
References

- Abbot, R., Albach, D., Ansell, S., et al. (2013). Hybridization and speciation. *Journal of Evolutionary Biology*, **26**, 229–246.
- Agrawal, A.F. (2001). Sexual selection and the maintenance of sexual reproduction. *Nature*, **411**, 692–695.
- Ahrens, C.W., Rymer, P.D., Stow, A., et al. (2018). The search for loci under selection: trends, biases and progress. *Molecular Ecology*, **27**, 1342–1356.
- Alatalo, R.V., Eriksson, D., Gustafsson, L., and Lundberg, A. (1990). Hybridization between pied and collared flycatchers—sexual selection and speciation theory. *Journal of Evolutionary Biology*, **3**, 375–389.
- Alatalo, R.V. and Gustafsson, L. (1988). Genetic component of morphological differentiation in coal tits under competitive release. *Evolution*, **42**, 200–203.
- Albertin, W. and Marullo, P. (2012). Polyploidy in fungi: evolution after whole-genome duplication. *Proceedings of the Royal Society B*, **279**, 2497–2509.
- Alcaide, M., Scordato, E.S.C., Price, T.D., and Irwin, D. (2014). Genomic divergence in a ring species complex. *Nature*, **511**, 83–85.
- Alerstam, T., Nilsson, S.G., and Ulfstrand, S. (1974). Niche organization during winter in woodland birds in Southern Sweden and the island of Gotland. *Oikos*, **25**, 321–330.
- Alexander, D.H., Novembre, J., and Lange, K. (2009). Fast model-based estimation of ancestry in unrelated individuals. *Genome Research*, **19**, 1655–1664.
- Amambua-Ngwa, A., Tetteh, K.K.A., Manske, M., et al. (2012). Population genomic scan for candidate signatures of balancing selection to guide antigen characterization in malaria parasites. *PLoS Genetics*, **8**, e1002992-14.
- Amoasii, L., Hildyard, J., Li, H., and Sanchez-Ortiz, E. (2018). Gene editing restores dystrophin expression in a canine model of Duchenne muscular dystrophy. *Science*, **362**, 86–91.
- Amoasii, L., Long, C., Li, H., et al. (2017). Single-cut genome editing restores dystrophin expression in a new mouse model of muscular dystrophy. *Science Translational Medicine*, **9**, eaan8081.
- Andersson, M. (1994). *Sexual Selection*. Princeton University Press, Princeton, NJ, USA.
- Andersson, M.B. (1982). Female choice selects for extreme tail length in a widowbird. *Nature*, **299**, 818–820.
- Andres, J.A., Maroja, L.S., and Harrison, R.G. (2008). Searching for candidate speciation genes using a proteomic approach: seminal proteins in field crickets. *Proceedings of the Royal Society B*, **275**, 1975–1983.
- Andrews, K.R., Good, J.M., Miller, M.R., Luikart, G., and Hohenlohe, P.A. (2016). Harnessing the power of RADseq for ecological and evolutionary genomics. *Nature Reviews Genetics*, **17**, 81–92.
- Arnegard, M.E., McGee, M.D., and Matthews, B., et al. (2014). Genetics of ecological divergence during speciation. *Nature*, **511**, 307–311.
- Arnqvist, G. (2014). Cryptic female choice. In: D.M. Shuker and L.W. Simmons (eds), *The Evolution of Insect Mating Systems*, pp. 204–220. Oxford University Press, Oxford, UK.
- Arnqvist, G. and Rowe, L. (2013). *Sexual Conflict*. Princeton University Press, Princeton, NJ, USA.
- Avent, N.D. and Reid, M.E. (2000). The Rh blood group system: a review. *Blood*, **95**, 375–387.
- Avery, O.T., MacLeod, C.M., and McCarty, M. (1944). Studies on the chemical nature of the substance inducing transformation of pneumococcal types: Induction of transformation by a desoxyribonucleic acid fraction isolated from pneumococcus type III. *Journal of Experimental Medicine*, **79**, 137–158.
- Avise, J.C. (2000). *Phylogeography: The History and Formation of Species*. Harvard University Press, Cambridge, MA, USA.
- Avise, J.C. (2009). Phylogeography: retrospect and prospect. *Journal of Biogeography*, **36**, 3–15.
- Avise, J.C., Giblin-Davidson, C., Laerm, J., Patton, J.C., and Lansman, R.A. (1979). Mitochondrial DNA clones and matriarchal phylogeny within and among geographic populations of the pocket gopher, *Geomys pinetis*. *Proceedings of the National Academy of Sciences of the USA*, **76**, 6694–6698.

- Axelrod, R. (1984). *The Evolution of Cooperation*. Basic Books, New York, USA.
- Bachtrog, D., Hom, E., Wong, K.M., and de Jong, P. (2008). Genomic degradation of a young Y chromosome in *Drosophila miranda*. *Genome Biology*, **9**, R30.
- Bailey, R.L., Tesaker, M.R., Trier, C.N., and Sætre, G.-P. (2015). Strong selection on male plumage in a hybrid zone between a hybrid bird species and one of its parents. *Journal of Evolutionary Biology*, **28**, 1257–1269.
- Baird, N.A., Etter, P.D., Atwood, T.S., et al. (2008). Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS One*, **3**, e3376.
- Baird, S.J.E. (2017). The impact of high-throughput sequencing technology on speciation research: maintaining perspective. *Journal of Evolutionary Biology*, **30**, 1482–1487.
- Baird, S.J.E., Barton, N.H., and Etheridge, A.M. (2003). The distribution of surviving blocks of an ancestral genome. *Theoretical Population Biology*, **64**, 451–471.
- Baldassarre, D.T., White, T.A., Karubian, J., and Webster, M.S. (2014). Genomic and morphological analysis of a semipermeable avian hybrid zone suggests asymmetrical introgression of a sexual signal. *Evolution*, **68**, 2644–2657.
- Baldwin, J.M. (1896). A new factor in evolution. *The American Naturalist*, **30**, 441–451.
- Baquero, F. and Blázquez, J. (1997). Evolution of antibiotic resistance. *Trends in Ecology & Evolution*, **12**, 482–487.
- Barrett, R.D.H., Rogers, S.M., and Schluter, D. (2008). Natural selection on a major armor gene in threespine stickleback. *Science*, **322**, 255–257.
- Bartlett, J.M.S. and Stirling, D. (2003). A short history of the polymerase chain reaction. In: J. M. S. Bartlett and D. Stirling (eds) *Methods in Molecular Biology, Vol 226: PCR Protocols, 2nd edition*. Humana Press Inc., Totowa, NJ, USA.
- Barton, N.H. and Charlesworth, B. (1984). Genetic revolutions, founder effects, and speciation. *Annual Reviews in Ecology and Systematics*, **15**, 133–164.
- Barton, N.H. and Gale, K.S. (1993). Genetic analysis of hybrid zones. In: R.G. Harrison *Hybrid Zones and the Evolutionary Process*, pp. 13–45. Oxford University Press, Oxford, UK.
- Barton, N.H. and Hewitt, G.M. (1985). Analysis of hybrid zones. *Annual Reviews in Ecology and Systematics*, **16**, 113–148.
- Bateson, W. (1909). Heredity and variation in modern lights. In: A.C. Seward (ed.) *Darwin and Modern Science*. Cambridge University Press, Cambridge, UK.
- Baum, D.A. and Shaw, K.L. (1995). Genealogical perspectives on the species problem. In: P.C. Hoch and A.G. Stephenson (eds) *Experimental and Molecular Approaches to Plant Biosystematics*, pp. 289–303. Monographs in Systematic Botany, Missouri Botanical Garden, St. Louis, MO, USA.
- Bazin, E., Glémin, S., and Galtier, N. (2006). Population size does not influence mitochondrial genetic diversity in animals. *Science*, **312**, 570–572.
- Beaumont, M.A. and Balding, D.J. (2004). Identifying adaptive genetic divergence among populations from genome scans. *Molecular Ecology*, **13**, 969–980.
- Beaumont, M.A. and Nichols, R.A. (1996). Evaluating loci for use in the genetic analysis of population structure. *Proceedings of the Royal Society B*, **263**, 1619–1626.
- Belancio, V.P., Deininger, P.L., and Roy-Engel, A.M. (2009). LINE dancing in the human genome: transposable elements and disease. *Genome Medicine*, **1**, 97.
- Belancio, V.P., Hedges, D.J., and Deininger, P.L. (2008). Mammalian non-LTR retrotransposons: for better or worse, in sickness and in health. *Genome Research*, **18**, 343–358.
- Beldade, R., Holbrook, S.J., Schmitt, R.J., Planes, S., Malone, D., and Bernardi, G. (2012). Larger female fish contribute disproportionately more to self-replenishment. *Proceedings of the Royal Society B*, **279**, 2116–2121.
- Bell, G. (1982). *The Masterpiece of Nature: The Evolution and Genetics of Sexuality*. Croom Helm, London, UK.
- Bell, M. (1994). Paleobiology and evolution of threespine stickleback. In: M. Bell and S.A. Foster *The Evolutionary Biology of the Threespine Stickleback*. Oxford University Press, Oxford, UK.
- Bell, M.A., Aguirre, W.E., and Buck, N.J. (2004). Twelve years of contemporary armor evolution in a threespine stickleback population. *Evolution*, **58**, 814–824.
- Bell, S.D. and Jackson, S.P. (1998). Transcription and translation in Archaea: a mosaic of eukaryal and bacterial features. *Trends in Microbiology*, **6**, 222–228.
- Belton, J.-M., McCord, R.P., Gibcus, J.H., et al. (2012). Hi-C: A comprehensive technique to capture the conformation of genomes. *Methods*, **58**, 268–276.
- Benson, W.W. (1972). Natural selection for Müllerian mimicry in *Heliconius erato* in Costa Rica. *Science*, **176**, 936–939.
- Berget, S.M., Moore, C., and Sharp, P.A. (1977). Spliced segments at the 5' terminus of adenovirus 2 late mRNA. *Proceedings of the National Academy of Sciences of the USA*, **74**, 3173–3175.
- Berner, D., Grandchamp, A.-C., and Hendry, A.P. (2009). Variable progress toward ecological speciation in parapatry: stickleback across eight lake-stream transitions. *Evolution*, **63**, 1740–1753.
- Bernstein, H., Byerly, H.C., Hopf, F.A., and Michod, R.E. (1985). Genetic damage, mutation, and the evolution of sex. *Science*, **299**, 1277–1281.
- Bertorelle, G., Benazzo, A., and Mona, S. (2010). ABC as a flexible framework to estimate demography over space and time: some cons, many pros. *Molecular Ecology*, **19**, 2609–2625.

- Betto-Colliard, C., Hofmann, S., Sermier, R., Perrin, N., and Stöck, M. (2018). Profound genetic divergence and asymmetric parental genome contributions as hallmarks of hybrid speciation in polyploid toads. *Proceedings of the Royal Society B*, **285**, 20172667.
- Birkhead, T.R. and Møller, A.P. (1998). *Sperm Competition and Sexual Selection*. Academic Press, New York.
- Blake, C.C. (1979). Exons encode protein functional units. *Nature*, **277**, 598.
- Boag, P.T. (1983). The heritability of external morphology in Darwin's ground finches (*Geospiza*) on Isla Daphne Major, Galápagos. *Evolution*, **37**, 877–894.
- Bono, J.M., Olesnick, E.C., and Matzkin, L.M. (2015). Connecting genotypes, phenotypes and fitness: harnessing the power of CRISPR/Cas9 genome editing. *Molecular Ecology*, **24**, 3810–3822.
- Boveri, T.H. (1904). *Ergebnisse über die Konstitution der Chromatischen Substanz des Zellkerns*. Verlag von Gustav Fischer, Jena, Germany. University Press, Princeton, NJ, USA.
- Boyle, E.A., Li, Y.L., and Pritchard, J.K. (2017). An expanded view of complex traits: from polygenic to omnigenic. *The Cell*, **169**, 1177–1186.
- Brochmann, C., Bryusting, A.K., and Alsos, I.G. (2004). Polyploidy in arctic plants. *Biological Society of the Linnean Society*, **82**, 521–536.
- Broman, K. and Sen, S. (2009). *A Guide to QTL Mapping with R/qtl*. Springer, New York, USA.
- Brown, W.L. and Wilson, E.O. (1956). Character displacement. *Systematic Zoology*, **5**, 49–64.
- Browning, S.R. and Browning, B.L. (2007). Rapid and accurate haplotype phasing and missing data inference for whole genome association studies by use of localized haplotype clustering. *American Journal of Human Genetics*, **81**, 1084–1097.
- Brunet, M., Guy, F., Pilbeam, D., et al. (2002) A new hominid from the Upper Miocene of Chad, Central Africa. *Nature*, **418**, 145–151.
- Buenrostro, J.D., Giresi, P.G., Zaba, L.C., Chang, H.Y., and Greenleaf, W.J. (2013). Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. *Nature Methods*, **10**, 1213–1218.
- Burki, F. (2014). The Eukaryotic Tree of Life from a Global Phylogenomic Perspective. *Cold Spring Harbor Perspectives in Biology*, **6**, a016147.
- Burri, R., Nater, A., Kawakami, T., et al. (2015). Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers. *Genome Research*, **25**, 1656–1665.
- Bush, G.L. (1966). The taxonomy, cytology and evolution of the genus *Rhagoletis* in North America (Diptera, Tephritidae). *Bulletin of the Museum of Comparative Zoology, Harvard University*, **134**, 431–562.
- Butlin, R.K. and Smadja, C.M. (2018). Coupling, reinforcement and speciation. *American Naturalist*, **191**, 155–172.
- Cann, R.L., Stoneking, M., and Wilson, A.C. (1987). Mitochondrial-DNA and Human-Evolution. *Nature*, **325**, 31–36.
- Carlborg, Ö., Jacobsson, L., Åhngren, P., Siegel, P., and Andersson, L. (2006). Epistasis and the release of genetic variation during long-term selection. *Nature Genetics*, **38**, 418–420.
- Carlsson, M. and Carlsson, A. (1990). Interactions between glutamatergic and monoaminergic systems within the basal ganglia—implications for schizophrenia and Parkinson's disease. *Trends in Neuroscience*, **13**, 272–274.
- Carneiro, M., Albert, F.W., Afonso, S., et al. (2014) The genomic architecture of population divergence between subspecies of the European rabbit. *PLoS Genetics*, **10**, e1003519.
- Carter, A.J.R., Hermisson, J., and Hansen, T.F. (2005). The role of epistatic gene interactions in the response to selection and the evolution of evolvability. *Theoretical Population Biology*, **68**, 179–196.
- Chan, Y.F., Marks, M.E., Jones, F.C., et al. (2010). Adaptive evolution of pelvic reduction in sticklebacks by recurrent deletion of a *pitx1* enhancer. *Science*, **327**, 302–305.
- Chargaff, E. (1950). Chemical specificity of nucleic acids and mechanisms of their enzymatic degradation. *Experientia*, **6**, 201–209.
- Charlesworth, B. (1998). Measures of divergence between populations and the effect of forces that reduce variability. *Molecular Biology and Evolution*, **15**, 538–543.
- Charlesworth, B., Coyne, J.A., and Barton, N.H. (1987). The relative rates of evolution of sex chromosomes and autosomes. *The American Naturalist*, **130**, 113–146.
- Charlesworth, B., Nordborg, M., and Charlesworth, D. (1997). The effects of local selection, balanced polymorphism and background selection on equilibrium patterns of genetic diversity in subdivided populations. *Genetics Research*, **70**, 155–174.
- Chen, S.-H., Habib, G., Yang, C.-Y., et al. (1987). Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in-frame stop codon. *Science*, **238**, 363–366.
- Chow, L.T., Gelinis, R.E., Broker, T.R., and Roberts, R.J. (1977). An amazing sequence arrangement at the 5' ends of adenovirus 2 messenger RNA. *The Cell*, **12**, 1–8.
- Ciomborowska, J., Rosikiewicz, W., Szklarczyk, D., Makalowski, W., and Makalowska, I. (2013). "Orphan" retrogenes in the human genome. *Molecular Biology and Evolution*, **30**, 384–396.
- Clark, P.D. and Pazdernik, N.J. (2012). *Molecular Biology, 2nd edition*. Academic Press, Waltham MA, USA.

