

ICG PUBLICATIONS [formerly CGEB]: 2008 – present

Faculty members (**bold**), Adjunct & former Associates (*), trainees (underlined)

Year 2022:

- Banerjee *et al.* [incl. **F. Maguire**] (2022) Immunogenicity of convalescent and vaccinated sera against clinical isolates of ancestral SARS-CoV-2, beta, delta, and omicron variants. *Med NY* (Cell Press, Apr. 2022). doi: 10.1016/j.medj.2022.04.002.
- Bertrand, E.M., Bannon, C., Rapp, I.** (2022) Community Interaction Co-Limitation: Nutrient Limitation in a Marine Microbial Community Context. *Frontiers in Microbiology, in press.*
- Bjorndahl P, Bielawski JP, Liu L, Zhou W, Gu H. (2022) Novel Application of Survival Models for Predicting Microbial Community Transitions with Variable Selection for Environmental DNA. *Appl. Environ Microbiol.* 88(6): e0214621.
- Blaxter, M. *et al.* [incl. **Archibald, J. M.**]. 2022. Why sequence all eukaryotes? *Proc. Natl. Acad. Sci. USA* 119(4): e2115636118.
- Chen X, Wei W, Xiao X, Wallace D, Hu C, Zhang L, Batt J, Liu J, Gonsior M, Zhang Y, **LaRoche J**, Hill P, Xu D, Wang J, Jiao N, Zhang R. (2022) Heterogeneous viral contribution to dissolved organic matter processing in a long-term macrocosm experiment. *Environ Int.* 158: 106950.
- Doolittle, W.F.** (2022) All about levels: Transposable elements as selfish DNAs *and* drivers of evolution. *Biology and Philosophy, in press.*
- Duerschlag J, Mohr W, Ferdelman TG, **LaRoche J**, Desai D, Croot PL, Voß D, Zielinski O, Lavik G, Littmann S, Martínez-Pérez C, Tschitschko B, Bartlau N, Osterholz H, Dittmar T, Kuypers MMM. (2022) Niche partitioning by photosynthetic plankton as a driver of CO₂-fixation across the oligotrophic South Pacific Subtropical Ocean. *ISME J.* 16(2):465-476.
- Duguay BA, Herod A, Pringle ES, Monro SMA, Hetu M, Cameron CG, McFarland SA, McCormick C. (2022) Photodynamic inactivation of human coronaviruses. *Viruses* 14(1): 110.
- Ebenezer, V., Y Hu, O Carnicer, AJ Irwin, MJ Follows, ZV Finkel (2022) Elemental and macromolecular composition of the marine Chloropicophyceae, a major group of oceanic photosynthetic picoeukaryotes. *Limnology & Oceanography* 67: 540-551.
- Griffiths *et al.* (incl. **F. Maguire**) (2022) Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. *GigaScience* 11:giac003.
- Herod, A., Emond-Rheault, J-G, Tamber, S., Goodridge, L., Levesque, R.C., Rohde, J. (2022) Genomic and phenotypic analysis of SspH1 identifies a new Salmonella effector, SspH3. *Mol. Microbiol.* 117(4): 770-789.
- Ho, L.S.T., Susko, E.** (2022) Ancestral state reconstruction with large numbers of sequences and edge-length estimation. *J. Mathematical Biol.* 84:21.
- Ho, L.S.T., Dinh, V.** (2022) Searching for Minimal Optimal Neural Networks. *Statistics and Probability Letters* 183: 109353.
- Joy-Warren, H.L., A.C. Alderkamp, G.L. van Dijken, L.J. Jabre, **E.M. Bertrand**, E.N. Baldonado, M.W. Glickman, K.M. Lewis, R. Middag, K. Seyitmuhammedov, K.E. Lowry, W. van de Poll, K.R. Arrigo (2022) Springtime phytoplankton responses to light and iron availability along the western Antarctic Peninsula. *Limnology and Oceanography, Feb. 2022.*
- Karakach, T.K., F Taverna, J Barra** (2022) Error Modelled Gene Expression Analysis (EMOGEA) provides a superior overview of time course RNA-Seq Measurements and low count gene expression. *BioRxiv*; doi: <https://doi.org/10.1101/2022.02.18.481000>
- Kember M., Grandy S., Raudonis R., Cheng Z. (2022) Non-canonical host intracellular niche links to new antimicrobial resistance mechanism. *Pathogens* 11(2):220.
- Kennedy *et al.* [incl. **D. Gaston**] (2022) NAD⁺ depletion enhances rovirus-induced oncolysis in multiple myeloma. *Molecular Therapy Oncolytics* 24: 695-706.

- Kim JI, **Maguire F**, Tsang KK, Gouliouris T, Peacock SJ, McAllister TA, McArthur AG, **Beiko RG**. (2022) Machine Learning for Antimicrobial Resistance Prediction: Current Practice, Limitations, and Clinical Perspective. *Clin Microbiol Rev.*, May 25: e0017921.
- LaRoche, J.** and **Robicheau, B.M.** (2022) The Pelagic Light-Dependent Microbiome. In: Stal, L.J., Cretoiu, M.S. (Eds), *The Marine Microbiome. The Microbiomes of Humans, Animals, Plants, and the Environment*, Vol 3, Springer, Cham. https://doi.org/10.1007/978-3-030-90383-1_9. Book chapter.
- Lawniczak *et al.* [incl. **Archibald, J. M.**] 2022. Standards recommendations for the Earth BioGenome Project. *Proc. Natl. Acad. Sci. USA* 119, 4: e2115636118.
- Lee, BD; Gitter, A; Greene, CS; Raschka, S; **Maguire, F**; Titus, AJ; Kessler, MD; Lee, AJ.; Chevrette, MG.; Stewart, PA; Britto-Borges, T; Cofer, EM; Yu, K-H; Carmona, JJ; Fertig, EJ; Kalinin, AA; Signal, B; Lengerich, BJ; Triche, TJ; Boca, SM (2022) Ten Quick Tips for Deep Learning in Biology. *PLoS Comput. Biol.* 18(3): e1009803.
- Lewin *et al.* [incl. **Archibald, J. M.**] 2022. The Earth BioGenome Project 2020: starting the clock. *Proc. Natl. Acad. Sci. USA*. 119, 4: e2115636118.
- Li, ZK, Y Zhang, W Li, **AJ Irwin**, **ZV Finkel** (2022) Conservation and architecture of housekeeping genes in the model marine diatom *Thalassiosira pseudonana*. *New Phytologist* 234: 1363-76.
- Luo Y., Zhang W., Cheng Y., Lu Q., Guo Y., Wen G., Shao H., **Cheng Z.**, Luo Q., and Zhang T. (2022) Droplet digital PCR-based detection and quantification of GyrA Thr-86-Ile mutation based fluoroquinolone-resistant *Campylobacter jejuni*. *Microbiology Spectrum* 10(2): e02769-21.
- McCain, J.S.P. and **E.M. Bertrand** (2022) Phytoplankton antioxidant systems and their contributions to cellular elemental stoichiometry. *Limnology and Oceanography Letters* 7(2): 96-111.
- McCain, J.S.P., A.E. Allen, **E.M. Bertrand** (2022) Proteomic traits vary across taxa in a coastal Antarctic phytoplankton bloom. *ISME Journal* 16, 569–579.
- Moran, M., E. B. Kujawinski, W. F. Schroer, S. A. Amin, N.R. Bates, **E.M. Bertrand**, R. Braakman, C. T. Brown, M. W Covert, S. C Doney, S. T Dyhrman, A. S Edison, A.M. Eren, N. M. Levine, L. Li, A. C. Ross, M. A. Saito, A. E. Santoro, D. Segrè, A. Shade, M. B Sullivan, A. Vardi. (2022) Microbial metabolites in the marine carbon cycle. *Nature Microbiology* 7, 508-523.
- Muñoz-Gómez S.A., **Susko E.**, **Williamson K.**, Eme L., **Slamovits C.H.**, Moreira D., López-García P. and **Roger A.J.** (2022) Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known *Alphaproteobacteria*. *Nat. Ecol. Evol.* 6: 253-262.
- Mutshinda, CM, A Mishra, **ZV Finkel**, CE Widdicombe, **AJ Irwin** (2022) Bayesian two-part modeling of phytoplankton biomass and occurrence. *Hydrobiologia* 849: 1247-1300.
- Nearing JT**, **Douglas GM**, **Hayes M**, **MacDonald J**, **Desai D**, **McCormick N**, **Jones JMA**, **Wright R**, **Dhanani A**, **Comeau AM**, **Langille MGI** (2022). Microbiome differential abundance methods produce different results across 38 datasets. *Nature Communications* 13:342.
- Nguyen, C.V., **Ho, L.S.T.**, Xu, H., Dinh, V., Nguyen, B. (2022) Bayesian Pool-based Active Learning with Abstention Feedbacks. *Neurocomputing* 471: 242-250.
- Pérez S, Manosalva A, Colin N, González J, Habit E, **Ruzzante DE**, Górski K. (2022) Juvenile salmon influence on the diet of native Puye *Galaxias maculatus* in lakes and estuaries of Patagonian fjords. *Biological Invasions* 24: 81–92.
- Pesaranghader A, Matwin S, Sokolova M, Grenier JC, **Beiko RG**, Hussin J. (2022) deepSimDEF: deep neural embeddings of gene products and Gene Ontology terms for functional analysis of genes. *Bioinformatics* 38: 3051-3061.
- Robicheau, B.**, J. Tolman, **E.M. Bertrand**, **J. LaRoche** (2022) Highly resolved interannual phytoplankton community dynamics of the coastal Northwest Atlantic. *ISME Commun.* 2, 38.
- Rossi, M., Marco Oliva, Ben Langmead, **Travis Gagie**, Christina Boucher (2022) MONI: A Pangenomic Index for Finding Maximal Exact Matches. *J. Comput. Biol.* 29(2): 169-187.
- Rossi, M., Marco Oliva, Paola Bonizzoni, Ben Langmead, **Travis Gagie**, Christina Boucher (2022) Finding Maximal Exact Matches Using the r-Index. *J. Comput. Biol.* 29(2): 188-194.

- Salisbury SJ, McCracken GR, Perry R, Keefe D, Layton KKS, Kess T, Nugent CM, Bradbury IR, Koop BF, Ferguson MM, **Ruzzante DE** (2022). The genomic consistency of the loss of Anadromy in an Arctic Fish (*Salvelinus alpinus*). *The American Naturalist* 199(5): 617-635.
- Salisbury SJ, **Ruzzante DE**. (2022) Genetic causes and consequences of sympatric morph divergence in Salmonidae: a search for mechanisms. *Annual Reviews in Animal Biosciences*, 10: 81-106. <https://doi.org/10.1146/annurev-animal-051021-080709>
- Sanderson *et al.* [including **F. Maguire, R.G. Beiko**] (2022) Exploring the mobilome and resistome of *Enterococcus faecium* in a One Health context across two continents. *BioRxiv*; doi: <https://doi.org/10.1101/2022.04.11.487771>
- Smith P, Beaumont L, Bernacchi CJ, Byrne M, Cheung W, Conant RT, Cotrufo F, Feng X, Janssens I, Jones H, Kirschbaum MUF, Kobayashi K, **LaRoche J**, Luo Y, McKechnie A, Penuelas J, Piao S, Robinson S, Sage RF, Sugget DJ, Thackeray SJ, Way D, Long SP. (2022) Essential outcomes for COP26. *Global Change Biol.* 28(1):1-3.
- Sterling, S.M.**, Clair, T.A., Rotteveel, L., O'Driscoll, N., Houle, D., Halfyard, E., Keys, K. (2022) Kejimikujik calibrated catchments: A benchmark dataset for long-term impacts of terrestrial and freshwater acidification. *Hydrological Processes* 36(2): e14477.
- Tashyreva, D., **Simpson, A.G.B.**, Prokopchuk, G., Škodová-Sveráková, I, Butenko, A., Hammond, M., George, E.E., Flegontova, O., Záhonová, K., Faktorová, D., Yabuki, A., Horák, A., Keeling, P.J., Lukeš, J. (2022) Diplonemids – A review on “new” flagellates on the oceanic block. *Protist* 173: 125868.
- Tymoshuk KM, Delgado ML, McCracken GR, Alonso M, Górski K, Habit E, **Ruzzante DE**. (2022) Drainage reversal with no lineage expansion, a case of competitive exclusion? The genetics of *Galaxias maculatus* in two connected trans-Andean systems. *Biol. J. Linnean Soc.* 136(2): 213-225.
- Valenzuela-Aguayo F, McCracken GR, Manosalva A, Habit EA, **Ruzzante DE**. 2022. Connectivity, diversity, and hybridization between two endemic fish species (genus *Percilia*) in a complex temperate landscape. *Conservation Genetics* 23: 23-33.
- Valenzuela-Valderas, K.N., Moreno-Hagelsieb, G.M., **Rohde, J.R.**, Garduno, R.A. (2022). The Functional Differences between the GroEL Chaperonin of *Escherichia coli* and the HtpB Chaperonin of *Legionella pneumophila* Can Be Mapped to Specific Amino Acid Residues. *Biomolecules* 12(1): 59.
- van Lersel, L., Janssen, R., Jones, M., Murakami, Y., **Zeh, N.** (2022) A practical fixed-parameter algorithm for constructing tree-child networks from multiple binary trees. *Algorithmica* 84: 917-960.
- Vasquez-Rifo A., Cook J., McEwan D.L., Shikara D., Ausubel F.M., Di Cara F., **Cheng Z.** (2022) ABCDs of the relative contributions of *Pseudomonas aeruginosa* quorum sensing systems to virulence in diverse non-vertebrate hosts. *mBio* 13(2): e0041722.
- Verburgt, C., **KA Dunn, JP Bielawski**, AR Otley, MB Heyman, W Sunseri, D Shouval, A Levine, T de Meij, JS Hyams, LA Denson, S Kugathasan, MA Benninga, WJ de Jonge, JE Van Limbergen* (2022) P711 stool microbiome communities predict remission in pediatric Crohn's disease patients even after start of treatment. *Journal of Crohn's and Colitis* 16(1): i608-i608.
- Wijesundara N.M., Lee S.F., Davidson R., **Cheng Z.**, and Rupasinghe V.H.P. (2022) Carvacrol suppresses inflammatory biomarkers production by lipoteichoic acid and peptidoglycan-stimulated human tonsil epithelial cells. *Molecules* 14(3):503.
- Youssef N., Susko E., Roger A.J. and Bielawski J.P.** (2022) Evolution of amino acid propensities under stability-mediated epistasis. *Mol. Biol. Evol.* 39(3): msac030.
- Zhang, X., Hu, Y., Eme, L., Maruyama, S., Eveleigh, R. J. M., Curtis, B. A., Sibbald, S. J., Hopkins, J. F., Filloramo, G. V., van Wijk, K., & Archibald, J. M.** 2022. TreeTuner: A pipeline for minimizing redundancy and complexity in large phylogenetic datasets. *STAR Protocols* 3: 101175.

Year 2021:

- Baldwin SJ, Slaine PD, Keltie E, Palit S, McKinnell SL, Longpre BE, Ko KR, Green J, Markle G, Kim JS, **McCormick C.**, Frampton JP. (2021) Non-Woven Textiles Formed from Contact-Drawn Poly(Ethylene Oxide) Nanofibers Provide Tunable Filtration and Virucidal Properties via Entrapment of Silver Nanoparticles. *ACS Applied Polymer Materials* 3(8): 4245-55.
- Bastide, P., **Ho, L.S.T.**, Baele, G., Lemey, P., Suchard, M.A. (2021) Efficient Bayesian inference of general Gaussian models on large phylogenetic trees. *Ann. Appl. Stat.* 15(2): 971-997.
- Behnke, J., Cohen, A.M., **LaRoche, J.** (2021) N-linked glycosylation enzymes in the diatom *Thalassiosira oceanica* exhibit a diel cycle in transcript abundance and favor for NXT-type sites. *Sci. Rep.* 11: 3227.
- Bernardino, M. and **R.G. Beiko** (2021) Genome-scale prediction of bacterial promoters. 2021 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), pp. 01-08, doi: 10.1109/CIBCB49929.2021.9562938.
- Bhatia, M.P., S Waterman, DO Burgess, PL Williams, RM Bundy, T Mellett, M Roberts, **Bertrand, EM** (2021) Glaciers and Nutrients in the Canadian Arctic Archipelago Marine System. *Global Biogeochem. Cycles* 35(8): e2021GB006976.
- Blais, C., **Archibald, J.M.** (2021) The past, present and future of the Tree of Life. *Curr. Biol.* 31: R314-321.
- Bôto, M.L., Magalhães, C., Perdigão, R., Alexandrino, D.A.M., Fernandes, J.P., Bernabeu, A.M., Ramos, S., Carvalho, M.F., Semedo, M., **LaRoche, J.**, Almeida, C.M.R., Mucha, A.P. (2021) Harnessing the potential of native microbial communities for bioremediation of oil spills in the Iberian Peninsula NW Coast. *Front. Microbiol.* 12: 633659.
- Brunet, T.D.P., **Doolittle, W.F.**, **Bielawski, J.P.** (2021) The role of purifying selection in the origin and maintenance of complex function. *Studies Hist. Phil. Biol. Biomed. Sci. C.* 87: 125-135.
- Carnicer, O., **AJ Irwin, ZV Finkel** (2021) Traits influence dinoflagellate C:N:P. *Eur. J Phycology* 57: 154-165.
- Cook, J., Douglas, G.M., Zhang, J., Glick, B.R., **Langille, M.G.I.**, Liu, K., **Cheng, Z.** (2021) Transcriptomic profiling of *Brassica napus* responses to *Pseudomonas aeruginosa*. *Innate Immunity*, 27(2): 143-157.
- Cram JA, **Gray MW**, McFarland K, Hollins A. (2021) Microbiota of *Crassostrea virginica* larvae during a hatchery crash and under normal production: Amplicon sequence data. *Data Brief* 40:107755.
- Daboor, S., **Rohde, J.R.**, **Cheng Z.** (2021) Disruption of the extracellular polymeric network of *Pseudomonas aeruginosa* biofilms by alginate lyase enhances pathogen eradication by antibiotics. *J. Cystic Fibrosis* 20(2):264-270.
- Daboor, S., Raudonis R., and **Cheng Z.** (2021) Characterizations of the viability and gene expression of dispersal cells from *Pseudomonas aeruginosa* biofilms released by alginate lyase and tobramycin. *PLoS One* 16(10): e0258950.
- Davies T, Watts S, McClure K, Migicovsky Z, **Myles S** (2021) Phenotypic divergence between the cultivated apple (*Malus domestica*) and its primary wild progenitor (*Malus sieversii*). *PLoS ONE* 17(3): e0250751.
- DeClercq V, Nearing JT, **Langille MGI** (2021) Investigation of the impact of commonly used medications on the oral microbiome of individuals living without major chronic conditions. *PLoS One*, 16(12): e0261032.
- Dinh, V., **Ho, L.S.T.** (2021). Convergence of maximum likelihood supertree reconstruction. *AIMS Mathematics* 6(8): 8870-8883
- Doolittle, W.F.** and Neto, C.A. (2021) A chemostat model for evolution by persistence, clade selection and its explanatory autonomy. *Philosophy of Science*, *in press*.
- Doolittle, W.F. (2021) All about levels: Transposable elements as selfish DNAs and drivers of evolution. *Biol. Philos.*, *in press*.

- Douglas, G.M., Langille, MGI (2021) A primer and discussion on DNA-based microbiome data and related bioinformatic analyses. *Peer Community Journal* 1: e5.
- Dunn, K.A., Connors, J., Bielawski, J.P., Nearing, J.T., Langille, MGI, Van Limbergen, J.*, Fernandez, C.V., MacDonald, T., Kulkarni, K. (2021) Investigating the gut microbial community and genes in children with differing levels of change in serum asparaginase activity during pegaspargase treatment for acute lymphoblastic leukemia. *Leuk. Lymphoma* 62: 927-936.
- Dunn, K.A., Forbrigger Z, Connors J, Rahman M, Cohen A, Van Limbergen J.*, Langille MGI, Stadnyk AW, Bielawski JP, Penny S, MacDonald T, Kulkarni K (2021) Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. *Leukemia & Lymphoma*, 62(13):3244-3255.
- Einfeldt, A.L., Kess, T., Wringe, B., Bradbury, I.R., Fisher, J., den Heyer, C., **Ruzzante, D.E.**, Bentzen, P. (2021) Chromosome level reference of Atlantic halibut *Hippoglossus hippoglossus* provides insight into the evolution of sexual determination systems. *Mol. Ecol. Resources* 21: 1686-1696.
- Ettahi, K., Lhee, D.H., Sung, J.Y., **Simpson, A.G.B.**, Park, J.S., Yoon, H.S. (2021) Evolutionary history of mitochondrial genomes in Discoba, including the extreme halophile *Pleurostomum flabellatum* (Heterolobosea). *Genome Biol. Evol.* 13: evaa241.
- Filloramo, G.V., Blanche, E., Curtis, B.A., Archibald, J.M. (2021) Re-examination of two diatom reference genomes using long-read sequencing. *BMC Genomics* 22: 379.
- Fürst-Jansen, J. M. R., de Vries, S. von Schwartzberg, K. **Archibald, J. M.** & de Vries, J. (2021) Submergence of the filamentous Zygnematophyceae *Mougeotia* induces differential gene expression patterns associated with photosynthesis. *Protoplasma*, Dec. 22 doi: 10.1007/s00709-021-01730-1.
- González-Morales, N.**, Océane Marescal, Szilárd Szikora, Miklos Erdelyi, Péter Bíró, Tuana Mesquita, József Mihály, Frieder Schöck (2021) Oxoglutarate dehydrogenase coordinates myofibril growth by maintaining amino acid homeostasis. *bioRxiv*; doi: <https://doi.org/10.1101/2021.12.13.472149>.
- Haas, S., Robicheau, B.M., Subhadeep Rakshit, Tolman, J., Algar, C.K., **LaRoche, J.**, Wallace, D.W.R. (2021) Physical mixing in coastal waters controls and decouples nitrification via biomass dilution. *PNAS* 118(18): e2004877118.
- Hart, K.A., Kennedy, G.W., **Sterling, S.M.** (2021) Distribution, Drivers, and Threats of aluminum in groundwater in Nova Scotia, Canada. *Water* 13: 1578.
- Herman EK, Greninger A, van der Giezen M, Ginger ML, Ramirez-Macias I, Miller HC, Morgan MJ, Tsaousis AD, Velle K, Vargová R, Záhonová K, Najle SR, MacIntyre G, Muller N, Wittwer M, Zysset-Burri DC, Eliáš M, **Slamovits CH**, Weirauch MT, Fritz-Laylin L, Marciano-Cabral F, Puzon GJ, Walsh T, Chiu C, Dacks JB. (2021) Genomics and transcriptomics yields a system-level view of the biology of the pathogen *Naegleria fowleri*. *BMC Biol.* 19(1):142.
- Heiss, A.A., Warring, S.D., Lukacs, K., Favate, J., Yang, A., Gyaltsen, Y., Filardi, C., **Simpson, A.G.B.**, Kim, E. (2021) *Imasa heleensis* gen. nov. sp. nov., a deep-branching marine malawimonad and possible key taxon in understanding early eukaryotic evolution. *J. Euk. Microbiol.* 68: e12837.
- Horvath, R., Hawe, N., Lam, C., Mestnikov, K., Eji-Lasisi, M., **Rohde, J.**, Sadowski, I. (2021) TORC1 signaling modulates Cdk8-dependent *GAL* gene expression in *Saccharomyces cerevisiae*. *Genetics* 219(4): iyab168.
- Horváthová L, Žárský V, Pánek T, Derelle R, Pyrih J, Motyčková A, Klápšťová V, Vinopalová M, Marková L, Voleman L, Klimeš V, Petruš M, Vaitová Z, Čepička I, Hryzáková K, Harant K, **Gray MW**, Chami M, Guilvout I, Francetic O, Lang BF, Vlček Č, Tsaousis AD, Eliáš M, Doležal P. (2021) Analysis of diverse eukaryotes suggests the existence of an ancestral mitochondrial apparatus derived from the bacterial type II secretion system. *Nat Commun.* 12(1): 2947.
- Huang, Y., Ragush, C.M., Johnston, L.H., Hall, M.W., **Beiko, R.G.**, Jamieson, R.C., Truelstrup, H.L. (2021) Changes in Bacterial Communities During Treatment of Municipal Wastewater in Arctic Wastewater Stabilization Ponds. *Frontiers in Water* 3: 710853.
- Inkpen, S.A. and Doolittle, W.F. (2021) Adaptive regeneration across scales: Replicators and interactors from limbs to forests. *Philosophy, Theory and Practice in Biology* 13: 1.

- Jabre, L., A. E. Allen, J. S. P. McCain, J. P. McCrow, N. Tenenbaum, J. L. Spackeen, R. E. Sipler, B. R. Green, D. A. Bronk, D. A. Hutchins, **E. M. Bertrand** (2021) Molecular underpinnings and biogeochemical consequences of enhanced diatom growth in a warming Southern Ocean. *PNAS* 118 (30): e2107238118.
- Jiao, N. *et al.* [34 authors incl. **J. LaRoche**] (2021) Correcting a major error in assessing organic carbon pollution in natural waters. *Sci. Adv.* 7: eabc7318.
- Karimi, K., Farid, A.H., **Myles, S.**, Miar, Y. (2021) Detection of selection signatures for response to Aleutian mink disease virus infection in American mink. *Sci. Rep.* 11(1): 2944.
- Kenney, T., Gu, H.**, Huang, T. (2021) Poisson PCA: Poisson Measurement Error corrected PCA, with application to microbiome data. *Biometrics* 77(4): 1369-1384.
- Kess, T., Dempson JB, Lehnert SJ, Layton K, Einfeldt A, Bentzen P, Salisbury SJ, Messmer A, Duffy S, **Ruzzante DE**, Nugent CM, Ferguson MM, Leong JS, Koop BF, Bradbury IR. (2021) Genomic basis of extreme deep-water adaptation in sympatric Arctic charr (*Salvelinus alpinus*) morphs. *Molecular Ecology*, 30(18): 4415-4432.
- Kess, T., Einfeldt, A.L., Wringe, B., Lehnert, S.J., Layton, K.K.S., McBride, M., Robert, D., Fisher, J., Le Bris, A., den Heyer, C., Shackell, N., **Ruzzante, D.E.**, Bentzen, P., Bradbury, I.R. (2021) A putative structural variant and environmental variation associated with genomic divergence across the Northwest Atlantic in Atlantic Halibut. *ICES J. Marine Sci.* 78: 2371-2384.
- Lawniczak, M.K. *et al.* [50+ co-authors incl. **Archibald, J.M.**] (2021) Standards recommendations for the Earth BioGenome Project. *Cell Genomics, in press.*
- Lax, G., Kolisko, M., Eglit, Y., Lee, W.J., Yubuki, N., Karnkowska, A., Leander, B.S., Burger, G., Keeling, P.J., **Simpson, A.G.B.** (2021) Multigene phylogenetics of euglenids based on single-cell transcriptomics of diverse phagotrophs. *Mol. Phylogenet. Evol.* 159: 107088.
- Layton, K.K.S., Snelgrove, P.V.R., Dempson, J.B., Kess, T., Lehnert, S.J., Bentzen, P., Duffy, S.J., Messmer, AM, Stanley, R.R.E., DiBacco, C., Salisbury, S.J., **Ruzzante, D.E.**, Nugent, C.M., Ferguson, M.M., Leong, J.S., Koop, B., Bradbury, I.R. (2021) Genomic evidence of past and future climate-linked loss in a migratory Arctic fish. *Nature Climate Change* 11: 158-165.
- Lewin, H.A. *et al.* [120+ authors incl. **Archibald, J.M.**] 2021 The Earth BioGenome Project 2020: starting the clock. *Cell Genomics, in press.*
- Li, Z-K., Li, W., Zhang, Y., Hu, Y., Sheward, R., **Irwin, A.J.**, **Finkel, Z.V.** (2021) Dynamic photophysiological stress response of a model diatom to ten environmental stresses. *J Phycol.* 57:484-495.
- Liang, Y., Bretherton, L., Brown, C.M., Passow, U., Quigg, A.S., **Irwin, A.J.**, **Finkel, Z.V.** (2021) Transcriptome-wide responses of aggregates of the diatom *Odontella aurita* to oil. *Mar. Ecol. Prog. Ser.* 671: 67-79.
- Liu, L., **Gu, H.**, Van Limbergen, J.*, **Kenney, T.** (2021) SuRF: a new method for sparse variable selection, with application in microbiome data analysis. *Stat. in Medicine* 40: 897–919.
- MacNeil L, Missan S, Luo J, Trappenberg T, **LaRoche J.** (2021) Plankton classification with high-throughput submersible holographic microscopy and transfer learning. *BMC Ecol Evol.* 21(1): 1-11.
- Maculins *et al.* [22 authors incl. **Rohde, J.**] (2021) Multiplexed proteomics of autophagy-deficient murine macrophages reveals enhanced antimicrobial immunity via the oxidative stress response. *Elife* 10: e62320.
- McCain, J.S.P., Tagliabue, A., **Susko, E.**, Achterberg, E.P., Allen, E., **Bertrand, E.M.** (2021). Cellular costs underpin micronutrient limitation in phytoplankton. *Science Advances* 7: eabg6501.
- McCormick, N, Earle M, Ha C, Hakes L, Evans A, Anderson L, Stoddart AK, **Langille MGI**, Gagnon GA. (2021) Biological and physico-chemical mechanisms accelerating the acclimation of Mn-removing biofilters. *Water Res.* 207:117793.
- McGinty, N., A Barton, DG Johns, **ZV Finkel**, **AJ Irwin** (2021) Niche conservation in copepods between ocean basins. *Ecography* 44: 1653-1664.

