation. *Ibis*, **152**, 724–46.
- Tognon, M., Köhler, T., Gdaniec, B.G., Hao, Y., Lam, J.S., Beaume, M., Luscher, A., Buckling, A., van Delden, C. 2017. Co-evolution with *Staphylococcus aureus* leads to lipopolysaccharide alterations in *Pseudomonas aeruginosa*. *ISME Journal*, **11**, 2233–2243.

- Tomasetto, F., Tylianakis, J. M., Reale, M., Wratten, S., and Goldson, S. L. 2017. Intensified agriculture favors evolved resistance to biological control. *Proceedings of the National Academy of Sciences of the United States of America*, **114**, 3885–90.
- Torresen, O. K., Star, B., Jentoft, S., et al. 2017. An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. *BMC Genomics*, **18**, 95.
- Turissini, D. A., McGuire, J. A., Patel, S. S., David, J. R., and Matute, D. R. 2018. The rate of evolution of postmating–prezygotic reproductive isolation in *Drosophila*. *Molecular Biology and Evolution*, **35**, 312–34.
- Turner, B., Paun, O., Munzinger, J., Duangjai, S., Chase, M. W., and Samuel, R. 2013. Analyses of amplified fragment length polymorphisms (AFLP) indicate rapid radiation of *Diospyros* species (Ebenaceae) endemic to New Caledonia. *BMC Evolutionary Biology*, **13**, 269.
- Urwin, R. and Maiden, M. C. J. 2003. Multi-locus sequence typing: a tool for global epidemiology. *Trends in Microbiology*, **11**, 479–87.
- Valente, L. M., Reeves, G., Schnitzler, J., et al. 2010. Diversification of the African genus *Protea* (Proteaceae) in the Cape biodiversity hotspot and beyond: equal rates in different biomes. *Evolution*, **64**, 745–59.
- Valente, L. M., Britton, A. W., Powell, M. P., Papadopoulos, A. S. T., Burgoyne, P. M., and Savolainen, V. 2014. Correlates of hyperdiversity in southern African ice plants (Aizoaceae). *Botanical Journal of the Linnean Society*, **174**, 110–29.
- Van Dam, P., Fokkens, L., Ayukawa, Y., et al. 2017. A mobile pathogenicity chromosome in *Fusarium oxysporum* for infection of multiple cucurbit species. *Scientific Reports*, **7**, 9042.
- Van Moorsel, S. J., Hahl, T., Wagg, C., et al. 2018. Community evolution increases plant productivity at low diversity. *Ecology Letters*, **21**, 128–37.
- Venturelli, O. S., Carr, A. V., Fisher, G., et al. 2018. Deciphering microbial interactions in synthetic human gut microbiome communities. *Molecular Systems Biology*, **14**, e8157.
- Vieira, C., D'Hondt, S., De Clerck, O., and Payri, C. E. 2014. Toward an inordinate fondness for stars, beetles and *Lobophora*? Species diversity of the genus *Lobophora* (Dictyotales, Phaeophyceae) in New Caledonia. *Journal of Phycology*, **50**, 1101–19.
- Voje, K. L., Holen, O. H., Liow, L. H., and Stenseth, N. C. 2015. The role of biotic forces in driving macroevolution: beyond the Red Queen. *Proceedings of the Royal Society B: Biological Sciences*, **282**, 20150186.
- Vonlanthen, P., Bittner, D., Hudson, A. G., et al. 2012. Eutrophication causes speciation reversal in whitefish adaptive radiations. *Nature*, **482**, 357–62.
- Vos, M. and Didelot, X. 2009. A comparison of homologous recombination rates in bacteria and archaea. *ISME Journal*, **3**, 199–208.
- Wade, M. J. and Kalisz, S. 1990. The causes of natural-selection. *Evolution*, **44**, 1947–55.
- Wagner, C. E., Harmon, L. J., and Seehausen, O. 2012. Ecological opportunity and sexual selection together predict adaptive radiation. *Nature*, **487**, 366–9.
- Wagner, C. E., Harmon, L. J., and Seehausen, O. 2014. Cichlid species–area relationships are shaped by adaptive radiations that scale with area. *Ecology Letters*, **17**, 583–92.
- Wallace, S. J., Morris-Pocock, J. A., Gonzalez-Solis, J., Quillfeldt, P., and Friesen, V. L. 2017. A phylogenetic test of sympatric speciation in the Hydrobatinae (Aves: Procellariiformes). *Molecular Phylogenetics and Evolution*, **107**, 39–47.