- Clutton-Brock, T.H., Guinness, F.E., and Albon, S.E. (1982). *Red Deer: Behaviour and Ecology of Two Sexes*. Edinburgh University Press, Edinburgh, UK.
- Colosimo, P.F., Hosemann, K.E., Balabhadra, S., et al. (2005). Widespread parallel evolution in sticklebacks by repeated fixation of Ectodysplasin alleles. *Science*, **307**, 1928–1933.
- Colosimo, P.F., Peichel, C.L., Nereng, K., et al. (2004). The genetic architecture of parallel armor plate reduction in threespine sticklebacks. *PLoS Biology*, **2**, e109.
- Cameron, J.M., Williford, A., Kliman, R.M. (2007). The Hill–Robertson effect: evolutionary consequences of weak selection and linkage in finite populations. *Heredity*, **100**, 19–31.
- Compeau, P.E.C., Pevzner, P.A., and Tesler, G. (2011). How to apply de Bruijn graphs to genome assembly. *Nature Biotechnology*, **29**, 987–991.
- Cook, L.M. (2003). The rise and fall of the *carbonaria* form of the peppered moth. *The Quarterly Review of Biology*, **78**, 399–417.
- Cooney, C.R., Bright, J.A., Capp, E.J.R., et al. (2017). Mega-evolutionary dynamics of the adaptive radiation of birds. *Nature*, **542**, 1–16.
- Corradi, N., Pombert, J.F., Farinelli, L., Didier, E.S., and Keeling, P.J. (2010). The complete sequence of the smallest known nuclear genome from the microsporidian *Encephalitozoon intestinalis*. *Nature Communications*, **1**, 77.
- Cortijo, S., Wardenar, R., Colomé-Tatché, M., et al. (2014). Mapping the epigenetic basis of complex traits. *Science*, **343**, 1145–1148.
- Coyne, J.A. and Orr, H.A. (1989). Two rules of speciation. In: D. Otte and J.A. Endler (eds) *Speciation and its Consequences*, pp. 180–207. Sinauer Associates, Sunderland, MA, USA.
- Coyne, J.A. and Orr, H.A. (2004). *Speciation*. Oxford University Press, Oxford, UK.
- Cracraft, J. (1989). Speciation and its ontology: The empirical consequences of alternative species concepts for understanding patterns and processes of differentiation. In: D. Otte and J.A. Endler (eds) *Speciation and its Consequences*, pp. 29–59. Sinauer Associates, Sunderland, MA, USA.
- Crick, F.H.C. (1958). On protein synthesis. *Symposia of the Society for Experimental Biology*, **12**, 138–163.
- Crick, F.H.C. (1988). *What Mad Pursuit: A Personal View on Scientific Discovery*. Basic Books, New York, USA.
- Cruikshank, 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**, 3133–3157.
- Currie, C.R., Scott, J.A., Summerbell, R.C., and Malloch, D. (1999). Fungus-growing ants use antibiotic-producing bacteria to control garden parasites. *Nature*, **398**, 701–704.
- Cutter, A.D. and Payseur, B.A. (2013). Genomic signatures of selection at linked sites: unifying the disparity among species. *Nature Reviews Genetics*, **14**, 262–264.
- Darvasi, A. (1998). Experimental strategies for the genetic dissection of complex traits in animal models. *Nature Genetics*, **18**, 19–24.
- Darwin, C. (1859). *On the Origin of Species by Means of Natural Selection, or the Preservation of Favored Races in the Struggle for Life*. Modern Library, New York, USA.
- Darwin, C. (1871). *The Descent of Man, and Selection in Relation to Sex*. Jon Murray, London, UK.
- Darwin, C. (1876). *Cross and Self-fertilization of Plants*. John Murray, London, UK.
- Darwin, C. and Wallace, A.R. (1858). On the tendency of species to form varieties; and on the perpetuation of varieties and species by natural means of selection. *Journal of the Proceedings of the Linnean Society of London, Zoology*, **3**, 45–62.
- Davey, J.W., Hohenlohe, P.A., Etter, P.D., Boone, J.Q., Catchen, J.M., and Blaxter, M.L. (2011). Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nature Reviews Genetics*, **12**, 499–510.
- Dawkins, R. (1976). *The Selfish Gene*. Oxford University Press, Oxford, UK.
- Dawkins, R. (1986). *The Blind Watchmaker*. Norton & Company Ltd, London, UK.
- Day, R.L., Laland, K.N., and Odling-Smee, J. (2003). Rethinking adaptation: The niche-construction perspective. *Perspectives in Biology and Medicine*, **46**, 80–95.
- de Queiroz, K. and Donoghue, M.J. (1990). Phylogenetic systematics or Nelson's version of cladistics? *Cladistics*, **6**, 61–75.
- de Sousa Abreu, R., Penalva, L.O., Marcotte, E.M., and Vogel, C. (2009). Global signatures of protein and mRNA expression levels. *Molecular BioSystems*, **5**, 1512–1526.
- de Vries, H. (1900). *The Mutation Theory: Experiments and Observation on the Origin of Species in the Vegetable*, Vol. 1. Classical Reprint 2012, Forgotten Books, London.
- de Vries, H. (1903). *The Mutation Theory: Experiments and Observation on the Origin of Species in the Vegetable*, Vol. 2. Classical Reprint 2013, Forgotten Books, London.
- Dean, A.M. and Thornton, J.W. (2007). Mechanistic approaches to the study of evolution: the functional synthesis. *Nature Reviews Genetics*, **8**, 675–688.
- Dekker, J., Belmont, A.S., Guttman, M., et al. (2017). The 4D nucleome project. *Nature*, **549**, 219–226.
- Delaneau, O., Howie, B., Cox, A., Zagury, J.-F., and Marchini, J. (2013). Haplotype estimation using sequence reads. *American Journal of Human Genetics*, **93**, 687–696.
- Delmore, K.E. and Irwin, D.E. (2014). Hybrid songbirds employ intermediate routes in a migratory divide. *Ecology Letters*, **17**, 1211–1218.

- Delsuc, F., Brinkmann, H., and Philippe, H. (2005). Phylogenomics and the reconstruction of the tree of life. *Nature Reviews Genetics*, **6**, 361–375.
- Der Sarkissian, C., Ermini, L., Schubert, M., et al. (2015). Evolutionary genomics and conservation of the endangered Przewalski's horse. *Current Biology*, **25**, 2577–2583.
- Diz, A.P., Martínez-Fernández, M., and Rolán-Alvarez, E. (2012). Proteomics in evolutionary ecology: linking the genotype with the phenotype. *Molecular Ecology*, **21**, 1060–1080.
- Dobzhansky, T. (1934). Studies on hybrid sterility. I. spermatogenesis in pure and hybrid *Drosophila pseudoobscura*. *Zeitschrift für Zellforschung und Mikroskopische Anatomie*, **21**, 169–221.
- Dobzhansky, T. (1937). *Genetics and the Origin of Species*. Reprint, 1982 by Columbia University Press, New York, USA.
- Dobzhansky, T. (1940). Speciation as a stage in evolutionary divergence. *American Naturalist*, **74**, 312–321.
- Donohue, K. (2013). Development in the wild: Phenotypic plasticity. *Annual Plant Reviews*, **45**, 321–356.
- Doolittle, W.F. (1978). Genes in pieces: were they ever together? *Nature*, **272**, 581–582.
- Doolittle, W.F. (2013). Is junk DNA bunk? A critique of ENCODE. *Proceedings of the National Academy of Sciences of the USA*, **110**, 5294–5300.
- Doolittle, W.F. and Stoltzfus, A. (1993) Molecular evolution. Genes-in-pieces revisited. *Nature*, **361**, 403.
- Dulai, K.S., von Dornum, M., Mollon, J.D., and Hunt, D.M. (1999). The evolution of trichromatic color vision by opsin gene duplication in New World and Old World primates. *Genome Research*, **9**, 629–638.
- Dunn, C.W., Hejnol, A., Matus, D.Q., et al. (2008). Broad phylogenomic sampling improves resolution of the animal tree of life. *Nature*, **452**, 745–749.
- Dunn, C.W. and Munro, C. (2016). Comparative genomics and the diversity of life. *Zoologica Scripta*, **45**, 5–13.
- Dunning Hotopp, J.C. (2011). Horizontal gene transfer between bacteria and animals. *Trends in Genetics*, **27**, 157–163.
- Eberhard, W.G. (1996). *Female Control: Sexual Selection by Cryptic Female Choice*. Princeton University Press, Princeton, NJ, USA.
- Edelson, E. (1999). *Gregor Mendel: And the Roots of Genetics*. Oxford University Press, New York, USA.
- Edwards, S.V., Potter, S., Schmitt, C.J., Bragg, J.G., and Moritz, C. (2016). Reticulation, divergence, and the phylogeography–phylogenetics continuum. *Proceedings of the National Academy of Sciences of the USA*, **113**, 8025–8032.
- Ehrlich, P.R. and Raven, P.H. (1964). Butterflies and plants: a study in coevolution. *Evolution*, **18**, 586–608.
- Eichler, E.E., Flint, J., Gibson, G., Kong, A., Leal, S.M., Moore, J.H., and Nadeau, J.H. (2010). Missing heritability and strategies for finding the underlying causes of complex disease. *Nature Reviews Genetics*, **11**, 446–450.
- Eisen, J.A. and Fraser, C.M. (2003). Phylogenomics: Intersection of evolution and genomics. *Science*, **300**, 1706–1707.
- Ekblom, R. and Wolf, J.B.W. (2014). A field guide to whole-genome sequencing, assembly and annotation. *Evolutionary Applications*, **7**, 1026–1042.
- Eldredge, N. and Gould, S.J. (1972). Punctuated equilibria: an alternative to phyletic gradualism. In: T.J.M. Schopf (ed.) *Models in Paleobiology*, pp 82–115. Freeman Cooper, San Francisco, USA.
- Elgvin, T.O., Trier, C.N., Tørresen, O.K., et al. (2017). The genomic mosaicism of hybrid speciation. *Science Advances*, **3**, e1602996.
- Ellegren, H. (2011). Sex chromosome evolution: recent progress and the influence of male and female heterogamety. *Nature Reviews Genetics*, **12**, 157–166.
- 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**, 756–760.
- Enattah, N.S., Sahi, T., Savilahti, E., Terwilliger, J.D., Peltonen, L., and Järvelä, I. (2002). Identification of a variant associated with adult-type hypolactasia. *Nature Genetics*, **30**, 233–237.
- Engel, M.S., Panian, J., Wiltschko, D., and Grimaldi, D.A. (2004). New light shed on the oldest insect. *Nature*, **427**, 627–630.
- English, A.C., Richards, S., Han, Y., et al. (2012). Mind the gap: Upgrading genomes with Pacific Biosciences RS long-read sequencing technology. *PLoS One*, **7**, e47768.
- Erickson, P.A., Ellis, N.A., and Miller, C.T. (2016). Microinjection for Transgenesis and Genome Editing in Threespine Sticklebacks. *Journal of Visualized Experiments*, **111**, e54055.
- Erwin, A.A., Galdos, M.A., Wickersheim, M.L., et al. (2015). piRNAs are associated with diverse transgenerational effects of gene and transposon expression in a hybrid dysgenic syndrome of *D. virilis*. *PLoS Genetics*, **11**, e1005332.
- Esvelt, K.M., Smidler, A.L., Catteruccia, F., and Church, G.M. (2014). Emerging technology: Concerning RNA-guided gene drives for the alteration of wild populations. *eLife*, **3**, e03401.
- Evanno, G., Regnaut, S., and Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology*, **14**, 2611–2620.
- Excoffier, L., Dupanloup, I., Huerta-Sánchez, E., Sousa, V.C., and Foll, M. (2013). Robust demographic inference

- from genomic and SNP data. *PLoS Genetics*, **9**, e1003905–17.
- Excoffier, L., Foll, M., Petit, R.J. (2009). Genetic consequences of range expansions. *Annual Review of Ecology, Evolution, and Systematics*, **40**, 481–501.
- Falconer, D.S. and Mackay, T.F.C. (1996). *Introduction to Quantitative Genetics*, 4th edition. Longmans Green, Harlow, Essex, UK.
- Falster, D.S. and Westoby, M. (2003). Plant height and evolutionary games. *Trends in Ecology & Evolution*, **18**, 337–343.
- Faria, R., Chaube, P., Morales, H.E., et al. (2018). Multiple chromosomal rearrangements in a hybrid zone between *Littorina saxatilis* ecotypes. *Molecular Ecology*. Accepted Author Manuscript. doi:10.1111/mec.14972
- Feder, J.L., Egan, S.P., and Nosil, P. (2012). The genomics of speciation-with-gene-flow. *Trends in Genetics*, **28**, 342–350.
- Feldman, M.W. and Otto, S.P. (1991). A comparative approach to the population-genetic theory of segregation distortion. *The American Naturalist*, **137**, 443–456.
- Felsenstein, J. (1974). The evolutionary advantage of recombination. *Genetics*, **78**, 737–756.
- Felsenstein, J. (1981). Skepticism towards Santa Rosalia, or why are there so few kinds of animals? *Evolution*, **35**, 124–138.
- Field, Y., Boyle, E.A., Telis, N., et al. (2016). Detection of human adaptation during the past 2000 years. *Science*, **354**, 760–764.
- Findlay, G.D., Yi, X., MacCoss, M.J., and Swanson, W.J. (2008). Proteomics reveals novel *Drosophila* seminal fluid proteins transferred at mating. *PLoS Biology*, **6**, e178.
- Finnegan, D.J. (2012). Retrotransposons. *Current Biology*, **22**, R432–R437.
- Firman, R.C. (2018). Postmating sexual conflict and female control over fertilization during gamete interaction. *Annals of the New York Academy of Sciences*, **1422**, 48–64.
- Fisher, R.A. (1918). The correlation between relatives on the supposition of Mendelian inheritance. *Transactions of the Royal Society of Edinburgh*, **52**, 399–433.
- Fisher, R.A. (1930). *The Genetical Theory of Natural Selection—A Complete Variorum Edition*, 1999. Oxford University Press, Oxford, UK.
- Fishman, L., Aagaard, J., and Tuthill, J.C. (2008). Toward the evolutionary genomics of gametophytic divergence: patterns of transmission ratio distortion in monkey-flowers (*Mimulus*) hybrids reveal a complex genetic basis for conspecific pollen precedence. *Evolution*, **62**, 2958–2970.
- Flicek, P. and Birney, E. (2009). Sense from sequence reads: methods for alignment and assembly. *Nature Methods*, **6**, S6–S12.
- Forterre, P. and Prangishvili, M. (2009). The origin of viruses. *Research in Microbiology*, **160**, 466–472.
- Fountain, T., Ravinet, M., Naylor, R., Reinhardt, K., and Butlin, R.K. (2016). A linkage map and QTL analysis for pyrethroid resistance in the bed bug *Cimex lectularis*. *Genes, Genomes, Genetics*, **6**, 4059–4066.
- Francioli, L.C., Polak, P.P., Koren, A., et al. (2015). Genome-wide patterns and properties of *de novo* mutations in humans. *Nature Genetics*, **47**, 822–826.
- Fu, Q., Hajdinjak, M., Moldovan, O.T., et al. (2015). An early modern human from Romania with a recent Neanderthal ancestor. *Nature*, **524**, 216–219.
- Fuiman, L.A. (1997). What can flatfish ontogenies tell us about pelagic and benthic lifestyles? *Journal of Sea Research*, **37**, 257–267.
- Galagan, J.E., Nusbaum, C., Roy, A., et al. (2002). The genome of *M. acetivorans* reveals extensive metabolic and physiological diversity. *Genome Research*, **12**, 532–542.
- Gardner, D. (2010). *Future Babble: Why Expert Predictions Fail and Why We Believe Them Anyway*. McClelland & Stewart, Toronto, Canada.
- Gaunitz, C., Fages, A., Hanghoj, K., and Albrechtsen, A. (2018). Ancient genomes revisit the ancestry of domestic and Przewalski's horses. *Science*, **360**, 111–114.
- Gautier, M., Klassmann, A., and Vitalis, R. (2016). REHH 2.0: a reimplement of the R package REHH to detect positive selection from haplotype structure. *Molecular Ecology Resources*, **17**, 78–90.
- Gavrilets, S. (2004). *Fitness Landscapes and the Origin of Species*. Princeton University Press, Princeton, NJ, USA.
- Gavrilets, S. (2014). Is sexual conflict an “engine of speciation”? *Cold Spring Harbor Perspectives in Biology*, **6**, a017723.
- Gemmell, N.J., Metcalf, V.J., and Allendorf, F.W. (2004). Mother's curse: the effect of mtDNA on individual fitness and population viability. *Trends in Ecology & Evolution*, **19**, 238–244.
- Gigord, L.D.B., Macnair, M.R., and Smithson, A. (2001). Negative frequency-dependent selection maintains a dramatic flower color polymorphism in the rewardless orchid *Dactylorhiza sambucina* (L.) Soð. *Proceedings of the National Academy of Sciences of the USA*, **98**, 6253–6255.
- Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D., and Pääbo, S. (2004). Loss of olfactory receptor genes coincides with the acquisition of full trichromatic vision in primates. *PLoS Biology*, **2**, e5.
- Gilbert, W. (1978). Why genes in pieces? *Nature*, **271**, 501.
- Girirajan, S. (2017). Missing heritability and where to find it. *Genome Biology*, **18**, 89.
- Gladyshev, E.A., Meselson, M., and Arkipova, I.R. (2008). Massive horizontal gene transfer in bdelloid rotifers. *Science*, **320**, 1210–1213.
- Glazer, A.M., Killingbeck, E.E., Mitros, T., Rokshar, D.S., and Miller, C.T. (2015). Genome assembly improvement and mapping convergently evolved skeletal traits in