- McGinty, N., Barton, A.D., Record, N.R., **Finkel, Z.V.**, Johns, D.G., Stock, C.A., **Irwin, A.J.** (2021) Anthropogenic climate change impacts on copepod trait biogeography. *Global Change Biol.* 27: 1431-1442.
- McKenna *et al.* [incl. **Archibald, J.M.**] 2021. The Aquatic Symbiosis Genomics Project: probing the evolution of symbiosis across the tree of life. *Wellcome Open Res.* 6:254.
- Migicovsky, Z., Gardner, K.M., Richards, C., Chao, C.T., Schwaninger, H.R., Fazio, G., Zhong, G.Y., **Myles, S.** (2021) Genomic consequences of apple improvement. *Horticulture Res.* 8:9.
- Migicovsky, Z., Yeats TH, Watts S, Song J, Forney CF, Burgher-MacLellan K, Somers DJ, Vrebalov J, van Velzen R, Giovannoni JG, Rose JKC, **Myles, S.** (2021) Apple ripening is controlled by a NAC transcription factor. *Frontiers in Genetics* 12:671300.
- Migicovsky, Z., Cousins P, Jordan LM, **Myles S.**, Striegler RK, Verdegaal P, Chitwood DH (2021) Grapevine rootstocks affect growth-related scion phenotypes. *Plant Direct* 5:e00324.
- Mirzayi C, *et al.* [incl. **Langille, MGI**] (2021) Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine* 27:1885-1892.
- More, K. **Simpson, A.G.B.** & Hess, S. (2021) Description of the marine predator *Sericomyxa perlucida* gen. et sp. nov., a cultivated representative of the deepest branching lineage of vampyrellid amoebae (Vampyrellida, Rhizaria). *Journal of Eukaryotic Microbiol.* 68: e12864.
- Nanjappa, D., Y Liang, L Bretherton, C Brown, A Quigg, **AJ Irwin, ZV Finkel** (2021) Contrasting transcriptomic responses of a microbial eukaryotic community to oil and dispersant. *Environmental Pollution* 288: 117774.
- Nearing, J.T., **Langille, MGI** (2021) Identifying biases and their potential solutions in human microbiome studies. *Microbiome* 9: 113.
- Novick, A., **Doolittle, W.F.** (2021) 'Species' without species. *Studies in History and Philosophy of Science* 87:72-80.
- Petrou, E.L., Fuentes-Pardo, A.P., Rogers, L.A., Orobko, M., Tarpey, C., Moss, M.L., Yang, D., Pitcher, T.J., Sandell, T., Lowry, D., **Ruzzante, D.E.**, Hauser, L. (2021) Functional genetic diversity in an exploited marine species and its relevance to management. *Proc. R. Soc. B.* 288: 20202398.
- Pipaliya, S., Santos, R., Salas-Leiva, D., Balmer, E.A., Wirdnam, C.D., **Roger, A.J.**, Hehl, A.B., Faso, C., Dacks, J.B. (2021) Unexpected organellar locations of ESCRT machinery in *Giardia intestinalis* and complex evolutionary dynamics spanning the transition to parasitism in the lineage Fornicata. *BMC Biol.* 19: article 167.
- Price, G.W., **Langille, M.G.I.**, **Yurgel, S.N.** (2021) Microbial co-occurrence network analysis of soils receiving short- and long-term applications of alkaline treated biosolids. *Sci. Total Environ.* 751: 141687.
- Prystupa, S., McCracken, G.R., Perry, R., **Ruzzante, D.E** (2021) Population abundance and structure in Yukon Arctic Grayling using genomics and Close-Kin Mark-Recapture. *Ecol. Evol.* 11: 4763-4773.
- Rakib, M.R.H., **Zeh, N.**, Milios, E. (2021) Efficient clustering of short text streams using online-offline clustering. *Proceedings of the 21st ACM Symposium on Document Engineering*, Article 5: 1-10.
- Roger, A.J.**, **Susko, E.**, Leger, M.M. (2021) Evolution: Reconstructing the timeline of eukaryogenesis. *Current Biol.* 31, R193–R196.
- Rotteveel, L., **Sterling, S.M.** (2021) The Surface Water Chemistry (SWatCh) database: A standardized global database of water chemistry to facilitate large-sample hydrological research. *Earth Syst. Sci. Data Discuss*, [preprint] <https://doi.org/10.5194/essd-2021-43>
- Rowarth, N.M., Curtis, B.A., Einfeldt, A.L., **Archibald, J.M.**, Lacroix, C.R., Gunawardena, A.H.L.A.N. (2021) RNA-Seq analysis reveals potential regulators involved in program cell death and remodeling of lace plant leaves (*Aponogeton madagascariensis*). *BMC Plant Biol.* 21: 375.
- Rybarski, A.E., Nitsche, F., Park, J.S., Filz, P., Schmidt, P., Kondo, R., **Simpson, A.G.B.**, Arndt, H. (2021) Revision of the phylogeny of Placididea (Stramenopiles): Molecular and morphological diversity of novel placidid protists from extreme aquatic environments. *European J. Protistology* 81: 125809.

- Saeidi, M., Milios, E. and **Zeh, N.** (2021) Graph convolutional networks for categorizing online harassment on Twitter. 20th IEEE International Conference on Machine Learning and Applications (ICMLA), pp. 946-951.
- Saeidi, M., Milios, E., **Zeh, N.** (2021) Graph representation learning in Document Wikification. In: Barney Smith, E.H., Pal, U. (Eds), Document Analysis and Recognition – ICDAR 2021 Workshops. Lecture Notes in Computer Science, Vol. 12917, Springer, Cham.
- Saeidi, M., Milios, E., **Zeh, N.** (2021) Contextualized knowledge base sense embeddings in Word Sense Disambiguation. In: Barney Smith, E.H., Pal, U. (eds), Document Analysis and Recognition – ICDAR 2021 Workshops. Lecture Notes in Computer Science, Vol. 12917, Springer, Cham.
- Salas-Leiva, D. E., Tromer, E. C., Curtis, B. A., Jerlstrom-Hultqvist, J., Kolisko, M., Yi, Z., Salas-Leiva, J. S., Gallot-Lavallée, L., Kops, J. J. P. L., **Archibald, J. M.**, **Simpson, A. G. B.** & Roger, A. J. (2021) Genomic analysis finds no evidence of canonical eukaryotic DNA processing systems in a free-living protist. *Nat. Comm.* 12:6003.
- Sibbald, S.J., Lawton, M., **Archibald, J.M.** (2021) Mitochondrial genome evolution in pelagophyte algae. *Genome Biol. Evol.* 13(3): evab018.
- Slaine, P.D., Kleer, M., Duguay, B.A., Pringle, E.S., Kadijk, E., Ying, S., Balgi, A., Roberge, M., **McCormick, C.**, Khaperskyy, D.A. (2021) Thiopurines activate an antiviral unfolded protein response that blocks influenza A virus glycoprotein accumulation. *J. Virol.* 95: e00453-21.
- Stairs C.W., Táborski P., Kolisko M., Pánek T., Eme L., Hradilová M., Vlček C., Jerlström-Hultqvist J., **Roger A.J.** and Čepička I. (2021) Anaeramoebae are a deeply divergent lineage of eukaryotes that clarify the transition from anaerobic mitochondria to hydrogenosomes. *Curr. Biol.* 31: 5605-5612.
- Sultan, M., Nearing, JT, Brown, JM, Hyyh, TT, Cruickshank, BM, Lamoureaux, E., Vidovic, D, Dahn, ML, Fernando, W, Coyle, KM, Giacomantonio, CA, **Langille, MGI**, Marcato, P. (2021) An in vivo genome-wide shRNA screen identifies BCL6 as a targetable paclitaxel resistance mediator in breast cancer. *Mol. Oncol.* 15(8): 2046-2064.
- Susko, E., Roger, A.J.** (2021). Long branch attraction biases in phylogenetics. *Syst. Biol.* 70: 838-843.
- Susko, E., Steel, M., Roger, A.J.** (2021) Conditions under which distribution of edge length ratios on phylogenetic trees can be used to order evolutionary events. *J. Theor. Biol.* 526: 110788.
- Tice AK, Žihala D, Pánek T, Jones RE, Salomaki E, Nenarokov S, Burki F, Eliáš M, Eme L, **Roger A.J.**, Rokas A, Shen X, Strasser JFH, Kolisko M, Brown MW. (2021) PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. *PLoS Biol.* 19(8): e3001365.
- Tsang, K.K, Maguire F., Zubyk, H.L, Chou, S. Edalatmand, A., Wright, G.D, **Beiko, R.G.**, McArthur, A.G. (2021) Identifying novel β -lactamase substrate activity through *in silico* prediction of antimicrobial resistance. *Microbial Genomics* 7(1): mengen000500.
- Valach, M., Gonzalez Alcazar, J.A., Sarrasin, M., Lang, B.F., **Gray, M.W.**, Burger, G. (2021) An unexpectedly complex mitoribosome in *Andalucia godoyi*, a protist with the most bacteria-like mitochondrial genome. *Mol. Biol. Evol.* 38(3): 788-804.
- van Lersel, L., Janssen, R., Jones, M., Murakami, Y., **Zeh, N.** (2021) A unifying characterization of tree-based networks and orchard networks using cherry covers. *Advances in Applied Math* 129: 102222.
- Verburgt, C., KA Dunn, **J Bielawski**, A Otley, M Heyman, W Sunseri, D Shouval, A Levine, T de Meij, J Hyams, L Denson, S Kugathasan, M Benninga, W de Jonge, J Van Limbergen* (2021) OP32 Stool microbiome communities predict remission in treatment-naïve Pediatric Crohn's Disease patients. *Journal of Crohn's and Colitis* 15 (Supplement 1): S030.
- Watts S, McElroy M, Migicovsky Z, Maassen H, van Velzen R, **Myles S** (2021) *Cannabis* labelling is associated with genetic variation in terpene synthase genes. *Nature Plants* 7:1330–1334.
- Watts S, Migicovsky Z, McClure K, Yu C, Amyotte B, Baker T, Bowlby D, Burgher-MacLellan K, Butler L, Donald RG, Fan L, Fillmore S, Flewelling J, Gardner K, Hodges M, Hughes T, Jagadeesan V, Lewis N, MacDonell E, MacVicar L, McElroy M, Money D, O'Hara M, Ong Q, Vinqvist-Tymchuk M, Rupasinghe HPV, DeLong JM, Forney CF, Song J, **Myles S** (2021) Quantifying apple diversity: a

phenomic characterization of Canada's Apple Biodiversity Collection. *Plants, People, Planet* 3(6): 747-760.

- Wijesundara, N.M., Lee, S.F., **Cheng, Z.**, Davidson, R., Rupasinghe, V.H.P. (2021) Carvacrol exhibits rapid bactericidal activity against *Streptococcus pyogenes* through cell membrane damage. *Sci. Reports* 11(1):1487.
- Williams, P.L., D Burgess, SN Waterman, M Roberts, **EM Bertrand**, M Bhatia (2021) Nutrient and Carbon Export from a Tidewater Glacier to the Coastal Ocean in the Canadian Arctic Archipelago. *Journal of Geophysical Research Biogeosci.* 126(9): e2021JG006289.
- Wright, R.J., Bosch, R., **Langille, MGI**, Gibson, M.I., Christie-Oleza, J.A. (2021) A multi-OMIC characterisation of biodegradation and microbial community succession within the PET plastisphere. *Microbiome* 9: 141.
- Wright, R.J., **Langille, MGI**, Walker, T.R. (2021) Food or just a free ride? A meta-analysis reveals the global diversity of the plastisphere. *ISME J.*, 15: 789-806.
- Wright, V., **Archibald, J.M.**, Beinart, R., Dawson, M.N., Hentschel, U., Keeling, P.J., Lopez, J.V., Martín-Durán, J.M., Petersen, J.M., Sigwart, J.D., Simakov, O., Sutherland, K.R., Sweet, M., Talbot, N., Thompson, A.W., Bender, S., Harrison, P.W., Rajan, J., Cochrane, G., Berriman, M., Lawniczak, M., Blaxter, M. (2021) The Aquatic Symbiosis Genomics Project. *Cell Genomics*, in press.
- Wringe, B., Bradbury, I.R., Fisher, J., den Heyer, C., **Ruzzante, D.E.**, Bentzen, P. (2021) Chromosome level reference of Atlantic halibut *Hippoglossus hippoglossus* provides insight into the evolution of sexual determination systems. *Mol. Ecol. Res.*, <https://doi.org/10.1111/1755-0998.13369>
- Youssef, N., **Susko, E.**, **Roger, A.J.** and **Bielawski, J.P.** (2021) Shifts in amino acid preferences as proteins evolve: a synthesis of experimental and theoretical work. *Protein Science* 30:2009-2028.
- Žárský, V., Klimeš V., Pačes J., Vlček C., Hradilová M., Beneš V., Nývltová E., Hrdý I., Pyrih J., Mach J., Barlow L., Stairs C.W., Eme L., Hall N., Eliáš M., Dacks J.B., **Roger, A.J.**, Tachezy J. (2021) The *Mastigamoeba balamuthi* genome and the nature of the free-living ancestor of *Entamoeba*. *Mol. Biol. Evol.* 38(6): 2240-2259.
- Zeng Q, Yang Z, Wang F, Li D, Liu Y, Wang D, Zhao X, Li Y, Wang Y, Feng X, Chen J, Li Y, Zheng Y, **Kenney T, Gu H**, Feng S, Li S, He Y, Xu X, Dai W. (2021) Association between metabolic status and gut microbiome in obese populations. *Microb. Genom.* 7(8):000639.
- Zhang, J., Cook, J., Nearing, J.T., Zhang, J., Raudonis, R., Glick, B.R., **Langille, M.G.I.**, **Cheng, Z.** (2021) Harnessing the plant microbiome to promote the growth of agricultural crops. *Microbiol. Res.* 245: 126690.
- Zhang, T., Li, C., Zhang, Z., Wang, C., **Roger, A.J.**, Gao, F. (2021) Characterization and comparative analyses of mitochondrial genomes in single-celled eukaryotes to shed light on the diversity and evolution of linear molecular architecture. *Int. J. Mol. Sci.* 22: 2546.
- Zhang, Y., Li, Z., Schulz, K.G., Hu, Y., **Irwin, A.J.**, **Finkel, Z.V.** (2021) Growth-dependent changes in elemental stoichiometry and macromolecular allocation in the coccolithophore *Emiliania huxleyi* under different environmental conditions. *Limnol. Oceanogr.* 66(8): 2999-3009.

Year 2020:

- Alcock *et al.* [24 authors incl. **Beiko, R.G.**] (2020) CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Res.* 48: D517-D525.
- Amirian, M.M.**, Towers, I., Jovanoski, Z., **Irwin, A.J.** (2020) Memory and mutualism in species sustainability: a time-fractional Lotka-Volterra model with harvesting. *Heliyon* 6(8): e04816.
- Archibald, J.M.** (2020) Quick Guide: Cryptomonads. *Curr. Biol.* 30: R1114-R1116.
- Attwood, KM, Robichaud A, Westhaver LP, Castle EL, Brandman DM, Balgi AD, Roberge M, Colp P, Croul S, Kim I, **McCormick C**, Corcoran JA, Weeks A. (2020) Raloxifene prevents stress granule dissolution, impairs translational control and promotes cell death during hypoxia in glioblastoma cells. *Cell Death Dis.* 11: 989.

- Behnke, J., LaRoche, J. (2020) Iron uptake proteins in algae and the role of Iron Starvation-Induced Proteins (ISIPs). *Eur. J. Phycol.* 55(3), 339-360.
- Benner, I., **Irwin, A.J.** and **Finkel, Z.V.** (2020) Capacity of the common Arctic picoeukaryote *Micromonas* to adapt to a warming ocean. *Limnol. Oceanogr. Letters* 5(2): 221-227.
- Bretherton, L., Hillhouse, J., Kamalanathan, M., Finkel, Z.V., Irwin, A.J. and Quigg, A. (2020) Trait-dependent variability of the response of marine phytoplankton to oil and dispersant exposure. *Marine Pollut. Bull.* 153: 110906.
- Burki, F., **Roger, A.J.**, Brown, M.W. and **Simpson, A.G.B.** (2020) The new tree of eukaryotes. *Trends Ecol. Evol.* 35: 43-55.
- Colp, M., Archibald, J.M. (2020) The language of symbiosis: insights from protist biology. In: *Cellular dialogues in the holobiont*, Bosch, T. and Hadfield, M. (Eds.), *CRC Press*. Invited book chapter.
- Connors, J., Dunn, K.A., Allott, J., Bandsma, R., Rashid, M., Otley, A.R., **Bielawski, J.P.** and *Van Limbergen, J. (2020) The relationship between fecal bile acids and microbiome community structure in pediatric Crohn's disease. *ISME J.* 14: 702-713.
- Crouse, A., Schramm, C., Emond-Rheault, J.G., Herod, A., Kerhoas, M., **Rohde, J.**, Gruenheid, S., Kukavica-Ibrulj, I., Boyle, B., Greenwood, C.M.T., Goodridge, L.D., Garduno, R., Levesque, R.C., Malo, D., Daigle, F. (2020) Combining whole-genome sequencing and multimodel phenotyping to identify genetic predictors of *Salmonella* Virulence. *mSphere* 5(3): e00293-20.
- Cui, T.T., Dawson, T.J., McLatchie, S., Dunn, K.A., **Bielawski, J.P.**, Walsh, D.A. (2020) Modelling free-living and particle-associated bacterial assemblages across the deep and hypoxic Lower St. Lawrence Estuary. *MSphere* 5(3): e00364-20.
- Delgado, M.L., Ruzzante, D.E. (2020) Investigating diadromy in fishes and its loss in an -omics era. *iScience* 23(12): 101837.
- Delgado, M.L., Manosalva, A., Urbina, M., Habit, E., Link, O., Ruzzante, D.E. (2020) Genomic basis of the loss of diadromy in *Galaxias maculatus*: insights from reciprocal transplant experiments. *Mol. Ecol.* 29: 4857–4870.
- de Vries, J., de Vries, S., Curtis, B.A., Zhou, H., Penny, S., Feussner, K., Pinto, D.M., Steinert, M., Cohen, A., von Schwanzenberg, K., Archibald, J.M. (2020) Heat stress response in the closest algal relatives of land plants reveals conserved stress signalling circuits. *Plant J.* 103: 1025-1048.
- de Vries, S., de Vries, J., Archibald, J.M., Slamovits, C.H. (2020) Comparative analyses of saprotrophy in *Salisapilia sapeloensis* and diverse plant pathogenic oomycetes reveal lifestyle-specific gene expression. *FEMS Microbiol. Ecol.* 96 (11), fiae184.
- Dinh, V., **Ho, L.S.T.** (2020) Consistent feature selection for analytic deep neural networks. *Neural Information Processing Systems (NeurIPS 2020)*, [arXiv:2010.08097v1](https://arxiv.org/abs/2010.08097v1)
- Doolittle, W.F.** (2020) Could this pandemic usher in evolution's next major transition?. *Curr. Biol.* 30: R846-R848.
- Doolittle, W.F.** (2020) Is the earth an organism?. *Aeon* (published Dec. 3).
- Doolittle, W.F.** (2020) Why I am not a creationist: the devil in the details. *Physics in Canada* 76: 1.
- Doolittle, W.F.** (2020) Evolution: Two domains of life or three? *Curr. Biol.* 30: R177-R179.
- Douglas, G.M., Bielawski, J.P., Langille, M.G.I. (2020) Re-evaluating the relationship between missing heritability and the microbiome. *Microbiome* 8: 87.
- Douglas, G.M., Maffei, V.J., Zaneveld, J., Yurgel, S.N., Brown, J.R., Taylor, C.M., Huttenhower, C., Langille, MGI (2020) PICRUSt2 for prediction of metagenome functions. *Nature Biotechnol.* 38:685-688.
- Faktorová D. *et al.* [95 authors incl. **Slamovits, CH**] (2020) Genetic tool development in marine protists: emerging model organisms for experimental cell biology. *Nat. Methods* 17(5):481-494.
- Finkel, Z.V., Irwin, A.J.** (2020) Phytoplankton. In Gargaud *et al.* (Eds), *Encyclopedia of Astrobiology*, Springer; 10.1007/978-3-642-27833-4_5416-1

- Finkel, Z.V.**, **Liang, Y.**, Nanjappa, D., **Bretherton, L.**, Brown, C.M., Quigg, A., **Irwin, A.J.** (2020) A ribosomal sequence-based oil sensitivity index for phytoplankton groups. *Marine Pollut. Bull.* 151: 110798.
- Gallot-Lavallée, L.**, **Archibald, J.M.** (2020) Spotlight: Phagocytosis in a shape-shifting bacterium. *Trends Microbiol.* 28, 429-430.
- Gallot-Lavallée, L.**, **Archibald, J.M.** (2020) Evolutionary Biology: Viral rhodopsins illuminate algal evolution. *Curr. Biol.* 30, R1469-1471.
- Gradone, J.C., Oliver, M.J., Davies, A.R., **Irwin, A.**, Moffat, C. (2020) Sea surface kinetic energy as a proxy for phytoplankton light limitation in the summer pelagic Southern Ocean. *J. Geophys. Res: Oceans* 125(3): e2019JC015646.
- Gray, M.W.**, Gopalan, V. (2020) Piece by piece: Building a ribozyme. *J. Biol. Chem.* 295: 2313-2323.
- Gray, M.W.**, Burger, G., Derelle, R., Klimes, V., Leger, M.M., Sarrasin, M., Vlcek, C., **Roger, A.J.**, Elias, M., Lang, B.F. (2020) The draft nuclear genome sequence and predicted mitochondrial proteome of *Andalucia godoyi*, a protist with the most gene-rich and bacteria-like mitochondrial genome. *BMC Biol.* 18: 22.
- Hassler, G., Tolkoﬀ, M.R., Allen, W.L., **Ho, L.S.T.**, Lemey, P., Suchard, M.A. (2020) Inferring phenotypic trait evolution on large trees with many incomplete measurements. *J. Amer. Stat. Assoc.*, DOI: 10.1080/01621459.2020.1799812
- Ho, L.S.T.**, Dinh, V., Matsen IV, F.A., Suchard, M.A. (2020). On the convergence of the maximum likelihood estimator for the transition rate under a 2-state symmetric model. *Journal Math. Biol.* 80(4): 1119–1138.
- Ho, L.S.T.**, Schaeffer, H., Tran, G., Ward, R. (2020). Recovery guarantees for polynomial coefficients from weakly dependent data with outliers. *J. Approx. Theory* 259: 105472.
- Ho, L.S.T.**, Nguyen, B.T., Dinh, V., Nguyen, D. (2020). Posterior concentration and fast convergence rates for generalized Bayesian learning. *Information Sci.* 538:372-383.
- Jabre, L.**, **Bertrand, E.M.** (2020) Interactive effects of iron and temperature on the growth of *Fragilariopsis cylindrus*. *Limnol. Oceanogr. Letters* 5: 363-370.
- Jabre, L.**, Allen, A.E., **McCain, J.S.P.**, McCrow, J.P., Tenenbaum, N., Spackeen, J.E., Sipler, R.E., Green, B.R., Bronk, D.A., Hutchins, D.A., **Bertrand, E.M.** (2020) Molecular underpinnings and biogeochemical consequences of enhanced diatom growth in a warming Southern Ocean. *PNAS*; doi:10.1073/pnas.2107238118.
- Johnston, B.P.**, **McCormick, C.** (2020) Herpes viruses and the unfolded protein response. *Viruses* 12(1): 17.
- Jones, C.M.A., Connors, J., **Dunn, K.A.**, **Bielawski, J.P.**, **Comeau, A.M.**, **Langille, M.G.I.**, *Van Limbergen, J. (2020) Bacterial taxa and functions are predictive of sustained remission following exclusive enteral nutrition in pediatric Crohn’s Disease. *Inflamm. Bowel Dis.* 26: 1026-1037.
- Jones, C.T.**, **Youssef, N.**, **Susko, E.**, **Bielawski, J.P.** (2020) A phenotype-genotype codon model for detecting adaptive evolution. *Syst. Biol.* 69: 722–738.
- Karimi, K., Farid A.H., Sargolzaei M., **Myles S.**, Miar Y. (2020) Linkage disequilibrium, effective population size and genomic inbreeding rates in American mink using denotyping-by-sequencing data. *Frontiers Genet.* 11:223.
- Kenney, T.**, **Gao, J.**, **Gu, H.** (2020) Application of OU processes to modelling temporal dynamics of the human microbiome, and calculating optimal sampling schemes. *BMC Bioinf.* 21: 450.
- Kim, J.I., Jeong, M., **Archibald, J.M.**, Shin, W. (2020) Comparative plastid genomics of non-photosynthetic chrysophytes: genome reduction and compaction. *Frontiers Plant Sci.* 11:572703.
- Kolisko, M., Flegontova, O., Karnkowska, A., **Lax, G.**, Maritz, J.M., Pánek, T., Táborský, P., Carlton, J.M., Čepička, I., Horák, A., Lukeš, J., **Simpson, A.G.B.**, Tai, V. (2020) EukRef-Excavates: Seven curated SSU ribosomal RNA gene databases. *Database* 2020: baaa80.