- Wang, I. J., Glor, R. E., and Losos, J. B. 2013. Quantifying the roles of ecology and geography in spatial genetic divergence. *Ecology Letters*, **16**, 175–82.
- Waterman, R. J., Bidartondo, M. I., Stofberg, J., et al. 2011. The effects of above- and belowground mutualisms on orchid speciation and coexistence. *The American Naturalist*, **177**, E54–68.
- Webster, A. J., Payne, R. J. H., and Pagel, M. 2003. Molecular phylogenies link rates of evolution and speciation. *Science*, **301**, 478.

- Weiner, A., Aurahs, R., Kurasawa, A., Kitazato, H., and Kucera, M. 2012. Vertical niche partitioning between cryptic sibling species of a cosmopolitan marine planktonic protist. *Molecular Ecology*, **21**, 4063–73.
- Weir, J. T. and Schluter, D. 2007. The latitudinal gradient in recent speciation and extinction rates of birds and mammals. *Science*, **315**, 1574–6.
- Wiedenbeck, J. and Cohan, F. M. 2011. Origins of bacterial diversity through horizontal genetic transfer and adaptation to new ecological niches. *FEMS Microbiology Reviews*, **35**, 957–76.
- Wiens, J. J. and Servedio, M. R. 2000. Species delimitation in systematics: inferring diagnostic differences between species. *Proceedings of the Royal Society B: Biological Sciences*, **267**, 631–6.
- Wiens, J. J., Engstrom, T. N., and Chippindale, P. T. 2006. Rapid diversification, incomplete isolation, and the ‘speciation clock’ in North American salamanders (genus *Plethodon*): testing the hybrid swarm hypothesis of rapid radiation. *Evolution*, **60**, 2585–603.
- Williams, G. C. 1992. *Natural Selection: Domains, Levels and Challenges*. Oxford: Oxford University Press.
- Wilson, C. G., Nowell, R. W., and Barraclough, T. G. 2018. Cross-contamination explains ‘inter and intraspecific horizontal genetic transfers’ between asexual bdelloid rotifers. *Current Biology*, **28**, 2436–444.
- Winstanley, C., O’Brien, S., and Brockhurst, M. A. 2016. *Pseudomonas aeruginosa* evolutionary adaptation and diversification in cystic fibrosis chronic lung infections. *Trends in Microbiology*, **24**, 327–37.
- Wood, J. L. A., Yates, M. C., and Fraser, D. J. 2016. Are heritability and selection related to population size in nature? Meta-analysis and conservation implications. *Evolutionary Applications*, **9**, 640–57.
- Wright, S. 1931. Evolution in Mendelian populations. *Genetics*, **16**, 97–159.
- Yablonovitch, A. L., Fu, J., Li, K. X., et al. 2017. Regulation of gene expression and RNA editing in *Drosophila* adapting to divergent microclimates. *Nature Communications*, **8**, 1570.
- Yang, Z. H. and Rannala, B. 2010. Bayesian species delimitation using multilocus sequence data. *Proceedings of the National Academy of Sciences of the United States of America*, **107**, 9264–9.
- Yin, Y. B., Zhang, H., Olman, V., and Xu, Y. 2010. Genomic arrangement of bacterial operons is constrained by biological pathways encoded in the genome. *Proceedings of the National Academy of Sciences of the United States of America*, **107**, 6310–15.
- Zhang, C., Zhang, D. X., Zhu, T. Q., and Yang, Z. H. 2011. Evaluation of a Bayesian coalescent method of species delimitation. *Systematic Biology*, **60**, 747–61.
- Zhang, J. J., Kapli, P., Pavlidis, P., and Stamatakis, A. 2013. A general species delimitation method with applications to phylogenetic placements. *Bioinformatics*, **29**, 2869–76.
- Zhao, L. P., Zhang, F., Ding, X. Y., et al. 2018. Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. *Science*, **359**, 1151–6.
- Zhao, S., Lieberman, T. D., Poyet, M., et al. 2017. Adaptive evolution within the gut microbiome of individual people. *bioRxiv*, doi: <https://doi.org/10.1101/208009>.
- Zuckermandl, E. and Pauling, L. B. 1962. Molecular disease, evolution, and genic heterogeneity. In: Kasha, M. and Pullman, B. (eds) *Horizons in Biochemistry*. New York: Academic Press.
- Zuppinge-Dingley, D., Schmid, B., Petermann, J. S., Yadav, V., De Deyn, G. B., and Flynn, D. F. B. 2014. Selection for niche differentiation in plant communities increases biodiversity effects. *Nature*, **515**, 108–11.