- stickleback with genotyping-by-sequencing. *Genes, Genomes, Genetics*, **5**, 1463–1472.
- Goldberg, E.E., Kohn, J.R., Lande, R., et al. (2010). Species selection maintains self-incompatibility. *Science*, **330**, 493–495.
- Golding, G.B. and Strobeck, C. (1980). Linkage disequilibrium in a finite population that is partially selfing. *Genetics*, **94**, 777–789.
- Gompert, Z. and Buerkle, C.A. (2016). What, if anything, are hybrids: enduring truths and challenges associated with population structure and gene flow. *Evolutionary Applications*, **9**, 909–923.
- Gompert, Z., Mandeville, E.G., and Buerkle, C.A. (2017). Analysis of population genomic data from hybrid zones. *Annual Review of Ecology, Evolution, and Systematics*, **48**, 207–229.
- Goodwin, S., McPherson, J.D., and McCombie, W.R. (2016). Coming of age: ten years of next-generation sequencing technologies. *Nature Reviews Genetics*, **17**, 333–351.
- Gould, S.J. (2002). *The Structure of Evolutionary Theory*. The Belknap Press of Harvard University Press, Cambridge, MA, USA.
- Grabherr, M.G., Haas, B.J., Yassour, M., et al. (2011). Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nature Biotechnology*, **29**, 644–652.
- Grafen, A. (1990). Biological signals as handicaps. *Journal of Theoretical Biology*, **144**, 517–546.
- Grahame, J.W., Wilding, C.S., and Butlin, R.K. (2006). Adaptation to a steep environmental gradient and an associated barrier to gene exchange in *Littorina saxatilis*. *Evolution*, **60**, 268–278.
- Grant, P.R. (1972). Convergent and divergent character displacement. *Biological Journal of the Linnean Society*, **4**, 36–98.
- Grant, P.R. and Grant, B.R. (2006). Evolution of character displacement in Darwin's finches. *Science*, **313**, 224–226.
- Grant, P.R. and Grant, B.R. (2011). *How and Why Species Multiply—The Radiation of Darwin's Finches*. Princeton University Press, Princeton, NJ, USA.
- Grasby, K.L., Verweij, K.J.H., Mosing, M.A., Zietch, B.P., and Medland, S.E. (2017). Estimating heritability from twin studies. In: R. Elston (ed.) *Statistical Human Genetics. Methods in Molecular Biology, vol 1666*. Humana Press, New York, USA.
- Green, R.E., Krause, J., Briggs, A.W., et al. (2010). A draft sequence of the Neandertal genome. *Science*, **328**, 710–722.
- Greenman, C., Stephens, P., Smith, R., et al. (2007). Patterns of somatic mutation in human cancer genomes. *Nature*, **446**, 153–158.
- Griffin, A.S. (2004). Social learning about predators: a review and prospectus. *Learning & Behavior*, **32**, 131–140.
- Guerrero, R.F. and Hahn, M.W. (2017). Speciation as a sieve for ancestral polymorphism. *Molecular Ecology*, **26**, 5262–5368.
- Guimaraes, P.R., Jr, Galetti, M., and Jordano, P. (2008). Seed dispersal anachronisms: Rethinking the fruits extinct megafauna ate. *PLoS One*, **3**, e1745.
- Gutenkunst, R.N., Hernandez, R.D., Williamson, S.H., and Bustamante, C.D. (2009). Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data. *PLoS Genetics*, **5**, e1000695–11.
- Hackett, S.J., Kimball, R.T., Reddy, S., et al. (2008). A phylogenomic study of birds reveals their evolutionary history. *Science*, **320**, 1763–1768.
- Haldane, J.B.S. (1922). Sex ratio and unisexual sterility in hybrid animals. *Journal of Genetics*, **12**, 101–109.
- Haldane, J.B.S. (1932). *The Causes of Evolution*. Reprint by Princeton University Press 1993, Princeton, NJ, USA.
- Hamilton, W.D. (1964a). The genetical evolution of social behaviour. I. *Journal of Theoretical Biology*, **7**, 1–16.
- Hamilton, W.D. (1964b). The genetical evolution of social behaviour. II. *Journal of Theoretical Biology*, **7**, 17–52.
- Hamilton, W.D. (1980). Sex versus non-sex versus parasite. *Oikos*, **35**, 282–290.
- Hamilton, W.D., Axelrod, R., and Tanese, R. (1990). Sexual reproduction as an adaptation to resist parasites (a review). *Proceedings of the National Academy of Sciences of the USA*, **87**, 3566–3573.
- Hansen, T.F. and Houle, D. (2008). Measuring and comparing evolvability and constraint in multivariate characters. *Journal of Evolutionary Biology*, **21**, 1201–1219.
- Hansen, T.F., Pélabon, C., and Houle, D. (2011). Heritability is not evolvability. *Evolutionary Biology*, **38**, 258.
- Hansen, T.F. and Wagner, G.P. (2001). Modelling genetic architecture: a multilinear model of gene interaction. *Theoretical Population Biology*, **59**, 61–86.
- Hardy, G.H. (1908). Mendelian proportions in a mixed population. *Science*, **18**, 49–50.
- Harold, D., Abraham, R., Hollingworth, P., et al. (2009). Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. *Nature Genetics*, **41**, 1088–1093.
- Harris, K. and Nielsen, R. (2013). Inferring demographic history from a spectrum of shared haplotype lengths. *PLoS Genetics*, **9**, e1003521.
- Hart, J.C. and Miller, C.T. (2017). Sequence-based mapping and genome editing reveal mutations in stickleback *hps5* cause oculocutaneous albinism and the casper phenotype. *Genes, Genomes, Genetics*, **7**, 3123–3131.
- Hasegawa, M., Kishino, H., and Yano, T.-A. (1985). Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *Journal of Molecular Evolution*, **22**, 160–174.

- Haynes, K.F., Gemeno, C., Yeargan, K.V., and Johnson, K.M. (2002). Aggressive chemical mimicry of moth pheromones by a bolas spider: how does this specialist predator attract more than one species of prey? *Chemoecology*, **12**, 99–105.
- Hedges, S.B., Marin, J., Suleski, M., Paymer, M., and Kumar, S. (2015). Tree of life reveals clock-like speciation and diversification. *Molecular Biology and Evolution*, **32**, 835–845.
- Hedrick, P.W. and Garcia-Dorado, A. (2016). Understanding inbreeding depression, purging and genetic rescue. *Trends in Ecology & Evolution*, **31**, 940–952.
- Helbig, A.J. (1991a). Inheritance of migratory direction in a bird species: a cross-breeding experiment with SE- and SW-migrating blackcaps (*Sylvia atricapilla*). *Behavioural Ecology and Sociobiology*, **28**, 9–12.
- Helbig, A.J. (1991b). SE- and SW-migrating blackcap (*Sylvia atricapilla*) populations in Central Europe: Orientation of birds in the contact zone. *Journal of Evolutionary Biology*, **4**, 657–670.
- Hellenthal, G., Busby, G., Band, G.B.J., et al. (2014). A genetic atlas of human admixture history. *Science*, **343**, 747–751.
- Hendry, A.P., Bolnick, D.I., Berner, D., and Peichel, C.L. (2009). Along the speciation continuum in sticklebacks. *Journal of Fish Biology*, **75**, 2000–2036.
- Hendry, A.P., Taylor, E.B., and McPhail, J.D. (2002). Adaptive divergence and the balance between selection and gene flow: Lake and stream stickleback in the Misty system. *Evolution*, **56**, 1199–1216.
- Henig, R.M. (2009). *The Monk in the Garden: The Lost and Found Genius of Gregor Mendel, the Father of Genetics*. Houghton Mifflin Company, Boston, New York, USA.
- Hermansen, J.S., Haas, F., Trier, C.N., et al. (2014). Hybrid speciation through sorting of parental incompatibilities in Italian sparrows. *Molecular Ecology*, **23**, 5831–5842.
- Hewitt, G.M. (2000). The genetic legacy of the Quaternary ice ages. *Nature*, **405**, 907–913.
- Hewitt, G.M. (2001). Speciation, hybrid zones and phylogeography—or seeing genes in space and time. *Molecular Ecology*, **10**, 537–549.
- Hickerson, M.J. (2014). All models are wrong. *Molecular Ecology*, **23**, 2887–2889.
- Hickerson, M.J., Carstens, B.C., Cavender-Bares, J., et al. (2010). Phylogeography's past, present, and future: 10 years after Avise, 2000. *Molecular Phylogenetics and Evolution*, **54**, 291–301.
- Higuchi, R., Bowman, B., Freiberger, M., Ryder, O.A., and Wilson, A.C. (1984). DNA-Sequences from the quagga, an extinct member of the horse family. *Nature*, **312**, 282–284.
- Hill, W.G. and Robertson, A. (1966). The effect on linkage on limits to artificial selection. *Genetic Research*, **8**, 269–294.
- Hirose, M., Hasegawa, A., Mochida, K., et al. (2017). CRISPR/Cas9-mediated genome editing in wild-derived mice: generation of tamed wild-derived strains by mutation of the *a* (nonagouti) gene. *Scientific Reports*, **7**, 42476.
- Ho, S.Y.W., Duchene, S., Molak, M., and Shapiro, B. (2015). Time-dependent estimates of molecular evolutionary rates: evidence and causes. *Molecular Ecology*, **24**, 6007–6012.
- Ho, S.Y.W., Shapiro, B., Phillips, M.J., Cooper, A., and Drummond, A.J. (2007). Evidence for time dependency of molecular rate estimates. *Systematic Biology*, **56**, 512–522.
- Hoban, S., Kelley, J.L., and Lotterhos, K.E. (2016). Finding the genomic basis of local adaptation: Pitfalls, practical solutions, and future directions. *American Naturalist*, **188**, 379–397.
- Hobolth, A., Dutheil, J.Y., Hawks, J., Schierup, M.H., and Mailund, T. (2011). Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection. *Genome Research*, **21**, 349–356.
- Hodgkinson, A. and Eyre-Walker, A. (2011). Variation in the mutation rate across mammalian genomes. *Nature Reviews Genetics*, **12**, 756–766.
- Hoekstra, H.E. and Coyne, J.A. (2007). The locus of evolution: evo devo and the genetics of adaptation. *Evolution*, **61**, 995–1016.
- Hoekstra, H.E., Drumm, K.E., and Nachman, M.W. (2004). Ecological genetics of adaptive color polymorphism in pocket mice: geographic variation in selected and neutral genes. *Evolution*, **58**, 1329–1341.
- Hohenlohe, P.A., Bassham, S., Etter, P.D., et al. (2010). Population genomics of parallel adaptation in threespine stickleback using sequenced RAD tags. *PLoS Genetics*, **6**, e1000862–23.
- Hollingsworth, P., Harold, D., Sims, R., et al. (2011). Common variants at ABVA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. *Nature Genetics*, **43**, 429–435.
- Holmquist, R., Jukes, T.H., and Moise, H. (1976). The evolution of the globin family genes: Concordance of stochastic and augmented maximum parsimony genetic distances for α hemoglobin, β hemoglobin and myoglobin phylogenies. *Journal of Molecular Biology*, **105**, 39–74.
- Hopkins, R., Guerrero, R.F., Rausher, M.D., and Kirkpatrick, M. (2014). Strong reinforcing selection in a Texas wildflower. *Current Biology*, **24**, 1–5.
- Hopkins, R. and Rausher, M.D. (2011). Identification of two genes causing reinforcement in the Texas wildflower *Phlox drummondii*. *Nature*, **469**, 411–414.
- Hopkins, R. and Rausher, M.D. (2012). Pollinator-mediated selection on flower color alleles drives reinforcement. *Science*, **335**, 1090–1092.
- Hori, M. (1993). Frequency-dependent natural selection in the handedness of scale-eating cichlid fish. *Science*, **260**, 216–219.