- Lax, G., Simpson, A.G.B. (2020) The molecular diversity of phagotrophic euglenids examined using single-cell methods. *Protist* 171: 125757.
- Layton, KKS, Dempson B., Snelgrove P.V.R., Duffy S.J., Messmer A.M., Paterson I.G., Jeffery N.W., Kess T., Horne J.B., Salisbury S.J., Ruzzante D.E., Bentzen P., Côté D., Nugent C.M., Ferguson M.M., Leong J.S., Koop B.F., Bradbury I.R. (2020) Resolving fine-scale population structure and fishery exploitation using sequenced microsatellites in a northern fish. *Evol. Applic.* 13: 1055-1068.
- Li, Z., Li, W., Zhang, Y., Hu, Y., Sheward, R., Irwin, A.J., Finkel, Z.V. (2020) Dynamic photophysiological stress response of a model diatom to ten environmental stresses. *J. Phycol.* 57: 484-495.
- Li, Z-K., Dai, G., Zhang, Y., Xu, K., Bretherton, L., Finkel, Z.V., Irwin, A.J., Juneau, P., Qiu, B-S. (2020) Photosynthetic adaptation to light availability shapes the ecological success of bloom-forming cyanobacterium *Pseudanabaena* to iron limitation. *J. Phycol.* 56: 1457-1467.
- Linquist, S., Doolittle, W.F., Palazzo, A.F. (2020) Getting clear about the F-word in genomics. *PLoS Genet.* 16(4): e1008702.
- Maguire, F., Baofeng, J., Gray, K.L., Wing, L., Venus, Y., Beiko R.G., Brinkman, F.S.L. (2020) Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic islands. *Microb. Genom.* 6(10): mgen000436.
- Matzov, D., Taoka, M., Nobe, Y., Yamauchi, Y., Halfon, Y., Asis, N., Zimmermann, E., Rozenberg, H., Bashan, A., Bhushan, S., Isobe, T., Gray, M.W., Yonath, A., Shalev-Benami, M. (2020) Cryo-EM structure of the highly atypical cytoplasmic ribosome of *Euglena gracilis*. *Nucleic Acids Res.* 48, 11750-11761.
- Mutshinda, C.M., Finkel, Z.V., Widdicombe, C.E., Irwin, A.J. (2020) A trait-based clustering for phytoplankton biomass modeling and prediction. *Diversity* 12: 295.
- Mutshinda, C.M., Irwin, A.J., Sillanpää, M.J. (2020) A Bayesian framework for robust quantitative trait locus mapping and outlier detection. *Int. J. Biostat.*, doi:10.1515/ijb-2019-0038
- Najle, S.R. et al. [incl. Slamovits, C.H.] (2020) Genome-wide transcriptional analysis of *Tetrahymena* thermophile response to exogenous cholesterol. *J. Eukaryot. Microbiol.* 67: 209-222.
- Nearing, J.T., DeClercq, V., Van Limbergen, J., Langille, MGI (2020) Assessing the variation within the oral microbiome of healthy adults. *mSphere* 5: e00451-20.
- Nejman, D. et al. [56 authors incl. Langille, M.G.I.] (2020) The human tumor microbiome is composed of tumor type-specific intracellular bacteria. *Science* 368(6494): 973-980.
- Novick, A., Doolittle, W.F. (2020) Horizontal persistence and the complexity hypothesis. *Biol. Philos.* 35: 2.
- Omar, T., Ziltenera P., Chamberlaina E., Cheng Z., Johnston B. (2020) Role of $\gamma\delta$ T cells in *Pseudomonas aeruginosa* lung infection. *Infect. Immun.* 88(6): e00171-20.
- Omta, A.W., Talmy, D., Inomura, K., Irwin, A.J., Finkel, Z.V., Sher, D., Liefer, J.D., Follows, M.J. (2020) Quantifying nutrient throughput and DOM production by algae in continuous culture. *J. Theor. Biol.* 494: 110214.
- Ontiveros, C.C., Sweeney C.L., Smith C., McIsaac S., Munoz S., Davidson R., McCormick C., Thomas N., Davis I., Stoddart A.K., Gagnon G.A. (2020) Characterization of a commercially-available, low pressure UV lamp as a disinfection system decontamination of common nosocomial pathogens on N95 Filtering Facepiece Respirator (FFR) material. *Env. Sci.: Water Res. Technol.* 6: 2089-2102.
- Palau, M., Piqué, N., Comeau, A.M., Douglas, G.M., Ramírez-Lázaro, M.J., Lario, S., Calvet, X., Langille, M.G.I., Miñana-Galbis, D. (2020) Detection of *Helicobacter pylori* microevolution and multiple infection from gastric biopsies by housekeeping gene amplicon sequencing. *Pathogens* 9(2): E97.
- Pang, Z., Raudonis R., McCormick C., Cheng Z. (2020) Early growth response 1 deficiency protects host against *Pseudomonas aeruginosa* lung infection. *Infect. Immun.* 88(1): e00678-719.
- Parenteau, M.T., Gu, H., Zebarth, B.J., Cambouris, A.N., Lafond, J., Nelson, A., Nyiraneza, J., Davidson, C., Lagüe, M., Galvez, J.H., Strömvik, M.V., Tai, H.H. (2020) Data mining nitrogen-responsive

- gene expression for source–sink relations and indicators of N status in potato. *Agronomy* 2020, 10(10): 1617.
- Peabody, M.A., Lau, W.Y.V., Hoad, G.R., Jia, B., Maguire, F., Gray, K.L., **Beiko, R.G.**, Brinkman, F.S.L. (2020) PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. *Bioinformatics* 36: 3043-3048.
- Price, G.W., **Langille, M.G.I.**, **Yurgel, S.N.** (2020) Microbial co-occurrence network analysis of soils receiving short- and long-term applications of alkaline treated biosolids. *Science of the Total Environ.* 751: 141687.
- Pringle, E.S., Robinson C.A., Crapoulet N., Monjo AL-A., Bouzanis K., Leidal A.M., Lewis S.M., Gaston D., Uniacke J., **McCormick C.** (2020) KSHV lytic mRNA is efficiently translated in the absence of eIF4F. *bioRxiv* 356162; online: <https://doi.org/10.1101/356162>
- Pringle, E.S., Wertman J., Melong N., Coombs A.J., Young A.L., O’Leary D., Veinotte C., Robinson C-A., Ha M.N., Dellaire G., Druley T.E., **McCormick C.**, Berman J.N. (2020) The zebrafish xenograft platform – a novel tool for modeling KSHV-associated diseases. *Viruses* 12(1): 12.
- Rahim, M.M., Parsons B., Price E.L., Slaine P.D., Chilvers B.L., Seaton G.S., Wight A., Medina-Luna D., Dey S., Grandy S.L., Anderson L.E., Zamorano C.N., Grandvaux N., Gaglia M.M., Kelvin A.A., Khapersky D.A., **McCormick C.**, Makrigiannis A.P. (2020) Defective influenza A virus RNA products mediate MAVS-dependent upregulation of human leukocyte antigen class I proteins. *J. Virol.* 94(13): 00165-20.
- Rotteveel, L., **Sterling, S.M.** (2020) Five aluminum seasonality regimes identified in chronically acidified rivers of Nova Scotia. *Environ. Sci. Technol.* 54: 807-817.
- Roy, A-S., Woehle, C., **LaRoche, J.** (2020) The transfer of the Ferredoxin gene from the chloroplast to the nuclear genome is ancient within the paraphyletic Genus *Thalassiosira*. *Front. Microbiol.* 11:523689.
- Ruzzante, D.E.**, Simons, A.P., McCracken, G.R., Habit, E., Walde, S.J. (2020) Multiple drainage reversal episodes and glacial refugia in a Patagonian fish revealed by sequenced microsatellites. *Proc. R. Soc. B* 287: 20200468.
- Salisbury, S.J., McCracken, G.R., Perry, R., Keefe, D., Layton, KKS, Kess, T., Nugent, C.M., Bradbury, I.R., Koop, B.F., Ferguson, M.M., **Ruzzante, D.E.** (2020) Limited genetic parallelism underlies recent, repeated incipient speciation in geographically proximate populations of an Arctic fish (*Salvelinus alpinus*). *Mol. Ecol.* 29: 4280-4294.
- Sibbald, S.J., **Archibald, J.M.** (2020) Genomic insights into plastid evolution. *Genome Biol. Evol.* 12(7): 978-990. Invited review article.
- Sibbald S.J., Eme L., **Archibald J.M.**, **Roger A.J.** (2020) Lateral gene transfer mechanisms and pan-genomes in eukaryotes. *Trends Parasitol.* 36: 927-941. Invited review article.
- Simpson A.G.B.** et. coll. (2020) Eukarya; Opisthokonta; Archaeplastida; Stramenopila; Alveolata; Rhizaria; Metamonada: Discoba; Discicristata; Euglenozoa. In de Queiroz, K., Cantino, P.D., Gauthier, J.A. (eds), *International Code of Phylogenetic Nomenclature, Companion Volume*, CRC Press.
- Sterling, S.M.**, MacLeod, S., Rotteveel, L., Hart, K., Clair, T.A., Halfyard, E.A., O'Brien, N.L. (2020). Ionic aluminium concentrations exceed thresholds for aquatic health in Nova Scotian rivers, even during conditions of high dissolved organic carbon and low flow. *Hydrol. Earth System Sci.* 24(10), 4763-4775.
- Stolz, M.L., **McCormick, C.** (2020) The bZIP proteins of oncogenic viruses. *Viruses* 12(1): 757.
- Susko, E.**, **Roger, A.J.** (2020) On the use of information criteria for model selection in phylogenetics. *Mol. Biol. Evol.* 37: 549-562.
- Tanifuji, G., Kamikawa, R., Moore, C.E., Mills, T., Onodera, N.T., Kashiyama, Y., **Archibald, J.M.**, Inagaki, Y., Hashimoto, T. (2020) Comparative plastid genomics of *Cryptomonas* species reveals fine-scale genomic responses to loss of photosynthesis. *Genome Biol Evol.* 12: 3926-3937.

- Valenzuela-Aguayo, F., McCracken, G.R., Manosalva, A., Habit, E., Ruzzante, D.E. (2020) Anthropogenic habitat fragmentation effects on connectivity, diversity and persistence of the endemic *Percilia irwini*, in the Biobío system in Chile. *Evol. Applic.* 13: 794-807.
- Vera-Escalona, I, Delgado, M.L., Habit, E, **Ruzzante, D.E.** (2020) Historical and contemporary diversity of galaxiids in South America: biogeographic and phylogenetic perspectives. *Diversity* 2020, 12: 304.
- Wandel, M.P., Kim, B-H, Park, E-S, Boyle, K.B., Nayak, K., Lagrange, B., Herod, A., Henry, T., Zilbauer, M., **Rohde, J.**, MacMicking, J.D., Randow, F. (2020) Guanylate-binding proteins convert cytosolic bacteria into caspase-4 signaling platforms. *Nature Immunol.* 21: 880-891.
- Wright, R.J., Langille, M.G.I., Walker, T.R. (2020) Food or just a free ride? A meta-analysis reveals the global diversity of the Plastisphere. *ISME J.* 15(3): 789-806.
- Wu, L., Zeng, T., Deligios, M., Milanesi, L., **Langille, MGI**, Zinellu, A., Rubino, S., Carru, C. and Kelvin, D. (2020) Age-related variation of bacterial and fungal communities in different body habitats across the young, elderly and centenarians in Sardinia. *mSphere* 5: e00558-19.
- Yazaki, E., Kume, K., Shiratori, T., Eglit, Y., Tanifuji, G., Harada, R., **Simpson, A.G.B.**, Ishida, K., Hashimoto, T., Inagaki, Y. (2020) Barthelonids represent a deep-branching metamonad clade with mitochondrion-related organelles predicted to generate no ATP. *Proc. Royal Soc. Series B.* 287: 20201538.
- Youssef, N., Susko, E., Bielawski, J.P. (2020) Consequences of stability-induced epistasis for substitution rates. *Mol. Biol. Evol.* 37: 3131–3148.
- Zhao, J., Azad, M.B., **Bertrand, E.M.** *et al.* (2020). Canadian Science Meets Parliament: Building relationships between scientists and policymakers. *Science and Public Policy*, <https://doi.org/10.1093/scipol/scz062>

Year 2019:

- Archibald, J.M.** (2019) Genomics reveals alga-associated cyanobacteria hiding in plain sight. *Proc. Natl. Acad. Sci. USA* 116: 15757-15759.
- Asman, A.K.M., Curtis, B.A. and **Archibald, J.M.** (2019) Nucleomorph small RNAs in cryptophyte and chlorarachniophyte algae. *Genome Biol. Evol.* 11: 1117-1134.
- Bolyen, E. *et al.* [100 authors, incl. **Langille, M.G.I., Douglas, G.M.**] (2019) Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat. Biotechnol.* 37: 852-857.
- Chen, W., Kenney, T., Bielawski, J.P. and **Gu, H.** (2019) Testing adequacy for DNA substitution models. *BMC Bioinformatics* 20: 349.
- Colp, M.J. and **Archibald, J.M.** (2019) Evolution: New protist predators under the sun. *Curr. Biol.* 29: R936-R938.
- DesRoches, C.T., Inkpen, S.A. and Green, T.L. (2019) The eroding artificial/natural distinction? Some consequences for ecology and economics. In M. Nagatsu and A. Ruzzante (Eds.), *Philosophy and Social Science: An Interdisciplinary Dialogue*, Bloomsbury Publishing, London, UK.
- de Vries, S., de Vries, J., Archibald, J.M. and **Slamovits, C.S.** (2019) Comparative analyses of saprotrophy in *Salisapilia sapeloensis* and diverse plant pathogenic oomycetes reveal lifestyle-specific gene expression. *FEMS Microbiol. Ecol.* 96: fiaa184.
- Doolittle, W.F.** (2019) Making evolutionary sense of Gaia. *Trends Ecol. Evol.* 34: 889-894.
- Doolittle, W.F.** (2019) Speciation without species: a final word. *Philos. Theory Practice Biol.* 11: 14.
- Douglas, G.M. and **Langille, M.G.I.** (2019) Current and promising approaches to identify horizontal gene transfer events in metagenomes. *Genome Biol. Evol.* 11: 2750-2766.
- Dunn, K.A., Kenny, T., Gu, H. and **Bielawski, J.P.** (2019) Improved inference of site-specific positive selection under a generalized parametric codon model when there are multinucleotide mutations and multiple nonsynonymous rates. *BMC Evol. Biol.* 19: 22.

- Frail-Gauthier, J.L., Mudie, P.J., **Simpson, A.G.B.** & Scott, D.B. (2019) Mesocosm and microcosm experiments on the feeding of temperate salt marsh foraminifera. *J. Foraminiferal Res.* 49: 259-274.
- Galindo, L.J., Torruella, G., Moreira, D., Eglit, Y., **Simpson, A.G.B.**, Völcker, E., Clauß, S. and López-García, P. (2019) Combined cultivation and single-cell approaches to the phylogenomics of nuclearioid amoebae, close relatives of fungi. *Philos. Trans. R Soc. Lond. B Biol. Sci.* 374: 20190094.
- Grisdale, C.J., Smith, D.R. and **Archibald, J.M.** (2019) Relative mutation rates in nucleomorph-bearing algae. *Genome Biol. Evol.* 11: 1045-1053.
- Haas, S., Desai, D.K., **LaRoche, J.**, Pawlowicz, R. and Wallace, D.W.R. (2019) Geomicrobiology of the carbon, nitrogen and sulphur cycles in Powell Lake: a permanently stratified water column containing ancient seawater. *Environ Microbiol.* 21(10): 3927-3952.
- Hess, S., Eme, L., **Roger, A.J.** and **Simpson, A.G.B.** (2019) A natural toroidal microswimmer with a rotary eukaryotic flagellum. *Nat. Microbiol.* 4: 1620-1626.
- Houfani, A.A., Větrovský, T., Navarrete, O.U., Štursová, M., Tláskal, V., **Beiko, R.G.**, Boucherba, N., Baldrian, P., Benallaoua, S. and Jorquera, M.A. (2019) Cellulase-hemicellulase activities and bacterial community composition of different soils from Algerian ecosystems. *Microb Ecol.* 77: 713-725.
- Jones, C.T., **Susko, E.** and **Bielawski, J.P.** (2019) Looking for Darwin in genomic sequences: Validity and success depends on the relationship between model and data. *Methods Mol. Biol.* 1910: 399-426.
- Jones, C.T., Youssef, N., **Susko, E.** and **Bielawski, J.P.** (2019) A phenotype-genotype codon model for detecting adaptive evolution. *Syst. Biol.*, Nov. 15; pii: syz075.
- Karnkowska, A., Treitli, S.C., Brzoň, O., Novák, L., Vacek, V., Soukal, P., Barlow, L.D., Herman, E.K., Pipaliya, S., Pánek, T., Žihala, D., Petrželková, R., Butenko, A., Eme, L., Stairs, C.W., **Roger, A.J.**, Eliáš, M., Dacks, J.B. and Hampl, V. (2019) The oxymonad genome displays canonical eukaryotic complexity in the absence of a mitochondrion. *Mol. Biol. Evol.* 36: 2292-2312.
- Kim, J.I., Shin, H., Škaloud, P., Jung, J., Yoon, H.S., **Archibald, J.M.** and Shin, W. (2019) Comparative plastid genomics of Synurophyceae: inverted repeat dynamics and gene content variation. *BMC Evol. Biol.* 19: 20.
- Lax, G., Lee, W.J., Eglit, Y. and **Simpson, A.G.B.** (2019) Ploetids represent much of the phylogenetic diversity of euglenids. *Protist* 170: 233-257.
- Leger, M.M., Kolisko, M., Stairs, C.W. and **Simpson, A.G.B.** (2019) Mitochondrion-related organelles in free-living protists. In J. Tachezy (Ed.), *Hydrogenosomes and mitosomes: Mitochondria of anaerobic eukaryotes*, 2nd edition, pp. 287-308, Springer Cham.
- Levine, A., Wine, E., Assa, A., Sigall Boneh, R., Shaoul, R., Kori, M., Cohen, S., Peleg, S., Shamali, H., On, A., Millman, P., Abramson, L., Ziv-Baran, T., Grant, S., Abitbol, G., Dunn, K.A., **Bielawski, J.P.** and *Van Limbergen, J. (2019) Crohn's Disease exclusion diet plus partial enteral nutrition induces sustained remission in a randomized controlled trial. *Gastroenterol.* 157: 440-450.
- Louropoulou, E., Gledhill, M., Browning, T.J., Desai, D.K., Barraqueta, J.M., Tonnard, M., Sarthou, G., Planquette, H., Bowie, A.R., Schmitz, R.A., **LaRoche, J.** and Achterberg, E.P. (2019) Regulation of the phytoplankton Heme *b* iron pool during the North Atlantic spring bloom. *Front Microbiol.* 10: 1566.
- Maguire, F., Rehman, M.A., Carrillo, C., Diarra, M.S. and **Beiko, R.G.** (2019) Identification of primary antimicrobial resistance drivers in agricultural nontyphoidal *Salmonella enterica* serovars by using machine learning. *mSystems* 4(4); pii: e00211-219.
- McCain, J.S.P. and **Bertrand, E.M.** (2019) Prediction and consequences of cofragmentation in metaproteomics. *J. Proteome Res.* 18: 3555-3566.

- Michl, S.C., Beyer, M., Ratten, J.M., Hasler, M., **LaRoche, J.** and Schulz, C. (2019) A diet-change modulates the previously established bacterial gut community in juvenile brown trout (*Salmo trutta*). *Sci Rep.* 9(1): 2339.
- Mingrone, J., Susko, E. and Bielawski, J.** (2019) ModL: exploring and restoring regularity when testing for positive selection. *Bioinformatics* 35: 2545-2554.
- More, K., Simpson, A.G.B. and Hess, S.** (2019) Two new marine species of Placopus (Vampyrellida, Rhizaria) that perforate the theca of Tetraselmis (Chlorodendroales, Viridiplantae). *J. Eukaryot. Microbiol.* 66: 560-573.
- Muñoz-Gómez, S.A., Durnin, K., Eme, L., Paight, C., Lane, C.E., Saffo, M.B. and Slamovits, C.H.** (2019) Nephromyces represents a diverse and novel lineage of the apicomplexa that has retained apicoplasts. *Genome Biol Evol.* 11(10): 2727-2740.
- Muñoz-Gómez, S.A., Hess, S., Burger, G., Lang, B.F., Susko, E., Slamovits, C.H. and Roger, A.J.** (2019) An updated phylogeny of the alphaproteobacteria reveals that the parasitic *Rickettsiales* and *Holosporales* have independent origins. *eLife* 8, pii: e42535.
- Nadukkalam Ravindran, P., Bentzen, P., Bradbury, I.R. and Beiko, R.G.** (2019) RADProc: A computationally efficient *de novo* locus assembler for population studies using RADseq data. *Mol. Ecol. Resour.* 19: 272-282.
- Najle, S.R., Hernández, J., Ocaña-Pallarès, E., García Siburú, N., Nusblat, A.D., Nudel, C.B., **Slamovits, C.H.** and Uttaro, A.D. (2019) Genome-wide transcriptional analysis of *Tetrahymena thermophile* response to exogenous cholesterol. *J. Eukaryot. Microbiol.* 67(2): 209-222.
- Nearing, J.T., Connors, J., Whitehouse, S., *Van Limbergen, J., Macdonald, T., Kulkarni, K. and Langille, M.G.I.** (2019) Infectious complications are associated with alterations in the gut microbiome in pediatric patients with acute lymphoblastic leukemia. *Front Cell. Infect. Microbiol.* 9: 28.
- Novick, A. and Doolittle, W.F.** (2019) How microbes “jeopardize” the modern synthesis. *PLoS Genet.* 15: e1008166.
- O’Malley, M.A., Leger, M.M., **Wideman, J.G.** and Ruiz-Trillo, I. (2019) Concepts of the last eukaryotic common ancestor. *Nature Ecol. Evol.* 3: 338-344.
- Paight, C., **Slamovits, C.H., Saffo, M.B. and Lane, C.E.** (2019) Nephromyces encodes a urate metabolism pathway and predicted peroxisomes, demonstrating that these are not ancient losses of Apicomplexans. *Genome Biol. Evol.* 11: 41-53.
- Saito, M.A., Bertrand, E.M., Duffy, M.E., Gaylord, D.A., Held, N.A., Hervey, W.J. 4th, Hettich, R.L., Jagtap, P.D., Janech, M.G., Kinkade, D.B., Leary, D.H., McIlvin, M.R., Moore, E.K., Morris, R.M., Neely, B.A., Nunn, B.L., Saunders, J.K., Shepherd, A.I., Symmonds, N.I. and Walsh, D.A.** (2019) Progress and challenges in ocean metaproteomics and proposed best practices for data sharing. *J. Proteome Res.* 18: 1461-1476.
- Sibbald, S.J., Hopkins, J.F., Filloramo, G.V. and Archibald, J.M.** (2019) Ubiquitin fusion proteins in algae: implications for cell biology and the spread of photosynthesis. *BMC Genomics* 20: 38.
- Simpson, A.G.B.** and Cepicka, I. (2019) Amitochondriate protists (Diplomonads, Parabasalids and Oxymonads). In *Encyclopedia of Microbiology*, 4th Edition, Elsevier.
- Singh *et al.* [21 authors, incl. **Langille, M.G.I.**] (2019) Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. *Nat. Commun.* 10: 89.
- Tikhonenkov, D.V., Jhin, S.H., **Eglit, Y., Miller, K., Plotnikov, A., Simpson, A.G.B. and Park, J.S.** (2019) Ecological and evolutionary patterns in the enigmatic protist genus Percolomonas (Heterolobosea; Discoba) from diverse habitats. *PLoS One* 14(8): e0216188.
- Wang, H.-C., Susko, E. and Roger, A.J.** (2019) The relative importance of modeling site pattern heterogeneity versus partition-wise heterotachy in phylogenomic inference. *Syst. Biol.* 68: 1003-1019.
- Wideman, J.G., Novick, A., Muñoz-Gomez, S. and Doolittle, W.F.** (2019) Neutral evolution of cellular phenotypes. *Curr. Op. Gen. Dev.* 58-59: 87-94.

- Wideman, J.G., Inkpen, S.A., **Doolittle, W.F.** and Redfield, R.J. (2019) Mutationism, not Lamarckism, captures the novelty of CRISPR-Cas. *Biol. Philos.* 34: 12.
- Wideman, J.G., Lax, G., Leonard, G., Milner, D.S., Rodríguez-Martínez, R., **Simpson, A.G.B.** and Richards, T.A. (2019) *Philos. Trans. R Soc. Lond. B Biol. Sci.* 374: 20190100.
- Willis, C., Desai, D. and **LaRoche, J.** (2019) Influence of 16S rRNA variable region on perceived diversity of marine microbial communities of the northern north Atlantic. *FEMS Microbiol. Lett.* 366: pii: fnz152.
- Wu, M., McCain, J.S.P., Rowland, E., Middag, R., Sandgren, M., Allen, A.E. and **Bertrand, E.M.** (2019) Manganese and iron deficiency in southern ocean *Phaeocystis antarctica* populations revealed through taxon-specific protein indicators. *Nat. Commun.* 10: 3582.
- Youssef, N., Budd, A. and **Bielawski, J.P.** (2019) Introduction to Genome Biology and Diversity. In *Evolutionary Genomics: Statistical and Computational Methods*, Maria Anisimova (ed.), 2nd edition, pp. 3-32, Humana Press.
- Yurgel, S.N., Nearing J.T., Douglas G.M. and **Langille M.G.I.** (2019) Metagenomic functional shifts to plant induced environmental changes. *Front Microbiol.* 10: 1682.
- Zorz, J., Willis, C., Comeau, A.M., **Langille, M.G.I.**, Johnson, C.L., Li, W.K.W. and **LaRoche, J.** (2019) Drivers of regional bacterial community structure and diversity in the northwest Atlantic Ocean. *Frontiers Microbiol.* 10: 281.

Year 2018:

- Archibald, J.M.** (2018) Evolution: scaling life's tree. *Nature* 560: 26-27. Invited book review.
- Archibald, J.M.** (2018) *Genomics. A Very Short Introduction.* Oxford University Press (VSI Series), 160 pp. ISBN: 978-0-19-878620-7.
- Asma, H.A., et al. [10 authors incl. **Beiko, R.G.**] (2018) Cellulase-Hemicellulase activities and bacterial community composition of different soils from Algerian ecosystems. *Microbial Ecology* 77(3), 713-725.
- Beiko, R.G.**, Hsiao, W., Parkinson, J., Eds. (2018) *Microbiome Analysis: Methods and Protocols*, Vol. 1849, Springer, USA [Edited Book]
- Bertrand, E.M.** (2018) Quantification of vitamin B12-related proteins in marine microbial systems using selected reaction monitoring mass spectrometry. *Methods Mol. Biol.* 1849: 87-98.
- Bradbury, I.R., Wringe, B.F., Watson, B., Paterson, I., Horne, J., **Beiko, R.G.**, Lehnert, S.J., Clément, M., Anderson, E.C., Jeffery, N.W., Duffy, S., Sylvester, E., Robertson, M. and Bentzen P. (2018) Genotyping-by-sequencing of genome-wide microsatellite loci reveals fine-scale harvest composition in a coastal Atlantic salmon fishery. *Evol. Appl.* 11: 918-930.
- Brown, M.W., Heiss, A.A., Kamikawa, R., Inagaki, Y., Yabuki, A., Tice, A.K., Shiratori, T., Ishida, K.I., Hashimoto, T., **Simpson, A.G.B.** and **Roger, A.J.** (2018) Phylogenomics places orphan protistan lineages in a novel eukaryotic super-group. *Genome Biol. Evol.* 10: 427-433.
- Brunet, T.D.P. and **Doolittle, W.F.** (2018) The generality of constructive neutral evolution. *Biol. Philos.* 33: 2.
- Brunson, J.K., McKinnie, S.M.K., Chekan, J.R., McCrow, J.P., Miles, Z.D., **Bertrand, E.M.**, Bielinski, V.A., Luhavaya, H., Oborník, M., Smith, G.J., Hutchins, D.A., Allen, A.E. and Moore, B.S. (2018) Biosynthesis of the neurotoxin domoic acid in a bloom-forming diatom. *Science* 361: 1356-1358.
- Buchwald R., Scheibling R.E. and **Simpson A.G.B.** (2018) Detection and quantification of a keystone pathogen in a coastal marine ecosystem. *Marine Ecol. Progress Series* 606: 79-90.
- Cenci, U., Sibbald, S.J., Curtis, B.A., Kamikawa, R., Eme, L., Moog, D., Henrissat, B., Maréchal, E., Chabi, M., Djemiel, C., **Roger, A.J.**, Kim, E. and **Archibald, J.M.** (2018) Nuclear genome sequence of the plastid-lacking cryptomonad *Goniomonas avonlea* provides insights in the evolution of secondary plastids. *BMC Biol.* 16: 137.
- Cheng, S., Melkonian, M., Smith, S.A., Brockington, S., **Archibald, J.M.**, Delaux, P.M., Li, F.W., Melkonian, B., Mavrodiev, E.V., Sun, W., Fu, Y., Yang, H., Soltis, D.E., Graham, S.W., Soltis,

- P.S., Liu, X., Xu, X. and Wong, G.K. (2018) 10KP: A phylodiverse genome sequencing plan. *Gigascience* 7: 1-9.
- Cruz-Reyes, J. and **Gray, M.W.** (Eds.) (2018) *RNA Metabolism in Mitochondria*, Vol. 34, *Nucleic Acids and Molecular Biology*, Springer International Publishing AG, part of Springer Nature. Book edited.
- DeClercq, V., **Langille, M.G.I.** and *Van Limbergen, J. (2018) Differences in adiposity and diet quality among individuals with inflammatory bowel disease in eastern Canada. *PLoS One* 13: e0200580.
- Del Campo J., Kolisko M., Boscaro V., Santoferrara L.F., Nenarokov S., Massana, R., Guillou L., **Simpson A.G.B.**, Berney C., de Vargas C., Brown M.W., Keeling P.J., Wegener Parfrey L. (2018) EukRef: Phylogenetic curation of ribosomal RNA to enhance understanding of eukaryotic diversity and distribution. *PLoS Biology*, 16: e2005849.
- de Vries, J. and **Archibald, J.M.** (2018) Quick guide: plastid genomes. *Curr. Biol.* 28: R336-R337.
- de Vries, J. and **Archibald, J.M.** (2018) Plant evolution: landmarks on the path to terrestrial life. *New Phytol.* 217: 1428-1434. Commissioned insight.
- de Vries, J. and **Archibald, J.M.** (2018) Plastid evolution: autonomy versus nuclear control. In: *Advances in Botanical Research*, Vol. 85 (Plastid Genome Evolution), pp. 1-28, Chaw, S.-M. & Jansen, R. (eds.). Invited book chapter.
- de Vries, J., Curtis, B.A., Gould, S.B. and **Archibald, J.M.** (2018) Embryophyte stress signalling evolved in the algal progenitors of land plants. *Proc. Natl. Acad. Sci. USA* 115: E3471-E3480. Journal Cover.
- de Vries, S., de Vries, J., von Dahlen, J.K., Gould, S.B., **Archibald, J.M.**, Rose, L.E. and **Slamovits, C.H.** (2018) On plant defense signalling networks and early land plant evolution. *Commun. Integr. Biol.* 11: e1486168.
- Dickson K, Liu S, Zhou J, **Langille MGI**, Holbein B, Lehmann C (2018) Selective sensitivity of the gut microbiome to iron chelators in polybacterial abdominal sepsis. *Medical Hypotheses* 120: 68-71.
- Dodbele, S., Jackman, J.E., and **Gray, M.W.** (2018) Mechanisms and evolution of mitochondrial tRNA 5'-editing. In *RNA Metabolism in Mitochondria* (Cruz-Reyes, J. and Gray, M.W., eds.), Vol. 34, *Nucleic Acids and Molecular Biology*, Springer International Publishing AG, pp. 177-198.
- Doolittle, W.F.** (2018) We simply cannot go on being so vague about 'function'. *Genome Biol.* 19: 223.
- Doolittle, W.F.** and Inkpen, S.A. (2018) Processes and patterns of interactions as units of selection: An introduction to ITSNTS thinking. *Proc. Natl. Acad. Sci. USA* 115: 4006-4014.
- Douglas GM, **Beiko RG**, **Langille MGI** (2018) Predicting the functional potential of the microbiome from marker genes using PICRUSt. *Methods in Molecular Biology*, Vol. 1849: 169-177.
- Douglas GM, Comeau AM, **Langille MGI**. (2018) Processing a 16S rRNA sequencing dataset with the Microbiome Helper workflow. In Beiko R, Parkinson J, and Hsiao W (eds.), *Microbiome Analysis: Methods and Protocols*, Springer Protocols: Methods in Molecular Biology, Vol. 1849, Humana Press. Book chapter.
- Douglas, G.M., Hansen, R., Jones, C.M.A., Dunn, K.A., Comeau, A.M., **Bielawski, J.P.**, Tayler, R., El-Omar, E.M., Russell, R.K., Hold, G.L., **Langille, M.G.I.** and *Van Limbergen, J. (2018) Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. *Microbiome* 6: 13.
- Dranse, H.J., Zheng, A., Comeau, A.M., **Langille, M.G.I.**, Zabel, B.A. and Sinal, C.J. (2018) The impact of chemerin or chemokine-like receptor 1 loss on the mouse gut microbiome. *PeerJ.* 6: e5494.
- Dunn, K.A., Andrews, K., Bashwih, R.O. and **Bielawski, J.P.** 2018. Bayesian Inference of Microbial Community Structure from Metagenomic data using BioMiCo. In *Microbiome Analysis: Methods and Protocols*, Beiko, R., Hsiao, Willina, & Parkinson, J. (eds), pp. 267-290, Humana Press.
- Goodwin, J.D., Lee, T.F., Kugrens P. and **Simpson, A.G.B.** (2018) *Allobodo chlorophagus* n. gen. n. sp., a kinetoplastid that infiltrates and feeds on the invasive alga *Codium fragile*. *Protist* 169: 911-925.
- Gray, M.W.** and Mootha, V.K. (2018) Evolutionary mitochondrial biology in titisee. *IUBMB Life* 70: 1184-1187.

- Hall, M. and **Beiko, R.G.** (2018) 16S rRNA gene analysis with QIIME2. *Methods Mol. Biol.* 1849: 113-129.
- Harding, T. and **Simpson, A.G.B.** (2018) Recent advances in halophilic protozoa research. *J. Eukaryot. Microbiol.* 65: 556-570.
- Heiss, A.A., Kolisko, M., Ekelund, F., Brown, M.W., **Roger, A.J.** and **Simpson, A.G.B.** (2018) Combined morphological and phylogenomic re-examination of malawimonads, a critical taxon for inferring the evolutionary history of eukaryotes. *Roy. Soc. Open Sci.* 5: 171707.
- Hleap, J.S. and **Blouin, C.** (2018) The response to selection in glycoside hydrolase family 13 structures: a comparative quantitative genetics approach. *PLoS One* 13: e0196135.
- Jones, C.T., Youssef, N., Susko, E. and Bielawski, J.P. (2018) Phenomenological load on model parameters can lead to false biological conclusions. *Mol. Biol. Evol.* 35: 1473-1488.
- Keddy, A. and **Beiko, R.G.** (2018) Investigating biogeographic patterns using point-based cartograms and the geographically coupled phylogenetic distance. *Global Ecology and Biogeography*, 27, 330-338.
- Kim, J.I., Yoon, H.S., Yi, G., Shin, W. and Archibald, J.M. (2018) Comparative mitochondrial genomics of cryptophyte algae: gene shuffling and dynamic mobile genetic elements. *BMC Genomics* 19: 275.
- Langille, M.G.I.** (2018) Exploring linkages between taxonomic and functional profiles of the human microbiome. *mSystems* 3: e00163-17.
- Langille, M.G.I., Ravel, J. and Fricke, W.F.** (2018) “Available upon request”: not good enough for microbiome data. *Microbiome* 6: 8.
- Lau, W.L., Vaziri, N.D., Nunes, A.C.F., Comeau, A.M., Langille, M.G.I., England, W., Khazaeli, M., Suematsu, Y., Phan, J. and Whiteson, K. (2018) The phosphate binder ferric citrate alters the gut microbiome in rats with chronic kidney disease. *J. Pharmacol. Exp. Ther.* 367: 452-460.
- Lax, G., Eglit, Y., Eme, L., Bertrand, E.M., Roger, A.J. and Simpson, A.G.B. (2018) Hemimastigophora is a novel supra-kingdom-level lineage of eukaryotes. *Nature* 564: 410-414.
- Leger, M.M., Eme, L., Stairs, C.W. and **Roger, A.J.** (2018) Demystifying eukaryote lateral gene transfer (Response to Martin 2017 DOI: 10.1002/bies.201700115). *Bioessays* 40: e1700242.
- Liu, C., Benjamin Wright, Emma Allen-Vercoe, Hong Gu, Beiko, R.G. (2018). Phylogenetic clustering of genes reveals shared evolutionary trajectories and putative gene functions. *Genome Biol. Evol.* 10, 2255-2265.
- Lukes, J., Wheeler, R., Jirsova, D., David, V. and **Archibald, J.M.** (2018) Massive mitochondrial DNA content in diplomonid and kinetoplastid protists. *IUBMB Life* 70: 1267-1274.
- Mariscal, C. and Doolittle, W.F. (2018) Life and life only: a radical alternative to life definitionism. *Synthese (online 11 July)*; <https://doi.org/10.1007/s11229-018-1852-2>
- Nadukkalam Ravindran, P., Bentzen, P., Bradbury, I.R. and Beiko R.G. (2018) PMERGE: Computational filtering of paralogous sequences from RAD-seq data. *Ecol. Evol.* 8(14): 7002-7013.
- Nearing, J.T., Douglas, G.M., Comeau, A.M. and Langille, M.G.I. (2018) Denoising the denoisers: an independent evaluation of microbiome sequence error-correction approaches. *PeerJ.* 6: e5364.
- Nowak, B.F. and **Archibald, J.M.** (2018) Opportunist but lethal: the mystery of Paramoebae. *Trends Parasitol.* 34: 404-419.
- Paerl, R.W., **Bertrand, E.M., Rowland, E., Schatt, P., Mehiri, M., Niehaus, T.D., Hanson, A.D., Riemann, L. and Bouget, F.** (2018) Carboxythiazole is a key microbial nutrient currency and critical component of thiamine biosynthesis. *Sci. Rep.* 8: 5940.
- Pyrihová, E., Motycková, A., Voleman, L., Wandyszewska, N., Fišer, R., Seydlová, G., **Roger, A., Kolisko, M. and Doležal, P.** (2018) A single tim translocase in the mitosomes of *Giardia intestinalis* illustrates convergence of protein import machines in anaerobic eukaryotes. *Genome Biol. Evol.* 10: 2813-2822.
- Raina, J.B., Eme, L., Pollock, F.J., Spang, A., **Archibald, J.M.** and Williams, T.A. (2018) Symbiosis in the microbial world: from ecology to genome evolution. *Biol. Open* 7(2): pii: bio032524.
- Roger, A.J.** (2018) Reply to ‘Eukaryote lateral gene transfer is Lamarckian.’ *Nature Ecol. Evol.* 2: 755.
- Roger, A.J.** (2018) Q & A. *Curr. Biol.* 28: R1233-R1234.

- Roger, A.J. and Susko, E.** (2018) Molecular clocks provide little information to date methanogenic Archaea. *Nature Ecol. Evol.* 2: 1676-1677.
- Spackeen, J., **Bertrand, E.M.**, Sipler, R., Hutchins, D.A., Allen, A.E., Bronk, D. (2018) Impact of temperature, CO₂, and iron on nutrient uptake by a late-season microbial community from the Ross Sea, Antarctica. *Aquatic Microbial Ecol.* 82:145-159.
- Spackeen, J., D. Bronk, R. Sipler, **Bertrand, E.M.**, D. A. Hutchins, A. E. Allen. (2018) Stoichiometric N:P ratios, temperature, and iron impact carbon and nitrogen uptake by Ross Sea microbial communities. *J. Geophysical Res.: Biogeosci.* 123: 2955-2975.
- Stairs, C.W., Eme, L., Muñoz-Gómez, S., Cohen, A., Delleire, G., Shepherd, J.N., Fawcett, J.P. and **Roger, A.J.** (2018) Microbial eukaryotes have adapted to hypoxia by horizontal acquisitions of a gene involved in rhodoquinone biosynthesis. *eLife* 7: e34292.
- Stanley, R.R.E, DiBacco, C., Lowen, B., **Beiko, R.G.**, Jeffery, N.W., Van Wyngaarden, M., Bentzen, P., Brickman, D., Benestan, L., Bernatchez, L., Johnson, C., Snelgrove, P.V.R., Wang, Z., Wringe, B.F. and Bradbury I.R. (2018) A climate-associated multispecies cryptic cline in the northwest Atlantic. *Sci. Adv.* 4: eaaq0929.
- Susko, E.**, Lincker, L. and **Roger, A.J.** (2018) Accelerated estimation of frequency classes in site-heterogeneous profile mixture models. *Mol. Biol. Evol.* 35: 1266-1283.
- Sylvester, E.V.A., Beiko, R.G., Bentzen, P., Paterson, I., Horne, J.B., Watson, B., Lehnert, S., Duffy, S., Clément, M., Robertson, M.J. and Bradbury, I.R. (2018) Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. *Mol. Ecol.* 27: 4026-4040.
- Tatters, A.O. *et al.* [incl. **Bertrand, E.M.**] (2018) Interactive effects of temperature, CO₂ and nitrogen source on a coastal California diatom assemblage. *J. Plankton Res.* 40(2): 151-164.
- Thilakarathna, WPDW, **Langille, MGI**, Rupasinghe, HPV (2018) “Polyphenol-based prebiotics and synbiotics: potential for cancer chemoprevention”. *Curr. Opin. in Food Sci.* 20: 51-57.
- Valach, M., Leveille-Kunst, A., **Gray, M.W.** and Burger, G. (2018) Respiratory chain Complex I of unparalleled divergence in diplomonads. *J. Biol. Chem.* 293: 16043-16056.
- van Wyngaarden, M., Snelgrove, P.V.R., DiBacco, C., Hamilton, L.C., Rodríguez-Ezpeleta, N., Zhan, L., **Beiko, R.G.** and Bradbury, I.R. (2018) Oceanographic variation influences spatial genomic structure in the sea scallop, *Placopecten magellanicus*. *Ecol. Evol.* 8: 2824-2841.
- Wang, H.-C., Minh, B.Q., Susko, E. and Roger, A.J. (2018) Modeling site heterogeneity with posterior mean site frequency profiles accelerates accurate phylogenomic estimation. *Syst. Biol.* 67: 216-235.
- Wideman, J.G. and Munoz-Gomez, S.A. (2018) Cell biology: functional conservation, structural divergence, and surprising convergence in the MICOS complex of Trypanosomes. *Curr. Biol.* 28: R1245-R1248.
- Yurgel, S.N., Douglas, G.M., Dusault, A., Percival, D. and **Langille, M.G.I.** (2018) Dissecting community structure in wild blueberry root and soil microbiome. *Frontiers Microbiol.* 9: 1187.

Year 2017:

- Alarcón, M.E., Jara-F.A., Briones, R.C., Dubey, A.K. and **Slamovits, C.H.** (2017) Gregarine infection accelerates larval development of the cat flea *Ctenocephalides felis* (Bouché). *Parasitol.* 144: 419-425.
- Archibald, J.M.** (2017) Evolution: Protein import in a nascent photosynthetic organelle. *Curr. Biol.* 27: R1004-R1006.
- Archibald, J.M., Simpson, A.G.B. and Slamovits, C.H.** (2017) Editors of *Handbook of the Protists (Second Edition)*, Springer Reference.
- Berney, C. *et al.* [25 authors incl. **Simpson, A.G.B.**] (2017) UniEuk: Time to speak a common language in protistology. *J. Eukaryot. Microbiol.* 64: 407-411.
- Browning, T.J., Achterberg, E.P., Rapp, I., Engel, A., **Bertrand, E.M.**, Tagliabue, A. and Moore, C.M. (2017) Nutrient co-limitation at the boundary of an oceanic gyre. *Nature* 551: 242-246.

- Caron, D.A. *et al.* [15 authors incl. **Archibald, J.M.**] (2017) Probing the evolution, ecology and physiology of marine protists using transcriptomics. *Nat. Rev. Microbiol.* 15: 6-20.
- Cenci, U., Moog, D. and Archibald, J.M. (2017) Origin and spread of plastids by endosymbiosis. In M. Grube, L. Muggia & J. Seckbach (Eds.), *Algal and Cyanobacteria Symbioses*, pp. 43-81, Springer-Verlag.
- Chan, C.X., **Beiko, R.G.** and Ragan, M.A. (2017) Scaling up the phylogenetic detection of lateral gene transfer events. *Methods Mol. Biol.* 1525: 421-432.
- Comeau, A.M., Douglas, G.M. and **Langille, M.G.** (2017) Microbiome Helper: a custom and streamlined workflow for microbiome research. *mSystems* 2: e00127.
- de Vries, J. and Archibald, J.M. (2017) Endosymbiosis: did plastids evolve from a freshwater cyanobacterium? *Curr. Biol.* 27: R103-105.
- de Vries, J., Archibald, J.M. and Gould, S.B. (2017) The carboxy terminus of YCF1 contains a motif conserved throughout >500Myr of streptophyte evolution. *Genome Biol. Evol.* 9: 473-479.
- de Vries, J., de Vries, S., Slamovits, C.H., Rose, L.E. and Archibald, J.M. (2017) How embryophytic is the biosynthesis of phenylpropanoids and their derivatives in streptophyte algae? *Plant Cell Physiol.* 58: 934-945.
- Doolittle, W.F.** (2017) Darwinizing Gaia. *J. Theor. Biol.* 434: 11-19.
- Doolittle, W.F.** (2017) Making the most of clade selection. *Phil. Sci.* 84: 275-295.
- Doolittle, W.F.** and Booth, A. (2017) It's the song, not the singer: an exploration of holobiosis and evolutionary theory. *Biol. Philos.* 32: 5-24.
- Doolittle, W.F.** and Brunet, T.D.P. (2017) On causal roles and selected effects: our genome is mostly junk. *BMC Biol.* 15: 116.
- Eme, L., Gentekaki, E., Curtis, B., Archibald, J.M. and Roger A.J. (2017) Lateral gene transfer in the adaptation of the anaerobic parasite *Blastocystis* to the gut. *Curr. Biol.* 27: 807-820.
- Finlayson-Trick, E.C.L., Getz, L.J., Slaine, P.D., Thornbury, M., Lamoureux, E., Cook, J., Langille, M.G.I., Murray, L.E., McCormick, C., Rohde, J.R. and Cheng, Z. (2017) Taxonomic differences of gut microbiomes drive cellulolytic enzymatic potential within hind-gut fermenting mammals. *PLoS One* 12: e0189404.
- Gentekaki, E., Curtis, B.A., Stairs, C.W., Klimeš, V., Eliáš, M., Salas-Leiva, D.E., Herman, E.K., Eme, L., Arias, M.C., Henrissat, B., Hilliou, F., Klute, M.J., Suga, H., Malik, S.B., Pightling, A.W., Kolisko, M., Rachubinski, R.A., Schlacht, A., Soanes, D.M., Tsaousis, A.D., Archibald, J.M., Ball, S.G., Dacks, J.B., Clark, C.G., van der Giezen, M. and Roger, A.J. (2017) Extreme genome diversity in the hyper-prevalent parasitic eukaryote *Blastocystis*. *PLoS Biol.* 15: e2003769.
- Gray, M.W.** (2017) Lynn Margulis and the endosymbiont hypothesis: 50 years later. *Mol. Biol. Cell* 28: 1285-1287.
- Hall, M.W., Rohwer, R.R., Perrie, J., McMahon, K.D. and Beiko, R.G. (2017) Ananke: Temporal clustering reveals ecological dynamics of microbial communities. *PeerJ* 5: e3812.
- Hall, M.W., Singh, N., Ng, K.F., Lam, D.K., Goldberg, M.B., Tenenbaum, H.C., Neufeld, J.D., Beiko, R.G. and Senadheera, D.B. (2017) Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. *NPJ Biofilms Microbiomes* 3, Article 2.
- Harding, T., Roger, A.J. and Simpson, A.G.B. (2017) Adaptations to high salt in a halophilic protist: differential expression and gene acquisitions through duplications and gene transfers. *Front Microbiol.* 8: 944.
- Heiss, A.A., Brown, M.W. and **Simpson, A.G.B.** (2017) Apusomonadida. In *Handbook of the Protists (Second Edition)*, Archibald, J.M., Simpson, A.G.B. & Slamovits, C. (Eds.), pp. 1619-1645, Springer Reference.
- Hoef-Emden, K. and **Archibald, J.M.** (2017) Cryptophyta (Cryptomonads). In *Handbook of the Protists (Second Edition)*, J.M. Archibald, A.G. Simpson & C. Slamovits (Eds), pp. 851-891, Springer Reference.
- Inkpen, S.A. (2017) Demarcating nature, defining ecology: Creating a rationale for the study of nature's 'primitive conditions'. *Perspect. Sci.* 25: 355-92.

- Inkpen, S.A. (2017) Are humans disturbing conditions in ecology? *Biol. Philos* 32: 51-71.
- Inkpen, S.A., Douglas, G.M., Brunet, T.D.P., Leuschen, K., Doolittle, W.F. and Langille, M.G.I. (2017) The coupling of taxonomy and function in microbiomes. *Biol. Philos.* 32: 1225-1243.
- Jeffery, N.W., DiBacco, C., Van Wyngaarden, M., Hamilton, L.C., Stanley, R.R.E., McKenzie, C., Nadukkalam Ravindran, P., Beiko, R.G. and Bradbury, I.R. (2017). RAD sequencing reveals genomewide divergence between independent invasions of the European green crab (*Carcinus maenas*) in the Northwest Atlantic. *Ecol. Evol.* 7: 2513-2524.
- Jeffery, N.W., Stanley, R.R.E., Wringe, B.F., Guijarro-Sabaniel, J., Bourret, V., Bernatchez, L., Bentzen, P., **Beiko, R.G.**, Gilbey, J., Clément, M. and Bradbury, I.R. (2017) Range-wide parallel climate-associated genomic clines in Atlantic salmon. *Roy. Soc. Open Sci.* 4: 171394.
- Jones, C.T., Youssef, N., Susko, E. and Bielawski, J.P. (2017) Shifting balance on a static mutation-selection landscape: a novel scenario of positive selection. *Mol. Biol. Evol.* 34: 391-407.
- Kamikawa, R., Moog, D., Zauner, S., Tanifuji, G., Ishida, K.I., Miyashita, H., Mayama, S., Hashimoto, T., Maier, U.G., **Archibald, J.M.** and Inagaki, Y. (2017) A non-photosynthetic diatom reveals early steps of reductive evolution in plastids. *Mol. Biol. Evol.* 34: 2355-2366.
- Kang, S., Tice, A.K., Spiegel, F.W., Silberman, J.D., Pánek, T., Cepicka, I., Kostka, M., Kosakyan, A., Alcântara, D.M., **Roger, A.J.**, Shadwick L.L., Smirnov A., Kudryavstev A., Lahr D.J.G. and Brown, M.W. (2017) Between a pod and a hard test: the deep evolution of amoebae. *Mol. Biol. Evol.* 34: 2258-2270.
- Kim, J.I., Moore, C.E., **Archibald, J.M.**, Bhattacharya, D., Yi, G., Yoon, H.S. and Shin, W. (2017) Evolutionary dynamics of Cryptophyte plastid genomes. *Genome Biol. Evol.* 9: 1859-1872.
- Lamoureux, E.V., Grandy, S.A. and Langille, M.G.I. (2017) Moderate exercise has limited but distinguishable effects on the mouse microbiome. *mSystems* 2(4): pii: e00006-17.
- Leander, B.S., Lax, G. Karnkowska, A. and **Simpson, A.G.B.** (2017) Euglenida. In *Handbook of the Protists (Second Edition)*, Archibald, J.M., Simpson, A.G.B. & Slamovits, C. (Eds.), pp. 1047-1088, Springer Reference.
- Leger, M.M., Kolisko, M., Kamikawa, R., Stairs, C.W., Kume, K., Čepicka, I., Silberman, J.D., Andersson, J.O., Xu, F., Yabuki, A., Eme, L., Zhang, Q., Takishita, K., Inagaki, Y., Simpson, A.G.B., Hashimoto, T. and Roger, A.J. (2017) Organelles that illuminate the origins of *Trichomonas* hydrogenosomes and *Giardia* mitosomes. *Nature Ecol. Evol.* 1: 0092.
- MacLellan, A., Moore-Connors, J., Grant, S., Cahill, L., **Langille, M.G.I.** and *Van Limbergen, J. (2017) The impact of exclusive enteral nutrition (EEN) on the gut microbiome in Crohn's Disease: A review. *Nutrients* 9: pii: E0447.
- Munoz-Gomez, S.A., Wideman, J.G., Roger, A.J. and Slamovits, C.H. (2017) The origin of mitochondrial cristae from alphaproteobacteria. *Mol. Biol. Evol.* 34: 943-956.
- Muñoz-Gómez, S.A., Mejía-Franco, F.G., Durnin, K., Colp, M., Grisdale, C.J., Archibald J.M. and Slamovits, C.H. (2017) The new red algal subphylum Proteorhodophytina comprises the largest and most divergent plastid genomes known. *Curr. Biol.* 27: 1677-1684.
- Pánek, T., Žihala, D., Sokol, M., Derelle, R., Klimeš, V., Hradilová, M., Zdrobilková, E., **Susko, E., Roger, A.J.**, Cepicka, I. and Eliáš, M. (2017) Nuclear genetic codes with a different meaning of the UAG and the UAA codon. *BMC Biol.* 15: 8.
- Pánek, T., **Simpson, A.G.B.**, Brown, M.W. and Dyer, B.D. (2017) Heterolobosea. In *Handbook of the Protists (Second Edition)*, Archibald, J.M., Simpson, A.G.B. & Slamovits, C. (Eds.), pp. 1005-1046, Springer Reference.
- Petkau, A., Mabon, P., Sieffert, C., Knox, N., Cabral, J., Weedmark, K., Zaheer, R., Katz, L.S., Nadon, C., Reimer, A., Taboada, E., **Beiko, R.G.**, Hsiao, W., Brinkman, F., Graham, M. and Van Domselaar, G. (2017) SNVPhyl: A single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. *Microb. Genom.* 3: e000116.
- Robicheau, B.M., **Susko, E.**, Harrigan, A.M. and Snyder, M. (2017) Ribosomal RNA genes contribute to the formation of pseudogenes and junk DNA in the human genome. *Genome Biol. Evol.* 9: 380-397.

- Roger, A.J., Munoz-Gomez, S.A.** and Kamikawa, R. (2017) The origin and diversification of mitochondria. *Curr. Biol.* 27: R1177-R1192.
- Sibbald, S.J.** and **Archibald, J.M.** (2017) More protist genomes needed. *Nature Ecol. Evol.* 1: 145.
- Sibbald, S.J., Cenci, U., Colp, M., Eglit, Y., O'Kelly, C.J.** and **Archibald, J.M.** (2017) Diversity and evolution of *Paramoeba spp.* and their kinetoplastid endosymbionts. *J. Eukaryot. Microbiol.* 64: 598-607.
- Simpson, A.G.B.** (2017) Jakobida. In *Handbook of the Protists (Second Edition)*, Archibald, J.M., Simpson, A.G.B. & Slamovits C. (Eds.), pp. 973-1003, Springer Reference.
- Simpson, A.G.B., Slamovits, C.H.** and **Archibald, J.M.** (2017) Protist diversity and eukaryote phylogeny (Introductory Chapter). In: *Handbook of the Protists (Second Edition)*, Archibald, J.M., Simpson, A.G.B. & Slamovits, C. (Eds.), pp. 1-21, Springer Reference.
- Spackeen, J.L., Sipler, R.E., Xu, K., Tatters A.O., Walworth, N.G., **Bertrand, E.M.**, McQuaid, J.B., Hutchins, D.A., Allen, A.A. and Bronk, D. (2017) Interactive effects of elevated temperature and CO₂ on nitrate, urea, and dissolved inorganic carbon uptake by a coastal California, USA, microbial community. *Marine Ecol. Progress Series* 577: 49-65.
- Stuart, Y.E., **Inkpen, S.A.**, Hopkins, R. and Bolnick, D.I. (2017) Character displacement is an evolutionary pattern. So what causes it? *Biol. J. Linnean Soc.* 121: 711-715.
- Sylvester, E.V.A.**, Bentzen, P., Bradbury, I.R., Clement, M., Pearce, J., Horne, J. and **Beiko, R.G.** (2017) Applications of random forest feature selection for fine-scale genetic population assignment. *Evol. Appl.* 11: 153-165.
- Takishita, K., Chikaraishi, Y., Tanifuji, G., Ohkouchi, N., Hashimoto, T., Fujikura, K. and **Roger, A.J.** (2017) Microbial eukaryotes that lack sterols. *J. Eukaryot. Microbiol.* 64: 897-900.
- Tanifuji, G., Cenci, U., Moog, D., Dean, S., Nakayama, T., **David, V.**, Fiala, I., **Curtis, B.A.**, **Sibbald, S.J.**, Onodera, N.T., **Colp, M.**, Flegontov, P., Johnson-MacKinnon, J., **McPhee, M.**, Inagaki, Y., Hashimoto, T., Kelly, S., Gull, K., Lukeš, J. and **Archibald, J.M.** (2017) Genome sequencing reveals metabolic and cellular interdependence in an amoeba-kinetoplastid symbiosis. *Sci. Rep.* 7: 11688.
- Yang, J., Harding, T., Kamikawa, R., Simpson, A.G.B.** and **Roger, A.J.** (2017) Mitochondrial genome evolution and a novel RNA editing system in deep-branching heteroloboseids. *Genome Biol. Evol.* 9: 1161-1174.
- Yurgel, S.N., **Douglas, G.M.**, **Comeau, A.M.**, Mammoliti, M., Dusault, A., Pecival, D. and **Langille, M.G.I.** (2017) Variation in bacterial and eukaryotic communities associated with natural and managed wild blueberry habitats. *Phytobiomes* 1: 102-113.
- Zhan, L., Paterson, I.G., Fraser, B.A., Watson, B., Bradbury, I.R., **Nadukkalam Ravindran, P.**, Reznick, D., **Beiko, R.G.** and Bentzen, P. (2017) Megasat: automated inference of microsatellite genotypes from sequence data. *Mol. Ecol. Resour.* 17: 247-256.

Year 2016:

- Archibald, J.M.** (2016) *One Plus One Equals One: Symbiosis and the Evolution of Complex Life*. 224 pp. Oxford University Press. ISBN: 978-0-19-966059-9 [Paperback with new Afterward].
- Baker, J.L., **Dunn, K.A.**, **Mingrone, J.**, Wood, B.A., Karpinski, B.A., Sherwood, C.C., Wildman, D.E., Maynard, T.M. and **Bielawski, J.P.** (2016) Functional divergence of the nuclear receptor *NR2C1* as a modulator of pluripotentiality during hominid evolution. *Genetics* 203: 905-922.
- Bielawski, J.P.**, Baker, J.L. and **Mingrone, J.** (2016) Inference of episodic changes in natural selection acting on protein coding sequences via CODEML. *Curr. Protoc. Bioinformatics* 54: 6.15.1-6.15.32.
- Booth, A., Mariscal, C.** and **Doolittle, W.F.** (2016) The modern synthesis in the light of microbial genomics. *Ann. Rev. Microbiol.* 70: 279-297.
- Brunet, T.D.** (2016) Aims and methods of biosteganography. *J. Biotechnol.* 226: 56-64.
- Castro, S.I., Hleap, J.S., Cárdenas, H.** and **Blouin, C.** (2016) Molecular organization of the 5S rDNA gene type II in elasmobranchs. *RNA Biol.* 13: 391-399.