- Hori, M., Ochi, H., and Kohda, M. (2007). Inheritance pattern of lateral dimorphism in two cichlids (a scale eater, *Perissodus microlepis*, and a herbivore, *Neolamprologus moorii*) in Lake Tanganyika. *Zoological Science*, **24**, 486–492.
- Hornett, E.A. and Wheat, C.W. (2012). Quantitative RNA-Seq analysis in non-model species: assessing transcriptome assemblies as a scaffold and the utility of evolutionary divergent genomic reference species. *BMC Genomics*, **13**, 361.
- Hosken, D.J. and Ward, P.I. (2001). Experimental evidence for testis size evolution via sperm competition. *Ecology Letters*, **4**, 10–13.
- Houle, D. (1992). Comparing evolvability and variability of quantitative traits. *Genetics*, **130**, 195–204.
- Howard, D.J. (1999). Conspecific sperm and pollen precedence and speciation. *Annual Review of Ecology and Systematics*, **30**, 109–132.
- Huber, H., Hohn, M.J., Rachel, R., Fuchs, T., Wimmer, V.C., and Stetter, K.O. (2002). A new phylum of Archaea represented by a nanosized hyperthermophilic symbiont. *Nature*, **417**, 63–67.
- Hudson, R.E., Aukema, J.E., Risper, C., and Roze, D. (2002). Altruism, cheating and anticheater adaptations in cellular slime molds. *The American Naturalist*, **160**, 31–43.
- Hudson, R.R., Kreitman, M., and Aguadé, M. (1987). A test of neutral molecular evolution based on nucleotide data. *Genetics*, **116**, 153–159.
- Hug, L.A., Baker, B.J., Anantharaman, K., et al. (2016). A new view of the tree of life. *Nature Microbiology*, **1**, 1–6.
- Husband, B.C. (2000). Constraints on polyploid evolution: a test of the minority exclusion principle. *Proceedings of the Royal Society B*, **267**, 217–223.
- Huxley, J. (1942). *Evolution—The Modern Synthesis*. Reprint, 2010 by MIT Press, Cambridge, MA, USA.
- Ibbotson, R.E., Hunt, D.M., Bowmaker, J.K., and Mollon, J.D. (1992). Sequence divergence and copy number of the middle- and longwave photopigment genes in Old World monkeys. *Proceedings of the Royal Society B*, **247**, 145–154.
- International Human Genome Sequencing Consortium (2001). Initial sequencing and analysis of the human genome. *Nature*, **409**, 860–921.
- Irwin, D.E., Bensch, S., Irwin, J.H., and Price, T.D. (2005). Speciation by distance in a ring species. *Science*, **307**, 414–416.
- Jacobs, G.H., Neitz, M., Deegan, J.F., and Neitz, J. (1996). Trichromatic colour vision in new world monkeys. *Nature*, **382**, 156–158.
- Jarvis, E.D., Mirarab, S., Aberer, A.J., et al. (2014). Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **346**, 1320–1331.
- 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**, 444–448.
- Jia, J., Zhao, S., Kong, X., et al. (2013). *Aegilops tauschii* draft genome sequence reveals a gene repertoire for wheat adaptation. *Nature*, **496**, 91–95.
- Jiang, W., Zhou, H., Bi, H., et al. (2013). Demonstration of CRISPR/Cas9/sgRNA-mediated targeted gene modification in *Arabidopsis*, tobacco, sorghum and rice. *Nucleic Acids Research*, **41**, e188.
- Jiggins, C.D., Salazar, C., Linares, M., and Mavárez, J. (2008). Hybrid trait speciation and *Heliconius* butterflies. *Philosophical Transactions of the Royal Society B*, **363**, 3047–3054.
- Johannesson, K., Butlin, R.K., Panova, M., and Westram, A.M. (2017). Mechanisms of divergence and speciation in *Littorina saxatilis*: Integrating knowledge from ecology and genetics with new data emerging from genomic studies. In: *Population Genomics*. Springer, Cham.
- Johnson, J.M., Castle, J., Garret-Engele, P., et al. (2003). Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays. *Science*, **302**, 2141–2144.
- Jones, F.C., Chan, Y.F., Schmutz, J., et al. (2012). A genome-wide SNP genotyping array reveals patterns of global and repeated species-pair divergence in sticklebacks. *Current Biology*, **22**, 83–90.
- Jones, M.R., Mills, L.S., Alves, P.C., et al. (2018). Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. *Science*, **360**, 1355–1358.
- Joyce, D.A., Lunt, D.H., Genner, M.J., Turner, G.F., Bills, R., and Seehausen, O. (2011). Repeated colonization and hybridization in Lake Malawi cichlids. *Current Biology*, **21**, R108–R109.
- Jukema, J. and Piersma, T. (2006). Permanent female mimics in a lekking shorebird. *Biology Letters*, **2**, 161–164.
- Kalisz, S., Vogler, D.W., and Hanley, K.M. (2004). Context-dependent autonomous self-fertilization yields reproductive assurance and mixed mating. *Nature*, **430**, 884–887.
- Kamm, J.A., Terhorst, J., and Song, Y.S. (2017). Efficient computation of the joint sample frequency spectra for multiple populations. *Journal of Computational and Graphical Statistics*, **26**, 182–194.
- Kashi, Y. and King, D.G. (2006). Simple sequence repeats as advantageous mutators in evolution. *Trends in Genetics*, **22**, 253–259.
- Kayser, M., Brauer, S., and Stoneking, M. (2003). A genome scan to detect candidate regions influenced by local natural selection in human populations. *Molecular Biology and Evolution*, **20**, 893–900.
- Kelleher, J., Etheridge, A.M., and McVean, G. (2016). Efficient coalescent simulation and genealogical analysis for large sample sizes. *PLoS Computational Biology*, **12**, e1004842–22.
- Kern, A.D. and Hahn, M.W. (2018). The neutral theory in light of natural selection. *Molecular Biology and Evolution*, **35**, 1366–1371.

- Ketting, R.F. (2011). The many faces of RNAi. *Developmental Cell*, **20**, 148–161.
- Kim, K.-W., Jackson, B.C., Zhang, H., et al. (2018). Black or red: A sex-linked colour polymorphism in a song bird is maintained by balancing selection. *BioRxiv*. doi: <http://dx.doi.org/10.1101/437111>
- Kimura, M. (1968). Evolutionary rate at the molecular level. *Nature*, **217**, 624–626.
- Kimura, M. (1983). *The Neutral Theory of Molecular Evolution*. Cambridge University Press, Cambridge, UK.
- King, J.L. and Jukes, T.H. (1969). Non-Darwinian evolution. *Science*, **164**, 788–798.
- Kingman, J.F.C. (1982a). On the genealogy of large populations. *Journal of Applied Probability*, **19**, 27–43.
- Kingman, J.F.C. (1982b). The coalescent. *Stochastic Processes and their Applications*, **13**, 235–248.
- Kingman, J.F.C. (2000). Origins of the coalescent 1974–1982. *Genetics*, **156**, 1461–1463.
- Kirk, G.S., Raven, J.E., and Schofield, M. (1983). *The Presocratic Philosophers—A Critical History with a Selection of Texts, 2nd edition*. Cambridge University Press, Cambridge, UK.
- Kirkpatrick, M. (1982). Sexual selection and the evolution of female choice. *Evolution*, **36**, 1–12.
- Kirkpatrick, M. (2010). How and why chromosomal inversions evolve. *PLoS One*, **8**, e1000501.
- Kitano, J., Bolnick, D.I., Beauchamp, D.A., et al. (2008). Reverse evolution of armor plates in the threespine stickleback. *Current Biology*, **18**, 769–774.
- Knowles, D.G. and McLysaght, A. (2009). Recent *de novo* origin of human protein-coding genes. *Genome Research*, **19**, 1752–1759.
- Knowles, L.L. (2009). Statistical phylogeography. *Annual Reviews of Ecology, Evolution, and Systematics*, **40**, 593–612.
- Kohn, M.H., Murphy, W.J., Ostrander, E.A., and Wayne, R.K. (2006). Genomics and conservation genetics. *Trends in Ecology & Evolution*, **21**, 629–637.
- Kohne, D.E. (1970). Evolution of higher-organism DNA. *Quarterly Review of Biophysics*, **3**, 327–375.
- Kondrashov, A. (1988). Deleterious mutations and the evolution of sexual reproduction. *Nature*, **336**, 435–440.
- Koonin, E.V. (2006). The origin of introns and their role in eukaryogenesis: a compromise solution to the intron-early versus introns-late debate? *Biology Direct*, **1**, 22.
- Koonin, E.V., Krupovic, M., and Yutin, N. (2015). Evolution of double-stranded DNA viruses of eukaryotes: from bacteriophages to transposons to giant viruses. *Annals of the New York Academy of Sciences*, **1341**, 10–24.
- Kubatko, L.S. and Degnan, J.H. (2007). Inconsistency of phylogenetic estimates from concatenated data under coalescence. *Systematic Biology*, **56**, 17–24.
- Kucharski, R., Maleszka, J., Foret, S., and Maleszka, R. (2008). Nutritional control of reproductive status in honeybees via DNA methylation. *Science*, **319**, 1827–1830.
- Küpper, C., Stocks, M., Risse, J.E., et al. (2016). A supergene determines highly divergent male reproductive morphs in the ruff. *Nature Genetics*, **48**, 79–83.
- Kusakabe, M., Ishikawa, A., Ravinet, M., et al. (2017). Genetic basis for variation in salinity tolerance between stickleback ecotypes. *Molecular Ecology*, **26**, 304–319.
- Kylafis, G. and Loreau, M. (2008). Ecological and evolutionary consequences of niche construction for its agent. *Ecology Letters*, **11**, 1072–1081.
- Kyriacou, C.P., Peixoto, A.A., Sandrelli, F., Costa, R., and Tauber, E. (2008). Clines in clock genes: fine tuning circadian rhythms to the environment. *Trends in Genetics*, **24**, 124–132.
- Kyrou, K., Hammond, A.M., Galizi, R., et al. (2018). A CRISPR–Cas9 gene drive targeting doublesex causes complete population suppression in caged *Anopheles gambiae* mosquitoes. *Nature Biotechnology*, **36**, 1062–1066.
- Laird, C.D., McConaughy, B.L., and McCarthy, B.J. (1969). Rate of fixation of nucleotide substitutions in evolution. *Nature*, **224**, 149–154.
- Lamarck, J.B.P.A.M. (1809). *Zoological Philosophy: An Exposition with Regard to the Natural History of Animals*. Reprint 2012, Cornell University Library Digital Collections.
- Lambert, J.C., Heath, S., Even, G., et al. (2009). Genome-wide association study identifies variants at CLU and CR1 associated with Alzheimer's disease. *Nature Genetics*, **41**, 1094–1099.
- Lamichhaney, S., Berglund, J., Almén, M.S., et al. (2015). Evolution of Darwin's finches and their beaks revealed by genome sequencing. *Nature*, **518**, 371–375.
- Lamichhaney, S., Fan, G., Widemo, F., et al. (2016). Structural genomic changes underlie alternative reproductive strategies in the ruff (*Philomachus pugnax*). *Nature Genetics*, **48**, 84–88.
- Lande, R. (1981). Models of speciation by sexual selection on polygenic traits. *Proceedings of the National Academy of Sciences of the USA*, **78**, 3721–3725.
- Lander, E.S., Linton, L.M., Birren, B., et al. (2001). Initial sequencing and analysis of the human genome. *Nature*, **409**, 860–921.
- Langer, D., Hain, J., Thuriaux, P., and Zillig, W. (1995). Transcription in archaea: similarity to that in eukarya. *Proceedings of the National Academy of Sciences of the USA*, **92**, 5768–5772.
- Langerhans, B.R. and DeWitt, T.J. (2002). Plasticity constrained: over-generalized induction cues cause maladaptive phenotypes. *Evolutionary Ecology Research*, **4**, 857–870.
- Larracuent, A.M. and Presgraves, D.C. (2012). The selfish segregation distorter gene complex of *Drosophila melanogaster*. *Genetics*, **192**, 33–53.

- Lawson, D.J., Hellenthal, G., Myers, S., and Falush, D. (2012). Inference of population structure using dense haplotype data. *PLoS Genetics*, **8**, e1002453–16.
- Lemmon, E.M. and Lemmon, A.R. (2013). High-throughput genomic data in systematics and phylogenetics. *Annual Review of Ecology, Evolution, and Systematics*, **44**, 99–121.
- Leonard, W.R., Snodgrass, J.J., and Robertson, M.L. (2007). Effects of brain evolution on human nutrition and metabolism. *Annual Review of Nutrition*, **27**, 311–327.
- Leslie, S., Winney, B., Hellenthal, G., et al. (2015). The fine-scale genetic structure of the British population. *Nature*, **519**, 309–314.
- Levene, P.A. (1917). The structure of yeast nucleic acid. *Journal of Biological Chemistry*, **31**, 591–598.
- Lewontin, R.C. (1964). The interaction of selection and linkage I. General considerations; heterotic models. *Genetics*, **49**, 49–67.
- Lewontin, R.C. and Kojima, K.-I. (1960). The evolutionary dynamics of complex polymorphisms. *Evolution*, **14**, 458–472.
- Lewontin, R.C. and Krakauer, J. (1973). Distribution of gene frequency as a test of the theory of the selective neutrality of polymorphisms. *Genetics*, **74**, 175–195.
- Lexer, C., Welch, M.E., Durphy, J.L., and Rieseberg, L.H. (2003). Natural selection for salt tolerance quantitative trait loci (QTLs) in wild sunflower hybrids: implications for the origin of *Helianthus paradoxus*, a diploid hybrid species. *Molecular Ecology*, **12**, 1225–1235.
- Librado, P., Fages, A., Gaunitz, C., et al. (2016). The evolutionary origin and genetic makeup of domestic horses. *Genetics*, **204**, 423–434.
- Librado, P., Gamba, C., Gaunitz, C., et al. (2017). Ancient genomic changes associated with domestication of the horse. *Science*, **356**, 442–445.
- Lifshytz, E. and Lindsley, D.L. (1972). The role of X-chromosome inactivation during spermatogenesis. *Proceedings of the National Academy of Sciences of the USA*, **69**, 182–186.
- Lindblad-Toh, K., Wade, C.M., Mikkelsen, T.S., et al. (2005). Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature*, **438**, 803–819.
- Linn, C., Jr, Feder, J.L., Nojima, S., Dambroski, H.R., Berlocher, S.H., and Roelofs, W. (2003). Fruit odor discrimination and sympatric host race formation in *Rhagoletis*. *Proceedings of the National Academy of Sciences of the USA*, **100**, 11490–11493.
- Long, T.A.F., Pischedda, A., Stewart, A.D., and Rice, W.R. (2009). A cost of sexual attractiveness to high-fitness females. *PLoS Biology*, **7**, e1000254.
- Lotterhos, K.E. and Whitlock, M.C. (2014). Evaluation of demographic history and neutral parameterization on the performance of F_{ST} outlier test. *Molecular Ecology*, **23**, 2178–2192.
- Lowry, D.B. and Willis, J.H. (2010). A widespread chromosomal inversion polymorphism contributes to a major life history transition, local adaptation, and reproductive isolation. *PLoS Biology*, **8**, e1000500.
- Luce, R.D. and Raiffa, H. (1957). *Games and Decisions; Introduction and Critical Survey*. Wiley, New York, USA.
- Lumley, A.J., Michalczyk, L., Kitson, J.J.N., et al. (2015). Sexual selection protects against extinction. *Nature*, **522**, 470–473.
- Lush, J.L. (1937). *Animal Breeding Plans*. Iowa State College Press, Ames, Iowa, USA.
- Lynch, M. (2010). Evolution of the mutation rate. *Trends in Genetics*, **28**, 345–352.
- Lynch, M., Ackerman, M.S., Gout, J.-F., et al. (2016). Genetic drift, selection and the evolution of the mutation rate. *Nature Reviews Genetics*, **17**, 704–714.
- MacHugh, D.E., Larson, G., and Orlando, L. (2017). Taming the past: ancient DNA and the study of animal domestication. *Annual Review of Animal Biosciences*, **5**, 329–351.
- Maddison, W.P. (1997). Gene trees in species trees. *Systematic Biology*, **46**, 523–536.
- Maher, B. (2008). Personal genomes: The case of missing heritability. *Nature*, **456**, 18–21.
- Mallet, J. (1989). The evolution of insecticide resistance: Have the insects won? *Trends in Ecology & Evolution*, **11**, 336–340.
- Mallet, J. (1995). A species definition for the Modern Synthesis. *Trends in Ecology & Evolution*, **10**, 294–299.
- Mallet, J. (2007). Hybrid speciation. *Nature*, **446**, 279–283.
- Man, P.Y.W., Turnbull, D.M., and Chinnery, P.F. (2002). Leber hereditary optic neuropathy. *Journal of Medical Genetics*, **39**, 162–169.
- Mank, J.E., Vicoso, B., Berlin, S., and Charlesworth, B. (2010). Effective population size and the faster-X effect. Empirical results and their interpretation. *Evolution*, **64**, 663–674.
- Manolio, T.A., Collins, F.S., Cox, N.J., et al. (2010). Finding the missing heritability of complex diseases. *Nature*, **461**, 747–753.
- Marchini, J., Cutler, D., Patterson, N., et al. (2006). A comparison of phasing algorithms for trios and unrelated individuals. *American Journal of Human Genetics*, **78**, 437–450.
- Marchini, J., Howie, B., Myers, S., McVean, G., and Donnelly, P. (2007). A new multipoint method for genome-wide association studies by imputation of genotypes. *Nature Genetics*, **39**, 906–913.
- Marchinko, K.B. and Schluter, D. (2007). Parallel evolution by correlated response: lateral plate reduction in threespine stickleback. *Evolution*, **61**, 1084–1090.

- Marcussen, T., Heier, L., Brysting, A.K., Oxelman, B., and Jakobsen, K.S. (2014). From gene trees to dated allopolyploid network: insights from the Angiosperm genus *Viola* (Violaceae). *Systematic Biology*, **64**, 84–101.
- Mardis, E.R. (2008). Next-generation DNA sequencing methods. *Annual Review of Genomics and Human Genetics*, **9**, 387–402.
- Marett, L., Jensen, J.M., Petersen, B., et al. (2017). Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. *Nature*, **548**, 87–91.
- Margulis, L. (1970). *Origin of Eukaryotic cells: Evidence and Research Implications for a Theory of the Origin and Evolution of Microbial, Plant, and Animal Cells on the Precambrian Earth*. New Haven, London.
- Marler, P. and Peters, S. (1977). Selective vocal learning in a sparrow. *Science*, **198**, 519–521.
- Marruffini, L.A. and Sontheimer, E.J. (2010). CRISPR interference: RNA-directed adaptive immunity in bacteria and archaea. *Nature Reviews Genetics*, **11**, 181–190.
- Marshall, J.A.R. (2011). Group selection and kin selection: formally equivalent approaches. *Trends in Ecology & Evolution*, **26**, 325–332.
- 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**, 1817–1828.
- Martin, S.H., Davey, J.W., and Jiggins, C.D. (2014). Evaluating the use of ABBA–BABA statistics to locate introgressed loci. *Molecular Biology and Evolution*, **32**, 244–257.
- Mason, A.S. and Pires, J.C. (2015). Unreduced gametes: meiotic mishap or evolutionary mechanism? *Trends in Genetics*, **31**, 5–10.
- Matute, D.R. (2010). Reinforcement of gametic isolation in *Drosophila*. *PLoS Biology*, **8**, e1000341.
- Mavárez, J., Salazar, C.A., Bermingham, E., Salcedo, C., Jiggins, C.D., and Linares, M. (2006). Speciation by hybridization in *Heliconius* butterflies. *Nature*, **441**, 868–871.
- Maynard Smith, J. (1964). Group selection and kin selection. *Nature*, **201**, 1145–1147.
- Maynard Smith, J. (1978). *The Evolution of Sex*. Cambridge University Press, Cambridge, UK.
- Maynard Smith, J. (1982). *Evolution and the Theory of Games*. Cambridge University Press, Cambridge, UK.
- Maynard Smith, J. (1989). *Evolutionary Genetics*. Oxford University Press, Oxford, UK.
- Maynard Smith, J. and Price, G.R. (1973). The logic of animal conflict. *Nature*, **246**, 15–18.
- Mayr, E. (1942). *Systematics and the Origin of Species*. Columbia University Press, New York, USA.
- Mayr, E. (1954). Change of genetic environment and evolution. In: J. Huxley, A.C. Hardy, E.B. Ford (eds) *Evolution as a Process*, pp 157–180. Allen & Unwin, London, UK.
- Mayr, E. (1982). *The Growth of Biological Thought: Diversity, Evolution and Inheritance*. The Belknap Press of Harvard University Press, Cambridge, MA, USA.
- McCauley, D.E. (2013). Paternal leakage, heteroplasmy, and the evolution of plant mitochondrial genomes. *New Phytologist*, **200**, 966–977.
- McClintock, B. (1950). The origin and behavior of mutable loci in maize. *Proceedings of the National Academy of Sciences of the USA*, **36**, 344–355.
- McCormack, J.E., Harvey, M.G., Faircloth, B.C., et al. (2013). A phylogeny of birds based on over 1,500 loci collected by target enrichment and high-throughput sequencing. *PLoS One*, **8**, e54848–11.
- McCutcheon, J.P. and Moran, N.A. (2012). Extreme genome reduction in symbiotic bacteria. *Nature Reviews Microbiology*, **10**, 13–26.
- McDonald, J.H. and Kreitman, M. (1991). Adaptive protein evolution at the *Adh* locus in *Drosophila*. *Nature*, **351**, 652–654.
- McKinnon, J.S. and Rundle, H.D. (2002). Speciation in nature: the threespine stickleback model systems. *Trends in Ecology & Evolution*, **17**, 480–488.
- McLysaght, A., Hokamp, K., and Wolfe, K.H. (2002). Extensive genomic duplication during early chordate evolution. *Nature Genetics*, **31**, 200–204.
- Mehdiabadi, N.J. and Schultz, T.R. (2010). Natural history and phylogeny of the fungus-farming ants (Hymenoptera: Formicidae: Myrmicinae: Attini). *Myrmecological News*, **13**, 37–55.
- Meier, J.I., Marques, D.A., Mwaiko, S., Wagner, C.E., Excoffier, L., and Seehausen, O. (2017b). Ancient hybridization fuels rapid cichlid fish adaptive radiations. *Nature Communications*, **8**, 14363.
- Meier, J.I., Marques, D.A., Wagner, C.E., Excoffier, L., and Seehausen, O. (2018). Genomics of parallel ecological speciation in Lake Victoria cichlids. *Molecular Biology and Evolution*, **35**, 1489–1506.
- Meier, J.I., Sousa, V.C., Marques, D.A., et al. (2017a). Demographic modelling with whole-genome data reveals parallel origin of similar *Pundamilia* cichlid species after hybridization. *Molecular Ecology*, **26**, 123–141.
- Meier, J.I., Vranken, N., Marques, D.A., et al. (2017c). Ancient hybridization fuels rapid cichlid fish adaptive radiations. *Nature Communications*, **8**, 14363.
- Meltz Steinberg, K., Schneider, V.A., and Church, D.M. (2017). Building and improving reference genome assemblies. *Proceedings of the IEEE*, **105**, 422–435.
- Mendel, G. (1865). *Versuche über Pflanzenhybriden—Zwei Abhandlungen, 1865*. Classic Reprint Series, Forgotten Books, London.
- Menzio, P., Piazza, A., and Cavalli-Sforza, L. (1978). Synthetic maps of human gene frequencies in Europeans. *Science*, **201**, 786–792.

- Metzker, M.L. (2010). Sequencing technologies—the next generation. *Nature Reviews Genetics*, **11**, 31–46.
- Meyer, C.A. and Liu, X.S. (2014). Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. *Nature Reviews Genetics*, **15**, 709–721.
- Michel, A.P., Sim, S., Powell, T.H.Q., Taylor, M.S., Nosil, P., and Feder, J.L. (2010). Widespread genomic divergence during sympatric speciation. *Proceedings of the National Academy of Sciences of the USA*, **107**, 9724–9729.
- Michod, R.E. (2007). Evolution of individuality during the transition from unicellular to multicellular life. *Proceedings of the National Academy of Sciences of the USA*, **104**, 8613–8618.
- Mills, R.E., Luttig, C.T., Larkins, C.E., Beauchamp, A., Tsui, C., Pittard, W.S., Devine, S.W. (2006). An initial map of insertion and deletion (INDEL) variation in the human genome. *Genome Research*, **16**, 1182–1190.
- Misof, B., Liu, S., Meusemann, K., et al. (2014). Phylogenomics resolves the timing and pattern of insect evolution. *Science*, **346**, 763–767.
- Mock, D.W. and Parker, G.A. (1997). *The Evolution of Sibling Rivalry*. Oxford Series in Ecology and Evolution, Oxford University Press, Oxford, UK.
- Moran, J.V., DeBerardinis, R.J., and Kazazian, H.H., Jr (1999). Exon shuffling by L1 retrotransposition. *Science*, **283**, 1530–1534.
- Morgan, L.T., Schmidt, O.G., Gelarden, I.A., Parrish, II, R.C., and Lively, C.M. (2011). Running with the Red Queen: Host-parasite coevolution selects for biparental sex. *Science*, **333**, 216–218.
- Morgan, T.H. (1911). The origin of five mutations in eye color in *Drosophila* and their modes of inheritance. *Science*, **33**, 534–537.
- Morgan, T.H., Sturtevant, A.H., Muller, H.J., and Bridges, C.B. (1915). *The Mechanism of Mendelian Heredity*. Henry Holt and Company, New York, USA.
- Morgante, M., Brunner, S., Pea, G., et al. (2005). Gene duplication and exon shuffling by helitron-like transposons generate intraspecies diversity in maize. *Nature Genetics*, **37**, 997–1002.
- Morozova, O., Hirst, M., and Marra, M.A. (2009). Applications of new sequencing technologies for transcriptome analysis. *Annual Review of Genomics and Human Genetics*, **10**, 135–151.
- Mueller, U.G., Gerardo, N.M., Aanen, D.K., Six, D.L., and Schultz, T.R. (2005). The evolution of agriculture in insects. *Annual Review of Ecology, Evolution, and Systematics*, **36**, 563–595.
- Müller, F. (1878). Über die Vortheile der Mimicry bei Schmetterlingen. *Zoologischer Anzeiger*, **1**, 54–55.
- Muller, H.J. (1932). Some genetic aspects of sex. *American Naturalist*, **66**, 118–138.
- Muller, H.J. (1940). Bearing of the *Drosophila* work on systematics. In: J. Huxley (ed.) *The New Systematics*, pp. 185–268. Clarendon Press, Oxford, UK.
- Muller, H.J. (1964). The relation of recombination to mutational advance. *Mutation Research*, **1**, 2–9.
- Myhre, F. and Klepaker, T. (2009). Body armour and lateral-plate reduction in freshwater three-spined stickleback *Gasterosteus aculeatus*: adaptations to a different buoyancy regime? *Journal of Fish Biology*, **75**, 2062–2074.
- Nachman, M.W. (2001). Single nucleotide polymorphisms and recombination rate in humans. *Trends in Genetics*, **17**, 481–485.
- Nachman, M.W., Hoekstra, H.E., D'Agostino, S.L. (2003). The genetic basis of adaptive melanism in pocket mice. *Proceedings of the National Academy of Sciences of the USA*, **100**, 5268–5273.
- Nadachowska-Brzyska, K., Burri, R., Olason, P.I., et al. (2013). Demographic divergence history of pied flycatcher and collared flycatcher inferred from whole-genome re-sequencing data. *PLoS Genetics*, **9**, e1003942–14.
- Nagarajan, N. and Pop, M. (2013). Sequence assembly demystified. *Nature Reviews Genetics*, **14**, 157–167.
- Naisbit, R.E., Jiggins, C.D., and Mallet, J. (2001). Disruptive sexual selection against hybrids contributes to speciation between *Heliconius cydno* and *Heliconius melpomene*. *Proceedings of the Royal Society B*, **268**, 1849–1854.
- Nakayama, H., Nakayama, N., Seiki, S., et al. (2014). Regulation of the KNOX-GA gene module induces heterophyllic alteration in North American lake cress. *The Plant Cell*, **26**, 4733–4748.
- Narasimhan, V.M., Rahbari, R., Scally, A., et al. (2017). Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. *Nature Communications*, **8**, 303.
- Nei, M. (1987). *Molecular Evolutionary Genetics*. Columbia University Press, New York, USA.
- Nei, M. and Li, W.-H. (1979). Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences of the USA*, **76**, 5269–5273.
- Nelson, K.E., Clayton, R.A., Gill, S.R., et al. (1999). Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*. *Nature*, **399**, 323–329.
- Nicotra, A.B., Atkin, O.K., Bonser, S.P., et al. (2010). Plant phenotypic plasticity in a changing climate. *Trends in Plant Science*, **15**, 684–692.
- Nielsen, R., Akey, J.M., Jakobsson, M., et al. (2017). Tracing the peopling of the world through genomics. *Nature*, **541**, 302–310.
- Noonan, J.P., Coop, G., Kudaravalli, S., et al. (2006). Sequencing and analysis of Neanderthal genomic DNA. *Science*, **314**, 1113–1118.