- Cenci, U., Moog, D., Curtis, B.A., Tanifuji, G., Eme, L., Lukes, J. and **Archibald, J.M.** (2016) Heme pathway evolution in kinetoplastid protists. *BMC Evol. Biol.* 16: 109.
- Cenci, U., Ducatez, M., Kadouche, D., Colleoni, C. and Ball, S.G. (2016) Was the Chlamydial adaptative strategy to Tryptophan starvation an early determinant of plastid endosymbiosis? *Front. Cell Infect. Microbiol.* 6: 67.
- Dacks, J., Field, M., Buick, R., Eme, L., Gribaldo, S., **Roger, A.J.**, Brochier, C. and Devos, D.P. (2016) The changing view of eukaryogenesis - fossils, cells, lineages and how they all come together. *J. Cell Sci.* 129: 3695-3703.
- David, V. and **Archibald, J.M.** (2016) Evolution: Plumbing the depths of diplomemid diversity. *Curr. Biol.* 26: R1290-1292.
- de Vries, J., Stanton, A., **Archibald, J.M.** and Gould, S.B. (2016) Streptophyte terrestrialization in light of plastid evolution. *Trends Plant Sci.* 21: 467-476.
- Dunn, K.A., Moore-Connors, J., MacIntyre, B., Stadnyk, A.W., Thomas, N.A., Noble, A., Mahdi, G., Rashid, M., Otley, A.R., **Bielawski, J.P.** and *Van Limbergen, J. (2016) Early changes in microbial community structure are associated with sustained remission after nutritional treatment of pediatric Crohn's Disease. *Inflamm. Bowel Dis.* 22: 2853-2862.
- Dunn, K.A., Moore-Connors, J., MacIntyre, B., Stadnyk, A.W., Thomas, N.A., Noble, A., Mahdi, G., Rashid, M., Otley, A.R., **Bielawski, J.P.** and *Van Limbergen, J. (2016) The gut microbiome of pediatric Crohn's Disease patients differs from healthy controls in genes that can influence the balance between a healthy and dysregulated immune response. *Inflamm. Bowel Dis.* 22: 2607-2618.
- Doolittle, W.F.** and Brunet, T.D. (2016) What is the tree of life?. *PLoS Genet.* 12: e1005912.
- Eme, L. and **Doolittle, W.F.** (2016) Microbial evolution: Xenology (apparently) trumps paralogy. *Curr. Biol.* 26: R1181-1183.
- Gawryluk, R., Kamikawa, R., Stairs, C.W., Brown, M.W., Silberman, J.D. and **Roger, A.J.** (2016) The earliest stages of mitochondrial adaptation to low oxygen revealed in a novel rhizarian. *Curr. Biol.* 26: 2729-2738.
- Grisdale, C.J. and **Archibald, J.M.** (2016) Secondary and tertiary endosymbiosis. In: *Reference Module in Life Sciences*, Elsevier Publishing. 10.1016/B978-0-12-809633-8.13107-3.
- Groussin, M., Boussau, B., Szöllosi, G.J., Eme, L., Gouy, M., Brochier-Armanet, C. and Daubin, V. (2016) Gene acquisitions from bacteria at the origins of major archaeal clades are vastly overestimated. *Mol. Biol. Evol.* 33: 305-310.
- Hajibabaei, M., Baird, D.J., Fahner, N.A., **Beiko, R.** and Golding, G.B. (2016) A new way to contemplate Darwin's tangled bank: how DNA barcodes are reconnecting biodiversity science and biomonitoring. *Philos Trans. R. Soc. Lond. B. Biol. Sci.* 371: 20150330.
- Hamann, E., Gruber-Vodicka, H., Kleiner, M., Tegetmeyer, H., Riedel, D., Littmann, S., Chen, J., Milucka, J., Viehweger, B., Becker, K., Dong, X., Stairs, C.W., Hinrichs, K., Brown, M.W., **Roger, A.J.** and Strous, M. (2016) Environmental Breviatea harbor mutualistic *Arcobacter* epibionts. *Nature* 534: 254-258.
- Harding, T., Brown, M.W., **Simpson, A.G.** and **Roger, A.J.** (2016) Osmoadaptive strategy and its molecular signature in obligately halophilic heterotrophic protists. *Genome Biol. Evol.* 8: 2241-2258.
- Hleap, J.S. and **Blouin, C.** (2016) The semantics of the modular architecture of protein structures. *Curr. Prot. Peptide Sci.* 17: 62-71.
- Inkpen, S.A. and **Doolittle, W.F.** (2016) Molecular phylogenetics and the perennial problem of homology. *J. Mol. Evol.* 83: 184-192.
- Kamikawa, R., Shiratori, T., Ishida, K., Miyashita, H. and **Roger, A.J.** (2016) Group II intron-mediated trans-splicing in the gene-rich mitochondrial genome of an enigmatic eukaryote, *Diphyllleia rotans*. *Genome Biol. Evol.* 8: 458-466.
- Karnkowska, K., Vacek, V., Zubáčová, Z., Treitli, S., Petrželková, R., Eme, L., Novák, N., Žárský, V., Barlow, L., Herman, H., Soukal, P., Hroudová, M., Doležal, P., Stairs, C.W., **Roger, A.J.**, Elias, M.,

- Dacks, J., Vlček, C. and Hampl, V. (2016) A eukaryote without a mitochondrial organelle. *Curr. Biol.* 26: 1274-84.
- Kureshi, N., Abidi, S.S. and **Blouin, C.** (2016) A predictive model for personalized therapeutic interventions in non-small cell lung cancer. *IEEE J. Biomed. Health Inform.* 20: 424-431.
- Leger, M.M., Eme, L., Hug, L.A. and **Roger, A.J.** (2016) Novel hydrogenosomes in the microaerophilic jakobid *Stygiella incarcerata*. *Mol. Biol. Evol.* 33: 2318-2336. [Corrigendum correction in *Mol. Biol. Evol.* (2017) 34(4): 1027.
- Miller, R.R., **Langille, M.G.**, Montoya, V., Crisan, A., Stefanovic, A., Martin, I., Hoang, L., Patrick, D.M., Romney, M., Tyrrell, G., Jones, S.J.M., Brinkman, F.S.L. and Tang, P. (2016) Genomic analysis of a serotype 5 *Streptococcus pneumoniae* outbreak in Canada, 2005-2009. *Can J. Infect. Dis. Med. Microbiol.* 2016: 5381871.
- Mingrone, J., **Susko, E.** and **Bielawski, J.** (2016) Smoothed bootstrap aggregation for assessing selection pressure at amino acid sites. *Mol. Biol. Evol.* 33: 2976-2989.
- Moore-Connors, J.M., Dunn, K.A., **Bielawski, J.P.** and *Van Limbergen, J. (2016) Novel strategies for applied metagenomics. *Inflamm. Bowel Dis.* 22: 709-718.
- Munoz-Gomez, S.A. and **Roger, A.J.** (2016) Leaving negative ancestors behind. *eLIFE* 5: e20061.
- Navia, A.F., Mejía-Falla, P. A. and Hleap, J.S. (2016) Zoogeography of the elasmobranchs in the Colombian Pacific Ocean and Caribbean Sea. *Neotrop. Ichthyol.* 14: e140134.
- Novák, L., Zubáčová, Z., Karnkowska, A., Kolisko, M., Hroudová, M., Stairs, C.W., **Simpson, A.G.**, Keeling, P.J., **Roger, A.J.**, Čepička, I. and Hampl, V. (2016) Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. *BMC Evol. Biol* 16: 197.
- Pánek, T., Zadrožilková, E., Walker, G., Brown, M.W., Gentekaki, E., Hroudová, M., Kang, S., **Roger, A.J.**, Tice, A.K., Vlček, Č. and Čepička I. (2016) First multigene analysis of Archamoebae robustly reveals its phylogeny and shows that Entamoebidae represents a deep lineage of the group. *Mol. Phylogenet. Evol.* 98: 41-51.
- Park, J.S. and **Simpson, A.G.** (2016) Characterization of a deep-branching Heterolobosean, *P. turkanaensis* n. sp., isolated from a non-hypersaline habitat, and ultrastructural comparison of cysts and amoebae among Pharyngomonas strains. *J. Eukaryot. Microbiol.* 63: 100-111.
- Pesaranghader, A., Matwin, S., Sokolova, M. and **Beiko R.G.** (2016) simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. *Bioinformatics* 32: 1380-1387.
- Rutherford, K., Meehan, C.J., **Langille, M.G.**, Tyack, S.G., McKay, J.C., McLean, N.L., Benkel, K., **Beiko, R.G.** and Benkel, B. (2016) Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. *Poult. Sci.* 95: 2250-2258.
- Sierra, R., Cañas-Duarte, S.J., Burki, F., Schwelm, A., Fogelqvist, J., Dixelius, C., González-García, L.N., Gile, G.H., **Slamovits, C.H.**, Klopp, C., Restrepo, S., Arzul, I. and Pawlowski J. (2016) Evolutionary origins of rhizarian parasites. *Mol. Biol. Evol.* 33: 980-983.
- Simpson, A.G.B.** and Eglit, Y. (2016) Protist diversification. In R.M. Kliman (Ed.), *Encyclopedia of Evolutionary Biology*, Vol. 3, pp. 344-360, Academic Press.
- Susko, E.** (2016) Support measures, phylogenetic tree. In R.M. Kliman (Ed.), *Encyclopedia of Evolutionary Biology*, Vol. 3, pp. 256-260, Academic Press.
- Tanifuji, G., **Archibald, J.M.** and Hashimoto, T. (2016) Comparative genomics of mitochondria in chlorarachniophyte algae: endosymbiotic gene transfer and organellar genome dynamics. *Sci. Rep.* 6: 21016.
- Wang, H.C., **Susko, E.** and **Roger, A.** (2016) Split-specific bootstrap measures for quantifying phylogenetic stability and the influence of taxon selection. *Mol. Phylogenet. Evol.* 105: 114-125.
- Whidden, C., **Beiko, R.G.** and *Zeh, N. (2016) Fixed-parameter and approximation algorithms for maximum agreement forests of multifurcating trees. *Algorithmica* 74: 1019-1054.

- Wideman, J.G. and Munoz-Gomez, S.A. (2016) The evolution of ERMIONE in mitochondrial biogenesis and lipid homeostasis: an evolutionary view from comparative cell biology. *BBA – Molecular and Cell Biology of Lipids* 1861: 900-912.
- Xu, F., Jerlström-Hultqvist, J., Kolisko, M., **Simpson, A.G.**, **Roger, A.J.**, Svärd, S.G. and Andersson, J.O. (2016) On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad *Trepomonas* sp. PC1. *BMC Biol.* 14: 62. [Erratum in *BMC Biol.* (2016) 14: 77].

Year 2015:

- Archibald, J.M.** (2015) Evolution: Gene transfer in complex cells. *Nature* 524: 423-424.
- Archibald, J.M.** (2015) Genomic perspectives on the birth and spread of plastids. *Proc. Natl. Acad. Sci. USA* 112: 10147-10153.
- Archibald, J. M.** (2015) Endosymbiosis and eukaryotic cell evolution. *Curr. Biol.* 25: R911-921.
- Beiko, R.G.** (2015) Microbial malaise: how can we classify the microbiome? *Trends Microbiol.* 23: 671-679.
- Bertrand, E.M. et al.** [12 co-authors] (2015) Phytoplankton-bacterial interactions mediate micronutrient colimitation at the coastal Antarctic sea ice edge. *Proc. Natl. Acad. Sci. USA* 112: 9938-9943.
- Booth, A. and **Doolittle, W.F.** (2015) Eukaryogenesis, how special really? *Proc. Natl. Acad. Sci. USA* 112: 10278-85.
- Booth, A. and **Doolittle, W.F.** (2015) Reply to Lane and Martin: Being and becoming eukaryotes. *Proc. Natl. Acad. Sci. USA* 112: E4824.
- Brunet, T.D. and **Doolittle, W.F.** (2015) Multilevel selection theory and the evolutionary functions of transposable elements. *Genome Biol. Evol.* 7: 2445-2457.
- Buchwald, R.T., Feehan, C.J., Scheibling, R.E. & **Simpson, A.G.B.** (2015) Low temperature tolerance of a sea urchin pathogen: implications for benthic community dynamics in a warming ocean. *J. Exp. Marine Biol. Ecol.* 469: 1-9.
- David, V., Flegontov, P., Gerasimov, E., Tanifuji, G., Hashimi, H., Logacheva, M.G., Maruyama, S., Onodera, N.T., **Gray, M.W.**, **Archibald, J.M.** and Lukeš, J. (2015) Gene loss and error-prone RNA editing in the mitochondrion of *Perkinsela*, an endosymbiotic kinetoplastid. *MBio* 6: e01498-15.
- Dhanani, A.S., Block, G., Dewar, K., Forgetta, V., Topp, E., **Beiko, R.G.** and Diarra, M.S. (2015) Genomic comparison of non-typhoidal *Salmonella enterica* Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky isolates from broiler chickens. *PLoS One* 10: e0128773.
- Dhillon, B., Laird, M., Shay, J., Winsor, G., Lo, R., Nizam, F., Sheldon, P., Waglechner, N., McArthur, A., **Langille, M.G.I.** and Brinkman, F.S.L. (2015) IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis. *Nucleic Acids Res.* 43: W104-108.
- Doolittle, W.F.** (2015) Rethinking the Tree of Life. *Microbe* 10: 319-323.
- El-Swais, H., Dunn, K.A., **Bielawski, J.P.**, Li, W.K. and Walsh, D.A. (2015) Seasonal assemblages and short-lived blooms in coastal north-west Atlantic Ocean bacterioplankton. *Environ. Microbiol.* 17: 3642-3661.
- Eme, L. and **Doolittle, W.F.** (2015) Archaea. *Curr. Biol.* 25: R851-855.
- Eme, L. and **Doolittle, W.F.** (2015) Microbial diversity: a bonanza of phyla. *Curr. Biol.* 25: R227-R230.
- Garvin, M.R., **Bielawski, J.P.**, Sazanov, L.A. and Gharrett, A.J. (2015) Review and meta-analysis of natural selection in mitochondrial complex I in metazoans. *J. Zool. Syst. Evol. Res.* 53: 1-17.
- Gawryluk, R., Eme, L. and **Roger, A.J.** (2015) Gene fusion, fission, lateral transfer, and loss: not-so-rare events in the evolution of eukaryotic ATP citrate lyase. *Mol. Phylogenet. Evol.* 91: 12-16.
- Gile, G.H., Moog, D., **Slamovits, C.H.**, Maier, U.G. and **Archibald, J.M.** (2015) Dual organellar targeting of aminoacyl-tRNA synthetases in Diatoms and Cryptophytes. *Genome Biol. Evol.* 7: 1728-1742.
- Gile, G.H., James, E.R., Okamoto, N., Carpenter, K.J., Scheffrahn, R.H. and Keeling, P.J. (2015) Molecular evidence for the polyphyly of macrotricomonas (Parabasalia: Cristamonadea) and a proposal for *Macrotrichomonoides* n. gen. *J. Eukaryot. Microbiol.* 62: 494-504.

- Gray, M.W.** (2015) Mosaic nature of the mitochondrial proteome: Implications for the origin and evolution of mitochondria. *Proc. Natl. Acad. Sci. USA* 112: 10133-10138.
- Heiss, A.A., Lee, W.J., Ishida, K. and Simpson, A.G.** (2015). Cultivation and characterization of new species of apusomonads (the sister group to opisthokonts), including close relatives of Thecamonas (*Chelonomonas* n. gen.). *J. Eukaryot. Microbiol.* 62: 637-649.
- Hester, C.M., Jala, V.R., Langille, M.G.I., Umar, S., Greiner, K.A. and Haribabu, B.** (2015) Fecal microbes, short chain fatty acids, and colorectal cancer across racial/ethnic groups. *World J. Gastroenterol.* 21: 2759-2769.
- Keeling, P.J., McCutcheon J.P. and Doolittle, W.F.** (2015) Symbiosis becoming permanent: Survival of the luckiest. *Proc. Natl. Acad. Sci. USA* 112: 10101-10103.
- Kirby, W.A., Tikhonenkov, D.V., Mylnikov, A.P., Janouškovec, J., Lax, G., and Simpson, A.G.B.** (2015) Characterisation of *Tulamoeba bucina* n. sp., an extremely halotolerant amoeboflagellate heterolobosean belonging to the *Tulamoeba-Pleurostomum* clade (*Tulamoebidae* n. fam.). *J. Euk. Microbiol.* 62: 227-238.
- Laird, M.R., Langille, M.G.I. and Brinkman, F.S.L.** (2015) GenomeD3Plot: A library for rich, interactive visualizations of genomic data in web applications. *Bioinformatics* 31: 3348-3349.
- Lau, J.B., Stork, S., Moog, D., Sommer, M.S. and Maier U.G.** (2015) N-terminal lysines are essential for protein translocation via a modified ERAD-system in complex plastids. *Mol. Microbiol.* 96: 609-620.
- Lee, P.A., Bertrand, E.M., Saito, M.A. and DiTullio, G.R.** (2015) Influence of vitamin B12 availability on oceanic dimethylsulfide and dimethylsulfoniopropionate. *Environ. Chem.* 13: 293-301.
- Leger, M.M., Petru, M., Žárský, V., Eme, L., Vlček, Č., Harding, T., Lang, B.F., Eliáš, M., Doležal, P. and Roger, A.J.** (2015) An ancestral bacterial division system is widespread in eukaryotic mitochondria. *Proc. Natl. Acad. Sci. USA* 112: 10239-46.
- Mariscal, C.** (2015) Universal biology: Assessing universality from a single example. In *The Impact of Discovering Life Beyond Earth*, S.J. Dick (Ed.), pp. 113-126, Cambridge University Press.
- Mariscal, C. and Doolittle, W.F.** (2015) Eukaryotes first: how could that be? *Phil. Trans. R. Soc. Lond. B.* 370: 20140322.
- Meehan, C.J., Langille, M.G. and Beiko, R.G.** (2015) Frailty and the microbiome. *Interdiscip. Topics Gerontol. Geriatr.* 41: 54-65.
- Moog, D., Stork, S., Reislöhner, S., Grosche, C. and Maier, UG** (2015) In vivo localization studies in the stramenopile alga *Nannochloropsis oceanica*. *Protist* 166: 161-171.
- Moog, D., Rensing, S.A., Archibald, J.M., Maier, U.-G. and Ullrich, K.K.** (2015) Localization and evolution of putative triose phosphate translocators in the diatom *Phaeodactylum tricornutum*. *Genome Biol. Evol.* 7: 2955-2969.
- Muñoz-Gómez, S.A., Slamovits, C.H., Dacks, J.B. and Wideman, J.G.** (2015) The evolution of MICOS: Ancestral and derived functions and interactions. *Commun. Integr. Biol.* 8: e1094593.
- Muñoz-Gómez, S.A., Slamovits, C.H., Dacks, J.B., Baier, K.A., Spencer, K.D., Wideman, J.G.** (2015) Ancient homology of the mitochondrial contact site and cristae organizing system points to an endosymbiont origin of mitochondrial cristae. *Curr. Biol.* 25: 1489-1495.
- Ning, J. and Beiko, R.G.** (2015) Phylogenetic approaches to microbial community classification. *Microbiome* 3: 47.
- Nýlvltová, E., Stairs, C.W., Hrdý, I., Rídl, J., Mach, J., Pačes, J., Roger, A.J. and Tachezy, J.** (2015) Lateral gene transfer and gene duplication played a key role in the evolution of *Mastigamoeba balamuthi* hydrogenosomes. *Mol. Biol. Evol.* 32: 1039-1055.
- Paerl, R.W., Bertrand, E.M., Allen, A.E., Palenik, B. and Azam, F.** (2015) Vitamin B1 ecophysiology of marine picoeukaryotic algae: Strain-specific differences and a new role for bacteria in vitamin cycling. *Limnol. Oceanogr.* 60: 215-228.
- Park, J.S. and Simpson, A.G.** (2015) Diversity of heterotrophic protists from extremely hypersaline habitats. *Protist* 166: 422-437.

- Powell, R. and Mariscal, C. (2015) Convergent evolution as a natural experiment: the tape of life reconsidered. *Interface Focus* 5: 20150040.
- Safatli, A. and **Blouin, C.** (2015). Phylogeny: an open-source Python framework for phylogenetic tree reconstruction and search space heuristics. *PeerJ Comput. Sci.* 1:e9.
- Scharf, C. *et al.* [30 authors incl. C. Mariscal] (2015) A strategy for origins of life research. *Astrobiology* 15: 1031-1042.
- Shafiei, M., Dunn, K.A., Boon, E., MacDonald, S.M., Walsh, D.A., *Gu, H. and Bielawski, J.P. (2015) BioMiCo: a supervised Bayesian model for inference of microbial community structure. *Microbiome* 3: 8.
- Sharpe, S.C., Eme, L., Brown, M.W. and Roger, A.J. (2015) Timing the origins of multicellular eukaryotes through phylogenomics and relaxed molecular clock analyses. In *Evolutionary Transitions to Multicellular Life, Advances in Marine Genomics 2*, I. Ruiz-Trillo and A.M. Nedelcu (Eds.), pp. 3-29, Springer Science.
- Stairs, C.W., Leger, M.M. and Roger, A.J. (2015) Diversity and origins of anaerobic metabolism in mitochondria and related organelles. *Philos. Trans. R. Soc. Lond. B. Biol. Sci.* 370: 20140326.
- Stark, M.R., Dunn, E.A., Dunn, W.S.C., Grisdale, C.J., Daniele, A.R., Halstead, M.R., Fast, N.M. and Rader, S.D. (2015) Dramatically reduced spliceosome in *Cyanidioschyzon merolae*. *Proc. Natl. Acad. Sci. USA* 112: E1191-E1200.
- Susko, E.** (2015). Bayesian long branch attraction bias and corrections. *Syst. Biol.* 64: 243-255.
- Tai, V., Gile, G.H., Pan, J., James, E.R., Carpenter, K.J., Scheffrahn, R.H., Keeling, P.J. (2015) The phylogenetic position of *Kofoidia loriculata* (Parabasalia) and its implications for the evolution of the Cristamonadea. *J. Euk. Microbiol.* 62: 255-259.
- Torruella, G., de Mendoza, A., Grau-Bové, X., Antó, M., Chaplin, M.A., del Campo, J., Eme L., Pérez-Cordón, G., Whipps, C.M., Nichols, K.M., Paley, R., Roger, A.J., Sitjà-Bobadilla, A., Donachie, S. and Ruiz-Trillo, I. (2015) Phylogenomics reveals convergent evolution of lifestyles in close relatives of animals and fungi. *Curr. Biol.* 25: 2404-2410.
- Waldbusser, G.G., Hales, B., Langdon, C.J., Haley, B.A., Schrader, P., Brunner, E.L., Gray, M.W., Miller, C.A., Gimenez, I. and Hutchinson, G. (2015) Ocean acidification has multiple modes of action on bivalve larvae. *PLoS One* 10: e0128376.
- Wong, D.H.J. and Beiko, R.G. (2015) Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. *BMC Genomics* 16: 526.
- Xu, X., Dunn, K.A. and *Field, C. (2015) A robust ANOVA approach to estimating a phylogeny from multiple genes. *Mol. Biol. Evol.* 32: 2186-2194.
- Zhang, Q., Táborský, P., Silberman, J.D., Pánek, T., Čepička, I. and Simpson, A.G. (2015) Marine isolates of *Trimastix marina* form a Plesiomorphic deep-branching lineage within Preaxostyla, separate from other known Trimastigids (Paratrimastix n. gen.). *Protist* 166: 468-491.

Year 2014:

- Abad, M.G., Long, Y., Kinchen, D., Schindel, E.T., Gray, M.W. and Jackman, J.E. (2014) Mitochondrial tRNA 5'-editing in *Dictyostelium discoideum* and *Polysphondylium pallidum*. *J. Biol. Chem.* 289: 15155-15165.
- Alonso-Sáez, L., Zeder, M., Harding, T., Pernthaler, J., Lovejoy, C., Bertilsson, S. and Pedrós-Alió, C. (2014) Winter bloom of a rare betaproteobacterium in the Arctic Ocean. *Front. Microbiol.* 5: 425.
- Archibald, J.M.** (2014) *One Plus One Equals One: Symbiosis and the Evolution of Complex Life.* 224 pp. Oxford University Press.
- Archibald, J.M.** (2014) The cellular revolution. *The Scientist* 12: 74.
- Boon, E., Meehan, C.J., Whidden, C., Wong, D.H., Langille, M.G. and Beiko, R.G. (2014) Interactions in the microbiome: communities of organisms and communities of genes. *FEMS Microbiol. Rev.* 38: 90-118.

- Brunet, T.D.P. and **Doolittle, W.F.** (2014) Getting “function” right. *Proc. Natl. Acad. Sci. USA* 111: E3365.
- Doolittle, W.F.** (2014) How natural a kind is ‘eukaryote?’. *Cold Spring Harb. Perspect. Biol.* 6: pii: a015974.
- Doolittle, W.F.** (2014) The trouble with (group II) introns. *Proc. Natl. Acad. Sci. USA* 111: 6536-6537.
- Doolittle, W.F.**, Brunet, T.D.P., Linquist, S. and Gregory, T.R. (2014) Distinguishing between “function” and “effect” in genome biology. *Genome Biol. Evol.* 6: 1234-1237.
- Doolittle, W.F.** (2014) Natural selection through survival alone, and the possibility of Gaia. *Biol. Philos.* 29: 415-423.
- Eme, L., Sharpe, S.C., Brown, M.W. and **Roger, A.J.** (2014) On the age of eukaryotes: evaluating evidence from fossils and molecular clocks. *Cold Spring Harb. Perspect. Biol.* 6: pii: a016139
- Filker, S., Kaiser, M., Rosselló-Móra, R., Dunthorn, M., Lax, G. and Stoeck, T. (2014) “Candidatus Haloectosymbiotes riaformosensis” (Halobacteriaceae), an archaeal ectosymbiont of the hypersaline ciliate *Platynematum salinarum*. *Syst Appl. Microbiol.* 37: 244–251.
- Gawryluk, R.M.R., Chisholm, K.A., Pinto, D.M. and **Gray, M.W.** (2014) Compositional complexity of the mitochondrial proteome of a unicellular eukaryote (*Acanthamoeba castellanii*, supergroup Amoebozoa) rivals that of animals, fungi, and plants. *J. Proteomics* 109C: 400-416.
- Gentekaki, E., Kolisko, M., Boscaro, V., Bright, K.J., Dini, F., Di Giuseppe, G., Gong, Y., Miceli, C., Modeo, L., Molestina, R.E., Petroni, G., Pucciarelli, S., **Roger, A.J.**, Strom, S.L. and Lynn, D.H. (2014) Large-scale phylogenomic analysis reveals the phylogenetic position of the problematic taxon Protocruzia and unravels the deep phylogenetic affinities of the ciliate lineages. *Mol. Phylogenet. Evol.* 78C: 36-42.
- Gile, G. and **Slamovits, C.H.** (2014) Transcriptomic analysis reveals evidence for a cryptic plastid in the colpodellid *Voromonas pontica*, a close relative of chromerids and apicomplexan parasites. *PLoS One* 9: e96258.
- Gray, M.W.** (2014) The pre-endosymbiont hypothesis: a new perspective on the origin and evolution of mitochondria. *Cold Spring Harb. Perspect. Biol.* 6: pii: a016097.
- Gray, M.W.** (2014) Organelle evolution, fragmented ribosomal RNAs, and Carl. *RNA Biol.* 11: 213-216.
- Gray, M.W.** (2014) Mitochondrial genomes. In *Molecular Life Sciences: An Encyclopedic Reference*, R.D. Wells *et al.* (Eds), Springer.
- Hahn, M.W., Schmidt, J., Taipale, S.J., **Doolittle, W.F.** and Koll, U. (2014). *Rhodoluna laticola* gen. nov., sp. nov., a planktonic freshwater bacterium with a stream-lined genome. *Int. J. Syst. Evol. Microbiol.* 64: 3254-3263.
- Hirakawa, Y., Suzuki, S., **Archibald, J.M.**, Keeling, P.J. and Ishida, K. (2014) Overexpression of molecular chaperone genes in nucleomorph genomes. *Mol. Biol. Evol.* 31: 1437-1443.
- Hleap, J.S. and **Blouin, C.** (2014) Inferring meaningful communities from topology-constrained correlation networks. *PLoS One* 9: e113438.
- Kamikawa, R., Kolisko, M., Nishimura, Y., Yabuki, A., Brown, M.W., Ishikawa, S.A., Ishida, K., **Roger, A.J.**, Hashimoto, T. and Inagaki, Y. (2014) Gene content evolution in Discobid mitochondria deduced from the phylogenetic position and complete mitochondrial genome of *Tsukubamonas globosa*. *Genome Biol. Evol.* 6: 306-315.
- Keeling, P.J. *et al.* (81 authors, incl. **Archibald, J.A.**, **Simpson, A.G.B.** and **Slamovits, C.H.**) (2014) The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): Illuminating the functional diversity of eukaryotic life in the oceans through transcriptome sequencing. *PLoS Biol.* 12: e1001889.
- Klimeš, V., Gentekaki, E., **Roger A.J.** and Eliáš, M. (2014) A large number of nuclear genes in the human parasite *Blastocystis* require mRNA polyadenylation to create functional termination codons. *Genome Biol. Evol.* 6: 1956-1961.
- Langille, M.G.**, **Meehan, C.J.**, **Koenig, J.E.**, **Dhanani, A.S.**, Rose, R.A., Howlett, S.E. and **Beiko, R.G.** (2014) Microbial shifts in the aging mouse gut. *Microbiome* 2:50.