- Noor, M.A.F. and Bennett, S.M. (2009). Islands of speciation or mirages in the desert? Examining the role of restricted recombination in maintaining species. *Heredity*, **103**, 439–444.
- Nosil, P. (2012). *Ecological Speciation*. Oxford Series in Ecology and Evolution. Oxford University Press, Oxford, UK.
- Nosil, P., Funk, D.J., and Ortiz-Barrientos, D. (2009). Divergent selection and heterogeneous genomic divergence. *Molecular Ecology*, **18**, 375–402.
- Novembre, J. and Di Rienzo, A. (2009). Spatial patterns of variation due to natural selection in humans. *Nature Reviews Genetics*, **10**, 745–755.
- Novembre, J., Johnson, T., Bryc, K., et al. (2008). Genes mirror geography within Europe. *Nature*, **456**, 98–101.
- Novembre, J. and Stephens, M. (2008). Interpreting principal component analyses of spatial population genetic variation. *Nature Genetics*, **40**, 646–649.
- Nowak, M.A., Tarnita, C.E., and Wilson, E.O. (2010). The evolution of eusociality. *Nature*, **466**, 1057–1062.
- O'Brien, S.J., Haussler, D., and Ryder, O. (2014). The birds of Genome10K. *GigaScience*, **3**, 1214–1215.
- O'Brown, N.M., Summers, B.R., Jones, F.C., Brady, S.D., and Kingsley, D.M. (2015). A recurrent regulatory change underlying altered expression and Wnt response of the stickleback armor plates gene *EDA*. *eLife*, **4**, e05290.
- O'Connell, J., Gurdasani, D., Delaneau, O., et al. (2014). A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **10**, e1004234–21.
- O'Dea, A., Lessios, H.A., Coates, A.G., et al. (2016). Formation of the Isthmus of Panama. *Science Advances*, **2**, e1600883.
- O'Donovan, M.C. (1993). A novel gene containing a trinucleotide repeat that is expanded and unstable on Huntington's disease chromosomes. *Cell*, **72**, 971–983.
- Obbard, D.J., Gordon, K.H.J., Buck, A.H., and Jiggins, F.M. (2009). The evolution of RNAi as a defense against viruses and transposable elements. *Philosophical Transactions of the Royal Society B*, **364**, 99–115.
- Ohno, S. (1970). *Evolution by Gene Duplication*. Springer-Verlag, New York, USA.
- Ohta, T. (1973). Slightly deleterious mutant substitutions in evolution. *Nature*, **246**, 96–98.
- Orlando, L., Gilbert, M.T.P., and Willerslev, E. (2015). Reconstructing ancient genomes and epigenomes. *Nature Reviews Genetics*, **16**, 395–408.
- Orr, H.A. (1996). Dobzhansky, Bateson, and the genetics of speciation. *Genetics*, **144**, 1331–1335.
- Otto, S.P. and Whitton, J. (2000). Polyploid incidence and evolution. *Annual Review of Genetics*, **34**, 401–437.
- Owens, I.P.F., Bennet, P.M., and Harvey, P.H. (1999). Species richness among birds: body size, life history, sexual selection or ecology? *Proceedings of the Royal Society B*, **266**, 933–939.
- Ozsolak, F. and Milos, P.M. (2010). RNA sequencing: advances, challenges and opportunities. *Nature Reviews Genetics*, **12**, 87–98.
- Pääbo, S. (1985). Molecular-cloning of ancient Egyptian mummy DNA. *Nature*, **314**, 644–645.
- Pace, N.R. (2006). Time for a change. *Nature*, **441**, 289.
- Page, R. and Holmes, E.C. (1998). *Molecular Evolution: A Phylogenetic Approach*. Blackwell Publishing, Oxford, UK.
- Palacio-López, K., Beckage, B., Scheiner, S., and Molofsky, J. (2015). The ubiquity of phenotypic plasticity in plants: a synthesis. *Ecology & Evolution*, **5**, 3389–3400.
- Palopoli, M.F. (2000). Genetic partners in crime: Evolution of an ultraselfish supergene that specializes in sperm sabotage. In: J.B. Wolf, E.D. Brodie III, and M.J. Wade (eds) *Epistasis and the Evolutionary Process*. Oxford University Press, New York, USA.
- Palumbi, S.R. (1998). Species formation and the evolution of gamete recognition loci. In: D.J. Howard and S.F. Berlocher (eds), *Endless Forms: Species and Speciation*, pp 271–278. Oxford University Press, Oxford, UK.
- Panhuis, T.M., Butlin, R., Zuk, M., and Tregenza, T. (2001). Sexual selection and speciation. *Trends in Ecology & Evolution*, **16**, 364–371.
- Pardo-Diaz, C., Salazar, C., Baxter, S.W., et al. (2012). Adaptive introgression across species boundaries in *Heliconius* butterflies. *PLoS Genetics*, **8**, e1002752.
- Park, P.J. (2009). ChIP-seq: advantages and challenges of a maturing technology. *Nature Reviews Genetics*, **10**, 669–680.
- Parker, G.A. (1970). Sperm competition and its evolutionary consequence in the insects. *Biological Reviews*, **45**, 525–567.
- Paten, B., Novak, A.M., Eizenga, J.M., and Garrison, E. (2017). Genome graphs and the evolution of genome inference. *Genome Research*, **27**, 665–676.
- Patterson, N., Price, A.L., and Reich, D. (2006). Population structure and eigenanalysis. *PLoS Genetics*, **2**, e190.
- Patthy, L. (1999). Genome evolution and the evolution of exon-shuffling—a review. *Gene*, **238**, 103–114.
- Payseur, B.A., Peicheng, J., and Haasl, R.J. (2011). A genomic portrait of human microsatellite variation. *Molecular Biology and Evolution*, **28**, 303–312.
- Payseur, B.A., Presgraves, D.C., and Filatov, D.A. (2018). Sex chromosomes and speciation. *Molecular Ecology*, **27**, 3745–3748.
- Peichel, C.L., Nereng, K.S., Ohgi, K.A., et al. (2001). The genetic architecture of divergence between threespine stickleback species. *Nature*, **414**, 901–905.
- Pellicer, J., Fay, M.F., and Leitch, I.J. (2010). The largest eukaryotic genome of them all? *Botanical Journal of the Linnean Society*, **164**, 10–15.
- Pérez-Palma, E., Bustos, B.I., Villamán, C.F., et al. (2014). Overrepresentation of glutamate signaling in Alzheimer's disease: network-based pathway enrichment using

- meta-analysis of genome-wide association studies. *PLoS One*, **9**, e95413.
- Pfennig, D.W. and Pfennig, K.S. (2012). Development and evolution of character displacement. *Annals of the New York Academy of Sciences*, **1256**, 89–107.
- Pfenniger, M. and Schwenk, K. (2007). Cryptic animal species are homogeneously distributed among taxa and biogeographical regions. *BMC Evolutionary Biology*, **7**, 121.
- Phadnis, N. and Orr, H.A. (2009). A single gene causes both male sterility and segregation distortion in *Drosophila* hybrids. *Science*, **323**, 376–379.
- Phillips, P.C. (2008). Epistasis—the essential role of gene interactions in the structure and evolution of genetic systems. *Nature Reviews Genetics*, **9**, 855–867.
- Poelstra, J.W., Vijay, N., Bossu, C.M., et al. (2014). The genomic landscape underlying phenotypic integrity in the face of gene flow in crows. *Science*, **344**, 1410–1414.
- Poelstra, J.W., Vijay, N., Hoepfner, M.P., and Wolf, J.B.W. (2015). Transcriptomics of colour patterning and coloration shifts in crows. *Molecular Ecology*, **24**, 4617–4628.
- Pop, M. (2009). Genome assembly reborn: recent computational challenges. *Briefings in Bioinformatics*, **10**, 354–366.
- Posada, D. and Crandall, K. (2001). Intraspecific gene genealogies: trees grafting into networks. *Trends in Ecology & Evolution*, **16**, 37–45.
- Poulter, M., Hollox, E., Harvey, C.B., et al. (2003). The causal element for the lactase persistence/non-persistence polymorphism is located in a 1 Mb region of linkage disequilibrium in Europeans. *Annals of Human Genetics*, **67**, 298–311.
- Prangishvili, D., Albers, S.-V., Holz, S., et al. (1998). Conjugation in Archaea: frequent occurrence of conjugative plasmids in *Sulfolobus*. *Plasmid*, **40**, 190–202.
- Presgraves, D.C. (2008). Sex chromosomes and speciation in *Drosophila*. *Trends in Genetics*, **24**, 336–343.
- Presgraves, D.C. (2010). The molecular evolutionary basis of species formation. *Nature Reviews Genetics*, **11**, 175–180.
- Price, T.D., Qvarnström, A., and Irwin, D.E. (2003). The role of phenotypic plasticity in driving genetic evolution. *Proceedings of the Royal Society B*, **270**, 1433–1440.
- Pritchard, J.K., Stephens, M., and Donnelly, P. (2000). Inference of population structure using multilocus genotype data. *Genetics*, **155**, 945–959.
- Provan, J. and Bennett, K. (2008). Phylogeographic insights into cryptic glacial refugia. *Trends in Ecology & Evolution*, **23**, 564–571.
- Prum, R.O., Berv, J.S., Dornburg, A., et al. (2015). A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. *Nature*, **526**, 569–573.
- Pryke, S. (2010). Sex chromosome linkage of mate preference and color signal maintains assortative mating between interbreeding finch morphs. *Evolution*, **64**, 1301–1310.
- Pusey, A.E. (1987). Sex-biased dispersal and inbreeding avoidance in birds and mammals. *Trends in Ecology & Evolution*, **2**, 295–299.
- Quinn, G.P. and Keough, M.J. (2002). *Experimental Design and Data Analysis for Biologists*. Cambridge University Press, Cambridge, UK.
- Qvarnström, A. and Bailey, R.I. (2009). Speciation through linkage of sex-linked genes. *Heredity*, **102**, 4–15.
- Racimo, F., Sankararaman, S., Nielsen, R., and Huerta-Sánchez, E. (2015). Evidence for archaic adaptive introgression in humans. *Nature Reviews Genetics*, **16**, 359–371.
- Raeymaekers, J.A.M., van Houdt, J.K.J., Larmuseau, M.H.D., Geldof, S., Volckaert, F.A.M. (2006). Divergent selection as revealed by P_{ST} and QTL-based F_{ST} in three-spined stickleback (*Gasterosteus aculeatus*) populations along a coastal-inland gradient. *Molecular Ecology*, **16**, 891–905.
- Raeymaekers, J.A.M., Konijnendijk, N., Larmuseau, M.H.D., Hellemans, B., De Meester, L., and Volckaert, F.A.M. (2014). A gene with major phenotypic effects as a target for selection vs. homogenizing gene flow. *Molecular Ecology*, **23**, 162–181.
- Rand, D.M. and Kann, L.M. (1996). Excess amino acid polymorphism in mitochondrial DNA: Contrasts among genes from *Drosophila*, mice, and humans. *Molecular Biology and Evolution*, **13**, 735–748.
- Randler, C. (2007). Assortative mating of carrion *Corvus corone* and hooded crows *C. cornix* in the hybrid zone in Eastern Germany. *Ardea*, **95**, 143–149.
- Rannala, B. and Yang, Z. (2008). Phylogenetic inference using whole genomes. *Annual Review of Genomics and Human Genetics*, **9**, 217–231.
- Ravindran, P. (2012). Barbara McClintock and the discovery of jumping genes. *Proceedings of the National Academy of Sciences of the USA*, **109**, 20198–20199.
- Ravinet, M., Elgvin, T.O., Trier, C.N., Aliabadian, M., Gavilov, A., and Sætre, G.-P. (2018b). Signatures of human-commensalism in the house sparrow genome. *Proceedings of the Royal Society B*, **285**, 20181246.
- Ravinet, M., Faria, R., Butlin, R.K., et al. (2017). Interpreting the genomic landscape of speciation: a road map for finding barriers to gene flow. *Journal of Evolutionary Biology*, **30**, 1450–1477.
- Ravinet, M., Hynes, R., Poole, R., et al. (2015). Where the lake meets the sea: strong reproductive isolation is associated with adaptive divergence between lake resident and anadromous three-spined sticklebacks. *PLoS One*, **10**, e0122825.
- Ravinet, M., Westram, A., Johannesson, K., Butlin, R., André, C., Panova, M. (2016). Shared and nonshared genomic divergence in parallel ecotypes of *Littorina saxatilis* at a local scale. *Molecular Ecology*, **25**, 287–305.
- Ravinet, M., Yoshida, K., Shigenobu, S., Toyoda, A., Fujiyama, A., and Kitano, J. (2018a). The genomic

- landscape at a late stage of stickleback speciation: High genomic divergence interspersed by small localized regions of introgression. *PLoS Genetics*, **14**, e1007358.
- Reich, D., Green, R.E., Kircher, M., et al. (2010). Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature*, **468**, 1053–1060.
- Reiley, M.T., Faulkner, G.J., Dubnau, J., Ponomarev, I., and Gage, F.H. (2013). The role of transposable elements in health and diseases of the central nervous system. *Journal of Neuroscience*, **33**, 17577–17586.
- Repping, S., Skaletsky, H., Brown, L., et al. (2003). Polymorphism for a 1.6-Mb deletion of the human Y chromosome persists through balance between recurrent mutation and haploid selection. *Nature Genetics*, **35**, 247–251.
- Rice, S.H. (2004). *Evolutionary Theory—Mathematical and Conceptual Foundations*. Sinauer Associates, Sunderland, MA, USA.
- Rice, W.A. (1996). Sexually antagonistic male adaptation triggered by experimental arrest of female evolution. *Nature*, **361**, 232–234.
- Rice, W.A. and Holland, B. (1997). The enemies within: intergenomic conflict, interlocus contest evolution (ICE) and the intraspecific red queen. *Behavioral Ecology and Sociobiology*, **41**, 1–10.
- Riesch, R., Muschick, M., and Lindke, D. (2017). Transitions between phases of genomic differentiation during stick-insect speciation. *Nature Ecology & Evolution*, **1**, 0082.
- Rieseberg, L.H. (1991). Homoploid reticulate evolution in *Helianthus* (Asteraceae): evidence from ribosomal genes. *American Journal of Botany*, **78**, 1218–1237.
- Rieseberg, L.H., Raymond, O., Rosenthal, D.M., et al. (2003). Major ecological transitions in wild sunflowers facilitated by hybridization. *Science*, **301**, 1211–1216.
- Rieseberg, L.H. and Willis, J.H. (2007). Plant speciation. *Science*, **317**, 910–914.
- Riyahi, S., Hammer, Ø., Arbabi, T., et al. (2013). Beak and skull shapes of human commensal and non-commensal house sparrows *Passer domesticus*. *BMC Evolutionary Biology*, **13**, 200.
- Robertson, H.M. and Paterson, H.E.H. (1982). Mate recognition and mechanical isolation in *Enallagma* damselflies (Odonata: Coenagrionidae). *Evolution*, **36**, 243–250.
- Rockman, M.V. (2012). The QTN program and the alleles that matter for evolution: all that's gold does not glitter. *Evolution*, **66**, 1–17.
- Roesti, M., Hendry, A.P., Salzburger, W., and Berner, D. (2012). Genome divergence during evolutionary diversification as revealed in replicate lake-stream stickleback population pairs. *Molecular Ecology*, **21**, 2852–2862.
- Rokas, A. and Abbot, P. (2009). Harnessing genomics for evolutionary insights. *Trends in Ecology & Evolution*, **24**, 192–200.
- Rolán-Alvarez, E., Johannesson, K., and Erlandsson, J. (1997). The maintenance of a cline in the marine snail *Littorina saxatilis*: The role of home site advantage and hybrid fitness. *Evolution*, **51**, 1838–1847.
- Ronquist, F., van der Mark, P., and Huelsenbeck, J. (2009). Bayesian phylogenetic analysis using MrBayes. In: P. Lemey, M. Salemi, and A.-M. Vandamme (eds) *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*, pp. 210–265. Cambridge University Press, Cambridge, UK.
- Rowe, L., Chenoweth, S.F., and Agrawal, A.F. (2018). The genomics of sexual conflict. *American Naturalist*, **192**, 274–286.
- Rudkin, D.M., Young, G.A., and Nowlan, G.S. (2008). The oldest horseshoe crab: a new xiphosurid from late Ordovician Konservat-Lagerstätten deposits, Manitoba, Canada. *Palaeontology*, **51**, 1–9.
- Runemark, A., Hey, J., Hansson, B., and Svensson, E.I. (2011). Vicariance divergence and gene flow among islet populations of an endemic lizard. *Molecular Ecology*, **21**, 117–129.
- Runemark, A., Trier, C.N., Eroukhanoff, F., et al. (2018). Variation and constraints in hybrid genome formation. *Nature Ecology & Evolution*, **2**, 549–556.
- Runnegar, B. (1982). A molecular-clock date for the origin of animal phyla. *Lethaia*, **15**, 199–205.
- Sabeti, P.C., Reich, D.E., Higgins, J.M., et al. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature*, **419**, 832–837.
- Sabeti, P.C., Varilly, P., Fry, B., et al. (2007). Genome-wide detection and characterization of positive selection in human populations. *Nature*, **449**, 913–918.
- Sackton, T.B., Corbett-Detig, R.B., Nagaraju, J., Vaishna, L., Arunkuma, K.P., and Hartl, D.L. (2014). Positive selection drives faster-Z evolution in silkworms. *Evolution*, **68**, 2331–2342.
- Sæther, S.A., Sætre, G.-P., Borge, T., et al. (2007). Sex chromosome-linked species recognition and evolution of reproductive isolation in flycatchers. *Science*, **318**, 95–97.
- Sætre, G.-P. (2013). Hybridization is important in evolution, but is speciation? *Journal of Evolutionary Biology*, **26**, 256–258.
- Sætre, G.-P., Borge, T., Lindroos, K., et al. (2003). Sex chromosome evolution and speciation in *Ficedula* flycatchers. *Proceedings of the Royal Society B*, **270**, 53–59.
- Sætre, G.-P., Cuevas, A., Hermansen, J.S., et al. (2017). Rapid polygenic response to secondary contact in a hybrid species. *Proceedings of the Royal Society B*, **284**, 20170365.
- Sætre, G.-P., Riyahi, S., Aliabadian, M., et al. (2012). Single origin of human commensalism in the house sparrow. *Journal of Evolutionary Biology*, **25**, 788–796.

- Sætre, G.-P., Moum, T., Bureš, S., Král, M., Adamjan, M., and Moreno, J. (1997). A sexually selected character displacement in flycatchers reinforces premating isolation. *Nature*, **387**, 589–592.
- Salzberg, S.L., Phillippy, A.M., Zimin, A., et al. (2012). GAGE: A critical evaluation of genome assemblies and assembly algorithms. *Genome Research*, **22**, 557–567.
- Sander, J.D. and Joung, J.K. (2014). CRISPR-Cas systems for editing, regulating and targeting genomes. *Nature Biotechnology*, **32**, 347–355.
- Sanderson, M.J. (2008). Phylogenetic signal in the eukaryotic tree of life. *Science*, **321**, 121–123.
- Sanger, F., Nicklen, S., and Coulson, A.R. (1977). DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences of the USA*, **74**, 5463–5467.
- Santos, F.P., Santos, F.C., and Pacheco, J.M. (2018). Social norm complexity and past reputations in the evolution of cooperation. *Nature*, **555**, 242–245.
- Scally, A. and Durbin, R. (2012). Revising the human mutation rate: implications for understanding human evolution. *Nature Reviews Genetics*, **13**, 745–753.
- Scally, A., Dutheil, J.Y., Hillier, L.W., et al. (2012). Insights into hominid evolution from the gorilla genome sequence. *Nature*, **483**, 169–175.
- Schaefer, H.M. and Ruxton, G.D. (2009). Deception in plants: mimicry or perceptual exploitation? *Trends in Ecology & Evolution*, **24**, 676–685.
- Schemske, D.W. and Bradshaw, H.D. (1999). Pollinator preference and the evolution of floral traits in monkey flowers (*Mimulus*). *Proceedings of the National Academy of Sciences of the USA*, **96**, 11910–11915.
- Schielzeth, H., Kempnaers, B., Ellegren, H., and Forstmeier, W. (2012). QTL linkage mapping of zebra finch beak color shows an oligogenic control of a sexually selected trait. *Evolution*, **66**, 18–30.
- Schlichting, C.D. (2002). Phenotypic plasticity in plants. *Plant Species Biology*, **17**, 85–88.
- Schlichting, C.D. and Wund, M.A. (2014). Phenotypic plasticity and epigenetic marking: an assessment of evidence for genetic accommodation. *Evolution*, **68**, 656–672.
- Schluter, D. (2000a). Ecological character displacement in adaptive radiation. *American Naturalist*, **156**, S4–S16.
- Schluter, D. (2000b). *The Ecology of Adaptive Radiation*. Oxford University Press, Oxford, UK.
- Schluter, D. and Conte, G.L. (2009). Genetics and ecological speciation. *Proceedings of the National Academy of Sciences of the USA*, **106**, 9955–9962.
- Schmitz, R.J. (2014). The secret garden—epigenetic alleles underlie complex traits. *Science*, **343**, 1082–1083.
- Schmitz, R.J., Schultz, M.D., Urich, M.A., et al. (2013). Patterns of population epigenomic diversity. *Nature*, **495**, 193–198.
- Schrider, D.R. and Kern, A.D. (2016). S/HIC: Robust identification of soft and hard sweeps using machine learning. *PLoS Genetics*, **12**, e1005928–31.
- Schrider, D.R. and Kern, A.D. (2018). Supervised machine learning for population genetics: a new paradigm. *Trends in Genetics*, **34**, 301–312.
- Schubert, M., Jónsson, H., Chang, D., et al. (2014). Prehistoric genomes reveal the genetic foundation and cost of horse domestication. *Proceedings of the National Academy of Sciences of the USA*, **111**, E5661–E5669.
- Searcy, W.A., Marler, P., Peters, S.S. (1981). Species song discrimination in adult female song and swamp sparrows. *Animal Behaviour*, **29**, 997–1003.
- Seehausen, O. (2000). Explosive speciation rates and unusual species richness in haplochromine cichlid fishes: Effects of sexual selection. *Advances in Ecological Research*, **31**, 237–274.
- Seehausen, O. (2004). Hybridization and adaptive radiation. *Trends in Ecology & Evolution*, **19**, 198–207.
- Seehausen, O., Butlin, R.K., Keller, I., et al. (2014). Genomics and the origin of species. *Nature Reviews Genetics*, **15**, 176–192.
- Seehausen, O., Terai, Y., Magalhaes, I.S., et al. (2008). Speciation through sensory drive in cichlid fish. *Nature*, **455**, 620–626.
- Seehausen, O. and Wagner, C.E. (2014). Speciation in freshwater fishes. *Annual Reviews of Ecology, Evolution, and Systematics*, **45**, 621–651.
- Servedio, M.R. and Boughman, J.W. (2017). The role of sexual selection in local adaptation and speciation. *Annual Review of Ecology, Evolution, and Systematics*, **48**, 85–109.
- Servedio, M.R. and Noor, M.A.F. (2003). The role of reinforcement in speciation: theory and data. *Annual Review of Ecology, Evolution and Systematics*, **34**, 339–364.
- Servedio, M.R., Van Doorn, G.S., Kopp, M., Frame, A.M., and Nosil, P. (2011). Magic traits in speciation: “magic” but not rare? *Trends in Ecology & Evolution*, **26**, 389–397.
- Shalem, O., Sanjana, N.E., and Zhang, F. (2015). High-throughput functional genomics using CRISPR–Cas9. *Nature Reviews Genetics*, **16**, 299–311.
- Sharma, M.D., Wilson, A.J., and Hosken, D.J. (2016). Fisher’s sons’ effect in sexual selection: absent, intermittent or just low experimental power? *Journal of Evolutionary Biology*, **29**, 2464–2470.
- Shen, H., Li, J., Zhang, J., et al. (2013). Comprehensive characterization of human genome variation by high coverage whole-genome sequencing of forty four Caucasians. *PLoS One*, **8**, e59494.
- Shendure, J. and Ji, H. (2008). Next-generation DNA sequencing. *Nature Biotechnology*, **26**, 1135–1145.
- Siller, S. (2001). Sexual selection and the maintenance of sex. *Nature*, **411**, 689–692.

- Silventoinen, K., Kaprio, J., Lahelma, E., Viken, R.J., and Rose, R.J. (2003). Assortative mating by body height and BMI: Finnish twins and their spouses. *American Journal of Human Biology*, **15**, 620–627.
- Simpson, G.G. (1944). *Tempo and Mode in Evolution*. Reprint 1984 by Columbia University Press, New York, USA.
- Slagsvold, T. and Wiebe, K.L. (2007). Learning the ecological niche. *Proceedings of the Royal Society B*, **274**, 19–23.
- Slatkin, M. (1987). Gene flow and the geographic structure of natural populations. *Science*, **236**, 787–792.
- Slatkin, M. (1994). Linkage disequilibrium in growing and stable populations. *Genetics*, **137**, 331–336.
- Slatkin, M. (2008). Linkage disequilibrium—understanding the evolutionary past and mapping the medical future. *Nature Reviews Genetics*, **9**, 477–485.
- Slon, V., Mafessoni, F., Vernot, B., et al. (2018). The genome of the offspring of a Neanderthal mother and a Denisovan father. *Nature*, **561**, 1–12.
- Smadja, C.M. and Butlin, R.K. (2011). A framework for comparing processes of speciation in the presence of gene flow. *Molecular Ecology*, **20**, 5123–5140.
- Sober, E. and Wilson, D.S. (1998). *Unto Others – The Evolution and Psychology of Unselfish Behavior*. Harvard University Press, Cambridge, MA, USA.
- Soh, Y.Q.S., Alföldi, J., Pyntikova, T., et al. (2014). Sequencing the mouse y chromosome reveals convergent gene acquisition and amplification on both sex chromosomes. *Cell*, **159**, 800–813.
- Sousa, V. and Hey, J. (2013). Understanding the origin of species with genome-scale data: modelling gene flow. *Nature Reviews Genetics*, **14**, 404–414.
- Spielmann, M., Lupiáñez, D.G., and Mundlos, S. (2018). Structural variation in the 3D genome. *Nature Reviews Genetics*, **19**, 453–467.
- Stebbins, G.L. (1950). *Variation and Evolution in Plants*. Columbia University Press, New York, USA.
- Stebbins, G.L. (1971). *Processes of Organic Evolution*. Prentice-Hall, Englewood Cliffs, NJ, USA.
- Stelkens, R.B., Schmid, C., and Seehausen, O. (2015). Hybrid breakdown in cichlid fish. *PLoS One*, **10**, e0127207.
- Stoletzki, N. and Eyre-Walker, A. (2010). Estimation of the neutrality index. *Molecular Biology and Evolution*, **28**, 63–70.
- Stork, N.E. (2018). How many species of insects and other terrestrial arthropods are there on earth? *Annual Review of Entomology*, **63**, 31–45.
- Storz, J.F. (2005). Invited Review: Using genome scans of DNA polymorphism to infer adaptive population divergence. *Molecular Ecology*, **14**, 671–688.
- Stronen, A.V., Tessier, N., Jolicoeur, H., et al. (2012). Canid hybridization: contemporary evolution in human-modified landscapes. *Ecology & Evolution*, **2**, 2128–2140.
- Summers-Smith, D. (1988). *The Sparrows*. T & AD Poyser, Calton, UK.
- Sun, L., Wang, J., Zhu, X., et al. (2018). HpQTL: a geometric morphometric platform to compute the genetic architecture of heterophylly. *Briefings in Bioinformatics*, **19**, 603–612.
- Sutton, W.S. (1902). On the morphology of the chromosome group in *Brachystola magna*. *Biological Bulletin*, **4**, 24–39.
- Suzuki, M.M. and Bird, A. (2008). DNA methylation landscapes: provocative insights from epigenomics. *Nature Reviews Genetics*, **9**, 465–476.
- Swanson, W.J. and Vacquier, V.D. (2002). The rapid evolution of reproductive proteins. *Nature Reviews Genetics*, **3**, 137–144.
- Számádó, S. and Penn, D.J. (2015). Why does costly signaling evolve? Challenges with testing the handicap hypothesis. *Animal Behaviour*, **110**, e9–e12.
- Taberlet, P., Fumagalli, L., Wust-Saucy, A.G., and Cosson, J.F. (1998). Comparative phylogeography and postglacial colonization routes in Europe. *Molecular Ecology*, **7**, 453–464.
- Tajima, F. (1989). Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics*, **123**, 585–595.
- Takahashi, T. and Hori, M. (2008). Evidence of disassortative mating in a Tanganyikan cichlid fish and its role in the maintenance of intrapopulation dimorphism. *Biology Letters*, **4**, 497–499.
- Takayama, S. and Isogai, A. (2005). Self-incompatibility in plants. *Annual Reviews in Plant Biology*, **56**, 467–489.
- Tang, S. and Presgraves, D.C. (2015). Lineage-specific evolution of the complex Nup160 hybrid incompatibility between *Drosophila melanogaster* and its sister species. *Genetics*, **200**, 1245–1254.
- Taylor, C.C.W., Hare, R.M., and Barnes, J. (1999). *Greek Philosophers—Socrates, Plato, and Aristotle*. Oxford University Press, Oxford, UK.
- Taylor, P.D., Wild, G., and Gardner, A. (2007). Direct fitness or inclusive fitness: how shall we model kin selection? *Journal of Evolutionary Biology*, **20**, 301–309.
- Templeton, A.R. (2008). The reality and importance of founder speciation in evolution. *BioEssays*, **30**, 470–479.
- Terns, R.M. and Terns, M.P. (2014). CRISPR-based technologies: prokaryotic defense weapons repurposed. *Trends in Genetics*, **30**, 111–118.
- Tishkoff, S.A., Reed, F.A., and Ranciaro, A., et al. (2007). Convergent adaptation of human lactase persistence in Africa and Europe. *Nature Genetics*, **39**, 31–40.
- Toomey, M.B., Marques, C.I., Andrade, P., et al. (2018). A non-coding region near *Follistatin* controls head colour polymorphism in the Gouldian finch. *Proceedings of the Royal Society B*, **285**, 20181788.