- *Lee, R., Lai, H., Malik, S.B., Saldarriaga, J.F., Keeling, P.K. and **Slamovits, C.H.** (2014) Analysis of EST data of the marine protist *Oxyrrhis marina*, an emerging model for alveolates biology and evolution. *BMC Genomics* 15: 122.
- Lee, W.J. and **Simpson, A.G.B.** (2014) Morphological and molecular characterisation of *Notosolenus urceolatus* Larsen and Patterson 1990, a member of an understudied deep-branching euglenid group (petalomonads). *J. Euk. Microbiol.* 61: 463-479.
- Lee, W.J. and **Simpson, A.G.B.** (2014) Ultrastructure and molecular phylogenetic position of *Neometanema parovale* sp. nov. (*Neometanema* gen. nov.), a marine phagotrophic euglenid with skidding motility. *Protist* 165: 452-472.
- Lee, W.J., Miller, K. and **Simpson, A.G.B.** (2014) Morphological and molecular characterisation of a new species of *Stephanopogon*, *Stephanopogon pattersoni* n. sp. *J. Euk. Microbiol.* 61: 389-398.
- Levy Karin, E., **Susko, E.** and Pupko, T. (2014) Alignment errors strongly impact likelihood-based tests for comparing topologies. *Mol. Biol. Evol.* 31: 3057-3067.
- Liu, H., Keselj, V. and **Blouin, C.** (2014) Biological event extraction using subgraph matching. *Comput. Intelligence* 30: 600-635.
- Malagón, J.N., Ahuja, A., Sivapatham G., Hung, J., Lee, J., Muñoz-Gómez, S.A., Atallah, J., Singh, R. and Larsen, E. (2014) Evolution of *Drosophila* sex comb length illustrates the inextricable interplay between selection and variation. *Proc. Natl. Acad. Sci. USA* 111: E4103-4109.
- Maselli, G.A., **Slamovits, C.H.**, Bianchi, J.I., Vilarrasa-Blasi, J., Caño-Delgado, A.I. and Mora-García, S. (2014) Revisiting the evolutionary history and roles of protein phosphatases with Kelch-like domains in plants. *Plant Physiol.* 164: 1527-1541.
- McRose, D., Guo, J., Monier, A., Sudek, S., Wilken, S., Yan, S., Mock, T., **Archibald, J.M.**, Begley, T. P., Reyes-Prieto, A. and Worden A. Z. (2014) Alternatives to vitamin B₁ uptake revealed with discovery of riboswitches in multiple marine eukaryotic lineages. *ISME J.* 8: 2517-2529.
- Meehan, C.J. and **Beiko, R.G.** (2014) A phylogenomic view of ecological specialization in the Lachnospiraceae, a family of digestive tract-associated bacteria. *Genome Biol. Evol.* 6: 703-713.
- Nakayama, T., Kamikawa, R., Tanifuji, G., Kashiya, Y., Ohkouchi, N., **Archibald J.M.** and Inagaki, Y. (2014) Complete genome of a non-photosynthetic cyanobacterium in a diatom reveals recent adaptations to an intracellular lifestyle. *Proc. Natl. Acad. Sci. USA* 111: 11407-11412.
- O'Doherty, K.C., Neufeld, J.D., Brinkman, F.S.L., Gardner, H., Guttman, D.S. and **Beiko, R.G.** (2014) Opinion: Conservation and stewardship of the human microbiome. *Proc. Natl. Acad. of Sci. USA* 111: 14312-14313.
- Panek, T., **Simpson, A.G.B.**, Hampl, V. and Cepicka, I. (2014) *Creneis carolina* gen. et sp. nov. (Heterolobosea), a novel marine anaerobic protist with strikingly derived morphology and life cycle. *Protist* 165: 542-567.
- Parks, D.H., Tyson, G.W., Hugenholtz, P. and **Beiko, R.G.** (2014) STAMP: statistical analysis of taxonomic and functional profiles. *Bioinformatics* 30: 3123-3124.
- Shafiei, M., Dunn, K.A., Chipman, H., *Gu, H. and **Bielawski, J.P.** (2014) BiomeNet: A Bayesian model for inference of metabolic divergence among microbial communities. *PLoS Comput. Biol.* 10: e1003918.
- Stairs, C.W., Eme, L., Brown, M.W., Mutsaers, C., **Susko, E.**, Dellaire, G., Soanes, D.M., van der Giezen, M. and **Roger, A.J.** (2014). A SUF Fe-S cluster biogenesis system in the mitochondrion-related organelles of the anaerobic protist *Pygssuia*. *Curr. Biol.* 24: 1176-86.
- Susko, E.** (2014) Tests for two trees using likelihood methods. *Mol. Biol. Evol.* 31: 1029-1039.
- Tanifuji, G. and **Archibald, J.M.** (2014) Nucleomorph comparative genomics. In *Endosymbiosis*, W. Löffelhardt (Ed.), pp. 197-213, Springer Wein.
- Tanifuji, G., Onodera, N.T., Moore, C.E. and **Archibald, J.M.** (2014) Reduced nuclear genomes maintain high levels of gene transcription. *Mol. Biol. Evol.* 31: 625-635.
- Tanifuji, G., Onodera, N.T., Brown, M.W., Curtis, B.A., **Roger, A.J.**, Wong, G.K.-S., Melkonian, M. and **Archibald, J.M.** (2014) Nucleomorph and plastid genome sequences of the chlorarachniophyte

Lotharella oceanica: convergent reductive evolution and frequent recombination in nucleomorph-bearing algae. *BMC Genomics* 15: 374.

- Tsaousis, A.D., Gentekaki, E., Eme, L., Gaston, D. and **Roger, A.J.** (2014) Evolution of the cytosolic iron-sulfur cluster assembly machinery in *Blastocystis sp.* and other microbial eukaryotes. *Eukaryot. Cell* 13: 143-153.
- Valach, M., Burger, G., **Gray, M.W.** and Lang, B.F. (2014) Widespread occurrence of organelle genome-encoded 5S rRNAs including permuted molecules. *Nucleic Acids Res.* 42: 13764-13777.
- Wang, H.-C., **Susko, E.** and **Roger, A.J.** (2014) An amino acid substitution-selection model adjusts residue fitness to improve phylogenetic estimation. *Mol. Biol. Evol.* 31: 779-792.
- Whidden, C., *Zeh, N. and **Beiko, R.G.** (2014) Supertrees based on the subtree prune-and-regraft distance. *Syst. Biol.* 63: 566-581.
- Yoder, A.D., Chan, L.M., Dos Reis, M., Larsen, P.A., Campbell, C.R., Rasoloarison, R., Barrett, M., Roos, C., Kappeler, P., **Bielawski, J.** and Yang, Z. (2014) Molecular evolutionary characterization of a V1R subfamily unique to Strepsirrhine primates. *Genome Biol. Evol.* 6: 213-227.

Year 2013:

- Bay, R.A. and **Bielawski, J.P.** (2013) Inference of functional divergence among proteins when the evolutionary process is non-stationary. *J. Mol. Evol.* 76: 205-215.
- Bielawski, J.P.** (2013) Detecting the signatures of adaptive evolution in protein-coding genes. *Curr. Protoc. Mol. Biol.*, Chapter 19: Unit 19.1.
- Breglia, S.A., Yubuki, N. and Leander, B.S. (2013) Ultrastructure and molecular phylogenetic position of *Heteronema scaphurum*: a eukaryovorous euglenid with a cytoproct. *J. Eukaryot. Microbiol.* 60: 107-120.
- Brown, M.W. and Silberman, J.D. (2013) The non-dictyostelid sorocarpic amoebae. In *Dictyostelids. Evolution, Genomics and Cell Biology*, M. Romeralo et al. (Eds.), pp. 219-242, Springer-Verlag, Heidelberg, Germany.
- Brown, M.W., Sharpe, S.C., Silberman, J.D., Heiss, A.A., Lang, B.F., **Simpson, A.G.B.** and **Roger, A.J.** (2013) Phylogenomics demonstrates that breviate flagellates are related to opisthokonts and apusomonads. *Proc. Royal Soc. Biol. Sci.* 280: 20131755.
- Burger, G., **Gray, M.W.**, Forget, L. and Lang, B.F. (2013) Strikingly bacteria-like and gene-rich mitochondrial genomes throughout jakobid protists. *Genome Biol. Evol.* 5: 418-438.
- Dhillon, B.K., Chiu, T.A., Laird, M.R., **Langille, M.G.** and Brinkman, F.S. (2013) IslandViewer update: Improved genomic island discovery and visualization. *Nucleic Acids Res.* 41 (Web Server issue): W129-32.
- Doolittle, W.F.** (2013) Is junk DNA bunk? A critique of ENCODE. *Proc. Natl. Acad. Sci. USA* 110: 5294-5300.
- Doolittle, W.F.** (2013) The spliceosomal catalytic core arose in the RNA world ... or did it? *Genome Biol.* 14: 141.
- Doolittle, W.F.** (2013) Carl R. Woese [1928-2012]. *Current Biol.* 23: R183-185.
- Doolittle, W.F.** and Zhaxybayeva, O. (2013) What is a prokaryote? In: *The Prokaryotes – Vol. 1: Prokaryotic Biology and Symbiotic Associations*, E. Rosenberg et al. (Eds.), pp. 41-58, Springer-Verlag.
- Doolittle, W.F.**, Fraser, P., Gerstein, M.B., Graveley, B.R., Henikoff, S., Huttenhower, C., Oshlack, A., Ponting, C.P., Rinn, J.L., Schatz, M.C., Ule, J., Weigel, D. and Weinstock, G.M. (2013) Sixty years of genome biology. *Genome Biol.* 14: 113.
- Dunn, K.A., Jiang, W., *Field, C. and **Bielawski, J.P.** (2013) Improving evolutionary models for mitochondrial protein data with site-class specific amino acid exchangeability matrices. *PLoS One* 8: e55816.
- Eveleigh, R.J.M., Meehan, C.J., **Archibald, J.M.** and **Beiko, R.G.** (2013) Being *Aquifex aeolicus*: untangling a hyperthermophile's checkered past. *Genome Biol. Evol.* 5: 2478-2497.

- Feehan, C.J., Johnson-Mackinnon, J., Scheibling, R.E., Lauzon-Guay, J.-S. and **Simpson, A.G.B.** (2013) Validating the identity of *Paramoeba invadens*, the causative agent of recurrent mass mortality of sea urchins in Nova Scotia. *Diseases of Aquatic Organisms* 103: 209-227.
- Flegontov, P., Votycka, J., Skalicky, T., Logacheva, M.D., Penin, A.A., Tanifuji, G., Onodera, N.T., Kondrashov, A.S., **Archibald, J.M.** and Lukeš, J. (2013) *Paratrypanosoma*—a novel trypanosomatid. *Curr. Biol.* 23: 1787-1793.
- Gaston, D. and **Roger, A.J.** (2013) Functional divergence and convergent evolution in the plastid-targeted glyceraldehyde-3-phosphate dehydrogenases of diverse eukaryotic algae. *PLoS One* 8: e70396.
- Gile, G.H.**, Carpenter, K.J., James, E.R., Scheffrahn, R.H. and Keeling, P.J. (2013) Morphology and molecular phylogeny of *Staurojoenia mulleri* sp. nov. (Trichonymphida, Parabasalia) from the hindgut of the kalotermitid *Neotermes jouteli*. *J. Eukaryot. Microbiol.* 60: 203-213.
- Gray, M.W.** (2013) RNA Editing: Evolutionary Implications. In *Encyclopedia of Life Sciences. Citable Reviews in the Life Sciences*, pp. 1-7, John Wiley & Sons.
- Gray, M.W.** (2013) Organelles. In *Brenner's Encyclopedia of Genetics (2nd Ed.)*, S. Maloy and K. Hughes (Eds.), pp. 181-183, Academic Press.
- Gray, M.W.** (2013) Mitochondria. In *Brenner's Encyclopedia of Genetics (2nd Ed.)*, S. Maloy and K. Hughes (Eds.), pp. 430-432, Academic Press.
- Gray, M.W.** (2013) Mitochondrial DNA. In *Brenner's Encyclopedia of Genetics (2nd Ed.)*, S. Maloy and K. Hughes (Eds.), pp. 436-438, Academic Press.
- Gray, M.W.** (2013) Mitochondrial genome. In *Brenner's Encyclopedia of Genetics (2nd Ed.)*, S. Maloy and K. Hughes (Eds.), pp. 441-442, Academic Press.
- Gray, M.W.** (2013) Mitochondrial mutants. In *Brenner's Encyclopedia of Genetics (2nd Ed.)*, S. Maloy and K. Hughes (Eds.), pp. 446-447, Academic Press.
- Harding, T., Brown, M.W., Plotnikov, A., Selivanova, E., Park, J.S., Gunderson, J.H., Baumgartner, M., Silberman, J.D., **Roger, A.J.** and **Simpson, A.G.B.** (2013) Amoeba stages in the deepest branching heteroloboseans, including *Pharyngomonas*: Evolutionary and systematic implications. *Protist* 164: 272-286.
- Heiss, A.A., Walker, G. and **Simpson, A.G.B.** (2013) The microtubular cytoskeleton of the apusomonad *Thecamonas*, a sister lineage to the opisthokonts. *Protist* 164: 598–621.
- Hleap, J.S., **Susko, E.** and **Blouin, C.** (2013) Defining structural and evolutionary modules in proteins: a community detection approach to explore sub-domain architecture. *BMC Struct. Biol.* 13: 20.
- Kamikawa, R., Brown, M.W., Nishimura, Y., Sako, Y., Heiss, A.A., Yubuki, N., Gawryluk, R., **Simpson, A.G.B.**, **Roger, A.J.**, Hashimoto, T. and Inagaki, Y. (2013) Parallel re-modeling of EF-1 α function: divergent EF-1 α genes co-occur with EFL genes in diverse distantly related eukaryotes. *BMC Evol. Biol.* 13: e131.
- Kim, E. and **Archibald, J.M.** (2013) Ultrastructure and molecular phylogeny of the cryptomonad *Goniomonas avonlea* sp. nov. *Protist* 164: 160-182.
- Langille, M.G.I.**, Zaneveld, J., Caporaso, J.G., McDonald, D., Knights, D., Reyes, J.A., Clemente, J.C., Burkepille, D.E., Vega Thurber, R.L., Knight, R., **Beiko, R.G.** and Huttenhower, C. (2013) Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nature Biotech.* 31: 814-821.
- Lax, G. and **Simpson, A.G.B.** (2013) Combining molecular data with classical morphology for uncultured phagotrophic euglenids (Excavata); A single-cell approach. *J. Euk. Microbiol.* 60: 615-625.
- Leger, M.M., Gawryluk, R.M.R., **Gray, M.W.** and **Roger, A.J.** (2013) Evidence for a hydrogenosomal type anaerobic ATP generation pathway in *Acanthamoeba castellanii*. *PLoS One* 8: e6953.
- Lepetit, B., Sturm, S., Rogato, A., Gruber, A., Sachse, M., Falciatore, A., Kroth, P.G., Lavaud, J. (2013) High light acclimation in the secondary plastids containing diatom *Phaeodactylum tricorutum* is triggered by the redox state of the plastoquinone pool. *Plant Physiol.* 161: 853–865.

- Li, L., Nelson, C.J., Carrie, C., Gawryluk, R.M., Solheim, C., **Gray, M.W.**, Whelan, J. and Millar, A.H. (2013) Subcomplexes of ancestral respiratory complex I subunits rapidly turn over in *in vivo* as productive assembly intermediates in *Arabidopsis*. *J. Biol. Chem.* 288: 5707-5717.
- Maruyama, S., Eveleigh, R.J. and **Archibald, J.M.** (2013) Treetrimmer: a method for phylogenetic dataset size reduction. *BMC Res. Notes* 6: 145.
- O'Malley, M.A., **Simpson, A.G.B.** and **Roger, A.J.** (2013) The other eukaryotes in light of evolutionary protistology. *Biol. Philos.* 28: 299-330.
- Parks, D.H. and **Beiko, R.G.** (2013) Measures of phylogenetic differentiation provide robust and complementary insight into microbial communities. *ISME J.* 7: 173-183.
- Parks, D.H., Mankowski, T., Zangooui, S., Porter, M.S., Armanini, D.G., Baird, D.J., **Langille, M.G.** and **Beiko, R.G.** (2013) GenGIS 2: Geospatial analysis of traditional and genetic biodiversity, with new gradient algorithms and an extensible plugin framework. *PLoS One* 8: e69885.
- Pombert, J.-F., Smirnov, A., James, E.R., Janouškovec, J., **Gray, M.W.** and Keeling, P.J. (2013) The complete mitochondrial genome from an unidentified *Phalansterium* species. *Protist Genomics* 1: 26-32.
- Porter, M.S. and **Beiko, R.G.** (2013) SPANNER: Taxonomic assignment of sequences using pyramid matching of similarity profiles. *Bioinformatics* 29: 1858-1864.
- Rao, B.S., Mohammad, F., **Gray, M.W.** and Jackman, J.E. (2013) Absence of a universal element for tRNA^{His} identity in *Acanthamoeba castellanii*. *Nucleic Acids Res.* 41: 1885-1894.
- Slamovits, C.H.** (2013) Extreme genome reduction in microbial parasites. In: *Comparative Genomics in Neglected Human Parasites*, M.C. López-Camarillo & L.A. Marchat (Eds.), pp. 157-174, Nova Publishers.
- Smith, D.R., Hua, J., **Archibald, J.M.** and *Lee, R.W. (2013) Palindromic genes in the linear mitochondrial genome of the nonphotosynthetic green alga *Polytomella magna*. *Genome Biol. Evol.* 5: 1661-1667.
- Sturm, S., Engelken, J., Gruber, A., Vugrinec, S., Kroth, P.G., Adamska, I. and Lavaud, J. (2013) A novel type of light-harvesting antenna protein of red algal origin in algae with secondary plastids. *BMC Evol. Biol.* 13: 159.
- Suga, H., Chen, Z., de Mendoza, A., Sebé-Pedrós, A., Brown, M.W., Kramer, E., Carr, M., Kerner, P., Vervoort, M., Sánchez-Pons, N., Torruella, G., Derelle, R., Manning, G., Lang, B.F., Russ, C., Haas, B.J., **Roger, A.J.**, Nusbaum, C. and Ruiz-Trillo, I. (2013) The *Capsaspora* genome reveals a complex unicellular prehistory of animals. *Nat. Commun.* 4: 2325.
- Sunagar, K., Undheim, E.A.B., Chan, A.H.C., Koludarov, I., Muñoz-Gómez, S.A., Antunes, A. and Fry, B.G. (2013) Evolution stings: The origin and diversification of scorpion toxin peptide scaffolds. *Toxins* 5: 2456-2487.
- Susko, E.** (2013). Likelihood ratio tests with boundary constraints using data-dependent degrees of freedom. *Biometrika* 100: 1019-1023.
- Susko, E.** and **Roger, A.J.** (2013) Problems with estimation of ancestral frequencies under stationary models. *Syst. Biol.* 62: 330-338.
- Wang, H.-C., **Susko, E.** and **Roger, A.J.** (2013) The site-wise log-likelihood score is a good predictor of genes under positive selection. *J. Mol. Evol.* 76: 280-294.
- Whidden, C., **Beiko, R.G.**, and *Zeh, N. (2013) Fixed-parameter and approximation algorithms for maximum agreement forests. *SIAM J. Comput.* 42: 1431-1466.
- Wideman, J.G., Gawryluk, R.M.R., **Gray, M.W.** and Dacks, J.B. (2013) The ancient and widespread nature of the ER-Mitochondria encounter structure. *Mol. Biol. Evol.* 30: 2044-2049.
- Yubuki, N., **Simpson, A.G.B.** and Leander, B.S. (2013) Comprehensive ultrastructure of *Kipferlia bialata* provides evidence for character evolution within the Fornicata (Excavata). *Protist* 164: 423-439.
- Yubuki, N., **Simpson, A.G.B.** and Leander, B.S. (2013) Reconstruction of the feeding apparatus in *Postgaardia mariagerensis* provides evidence for character evolution within the Symbiontida (Euglenozoa). *Eur. J. Protist.* 49: 32-39.

Year 2012:

- Adl, SM, **Simpson, AGB**, Lane, CE, Lukes, J, Bass, D, Bowser, SS, Brown, MW, Burki, F, Dunthorn, M, Hampl, V, Heiss, A, Hoppenrath, M, Lara, E, Legall, L, Lynn, DH, McManus, H, Mitchell, EAD, Mozley-Stanridge, SE, Parfrey, LW, Pawlowski, J, Rueckert S, Shadwick LL, Schoch C, Smirnov A, Spiegel, FW (2012) The revised classification of eukaryotes. *J. Eukaryot. Microbiol.* 59: 429-493.
- Archibald, J.M.** (2012) Plastid origins. In: *Organelle Genetics: Evolution of Organelle Genomes and Gene Expression*, C. Bullerwell (Ed.), pp. 19-38, Springer-Verlag.
- Archibald, J.M.** (2012) The evolution of algae by secondary and tertiary endosymbiosis. In *Advances in Botanical Research*, G. Piganeau (Ed.), pp. 97-118, Elsevier Press.
- Archibald, JM** (2012) Lynn Margulis [1938-2011]. *Curr. Biol.* 22: R4-6.
- Brown, M.W., Silberman, J.D. and Spiegel, F.W. (2012) A contemporary evaluation of the acrasids (Acrasidae, Heterolobosea, Excavata). *Eur. J. Protistol.* 48: 103-123.
- Brown, M.W., Kolisko, M., Silberman, J.D. and **Roger, A.J.** (2012) Aggregative multicellularity evolved independently in the eukaryotic supergroup Rhizaria. *Curr. Biol.* 22: 1123-1127.
- Curtis, B.A. et al. [73 authors incl. G. Tanifuji, A. Gruber, S. Maruyama, G.H. Gile, J.F. Hopkins, R.J. Eveleigh, T. Nakayama, **R.G. Beiko**, E. Kim, S.B. Malik, **C.H. Slamovits**, **M.W. Gray**, **J.M. Archibald**] (2012) Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature* 492: 59-65.
- Doolittle, W.F.** (2012) Evolutionary biology: A ratchet for protein complexity. *Nature* 481: 270-271.
- Doolittle, W.F.** (2012) Microbial neopleomorphism. *Biology and Philosophy* 28: 351-378.
- Doolittle, W.F.** (2012) Postphylogenetics. In *Microbes and Evolution: The World That Darwin Never Saw*, R. Kolter & S. Maloy (Eds.), pp. 269-274, ASM Press, Washington.
- Doolittle, W.F.** (2012) Population genomics: how bacterial species form and why they don't exist. *Curr. Biol.* 22: R451-453.
- Doolittle, W.F.** (2012) Craig Venter's new life: The realization of some thought experiments in biological ontology. In *Thought Experiments in Science, Philosophy and the Arts*, M. Frappier, L. Meynell & J.R. Brown (Eds.), pp. 160-176, Routledge.
- Gawryluk, R.M., Chisholm, K.A., Pinto, D.M. and **Gray, M.W.** (2012) Composition of the mitochondrial electron transport chain in *Acanthamoeba castellanii*: structural and evolutionary insights. *Biochim. Biophys. Acta.* 1817: 2027-2037.
- Gile, G.H. and **Slamovits, C.H.** (2012) Phylogenetic position of *Lophomonas striata* Bütschli (Parabasalia) from the hindgut of the cockroach *Periplaneta americana*. *Protist* 163: 274-283.
- Gray, M.W.** (2012) Mitochondrial evolution. *Cold Spring Harb Perspect Biol.* 4: a011403.
- Gray, M.W.** (2012) Evolutionary origin of RNA editing. *Biochem.* 51: 5235-5242.
- Gray, M.W.** and **Archibald, J.M.** (2012) Origins of mitochondria and plastids. In: *Advances in photosynthesis and respiration (Genomics of Chloroplasts and Mitochondria)*, R. Bock & V. Knoop (Eds.), pp. 1-30, Springer.
- Gray, M.W.** and Beyer, A.L (2012) Ribonucleic acid (RNA). In *McGraw Hill Encyclopedia of Science & Technology (11th Ed.)*, McGraw-Hill Education.
- *Gu, H., Dunn, K.A. and **Bielawski, J.P.** (2012) Likelihood Based Clustering (LiBaC) for Codon Models. In *Codon Evolution: Mechanisms and Models*, G.M. Cannarozzi & A. Schneider (Eds.), pp. 60-72, Oxford University Press.
- Hleap, J.S., Mejía-Falla, P.A. and Cárdenas, H. (2012) Morphometric relationships of the round ray *Urotrygon rogersi*: quantitative implications under linear models. *Revista de Biología marina y oceanografía* 47: 35-50.
- Hopkins, J.F., Spencer, D.F., Laboissiere, S., Neilson, J.A., Eveleigh, R.J., Durnford, D.G., **Gray, M.W.** and **Archibald, J.M.** (2012) Proteomics reveals plastid- and periplastid-targeted proteins in the chlorarachniophyte alga *Bigeloviella natans*. *Genome Biol. Evol.* 4: 1391-1406.