- Tørresen, O.K., Star, B., Jentoft, S., et al. (2017). An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. *BMC Genomics*, **18**, 311.
- Trapnell, C., Roberts, A., Goff, L., et al. (2012). Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. *Nature Protocols*, **7**, 562–578.
- Trautwein, M.D., Wiegmann, B.M., Beutel, R., Kjer, K.M., and Yeates, D.K. (2012). Advances in insect phylogeny at the dawn of the postgenomic era. *Annual Review of Entomology*, **57**, 449–468.
- Trier, C.N., Hermansen, J.S., Sætre, G.-P., and Bailey, R.I. (2014). Evidence for mito-nuclear and sex-linked reproductive barriers between the hybrid Italian sparrow and its parent species. *PLoS Genetics*, **10**, e1004075.
- Trivers, R.L. (1971). The evolution of reciprocal altruism. *Quarterly Review of Biology*, **46**, 35–37.
- Trivers, R.L. (1972). Parental investment and sexual selection. In: B. Campbell (ed.) *Sexual Selection and the Descent of Man*, pp. 136–179. Heinemann, London, UK.
- Trucchi, E., Mazzarella, A.B., Gilfillan, G.D., et al. (2016). BsRADseq: screening DNA methylation in natural populations of non-model species. *Molecular Ecology*, **25**, 1697–1713.
- Turcotte, M.M. and Levine, J.M. (2016). Phenotypic plasticity and species coexistence. *Trends in Ecology & Evolution*, **31**, 803–813.
- Turelli, M. and Orr, H.A. (1995). The dominance theory of Haldane's rule. *Genetics*, **140**, 389–402.
- Turner, L.M. and Harr, B. (2014). Genome-wide mapping in a house mouse hybrid zone reveals hybrid sterility loci and Dobzhansky–Muller interactions. *eLife*, **3**, e02504.
- Turner, T.L., Hahn, M.W., and Nuzhdin, S.V. (2005). Genomic islands of speciation in *Anopheles gambiae*. *PLoS Biology*, **3**, e285–7.
- Turner, W.C., Kausrud, K.L., Krishnappa, Y.S., et al. (2014). Fatal attraction: vegetation responses to nutrient inputs attract herbivores to infectious anthrax carcass sites. *Proceedings of the Royal Society B*, **281**, 20141785.
- Twyford, A.D. and Friedman, J. (2015). Adaptive divergence in the monkey flower *Mimulus guttatus* is maintained by a chromosomal inversion. *Evolution*, **69**, 1476–1486.
- Udovic, D. (1980). Frequency-dependent selection, disruptive selection and the evolution of reproductive isolation. *The American Naturalist*, **116**, 621–641.
- Vacquier, V.D. and Swanson, W.J. (2011). Selection in the rapid evolution of gamete recognition proteins in marine invertebrates. *Cold Spring Harbor Perspectives in Biology*, **3**, a002931.
- Valcu, C.-M. and Kempenaers, B. (2015). Proteomics in behavioral ecology. *Behavioral Ecology*, **26**, 1–15.
- van Valen, L. (1973). A new evolutionary law. *Evolutionary Theory*, **1**, 1–30.
- van't Hof, A.E., Campagne, P., Rigden, D.J., et al. (2016). The industrial melanism mutation in British peppered moths is a transposable element. *Nature*, **534**, 102–105.
- Veeramah, K.R. and Hammer, M.F. (2014). The impact of whole-genome sequencing on the reconstruction of human population history. *Nature Reviews Genetics*, **15**, 149–162.
- Venter, J.C., Adams, M.D., Myers, E.W., et al. (2001). The sequence of the human genome. *Science*, **291**, 1304–1351.
- Verhoeven, K.J.F., vonHoldt, B.M., and Sork, V.L. (2016). Epigenetics in ecology and evolution: what we know and what we need to know. *Molecular Ecology*, **25**, 1631–1638.
- Verzijden, M.N., ten Cate, C., Servedio, M.R., et al. (2012). The impact of learning on sexual selection and speciation. *Trends in Ecology & Evolution*, **27**, 511–519.
- Via, S. and West, J. (2008). The genetic mosaic suggests a new role for hitchhiking in ecological speciation. *Molecular Ecology*, **17**, 4334–4345.
- Vicoso, B. and Charlesworth, B. (2006). Evolution on the X chromosome: unusual patterns and processes. *Nature Reviews Genetics*, **7**, 645–653.
- Vijay, N., Poelstra, J.W., Künstner, A., and Wolf, J.B.W. (2013). Challenges and strategies in transcriptome assembly and differential gene expression quantification. A comprehensive *in silico* assessment of RNA-seq experiments. *Molecular Ecology*, **22**, 620–634.
- Vitti, J.J., Grossman, S.R., and Sabeti, P.C. (2013). Detecting natural selection in genomic data. *Annual Review of Genetics*, **47**, 97–120.
- Vogel, C. and Marcotte, E.M. (2012). Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. *Nature Reviews Genetics*, **13**, 227–232.
- Voight, B.F., Kurdaravalli, S., Wen, X., and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *PLoS Biology*, **4**, e72.
- Voje, K.L. (2016). Tempo does not correlate with mode in the fossil record. *Evolution*, **70**, 2678–2689.
- Vonlanthen, P., Bittner, D., Hudson, A.G., et al. (2012). Eutrophication causes speciation reversal in whitefish adaptive radiations. *Nature*, **482**, 357–362.
- Wagh, K., Bhatia, A., Alexe, G., Reddy, A., Ravikumar, V., Seiler, M., Boemo, M., Yao, M., Cronk, L., Naqvi, A., Ganesan, S., Levine, A.J., and Bhanot, G. (2012). Lactase persistence and lipid pathway selection in the Maasai. *PLoS One*, **7**, e44751.
- Wagner, C.E., Keller, I., Wittwer, S., et al. (2013). Genome-wide RAD sequence data provide unprecedented resolution of species boundaries and relationships in the Lake Victoria cichlid adaptive radiation. *Molecular Ecology*, **22**, 787–798.

- Wall, J.D., Lohmueller, K.E., and Plagnol, V. (2009). Detecting ancient admixture and estimating demographic parameters in multiple human populations. *Molecular Biology and Evolution*, **26**, 1823–1827.
- Wang, Z., Gerstein, M., and Snyder, M. (2009). RNA-Seq: a revolutionary tool for transcriptomics. *Nature Reviews Genetics*, **10**, 57–63.
- Warzluff, W.F., Gongidi, P., Woods, K.R., and Maltais, L.J. (2002). The human and mouse replication-dependent histone genes. *Genomes*, **80**, 487–498.
- Watakabe, I., Hashimoto, H., Kimura, Y., et al. (2018). Highly efficient generation of knock-in transgenic medaka by CRISPR/Cas9-mediated genome engineering. *Zoological Letters*, **4**, 3.
- Watanabe, Y., Yokobori, S., Inabe, T., et al. (2002). Introns in protein coding genes in Archaea. *FEBS Letters*, **510**, 27–30.
- Waterhouse, P.M., Wang, M.-B., and Lough, T. (2001). Gene silencing as an adaptive defence against viruses. *Nature*, **411**, 834–842.
- Watson, J.D. and Crick, F.H.C. (1953). A structure for deoxyribose nucleic acid. *Nature*, **171**, 737–738.
- Watterson, G.A. (1975). On the number of segregating sites in genetical models without recombination. *Theoretical Population Biology*, **7**(2), 256–276.
- Webber, B.L., Raghu, S., and Edwards, O.R. (2015). Opinion: Is CRISPR-based gene drive a biocontrol silver bullet or global conservation threat? *Proceedings of the National Academy of Sciences of the USA*, **112**, 10565–10567.
- Weigand, H. and Leese, F. (2018). Detecting signatures of positive selection in non-model species using genomic data. *Zoological Journal of the Linnean Society*, **184**(2), 528–583.
- Weinberg, W. (1908). Über den nachweis der vererbung beim menschen. *Jahreshefte des Vereins für Vaterländische Naturkunde in Württemberg*, **64**, 368–382.
- Weir, B.S. and Cockerham, C.C. (1969). Group inbreeding with 2 linked loci. *Genetics*, **63**, 711–742.
- West, S.A., Griffin, A.S., and Gardner, A. (2007). Evolutionary explanations for cooperation. *Current Biology*, **17**, R661–R672.
- West-Eberhard, J. (1989). Phenotypic plasticity and the origins of diversity. *Annual Reviews in Ecology and Systematics*, **20**, 249–178.
- West-Eberhard, J. (2014). Darwin's forgotten idea: the social essence of sexual selection. *Neuroscience & Biobehavioral Reviews*, **46**, 501–508.
- Westram, A.M., Galindo, J., Rosenblad, M.A., Grahame, J.W., and Butlin, R.K. (2014). Do the same genes underlie parallel phenotypic divergence in different *Littorina saxatilis* populations? *Molecular Ecology*, **23**, 4603–4616.
- Westram, A.M., Panova, M., Galindo, J., Butlin, R.K. (2016). Targeted resequencing reveals geographical patterns of differentiation for loci implicated in parallel evolution. *Molecular Ecology*, **25**, 3169–3186.
- Westram, A.M., Rafajlović, M., Chaube, P. et al. (2018). Clines on the seashore: The genomic architecture underlying rapid divergence in the face of gene flow. *Evolution Letters*, **2**, 297–309.
- Westram, A.M. and Ravinet, M. (2017). Land ahoy? Navigating the genomic landscape of speciation while avoiding shipwreck. *Journal of Evolutionary Biology*, **30**, 1522–1525.
- White, M.A., Ané, C., Dewey, C.N., Larget, B.R., and Payseur, B.A. (2009). Fine-scale phylogenetic discordance across the house mouse genome. *PLoS Genetics*, **5**, e1000729.
- Whitlock, M.C., Phillips, P.C., Moore, F.B.G., and Tonsor, S.J. (1995). Multiple fitness peaks and epistasis. *Annual Review of Ecology and Systematics*, **26**, 601–621.
- Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S., and Buckler, E.S. (2002). Genetic diversity and selection in the maize starch pathway. *Proceedings of the National Academy of Sciences of the USA*, **99**, 12959–12962.
- Widemo, F. (1998). Alternative mating strategies in the ruff: a mixed ESS? *Animal Behaviour*, **56**, 329–336.
- Wilding, C.S., Butlin, R.K., and Grahame, J. (2001). Differential gene exchange between parapatric morphs of *Littorina saxatilis* detected using AFLP markers. *Journal of Evolutionary Biology*, **14**, 611–619.
- Wiley, C., Qvarnström, A., Andersson, G., Borge, T., and Sætre, G.-P. (2009). Postzygotic isolation over multiple generations of hybrid descendants in a natural hybrid zone: how well do single-generation estimates reflect reproductive isolation? *Evolution*, **63**, 1731–1739.
- Wilkinson, G.S. (1984). Reciprocal food sharing in the vampire bat. *Nature*, **308**, 181–184.
- Wilkinson, G.S. (1988). Reciprocal altruism in bats and other mammals. *Ethology and Sociobiology*, **9**, 85–100.
- Willerslev, E. and Cooper, A. (2005). Ancient DNA. *Proceedings of the Royal Society B*, **272**, 3–16.
- Williams, G.C. (1966). *Adaptation and Natural Selection*. Princeton University Press, Princeton, NJ, USA.
- Williams, G.C. (1975). *Sex and Evolution*. Princeton University Press, Princeton, NJ, USA.
- Williams, T.N., Mwangi, T.W., Wambua, S., Alexander, N.D., Kortok, M., Snow, R.W., and Marsh, K. (2005). Sick cell trait and the risk of *Plasmodium falciparum* malaria and other childhood diseases. *Journal of Infectious Diseases*, **192**, 178–186.
- Wilson, E.O. (2005). Kin selection as the key to altruism. *Social Research*, **72**, 159–166.
- Wistow, G.J., Mulders, J.W., and de Jong, W.W. (1987). The enzyme lactate dehydrogenase as a structural protein in avian and crocodylian lenses. *Nature*, **326**, 622–624.
- Woese, C.R., Kandler, O., Wheelis, M.L. (1990). Towards a natural system of organisms: Proposal for the domains Archaea, Bacteria, and Eucarya. *Proceedings of the National Academy of Sciences of the USA*, **87**, 4576–4579.

- Wolf, J.B.W., Bayer, T., Haubold, B., Scilhabel, M., Rosenstiel, P., and Tautz, D. (2010). Nucleotide divergence vs. gene expression differentiation: comparative transcriptome sequencing in natural isolates from the carrion crow and its hybrid zone with the hooded crow. *Molecular Ecology*, **19**, 162–175.
- Wolf, J.B.W. and Ellegren, H. (2017). Making sense of genomic islands of differentiation in light of speciation. *Nature Reviews Genetics*, **18**, 87–100.
- Wolfe, K.H. (2001). Yesterday's polyploids and the mystery of diploidization. *Nature Reviews Genetics*, **2**, 331–341.
- Wood, T.E., Takebayashi, N., Barker, M.S., Mayrose, I., Greenspoon, P.B., and Rieseberg, L.H. (2009). The frequency of polyploid speciation in vascular plants. *Proceedings of the National Academy of Sciences of the USA*, **106**, 13875–13879.
- Woodward, S.R., Weyand, N.J., and Bunnell, M. (1994). DNA-sequence from Cretaceous period bone fragments. *Science*, **266**, 1229–1232.
- Wrangham, R. and Conklin-Brittain, N. (2003). Cooking as a biological trait. *Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology*, **136**, 35–46.
- Wrangham, R., Jones, J.H., Laden, G., Pilbeam, D., and Conklin-Brittain, N. (1999). The raw and the stolen: Cooking and ecology of human origins. *Current Anthropology*, **40**, 567–594.
- Wright, A.E., Darolti, I., Bloch, N.I., et al. (2017). Convergent recombination suppression suggests role of sexual selection in guppy sex chromosome formation. *Nature Communications*, **8**, 14251.
- Wright, A.E., Fumagalli, M., Cooney, C.R., et al. (2018). Male-biased gene expression resolves sexual conflict through the evolution of sex-specific genetic architecture. *Evolution Letters*, **2**, 52–61.
- Wright, G.A., Baker, D.D., Palmer, M.J., et al. (2013). Caffeine in floral nectar enhances a pollinator's memory of reward. *Science*, **339**, 1202–1204.
- Wright, S. (1922). Coefficient of inbreeding and relationship. *American Naturalist*, **51**, 330–338.
- Wright, S. (1931). Evolution in Mendelian populations. *Genetics*, **16**, 97–159.
- Wright, S. (1932). The roles of mutation, inbreeding, cross-breeding and selection in evolution. *Proceedings of the 6th International Congress of Genetics*, **1**, 356–366.
- Wright, S. (1937). The distribution of gene frequencies in populations. *Proceedings of the National Academy of Sciences of USA*, **23**, 307–320.
- Wright, S. (1938). Size of population and breeding structure in relation to evolution. *Science*, **87**, 430–431.
- Wu, C.I. (2001). The genic view of the process of speciation. *Journal of Evolutionary Biology*, **14**, 851–865.
- Wynne-Edwards, V.C. (1962). *Animal Dispersion in Relation to Social Behavior*. Oliver & Boyd, London, UK.
- Xu, J., Bauer, D.E., Kerenyi, M.A., et al. (2013). Corepressor-dependent silencing of fetal hemoglobin expression by BCL11A. *Proceedings of the National Academy of Sciences of the USA*, **110**, 6518–6523.
- Yandell, M. and Ence, D. (2012). A beginner's guide to eukaryotic genome annotation. *Nature Reviews Genetics*, **13**, 329–342.
- Yang, C., Liang, W., Cai, Y., et al. (2010). Coevolution in action: Disruptive selection on egg colour in an avian brood parasite and its host. *PLoS One*, **5**, e10816.
- Yang, F., Fu, B., O'Brian, P.C.M., Nie, W., Ryder, O.A., and Ferguson-Smith, M.A. (2004). Refined genome-wide comparative map of the domestic horse, donkey and human based on cross-species chromosome painting: insight into the occasional fertility of mules. *Chromosome Research*, **12**, 65–76.
- Yang, Z. (2006). *Computational Molecular Evolution*. Oxford University Press, Oxford, UK.
- Yang, Z. (2014). *Molecular Evolution: A Statistical Approach*. Oxford University Press, Oxford, UK.
- Yang, Z., Goldman, N., and Friday, A. (1994). Comparison of models for nucleotide substitution used in maximum likelihood phylogenetic estimation. *Molecular Biology and Evolution*, **11**, 316–324.
- Yeates, S.E., Diamond, S.E., Einum, S., et al. (2013). Cryptic choice of conspecific sperm controlled by the impact of ovarian fluid on sperm swimming behavior. *Evolution*, **67**, 2523–2536.
- Yoshida, K., Ishikawa, A., Toyoda, A., et al. (2019). Functional divergence of a heterochromatin-binding protein during stickleback speciation. *Molecular Ecology*. <https://doi.org/10.1111/mec.14841>
- Young, D.L., Huyen, Y., and Allard, M.W. (1995). Testing the validity of the cytochrome B sequence from Cretaceous period bone fragments as dinosaur DNA. *Cladistics*, **11**, 199–209.
- Zahavi, A. (1975). Mate selection—a selection for a handicap. *Journal of Theoretical Biology*, **53**, 204–214.
- Zahavi, A. and Zahavi, A. (1997). *The Handicap Principle: A Missing Piece of Darwin's Puzzle*. Oxford University Press, New York, USA.
- Zhang, L., Mazo-Vargas, A., and Reed, R.D. (2017). Single master regulatory gene coordinates the evolution and development of butterfly color and iridescence. *Proceedings of the National Academy of Sciences of the USA*, **114**, 10707–10712.
- Zhang, X., Wang, H., Li, M., et al. (2014). Isolation of doublesex- and mab-3-related transcription factor 6 and its involvement in spermatogenesis in tilapia1. *Biology of Reproduction*, **91**, 1–10.
- Zimorski, V., Ku, C., Martin, W.F., and Gould, S.B. (2014). Endosymbiotic theory for organelle origins. *Current Opinion in Microbiology*, **22**, 38–48.
- Zuckerandl, E. and Pauling, L.B. (1962). Molecular disease, evolution, and genic heterogeneity. In: M. Kasha and B. Pullman (eds) *Horizons in Biochemistry*, pp. 189–225. Academic Press, New York, USA.