- Hug, L.A., **Beiko, R.G.**, Rowe, A.R., Richardson, R.E. and Edwards, E.A. (2012) Comparative metagenomics of three Dehalococcoides-containing enrichment cultures: the role of the non-dechlorinating community. *BMC Genomics* 13: 327.
- Jackman, J.E., Gott, J.M. and **Gray, M.W.** (2012) Doing it in reverse: 3'to-5' polymerization by the Thg1 superfamily. *RNA* 18: 886-899.
- Jiang, X., **Langille, M.G.I.**, Neches, R.Y., Elliot, M., Levin, S.A., Eisen, J.A., Weitz, J.S., Dushoff, J. (2012) Functional biogeography of ocean microbes revealed through non-negative matrix factorization. *PLoS One* 7: e43866.
- Langille, M.G.**, Meehan, C.J. and **Beiko, R.G.** (2012) Human microbiome: a genetic bazaar for microbes? *Curr. Biol.* 22: R20-22.
- Liberles, D. *et al.* (29 authors incl. **Roger, A.J.**) (2012) The interface of protein structure, protein biophysics, and molecular evolution. *Protein Sci.* 21:769-785.
- Lommer, M., Specht, M., Roy, A.S., Kraemer, L., Andreson, R., Gutowska, M.A., Wolf, J., Bergner, S.V., Schilhabel, M.B., Klostermeier, U.C., **Beiko, R.G.**, Rosenstiel, P., Hippler, M. and *LaRoche, J. (2012) Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. *Genome Biol.* 13: R66.
- Lynch, E.A., **Langille, M.G.I.**, Darling, A., Wilbanks, E.G., Haltiner, C., Shao, K.S.Y., Starr, M.O., Teiling, C., Harkins, T.T., Edwards, R.A., Eisen, J.A. and Facciotti, M.T. (2012) Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. *PLoS One* 7: e41389.
- MacDonald, N.J., Parks, D.H. and **Beiko, R.G.** (2012) Rapid identification of high-confidence taxonomic assignments for metagenomic data. *Nucleic Acids Res.* 40: e111.
- Maruyama, S. and **Archibald, J.M.** (2012) Endosymbiosis, gene transfer, and algal cell evolution. In: *Advances in Algal Cell Biology*, K. Heimann & C. Katsaros (Eds.), pp. 21-41, Walter de Gruyter.
- Meehan, C.J. and **Beiko, R.G.** (2012) Lateral gene transfer of an ABC transporter complex between major constituents of the human gut microbiome. *BMC Microbiol.* 12: 248.
- Moore, C.E., Curtis, B., Mills, T., Tanifuji, G. and **Archibald, J.M.** (2012) Nucleomorph genome sequence of the cryptophyte alga *Chroomonas mesostigmatica* CCMP1168 reveals lineage-specific gene loss and genome complexity. *Genome Biol. Evol.* 4: 1162-1175.
- Nakayama, T. and **Archibald, J.M.** (2012) Evolving a photosynthetic organelle. *BMC Biol.* 10: 35.
- Nakayama, T., Ishida, K. and **Archibald, J.M.** (2012) Broad distribution of TPI-GAPDH fusion proteins among eukaryotes: evidence for glycolytic reactions in the mitochondrion? *PLoS One* 7: e52340.
- Nesbø, C.L., Bradnan D.M., Adebusuyi A., Dlutek M., Petrus A.K., Foght J., **Doolittle W.F.** and Noll K.M. (2012) *Mesotoga prima* gen. nov., sp. nov., the first described mesophilic species of the Thermotogales. *Extremophiles* 16: 387-393.
- Onodera, N.T., Ryu, J., Durbic, T., Nislow, C., **Archibald, J.M.** and *Rohde, J.R. (2012) Genome sequence of *Shigella flexneri* serotype 5a strain M90T Sm. *J. Bacteriol.* 194: 3022.
- Park, J.S., De Jonckheere, J.F. and **Simpson, A.G.** (2012) Characterization of *Selenaion koniopes* n. gen., n. sp., an Amoeba that represents a major lineage with Heterolobosea, isolated from the Wieliczka salt mine. *J. Eukaryot. Microbiol.* 59: 601-613.
- Parks, D.H. and **Beiko, R.G.** (2012) Measuring community similarity with phylogenetic networks. *Mol. Biol. Evol.* 29: 3947-3958.
- Pawlowski J. *et al.* (32 authors incl. **Simpson, A.G.** and Gile, G.H.) (2012) CBOL protist working group: Barcoding eukaryotic richness beyond the animal, plant and fungal kingdoms. *PLoS Biol.* 10: e1001419.
- Roger, A.J.**, Kolisko, M. and **Simpson, A.G.B.** (2012) Phylogenomic analysis. In *Evolution of Virulence in Eukaryotic Microbes*, L.D. Sibley, B.J. Howlett, and J. Heitman (Eds.), pp. 44-69, Wiley-Blackwell.
- Schnittler, M., Novozhilov, Y.K., Romeralo, M., Brown, M.W., Fiore-Donno, A.M. (2012) Fruit body-forming protists: Myxomycetes and Myxomycete-like organisms Acrasia, Eumycetozoa. In W. Frey

(Ed.), *A. Engler's Syllabus of Plant Families*, 13th ed., pp. 40-88, Borntraeger Science Publishers, Berlin.

- Sharpton, T.J., Jospin, G., Wu, D., **Langille, M.G.I.**, Pollard, K.S. and Eisen, J.A. (2012) Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. *BMC Bioinformatics* 13: 624.
- Smith, S.E., Showers-Corneli, P., Dardenne, C.N., Harpending, H.H., Martin, D.P., **Beiko, R.G.** (2012) Comparative genomic and phylogenetic approaches to characterize the role of genetic recombination in mycobacterial evolution. *PLoS One* 7: e50070.
- Susko, E.** and **Roger, A.J.** (2012) The probability of correctly resolving a split as an experimental design criterion in phylogenetics. *Syst. Biol.* 61: 811-821.
- Takishita, K., Chikaraishi, Y., Leger, M.M., Kim, E., Yabuki, A., Ohkouchi, N. and **Roger, A.J.** (2012) Lateral transfer of tetrahymanol-synthesizing genes has allowed multiple diverse eukaryote lineages to independently adapt to environments without oxygen. *Biol. Direct* 7:5.
- Takishita, K., Kolisko, M., Komatsuzaki, H., Yabuki, A., Inagaki, Y., Cepicka, I., Smejkalová, P., Silberman, J.D., Hashimoto, T., **Roger, A.J.** and **Simpson, A.G.** (2012) Multigene phylogenies of diverse Carpediemonas-like organisms identify the closest relatives of 'amitochondriate' diplomonads and retortamonads. *Protist* 163: 344-355.
- Torruella, G., Derelle, R., Paps, J., Lang, B.F., **Roger, A.J.**, Shalchian-Tabrizi, K. and Ruiz-Trillo, I. (2012) Phylogenetic relationships within the Opisthokonta based on phylogenomic analyses of conserved single-copy protein domains. *Mol. Biol. Evol.* 29: 531-544.
- Tsaousis, A.D., Ollagnier de Choudens, S., Gentekaki, E., Long, S., Gaston, D., Stechmann, A., Vinella, D., Py, B., Fontecave, M., Barras, F., Lukeš, J. and **Roger, A.J.** (2012) Evolution of Fe/S cluster biogenesis in the anaerobic parasite *Blastocystis*. *Proc. Natl. Acad. Sci. USA* 109: 10426-10431.
- Tsaousis, A.D., Leger, M.L., Stairs, C.W. and **Roger, A.J.** (2012) The biochemical adaptations of mitochondrion-related organelles of parasitic and free-living microbial eukaryotes to low oxygen environments. In *Anoxia, Vol. 21: Cellular Origin, Life in Extreme Habitats and Astrobiology*, A.V. Altenbach, J.M. Bernhard & J. Seckbach (Eds.), pp. 51-81, Springer.
- Zhang, Q., **Simpson, A.G.B.** and Song, W. (2012) Insights into the phylogeny of systematically controversial haptorian ciliates (Ciliophora, Litostomatea) based on multigene analyses. *Proc. Roy. Soc., Series B*, 279: 2625-2635.
- Zhaxybayeva, O. *et al.* [20 authors incl. **Doolittle, W.F.**] (2012) Genome sequence of the mesophilic Thermotogales bacterium *Mesotoga prima* MesG1.Ag.4.2 reveals the largest Thermotogales genome to date. *Genome Biol. Evol.* 4: 700-708.
- Zou, L., **Susko, E.**, *Field, C. and **Roger, A.J.** (2012) Fitting nonstationary general-time-reversible models to obtain edge-lengths and frequencies for the Barry-Hartigan Model. *Syst. Biol.* 61: 927-940.

Year 2011:

- Abad, M.G., Long, Y., Willcox, A., Gott, J.M., **Gray, M.W.** and Jackman, J.E. (2011) A role for tRNAHis guanylyltransferase (Thg1)-like proteins from *Dictyostelium discoideum* in mitochondrial 5'-tRNA editing. *RNA* 17: 613-623.
- Archibald, J.M.** (2011) Origin of eukaryotic cells: 40 years on. *Symbiosis* 54: 69-86.
- Bay, R.A. and **Bielawski, J.P.** (2011) Recombination detection under evolutionary scenarios relevant to functional divergence. *J. Mol. Evol.* 73: 273-286.
- Beiko, R.G.** (2011) Telling the whole story in a 10,000-genome world. *Biology Direct* 6: 34.
- Bowman, S. *et al.* [20 authors incl. Curtis, B.A.] (2011) An integrated approach to gene discovery and marker development in Atlantic cod (*Gadus morhua*). *Marine Biotech* 13: 242-255.
- Brown, M.W., Silberman J.D. and Spiegel F.W. (2011) "Slime molds" among the Tubulinea (Amoebozoa): Molecular systematics and taxonomy of *Copromyxa*. *Protist* 162: 277-287.

- Chan, C.X., **Beiko, R.G.** and Ragan, M.A. (2011) Lateral transfer of genes and gene fragments in *Staphylococcus* extends beyond mobile elements. *J. Bacteriol.* 193: 3964-3977.
- Corradi, N. and **Slamovits, C.H.** (2011) The intriguing nature of microsporidian genomes *Brief Funct. Genomics* 10:115-124.
- Doolittle, W.F.**, Lukes, J., **Archibald, J.M.**, Keeling, P.J. and **Gray, M.W.** (2011) Comment on “Does constructive neutral evolution play an important role in the origin of cellular complexity?” *Bioessays* 33: 427-429.
- Flegontov, P., **Gray, M. W.**, Burger, G. and Lukeš, J. (2011) Gene fragmentation: a key to mitochondrial genome evolution in Euglenozoa? *Curr. Genet.* 57: 225-232.
- Garvin, M.R., **Bielawski, J.P.** and Gharrett, A.J. (2011) Positive Darwinian selection in the piston that powers proton pumps in Complex I of the mitochondria of Pacific salmon. *PLoS One* 6: e24127.
- Gaston, D., **Susko, E.** and **Roger, A.J.** (2011) A phylogenetic mixture model for the identification of functionally divergent protein residues. *Bioinformatics* 27: 2655-2663.
- Gile, G.H., James, E.R., Scheffrahn, R.H., Carpenter, K.J., and Keeling, P.J. (2011) Molecular and morphological analysis of the family Calonymphidae with a description of *Calonympha chia* sp. nov., *Snyderella kirbyi* sp. nov., *Snyderella swezyae* sp. nov. and *Snyderella yamini* sp. nov. *Int. Journal of Syst. Evol. Microbiol.* 61: 2547-2558.
- Gray, M.W.** (2011) The incredible shrinking organelle. *EMBO Reports* 12: 873.
- Halary, S., Malik, S.-B., Lildhar, L., **Slamovits, C.H.**, Hijri, M. and Corradi, N. (2011) Conserved meiotic machinery in *Glomus* spp., a putatively ancient asexual fungal lineage. *Genome Biol. Evol.* 3: 950-958.
- Hampl, V., Stairs, C.W. and **Roger A.J.** (2011) The tangled past of eukaryotic enzymes involved in anaerobic metabolism. *Mobile Genetic Elements* 3: 71-74.
- Harding, T., Jungblut, A.D., Lovejoy, C. and Vincent, W.F. (2011) Microbes in high Arctic snow and implications for the cold biosphere. *Appl. Environ. Microbiol.* 77: 3234-3243.
- Heiss, A.A., Walker, G. and **Simpson, A.G.** (2011) The ultrastructure of *Ancyromonas*, a eukaryote without supergroup affinities. *Protist* 162: 373-393.
- Kamikawa, R., Inagaki, Y., **Roger, A.J.** and Hashimoto, T. (2011) Splintrons in *Giardia intestinalis*: Spliceosomal introns in a split form. *Commun. Integr. Biol.* 4: 454-456.
- Kamikawa, R., Inagaki, Y., Tokoro, M., **Roger, A.J.** and Hashimoto, T. (2011) Split introns in the genome of a divergent eukaryote *Giardia intestinalis* are excised by spliceosome-mediated trans-splicing. *Curr. Biol.* 21: 311-315.
- Kerney, R., Kim, E., Hangarter, R., Heiss, A.A., Bishop, C.D. and Hall, B.K. (2011) Intracellular invasion of green algae in a salamander host. *Proc. Natl. Acad. Sci. USA* 108: 6497–6502.
- Kim, E., Harrison, J.W., Sudek, S., Jones, M.D.M., Wilcox, H.M., Richards, T.A., Worden, A.Z. and **Archibald, J.M.** (2011) Newly identified and diverse plastid-bearing branch on the eukaryotic tree of life. *Proc. Natl. Acad. Sci. USA* 108: 1496–1500.
- Koenig, J.E., Bourne, D.G., Curtis, B., Dlutek, M., Stokes, H.W., **Doolittle, W.F.** and Boucher, Y. (2011) Coral-mucus-associated *Vibrio* integrons in the Great Barrier Reef: genomic hotspots for environmental adaptation. *ISME J.* 5: 962-972.
- Long, S., Changmai, P., Tsaousis, A.D., Skalický, T., Verner, Z., Wen, Y.Z., **Roger, A.J.** and Lukeš, J. (2011) Stage-specific requirement for Isa1 and Isa2 proteins in the mitochondrion of *Trypanosoma brucei* and heterologous rescue by human and *Blastocystis* orthologues. *Mol. Microbiol.* 81: 1403-1418.
- Lowe, C.D., Keeling, P.J., Martin, L.E., **Slamovits, C.H.**, Watts, P.C. and Montagnes, D.J.S. (2011) Who is *Oxyrrhis marina*? Morphological and phylogenetic studies on an unusual dinoflagellate. *J. Plankton Res.* 33: 555-567.
- Lukes, J., **Archibald, J.M.**, Keeling, P.J., **Doolittle, W.F.** and **Gray, M.W.** (2011) How a neutral evolutionary ratchet can build cellular complexity. *IUBMB Life* 63: 528-537.

- Malik S.-B., Brochu, C.D., Bilic, I., Yuan, J., Hess, M., Logsdon, J.M. Jr. and Carlton, J.M. (2011) Phylogeny of parasitic Parabasalia and free-living relatives inferred from conventional markers vs. *Rpbl*, a single-copy gene. *PLoS One* 6: e20774.
- Maruyama, S., Suzuki, T., Weber, A.P.M., **Archibald, J. M.** and Nozaki, H. (2011) Eukaryote-to-eukaryote gene transfer gives rise to genome mosaicism in euglenids. *BMC Evol. Biol.* 11: 105.
- McInerney, J.O., Martin, W.F., Koonin, E.V., Allen, J.F., Galperin, M.Y., Lane, N., **Archibald, J.M.** and Embley, T.M. (2011) Planctomycetes and eukaryotes: a case of analogy not homology. *BioEssays* 33: 810-817.
- Mora, C., Tittensor, D.P., Adl, S. and **Simpson A.G.** and Worm, B. (2011) How many species are there on Earth and in the Ocean? *PLOS Biology* 9: e1001127.
- Park, J.S. and **Simpson A.G.** (2011) Characterization of *Pharyngomonas kirbyi* (=“*Macropharyngomonas halophila*” nomen nudum), a very deep-branching, obligately halophilic heterolobosean flagellate. *Protist* 162: 691-709.
- Parks, D.H., MacDonald, N.J. and **Beiko, R.G.** (2011) Classifying short genomic fragments from novel lineages using composition and homology. *BMC Bioinformatics* 12: 328.
- Richards, T.A. and **Archibald J.M.** (2011) Cell evolution: gene transfer agents and the origin of mitochondria. *Curr. Biol.* 21: R112-114.
- Saldarriaga, J., Gile, G.H., James, E.R., Horák, A., Scheffrahn, R.H., and Keeling, P.J. (2011) Morphology and molecular phylogeny of *Pseudotriconympha hertwigi* and *Pseudotriconympha paulistana* (Triconymphaea, Parabasalia) from neotropical rhinotermitids. *J. Eukaryot. Microbiol.* 58: 487-496.
- Schnare, M.N. and **Gray, M.W.** (2011) Complete modification maps for the small and large subunit rRNAs of *Euglena gracilis*: functional and evolutionary implications of contrasting patterns between the two rRNA components. *J. Mol. Biol.* 413: 66-83.
- Slamovits, C.H.** and Keeling, P.J., (2011) Contributions of *Oxyrrhis marina* to molecular biology, genomics and organelle evolution of dinoflagellates. *J. Plankton Res.* 33: 591-602.
- Slamovits, C.H.**, Okamoto, N., Burri, L. James, E. and Keeling, P.J. (2011) A bacterial proteorhodopsin proton pump in marine eukaryotes. *Nature Communications* 2:183.
- Spencer, D.F. and **Gray, M.W.** (2011) Ribosomal RNA genes in *Euglena gracilis* mitochondrial DNA: fragmented genes in a fragmented genome. *Mol. Genet. Genomics* 285: 19-31.
- Stairs, C.W., **Roger, A.J.**, and Hampl, V. (2011) Eukaryotic pyruvate formate lyase and its activating enzyme were acquired laterally from a firmicute. *Mol. Biol. Evol.* 28: 2087-2099.
- Stokesbury, M.J.W., Neilson, J.D., **Susko, E.** and Cooke, S.J. (2011) Estimating mortality of Atlantic bluefin tuna in an experimental recreational catch-and-release fishery. *Biol. Conserv.* 144: 2684-2691.
- Susko, E.** (2011) Improved least squares topology testing and estimation. *Syst. Biol.* 60: 668-675.
- Susko, E.** (2011) Large sample approximations of probabilities of correct evolutionary tree estimation and biases of maximum likelihood estimation. *Stat. Applic. Genet. Mol. Biol.* 10(1): Article 10.
- Tanifuji, G. (2011) Reductive genome evolution in nucleomorphs. *Jpn. J. Protozool.* 44: 89-102.
- Tanifuji, G., Kim, E., Onodera, N.T., Gibeault, R., Dlutek, M., Cawthorn, R.J., Fiala, I., Lukeš, J., Greenwood, S.J. and **Archibald, J.M.** (2011) Genomic characterization of *Neoparamoeba pemaquidensis* (Amoebozoa) and its kinetoplastid endosymbiont. *Eukaryot. Cell* 10: 1143–1146.
- Tanifuji, G., Onodera, N.T., Wheeler, T.J., Dlutek, M., Donaher, N. and **Archibald, J.M.** (2011) Complete nucleomorph genome sequence of the non-photosynthetic alga *Cryptomonas paramecium* reveals a core nucleomorph gene set. *Genome Biol. Evol.* 3: 44-54.
- Tong, J., Dolezal, P., Selkrig, J., Crawford, S., **Simpson, A.G.B.**, Noinaj, N., Buchanan, S.K., Gabriel, K. and Lithgow, T. (2011) Ancestral and derived protein import pathways in the mitochondrion of *Reclinomonas americana*. *Mol. Biol. Evol.* 28: 1581-1591.
- Tsaousis, A.D., Gaston, D., Stechmann, A., Walker, P.B., Lithgow, T. and **Roger, A.J.** (2011) A functional Tom70 in the human parasite *Blastocystis* sp.: Implications for the evolution of the

mitochondrial import apparatus. *Mol. Biol. Evol.* 28: 781-791.

Veillette, J., Lovejoy, C., Potvin, M., Harding, T., Jungblut, A.D., Antoniadou, D., Chénard, C., Suttle, C.A. and Vincent, W.F. (2011) Milne Fiord epishelf lake: a coastal Arctic ecosystem vulnerable to climate change. *Ecosci.* 18: 304-316.

Wang, H.-C., **Susko, E.** and **Roger, A.J.** (2011) Fast statistical tests for detecting heterotachy in protein evolution. *Mol. Biol. Evol.* 28: 2305-2315.

Wu, J. and **Susko, E.** (2011) A test for heterotachy using multiple pairs of sequences. *Mol. Biol. Evol.* 28: 1661-1673.

Zhaxybayeva, O. and **Doolittle, W.F.** (2011) Lateral gene transfer. *Curr. Biol.* 21: R242-R246.

Zou, L., **Susko, E.**, *Field, C. and **Roger, A.J.** (2011) The parameters of the Barry and Hartigan general Markov model are statistically nonidentifiable. *Syst. Biol.* 60: 872-875.

Year 2010:

Archibald, J.M. and Richards, T.A. (2010) Gene transfer: anything goes in plant mitochondria. *BMC Biol.* 8:147.

Barberà, M.J., Ruiz-Trillo, I., Tufts, J.Y., Bery, A., Silberman, J.D. and **Roger, A.J.** (2010) *Sawyeria marylandensis* (Heterolobosea) has a hydrogenosome with novel metabolic properties. *Eukaryot. Cell* 9: 1913-24.

Baurain, D., Brinkmann, H., Petersen, J., Rodríguez-Ezpeleta, N., Stechmann, A., Demoulin, V., **Roger, A.J.**, Burger, G., Lang, B.F. and Philippe, H. (2010) Phylogenomic evidence for separate acquisition of plastids in cryptophytes, haptophytes and stramenopiles. *Mol. Biol. Evol.* 27: 1698-1709.

Beiko, R.G. (2010) Gene sharing and genome evolution: Networks in trees and trees in networks. *Biol. Philos.* 25.4: 659-673.

Brown, M.W., Silberman, J.D. and Spiegel, F.W. (2010) A morphologically simple species of *Acrasis* (Heterolobosea, Excavata), *Acrasis helenhemmesae* n. sp. *J. Eukaryot. Microbiol.* 57: 346-353.

Bullerwell, C.E., Burger, G., Gott, J.M., Kourennaia, O., Schnare, M.N. and **Gray, M.W.** (2010) Abundant 5S rRNA-like transcripts encoded by the mitochondrial genome in amoebozoia. *Eukaryot. Cell* 9: 762-773.

Carlton, J.M., Malik, S.-B., Sullivan S.A., Sicheritz-Ponten, T., Tang P. and R.P. Hirt (2010) The genome of *Trichomonas vaginalis*. In *Anaerobic Parasitic Protozoa. Genomics and Molecular Biology*, C.G. Clark, P.J. Johnson & R.D. Adam (Eds.), pp. 45-80, Caister Academic Press.

Cocquyt, E., Gile, G.H., Leliaert, F., Verbruggen, H., Keeling, P.J. and De Clerck, O. (2010) Complex phylogenetic distribution of a non-canonical code in green algae. *BMC Evol. Biol.* 10: e327.

Curtis, B.A. and **Archibald, J.M.** (2010) A spliceosomal intron of mitochondrial DNA origin. *Curr. Biol.* 20: R919-920.

Curtis, B.A. and **Archibald, J.M.** (2010) Problems and progress in understanding the origins of mitochondria and plastids. In: *Symbiosis and Stress*, Seckbach, J. & Grube, M. (Eds.), pp. 41-62, Springer-Verlag.

Doolittle, W.F. (2010) The attempt on the life of the Tree of Life: science, philosophy and politics. *Biol. Philos.* 25: 455-473.

Doolittle, W.F. and Zhaxybayeva, O. (2010) Metagenomics and the units of biological organization. *Biosci.* 60: 102-112.

Gawryluk, R.M. and **Gray, M.W.** (2010) An ancient fission of mitochondrial cox1. *Mol. Biol. Evol.* 27: 7-10.

Gawryluk, R.M. and **Gray, M.W.** (2010) Evidence for an early evolutionary emergence of gamma-type carbonic anhydrases as components of mitochondrial respiratory complex I. *BMC Evol. Biol.* 10: 176.

- Gentekaki, E. and Lynn, D. (2010) Evidence for cryptic speciation in *Carchesium polypinum* Linnaeus 1758 (Ciliophora: Peritrichia) inferred from mitochondrial, nuclear, and morphological markers. *J. Eukaryot. Microbiol.* 57: 508-519.
- Graham, L.E., Kim, E., Arancibia-Avila, P., Graham, J.M. and Wilcox, L.E. (2010) Evolutionary and ecophysiological significance of sugar utilization by the peatmoss *Sphagnum compactum* (Sphagnaceae) and the common charophycean associates *Cylindrocystis brebissonii* and *Mougeotia* sp. (Zygnemataceae). *Amer. J. Botany* 97: 1–7.
- Gott, J.M., Somerlot, B.H. and **Gray, M.W.** (2010) Two forms of RNA editing are required for tRNA maturation in *Physarum* mitochondria. *RNA* 16: 482-488.
- Gray, M.W.** (2010) Re-thinking plastid evolution. *EMBO Reports* 11: 562-563.
- Gray, M.W.**, Lukes, J., **Archibald, J.M.**, Keeling, P.J. and **Doolittle, W.F.** (2010) Cell biology. Irremediable complexity? *Science* 330: 920-921.
- Heiss, A.A., Walker, G. and **Simpson, A.G.** (2010) Clarifying the taxonomic identity of phylogenetically important group of eukaryotes: *Planomonas* is a junior synonym of *Ancyromonas*. *J. Eukaryot. Microbiol.* 57: 285-293.
- Hjort, K., Goldberg, A.V., Tsaousis, A.D., Hirt, R.P. and Embley, T.M. (2010). Diversity and reductive evolution of mitochondria among microbial eukaryotes. *Philos. Trans Royal Society London B: Biol. Sci.* 365: 713-727.
- Holloway, C. and **Beiko, R.G.** (2010) Assembling networks of microbial genomes using linear programming. *BMC Evol. Biol.* 10: 360.
- Hopkins, J. and **Archibald, J.M.** (2010) Plastid evolution and the nuclear genomic 'footprint' of red and green algal endosymbionts. In: *Red Algae in the Genomics Age*, J. Seckbach & M. Grube, M. (Eds.), pp. 191-204, Springer-Verlag.
- Hug, L.A., Stechmann, A. and **Roger, A.J.** (2010) Phylogenetic distributions and histories of proteins involved in anaerobic pyruvate metabolism in eukaryotes. *Mol. Biol. Evol.* 27: 311-324.
- Kim, E. and **Archibald, J.M.** (2010) Plastid evolution: gene transfer and the maintenance of 'stolen' organelles. *BMC Biology* 8: 73.
- Kim, E., Park, J.S., **Simpson, A.G.**, Matsunaga, S., Watanabe, M., Murakami, A., Sommerfeld, K., Onodera, N.T. and **Archibald, J.M.** (2010) Complex array of endobionts in *Petalomonas sphagnophila*, a large heterotrophic euglenid protist from Sphagnum-dominated peatlands. *ISME Journal* 4: 1108-1120.
- Kim, E., Yubuki, N., Leander, B.S. and Graham, L.E. (2010) Ultrastructure and 18S rDNA phylogeny of *Apoikia lindahlia* comb. nov. (Chrysophyceae) and its epibiontic protists, *Filos agilis* gen. et sp. nov. (Bicosoecida) and *Nanos amicus* gen. et sp. nov. (Bicosoecida). *Protist* 161: 177–196.
- Kolisko, M., Silberman, J.D., Cepicka, I., Yubuki, N., Takishita, K., Yabuki, A., Leander, B.S., Inouye, I., Inagaki, Y., **Roger, A.J.** and **Simpson, A.G.** (2010) A wide diversity of previously undetected free-living relatives of diplomonads isolated from marine/saline habitats. *Environ. Microbiol.* 12: 2700-2710.
- Holloway, C. and **Beiko, R.G.** (2010) Assembling networks of microbial genomes using linear programming. *BMC Evol. Biol.* 10: 360.
- Langelaan, D.N., Wiczorek, M., **Blouin, C.** and Rainey, J.K. (2010) Improved helix and kink characterization in membrane proteins allows evaluation of kink sequence predictors. *J. Chem. Inf. Model.* 50: 2213-2220.
- Lovejoy, T.E. et al. (13 authors, incl. **W.F. Doolittle**) (2010) *Canadian Taxonomy: Exploring Biodiversity, Creating Opportunity*. Canadian Council of Academies Press, Government of Canada.
- Lynn, D.H. and **Simpson, A.G.** (2010) From the editors: Describing new taxa of unicellular protists. *J. Eukaryot. Microbiol.* 56: 403-405.
- MacDonald, N.J. and **Beiko, R.G.** (2010) Efficient learning of microbial genotype-phenotype association rules. *Bioinformatics* 26: 1834-1840.
- Martin, D.P. and **Beiko, R.G.** (2010) Genetic recombination and bacterial population structure. In:

Bacterial Population Genetics in Infectious Disease, D.A. Robinson, D. Falush, and E.J. Feil (Eds.), pp. 61-85, John Wiley & Sons.

- Nesbø, C.L., Kumaraswamy, R., Dlutek, M., **Doolittle, W.F.** and Foght, J. (2010) Searching for mesophilic Thermotogales bacteria: "mesotogas" in the wild. *Appl. Environ. Microbiol.* 76: 4896-4900.
- Park, J.S. and **Simpson, A.G.** (2010) Characterization of halotolerant Bicosoecida and Placididea (Stramenopila) that are distinct from marine forms, and the phylogenetic pattern of salinity preference in heterotrophic stramenopiles. *Environ. Microbiol.* 12:1173-1184.
- Park, J.S., Kolisko, M. and **Simpson, A.G.B.** (2010). Cell morphology and formal description of *Ergobibamus cyprinoides* n. gen., n. sp., another *Carpediemonas*-like relative of diplomonads. *J. Eukaryot. Microbiol.* 57: 520-528.
- Parks, D.H. and **Beiko, R.G.** (2010) Identifying biologically relevant differences between metagenomic communities. *Bioinformatics* 26: 715-721.
- Perry, S.C. and **Beiko, R.G.** (2010) Distinguishing microbial genome fragments based on their composition: evolutionary and comparative genomic perspectives. *Genome Biol. Evol.* 2: 117-131.
- Rowe, D.L., Dunn, K.A., Adkins, R.M. and R.L. Honeycutt. (2010) Molecular clock keeps dispersal hypothesis afloat: evidence for trans-Atlantic rafting by rodents. *J. Biogeography* 37: 305-324.
- Saffo, M.B., McCoy, A.M., Rieken, C. and **Slamovits, C.H.** (2010) Nephromyces, a beneficial apicomplexan symbiont in marine animals. *Proc. Natl. Acad. Sci. USA* 107: 16190-16195.
- Sangaralingam, A., **Susko, E.**, Bryant, D. and Spencer, M. (2010) On the artefactual parasitic eubacteria claim in conditioned logdet phylogenies: heterotachy and ortholog identification artefacts as explanations. *BMC Evol. Biol.* 10: 343.
- Sebé-Pedrós, A., **Roger, A.J.**, Lang, F.B., King, N. and Ruiz-Trillo, I. (2010) From the cover: Ancient origin of the integrin-mediated adhesion and signaling machinery. *Proc. Natl. Acad. Sci USA* 107: 10142-10147.
- Silver, T.D., Moore, C.E., and **Archibald, J.M.** (2010) Nucleomorph ribosomal DNA and telomere dynamics in chlorarachniophyte algae. *J. Eukaryot. Microbiol.* 57: 453-459.
- Slater, F.R., Johnson, C.R., Blackall, L.L., **Beiko, R.G.** and Bond, P.L. (2010) Monitoring associations between clade-level variation, overall community structure and ecosystem function in enhanced biological phosphorus removal (EBPR) systems using terminal-restriction fragment length polymorphism (T-RFLP). *Water Res.* 44: 4908-4923.
- Susko, E.** (2010) First-order correct bootstrap support adjustments for splits that allow hypothesis testing when using maximum likelihood estimation. *Mol. Biol. Evol.* 27: 1621-1629.
- Tanifuji, G. and **Archibald, J.M.** (2010) Actin gene family dynamics in cryptomonads and red algae. *J. Mol. Evol.* 71: 169-179.
- Tanifuji, G., Onodera, N.T. and Hara, Y. (2010) Nucleomorph genome diversity and its phylogenetic implications in cryptomonad algae. *Phycology Res.* 58: 230-237.
- Tsaousis, A.D., Stechmann, A., Hamblin, K.A., van der Giezen, M., Perez-Brocal, V. and Graham Clark, C. (2010). In *Anaerobic Parasitic Protozoa. Genomics and Molecular Biology*, C.G. Clark, P.J. Johnson & R.D. Adam (Eds.), pp. 205-220, Caister Academic Press.
- Volkman, G., Murphy, P.W., Rowland, E.E., Cronan, J.E. Jr., Liu, X.Q., **Blouin, C.** and Byers, D.M. (2010) Intein-mediated cyclization of bacterial acyl carrier protein stabilizes its folded conformation but does not abolish function. *J. Biol. Chem.* 285: 8605-8614.
- Whidden, C., **Beiko, R.G.** and *Zeh, N. (2010) Fast FPT algorithms for computing rooted agreement forests: Theory and experiments. In P. Festa (Ed.), *Experimental Algorithms. SEA 2010. Lecture Notes in Computer Science* 6049: 141-153, Springer.
- Wilson, S., **Simpson, A.G.B.** and Lynn, D.H. (2010) Maintaining journal figure quality. *J. Eukaryot. Microbiol.* 57: 285-293.
- Wu, J. and **Susko, E.** (2010) Rate-variation need not defeat phylogenetic inference through pairwise sequence comparisons. *J. Theoret. Biol.* 263: 587-589.

Year 2009:

- Archibald, J.M.** (2009) Genomics. Green evolution, green revolution. *Science* 324: 191-92.
- Archibald, J.M.** (2009) Secondary endosymbiosis. In *Encyclopedia of Microbiology*, M. Schaechter (Ed.), pp. 438-446, Elsevier.
- Archibald, J.M.** (2009) The origin and spread of eukaryotic photosynthesis—evolving views in light of genomics. *Botanica Marina* 52: 95-103.
- Archibald, J.M.** (2009) The puzzle of plastid evolution. *Curr. Biol.* 18: 663-665.
- Archibald, J.M.** and Lane, C.E. (2009) Going, going, not quite gone: nucleomorphs as a case study in nuclear genome reduction. *J. Hered.* 100: 582-590.
- Bae, Y., **Kim, E.**, L'Hernault, S.W. and Barr, M.M. (2009) The CIL-1 PI 5-phosphatase localizes TRP polycystins to cilia and activates sperm in *C. elegans*. *Curr. Biol.* 19: 1599–1607.
- Baptiste, E., O'Malley, M.A., **Beiko, R.G.**, Ereshefsky, M., Gogarten, J.P., Franklin-Hall, L., Lapointe, F.J., Dupré, J., Dagan, T., Boucher, Y. and Martin W. (2009) Prokaryotic evolution and the tree of life are two different things. *Biology Direct* 4: 34-54.
- Beiko, R.G.** and Ragan, M.A. (2009) Untangling hybrid phylogenetic signals - HGT and artifacts of phylogenetic reconstruction. *Methods Mol. Biol.* 532: 241-256.
- Blouin, C.**, **Perry, S.**, Lavell, A., **Susko, E.** and **Roger, A.J.** (2009) Reproducing the manual annotation of multiple sequence alignments using an SVM classifier. *Bioinformatics* 25: 3093-3098.
- Burki, F., Inagaki, Y., Brate, J., **Archibald, J.M.**, Keeling, P.J., Cavalier-Smith, T., Sakaguchi, M., Hashimoto, T., Horak, A., Kumar, S., Klaveness, D., Jakobsen, K.S., Pawlowski, J. and Shalchian-Tabrizi, K. (2009) Large-scale phylogenomic analyses reveal that two enigmatic protist lineages, *Telonemia* and *Centroheliozoa*, are related to photosynthetic chromalveolates. *Gen. Biol. Evol.* 1: 231-238.
- Chan, C.X, Darling, A.C., **Beiko, R.G.** and Ragan, M.A. (2009) Are protein domains modules of lateral genetic transfer? *PLoS One* 4: e4524.
- Chan, C.X., **Beiko, R.G.**, Darling, A.E. and Ragan, M.A. (2009) Lateral transfer of genes and gene fragments in prokaryotes. *Genome Biol. Evol.* 1: 429-438.
- Charette, J.M. and **Gray, M.W.** (2009) U3 snRNA genes are multi-copy and frequently linked to U5 snRNA genes in *Euglena gracilis*. *BMC Genomics* 10: 528.
- Curtis, B.A.** & **Archibald, J.M.** (2009) Problems and progress in understanding the origins of mitochondria and plastids. In *Symbioses and Stress*, J. Seckbach & M. Grube (Eds.), pp. 41-62, Springer-Verlag.
- Dipippo, J.L., Nesbo, C.L., Dahle, H., **Doolittle, W.F.**, Birkland, N.-K. and Noll, K.M. (2009) *Kosmotoga olearia* gen. nov., sp. nov., a thermophilic, anaerobic heterotroph isolated from oil production fluid. *Int. J. Syst. Evol. Microbiol.* 59: 2991-3000.
- Doolittle, W.F.** (2009) Eradicating typological thinking in prokaryotic systematics and evolution. In *Cold Spring Harb. Symp. Quant. Biol.* 74: 197-204.
- Doolittle, W.F.** (2009) The practice of classification and the theory of evolution, and what the demise of Darwin's Tree of Life Hypothesis means for both of them. *Phil. Trans. Roy. Soc. Lond. Series B*, 364: 2221-2228.
- Doolittle, W.F.** and **Zhaxybayeva, O.** (2009) On the origin of prokaryotic species. *Genome Res.* 19: 744-756.
- Donaher, N., **Tanifuji, G.**, Onodera, N.T., Malfatti, S.A., Chain, P.S.G., Hara, Y. and **Archibald, J.M.** (2009) The complete plastid genome sequence of the secondarily non-photosynthetic alga *Cryptomonas paramecium*: reduction, compaction, and accelerated evolutionary rate. *Genome Biol. Evol.* 1: 439-448.
- Dunn, K.A.**, **Bielawski, J.P.**, Ward, T.J., **Urquhart, C.** and *Gu, H. (2009) Reconciling ecological and genomic divergence among lineages of *Listeria* under an “extended mosaic genome concept.” *Mol. Biol. Evol.* 26: 2605-2615.

- Elias, M. and **Archibald, J.M.** (2009) The RFL family of small GTPases is an ancient eukaryotic invention probably functionally associated with the flagellar apparatus. *Gene* 442: 63-72.
- Elias, M. and **Archibald, J.M.** (2009) Sizing up the genomic footprint of endosymbiosis. *Bioessays* 31: 1273-1279.
- Gawryluk, R.M. and **Gray M.W.** (2009) A split and rearranged nuclear gene encoding the iron-sulfur subunit of mitochondrial succinate dehydrogenase in Euglenozoa. *BMC Res. Notes* 2: 16.
- Gaston, D., Tsaousis, A.D. and **Roger, A.J.** (2009) Predicting proteomes of mitochondria and related organelles from genomic and expressed sequence tag data. *Methods Enzymol.* 457: 21-47.
- Gray, M.W.** (2009) The path to RNA editing in plant mitochondria: the Halifax chapter. *IUBMB Life* 61: 1114-1117.
- Gray, M.W.** (2009) RNA editing in plant mitochondria: twenty years later. *IUBMB Life* 61: 1101-1104.
- Hapl, V., Hug, L., Leigh, J.W., Dacks, J.B., Lang, B.F., **Simpson, A.G.B.** and **Roger, A.J.** (2009) Phylogenetic analyses support the monophyly of Excavata and resolve relationships among eukaryotic “supergroups”. *Proc Natl Acad Sci USA* 106: 3859-3864.
- Jezbera, J., Sharma, A.K., Brandt, U., **Doolittle, W.F.** and Hahn, M.W. (2009) ‘*Candidatus Planktophila limnetica*’, an actinobacterium representing one of the most numerically important taxa in freshwater bacterioplankton. *Int. J. Syst. Evol. Microbiol.* 59: 2864-2869.
- Joss, M.J., Koenig, J.E., Labbate, M., Polz, M.F., Gillings, M.R., Stokes, H.W., **Doolittle W.F.** and Boucher, Y. (2009) ACID: annotation of cassette and integron data. *BMC Bioinformatics* 21: 118.
- Kamikawa, R., Sanchez-Perez, G.F., Sako, Y., **Roger, A.J.** and Inagaki, Y. (2009) Expanded phylogenies of canonical and non-canonical types of methionine adenosyltransferase reveal a complex history of these gene families in eukaryotes. *Mol. Phylogenet. Evol.* 53: 565-570.
- Kim, E. and **Archibald, J. M.** (2009) Diversity and evolution of plastids and their genomes. In *The Chloroplast-Interactions with the Environment*, A.S. Sandelius & H. Aronsson (Eds.), pp. 1-39, Springer.
- Koenig, J.E., Sharp, C., Dlutek, M., Curtis, B., Joss, M., Boucher, Y. and Doolittle, W.F. (2009) Integron Gene Cassettes and Degradation of Compounds Associated with Industrial Waste: The Case of the Sydney Tar Ponds. *PLoS One* 4: e5276.
- Lane, C.E. and **Archibald, J.M.** (2009) Reply to Bodyl, Stiller and Mackiewicz: Chromalveolate plastids: direct descent or multiple endosymbioses? *Trends Ecol. Evol.* 24: 121-122.
- Liu, H., Blouin, C. and Keselj, V. (2009) Identifying interaction sentences from biological literature using automatically extracted patterns. In *BioNLP '09 Proceedings of the Workshop on Current Trends in Biomedical Natural Language Processing*, pp. 133-141, Boulder, Colorado.
- MacDonald, N., Parks, D. and Beiko, R. (2009) SeqMonitor: Influenza analysis pipeline and visualization. *PLoS Currents Influenza* 1: RRN1040.
- Moore, C.E. and **Archibald, J.M.** (2009) Nucleomorph genomes. *Ann. Rev. Genet.* 43: 251-264.
- Morine, M., *Gu, H., Myers, R. and **Bielawski, J.P.** (2009) Trade-offs between efficiency and robustness in bacterial metabolic networks are associated with niche breadth. *J. Mol. Evol.* 68: 506-515.
- Nesbo, C.L., Baptiste, E., Curtis, B., Dahle, H., Lopez, P., Macleod, D., Dlutek, M., Bowman, S., Zhaxybayeva, O., Birkeland, N.K. and **Doolittle, W.F.** (2009) The genome of *Thermosiphon africanus* TCF52B: lateral genetic connections to the Firmicutes and Archaea. *J. Bacteriol.* 191: 1974-1978.
- Ota, S., Silver, T.D., **Archibald, J.M.** and Ishida, K.-I. (2009) *Lotharella oceanica* sp. nov.— a new planktonic chlorarachniophyte studied by light and electron microscopy. *Phycologia* 48: 317-325.
- Park, J.S., Kolisko, M., Heiss, A.A., Simpson, A.G.B. (2009) Light microscopic observations, ultrastructure, and molecular phylogeny of *Hicanonectes teleskopos* n.g., n.sp., a deep-branching relative of diplomonads. *J. Euk. Microbiol.* 56: 373-84.
- Park, J.S., Simpson, A.G.B., Brown, S. and Cho, B.C. (2009) Ultrastructure and molecular phylogeny of two heterolobosean amoebae. *Protist* 160: 265-283.

- Park, J.S., Vreeland, R.H., Cho, B.C., Lowenstein, T.K., Timofeeff, M.N. and Rosenzweig, W.D. (2009) Haloarchaeal diversity at 23, 121, and 419 MYA salts. *Geobiol.* 7: 515-523.
- Parks, D.H. and Beiko, R.G. (2009) Quantitative visualizations of hierarchically organized data in a geographic context. *Geoinformatics* 2009: 1-6.
- Parks, D.H., MacDonald, N. and Beiko, R. (2009) Tracking the evolution and geographic spread of influenza A. *PLoS Currents Influenza* 1: RRN1014.
- Parks, D.H., Porter, M., Churcher, S., Wang, S., Blouin, C., Whalley, J., Brooks, S. and Beiko, R.G. (2009) GenGIS: A geospatial information system for genomic data. *Genome Res.* 19: 1896-1904.
- Ragan, M.A. and Beiko, R.G. (2009) Lateral genetic transfer: open issues. *Philos. Trans. Royal Soc. London B Biol. Sci.* 364: 2241-2251.
- Roger, A.J. and Simpson, A.G.B. (2009) Evolution: revisiting the root of the eukaryote tree. *Curr Biol.* 19: R165-167.
- Schloss, P.D., Westcott, S.L., Ryabin, T., Hall, J.R., Hartman, M., Hollister, E.B., Lesniewski, R.A., Oakley, B.B., Parks, D.H., Robinson, C.J., Sahl, J.W., Stres, B., Thallinger, G.G., Van Horn, D.J. and Weber, C.F. (2009) Introducing mothur: open source, platform-independent, community-supported software for describing and comparing microbial communities. *Appl. Environ. Microbiol.* 75: 7537-7541.
- Sharma, A.K., Sommerfeld, K., Bullerjahn, G.S., Matteson, A.R., Wilhelm, S.W., Jezbera, J., Brandt, U., Doolittle, W.F. and Hahn, M.W. (2009) Actinorhodopsin genes discovered in diverse freshwater habitats and among cultivated freshwater Actinobacteria. *ISME* 3: 726-737.
- Simpson A.G. and Cepicka, I. (2009) Amitochondriate protists (Diplomonads, Parabasalids and Oxymonads). In *Encyclopedia of Microbiology*, 3rd Ed., pp. 545-557, Elsevier.
- Slamovits, C.H. and Keeling, P.J. (2009) Evolution of ultrasmall spliceosomal introns in highly reduced nuclear genomes. *Mol. Biol. Evol.* 26: 1699-1705.
- Susko, E. (2009) Bootstrap support is not first order correct. *Syst. Biol.* 58: 211-233.
- Susko, E. and Roger, A.J. (2009) Statistical analysis of expressed sequence tags. *Methods Mol. Biol.* 533: 277-87.
- Tanifuji, G. (2009) Have Diatoms ever possessed Prasinophyte-derived plastid? *Japan J. Phycol.* 57: 134-136.
- Walsh, D.A. and Sharma, A.K. (2009) Molecular phylogenetics: Testing evolutionary hypotheses. In *Bacteriophages: Methods and Protocols, Vol. 2: Molecular and Applied Aspects*, M. Clokie & A. Kropinski (Eds.), pp. 131-168, Humana Press.
- Wang, H., Susko, E. and Roger, A.J. (2009) PROCOV-SPR: maximum likelihood estimation of protein phylogeny under covarion models and site-specific covarion pattern analysis. *BMC Evol. Biol.* 9: 225.
- Whalley, J., Brooks, S. and Beiko, R.G. (2009) Radie: visualizing taxon properties and parsimonious mappings using a radial phylogenetic tree. *Bioinformatics* 25: 672-673.
- Wu, J. and Susko, E. (2009) General heterotachy and distance method adjustments. *Mol. Biol. Evol.* 26: 2689-2697.
- Zhaxybayeva, O. (2009) Detection and quantitative assessment of horizontal gene transfer. *Methods Mol. Biol.* 532: 195-213.
- Zhaxybayeva, O., Swithers, K., Lapierre, P., Fournier, G., Bickhard, D., DeBoy, R.T., Nelson, K.E., Nesbø, C.L., Doolittle, W.F., Gogarten, J.P. and Noll, K.M. (2009) On the chimeric nature, thermophilic origin and phylogenetic placement of the Thermotogales. *Proc. Natl. Acad. Sci. USA* 106: 5865-5870.
- Zhaxybayeva, O., Doolittle, W.F., Papke, R.T. and Gogarten, J.P. (2009) Intertwined evolutionary histories of marine *Synechococcus* and *Prochlorococcus marinus*. *Genome Biol. Evol.* 1: 325-329.

Year 2008:

- Archibald, J.M. (2008) Genome evolution: remnant algal genes in ciliates. *Curr. Biol.* 18: R663-R665.

- Archibald, J.M.** (2008) The eocyte hypothesis and the origin of eukaryotic cells. *Proc. Natl. Acad. Sci. USA* 51: 20049-20050.
- Bao, L., *Gu, H., Dunn, K.A. and **Bielawski, J.P.** (2008) Likelihood-based clustering (LiBaC) for codon models, a method for grouping sites according to similarities in the underlying process of molecular evolution. *Mol. Biol. Evol.* 25: 1995-2007.
- Baptiste, E., **Susko, E.**, Leigh, J., Ruiz-Trillo, I., Bucknam, J. and **Doolittle, W.F.** (2008) Alternative methods for concatenation of core genes indicate a lack of resolution in deep nodes of the prokaryotic phylogeny. *Mol. Biol. Evol.* 25: 83-91.
- Beiko, R.G.** (2008) Small but mighty: microbial communities and a second wave of genomics. *Can. Chem. News* 60: 10-13.
- Beiko, R.G.** and Ragan, M.A. (2008) Detecting lateral genetic transfer: a phylogenetic approach. *Methods Mol. Biol.* 452: 457-469.
- Beiko, R.G.**, **Doolittle, W.F.** and Charlebois, R.L. (2008) The impact of reticulate evolution on genome phylogeny. *Syst. Biol.* 57: 844-56.
- Beiko, R.G.**, Whalley, J., Wang, S., Clair, H., Smolyn, G., Churcher, S., Porter, M., **Blouin, C.** and Brooks, S. (2008) Spatial analysis and visualization of genetic biodiversity. *Free and Open Source Software for Geospatial (FOSS4G)*.
- Cavalier-Smith, T., Chao, E.E., Stechmann, A., Oates, B. and Nikolaev, S. (2008) Planomonadida ord. nov. (Apusozoa): ultrastructural affinity with *Micronuclearia podoventralis* and deep divergences within Planomonas gen. nov. *Protist* 159: 535-562.
- Chan, C.X., **Beiko, R.G.** and Ragan, M.A. (2008) Large-scale detection of recombination in nucleotide sequences. *AIP Conference Proceedings* 971: 101-104.
- Cuvelier, M. L., Ortiz, A., Kim, E., Moehlig, H., Richardson, D., Heidelberg, J.F., **Archibald, J.M.** and Worden, A. (2008) Widespread distribution of a unique marine protistan lineage. *Environ. Microbiol.* 10: 1621-1634.
- Doolittle, W.F.** (2008) Microbial evolution: stalking the wild bacterial species. *Curr. Biol.* 18: R565-567.
- Doolittle, W.F.**, Nesbo, C.L., Baptiste, E. and Zhaxybayeva, O. (2008) Lateral gene transfer. In *Evolutionary Genomics and Proteomics*, M. Pagel & A. Pomiankowski (Eds.), pp. 45-79, Sinauer.
- Fong, M. and **Archibald, J.M.** (2008) Evolutionary dynamics of light-independent protochlorophyllide oxidoreductase (LIPOR) genes in the secondary plastids of cryptophyte algae. *Eukaryot. Cell* 7: 550-553.
- Gogarten, P.J., Fournier, G. and Zhaxybayeva, O. (2008) Gene transfer and the reconstruction of life's early history from the molecular record. *Space Sci. Rev.* 135: 115-131.
- Hamblin, K., Standley, D.M., Rogers, M.B., Stechmann, A., **Roger, A.J.**, Maytum, R. and van der Giezen, M. (2008) Localization and nucleotide specificity of *Blastocystis* succinyl-CoA synthetase. *Mol. Microbiol.* 68: 1395-1405.
- Hamel, L., Nahar, N., Poptsova, M.S., Zhaxybayeva, O. and Gogarten, J.P. (2008) Unsupervised learning in detection of gene transfer. *J. Biomed. Biotech.* 2008: 472719.
- Hampl, V. and **Simpson, A.G.B.** (2008) Possible mitochondria-related organelles in poorly-studied 'amitochondriate' eukaryotes. In J. Tachezy (Ed.), *Hydrogenosomes and mitosomes: mitochondria of anaerobic eukaryotes*, pp. 265-282, Springer Verlag.
- Hampl, V., Silberman, J.D., Stechmann, A., Diaz-Triviño, S., Johnson, P.J. and **Roger, A.J.** (2008) Genetic evidence for a mitochondriate ancestry in the amitochondriate flagellate *Trimastix pyriformis*. *PLoS One* 3: e1383.
- Hickey, G., Dehne, F., Rau-Chaplin, A. and **Blouin, C.** (2008) SPR distance computation for unrooted trees. *Evol. Bioinform.* 4: 17-27.
- Hoef-Emden, K. and **Archibald, J.M.** (2008) Cryptomonads. In *Tree of Life Web Project*. <http://tolweb.org/Cryptomonads/>
- Keeling, P.J. and **Archibald, J.M.** (2008) Organelle evolution: What's in a name? *Curr. Biol.* 18: R345-R347.

- Keeling, P.J., Leander, B.S. and **Simpson A.G.** (2008) Eukaryotes. In *Tree of Life Web Project*. <http://www.tolweb.org/Eukaryotes/3>
- Khan, H.** and **Archibald, J.M.** (2008) Lateral transfer of introns in the cryptophyte plastid genome. *Nucleic Acids Res.* 36: 3043-3053.
- Kim, E.**, Lane, C.E., **Curtis, B.A.**, Kozera, C., Bowman, S. and **Archibald, J.M.** (2008) Complete sequence and analysis of the mitochondrial genome of *Hemiselmis andersenii* CCMP644 (Cryptophyceae). *BMC Genomics* 9: 215.
- Koenig, J.E.**, Boucher, Y., Charlebois, R.L., Nesbo, C., **Zhaxybayeva, O.**, Bapteste, E., Spencer, M., Stokes, H.W. and **Doolittle, W.F.** (2008) Integron-associated gene cassettes in Halifax Harbour: assessment of a mobile gene pool in marine sediments. *Environ. Microbiol.* 10: 1024-1038.
- Kolisko, M.**, **Cepicka, I.**, **Hampl, V.**, **Leigh, J.**, **Roger, A.J.**, Kulda, J., **Simpson, A.G.B.** and **Flegr, J.** (2008) Molecular phylogeny of diplomonads and enteromonads based on SSU rRNA, α -tubulin and HSP90 genes: implications for the evolutionary history of the double karyomastigont of diplomonads. *BMC Evol. Biol.* 8: 205.
- Lane, C.E. and **Archibald, J.M.** (2008) New members of the genus *Hemiselmis* (Cryptomonadales, Cryptophyceae). *J. Phycol.* 44: 339-450.
- Lane, C.E. and **Archibald, J.M.** (2008) The eukaryotic Tree of Life: endosymbiosis takes its TOL. *Trends Ecol. Evol.* 23: 268-275.
- Leander, B.S. and **Simpson A.G.B.** (2008) Euglenozoa. In *Tree of Life Web Project*. <http://www.tolweb.org/Euglenozoa/2405>
- Leigh, J.**, **Susko, E.**, Baumgartner, M. and **Roger, A.J.** (2008) Testing congruence in phylogenomic analysis. *Syst. Biol.* 57: 104-115.
- Lin, S., Zhang, H. and **Gray, M.W.** (2008) RNA editing in dinoflagellates and its implications for the evolutionary history of the editing machinery. In *RNA and DNA Editing: Molecular Mechanisms and Their Integration into Biological Systems*, H.C. Smith (Ed.), pp. 280-309, Wiley Press.
- Phipps, K., Lane, C.E., **Donaher, N.** and **Archibald, J.M.** (2008) Nucleomorph genome karyotype diversity in the cryptophyte genus *Cryptomonas*. *J. Phycol.* 44: 11-14.
- Ruiz-Trillo, I., **Roger, A.J.**, Burger, G., **Gray, M.W.** and Lang, B.F. (2008) A phylogenomic investigation into the origin of metazoa. *Mol. Biol. Evol.* 25: 664-672.
- Sanchez-Perez, G.**, **Hampl, V.**, **Simpson, A.G.B.** and **Roger, A.J.** (2008) A new divergent type of eukaryotic methionine adenosyltransferase is present in multiple distantly related secondary algal lineages. *J. Eukaryot. Microbiol.* 55: 374-381.
- Sharma, A.K.**, **Zhaxybayeva, O.**, Papke, R.T. and **Doolittle, W.F.** (2008) Actinorhodopsins: Proteorhodopsin-like gene sequences found predominantly in non-marine environments. *Environ Microbiol.* 10: 1039-56.
- Simpson A.G.** (2008) Jakobida. In *Tree of Life Web Project*. <http://www.tolweb.org/Jakobida/97407>
- Simpson, A.G.B.**, Perley, T.A. and Lara, E. (2008) Lateral transfer of the gene for a widely used marker, α -tubulin, indicated by a multi-protein study of the phylogenetic position of Andalucia (Excavata). *Mol. Phylogenet. Evol.* 47: 366-377.
- Stechmann, A.**, Hamblin, K., Perez-Brocad, V., **Gaston, D.**, Richmond, G.S., van der Giezen, M., Clark, C.G. and **Roger, A.J.** (2008) Organelles in *Blastocystis* that blur the distinction between mitochondria and hydrogenosomes. *Curr. Biol.* 18: 580-585.
- Sullivan, M.B., Coleman, M.L., Quinlivan, V., Rosenkrantz, J.E., Defrancesco, A.S., Tan, G., Fu, R., Lee, J.A., Waterbury, J.B., **Bielawski, J.P.** and Chisholm, S.W. (2008) Portal protein diversity and phage ecology. *Environ. Microbiol.* 10: 2810-2823.
- Susko, E.** (2008) On the distributions of bootstrap support and posterior distributions for a star tree. *Syst. Biol.* 57: 602-612.
- Wang, H.C.**, Li, K.M., **Susko, E.** and **Roger A.J.** (2008) A class frequency mixture model that adjusts for site-specific amino acid frequencies and improves inference of protein phylogeny. *BMC Evol. Biol.* 8: 331.

- Wang, H.C., **Susko, E.**, Spencer, M. and **Roger, A.J.** (2008) Topological estimation biases with covarion evolution. *J. Mol. Evol.* 66: 50-60.
- Ward, T.J., Ducey, T.F., Usgaard, T., Dunn, K.A. and **Bielawski, J.P.** (2008) Multilocus genotyping assays for single nucleotide polymorphism-based subtyping of *Listeria monocytogenes* isolates. *Appl. Environ. Microbiol.* 74: 7629-7642.
- Watkins, R.F. and **Gray M.W.** (2008) Sampling gene diversity across the supergroup Amoebozoa: large EST data sets from *A. castellanii*, *H. vermiformis*, *P. polycephalum*, *H. dachnaya* and *Hyperamoeba sp.* *Protist* 159: 269-281.
- Wu, J., **Susko, E.** and **Roger, A.J.** (2008) An independent heterotachy model and its implications for phylogeny and divergence time estimation. *Mol. Phylogenet. Evol.* 46: 801-806.