

Publications 2014: Research Themes and Activities

1 Genomics & Biomathematics

Clarke, A.C., S. Prost, J.L. Stanton, W.T.J. White, M.E. Kaplan, E. Matisoo-Smith & the Genographic Consortium. From cheek swabs to consensus sequences: an A to Z protocol for high-throughput DNA sequencing of complete human mitochondrial genomes. *BMC Genomics*. 15:68.

Catchpole, R.J. and Poole, A.M. (2014). Antibiotic genes spread far and wide. *eLife*. 3:e05244. doi: 10.7554/eLife.05244

Nelson-Sathi, S., Sousa, F.L., Röttger, M., Lozada-Chávez, N., Thiergart, T., Janssen, A., Bryant, D., Landan, G., Schönheit, P., Siebers, P., McInerney, J. & Martin, W.F. (2014). Origins of major archaeal clades correspond to gene acquisitions from bacteria. *Nature*. doi: 10.1038/nature13805.

Poole, A.M., Horinouchi, N., Catchpole, R.J., Si, D., Hibi, M., Tanaka, V. & Ogawa, J. (2014). The case for an early biological origin of DNA. *Journal of Molecular Evolution*. 79: 204-212.

Poole, A.M. & Gribaldo, S. (2014). Origin of Eukaryotes: how and when was the mitochondrion acquired? *Cold Spring Harbor Perspectives in Biology*, doi: 10.1101/cshperspect.a015990.

1A. Developing cutting-edge bioinformatic and biomathematical technologies for New Zealand

Amaris, A.J.R. & Cox, M.P. (2014). A Flexible Theoretical Representation for the Temporal Dynamics of Structured Populations as Paths on Polytope Complexes. *Journal of Mathematical Biology*. doi: 10.1007/s00285-014-0841-4.

Anderson, M.J. and Santana-Garcon, J. (2015). Measures of precision for dissimilarity-based multivariate analysis of ecological communities. *Ecology Letters*. 18: 66-73.

Bertels, F., Silander, O. K., Pachkov, M., Rainey, P. B. & van Nimwegen, E. (2014). Automated reconstruction of whole genome phylogenies from short sequence reads. *Molecular Biology and Evolution*. 31, 1077-1088. doi: 10.1093/molbev/msu088.

Bouckaert, R., Heled, J., Kühnert, D., Vaughan, T., Wu, C. H., Xie, D., ... & Drummond, A. J. (2014). BEAST 2: a software platform for Bayesian evolutionary analysis. *PLoS Computational Biology*. 10(4), e1003537.

Cordue, P., Linz, S., & Semple, C. (2014). Phylogenetic networks that display a tree twice. *Bulletin of Mathematical Biology*. 76, 2664-2679.

Fearnhead, P., Biggs, P., & French, N. (2014). Learning about recombination in *Campylobacter*. In: Sheppard, S., Méric, G. (Eds.), *Campylobacter Ecology and Evolution*. Horizon Scientific Press. 9-22.

Franz, E., Delaquis, P., Morabito, S., Beutin, L., Gobius, K., Rasko, D.A., Bono, J., French, N., Osek, J. & Lindstedt, B. A. (2014). Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin producing *Escherichia coli* (STEC) in global food production systems. *International Journal Food Microbiology*. 187, 57-72.

French, N., Yu, S., Biggs, P., Holland, B., Fearnhead, P., Binney, B., Fox, A., Grove-White, D.H., Leigh, J., Miller, W., Muellner, P. & Carter, P. (2014). Evolution of *Campylobacter* species in New Zealand. In: Sheppard, S., Méric, G. (Eds.), *Campylobacter Ecology and Evolution*. *Horizon Scientific Press*. 221-240.

Guillot, E.G. and Cox, M. P. (2014). SMARTPOP: Inferring the Impact of Social Dynamics on Genetic Diversity through High Speed Simulations. *BMC Bioinformatics*. 15:175.

Irshad, H., Cookson, A. & French, N.P. (2014). Distribution of *Escherichia coli* strains harbouring Shiga toxin-producing *E. coli* (STEC)-associated virulence factors (*stx1*, *stx2*, *eae*, *ehxA*) from very young calves in the North Island of New Zealand. *Epidemiology and Infection*. 142(12):2548-58.

Lindgreen, S., Umu, S.U., Lai, A.S-W., Eldai, H., Liu, W., McGimpsey, S., Wheeler, N., Biggs, P.J., Thomson, N.R., Barquist, L., Poole, A.M. & Gardner, P.P. (2014). Robust identification of noncoding RNA from transcriptomes requires phylogenetically-informed sampling. *PLoS Computational Biology*. 10, e1003907.

Prangle, D., Fearnhead, P., Cox, M.P., Biggs, P.J. & French, N.P. (2014). Semi-Automatic Selection of Summary Statistics for ABC Model Choice. *Statistical Applications in Genetics and Molecular Biology*. 13:67-82.

Steel, M. and Velasco, J. (2014). Axiomatic opportunities and obstacles for inferring a species tree from gene trees. *Systematic Biology*. 63(5): 772-778.

Smith, J., Steel, M. & Hordijk, W. (2014). Autocatalytic sets in a partitioned biochemical network. *Journal of Systems Chemistry*. 5:2.

Terlizzi, A., Anderson, M.J., Bevilacqua, S. & Ugland, K. (2014). Species-accumulation curves and taxonomic surrogates: an integrated approach for estimation of regional species richness. *Diversity and Distributions*. 20: 356-368.

1B. Using new genetic knowledge for molecular ecology and evolution

Abe, H. and Gemmell, N. J. (2014). Abundance, arrangement, and function of sequence motifs in the chicken promoters. *BMC Genomics*. 15, 900.

Alsohim, A. S., Taylor, T. B., Barrett, G. A., Gallie, J., Zhang, X.-X., Johnson, L. J., Altamirano-Junqueira, A. E., Rainey, P. B. & Jackson, R. W. (2014). The biosurfactant viscosin produced by *Pseudomonas fluorescens* SBW25 mediates in vitro spreading motility and plant growth promotion. *Environmental Microbiology*. doi: 10.1111/1462-2920.12469.

Baillie, S. M.; Ritchie, P. A. & Brunton, D. H. (2014). Population genetic connectivity of an endemic New Zealand passerine after large-scale local extirpations: a model of re-colonization potential. *IBIS*. 156(4): 826-839.

Davies, N., Field, D., Amaral-Zettler, L., Clark, M. S., Deck, J., Drummond, A., ... & Fuhrman, J. (2014). The founding charter of the Genomic Observatories Network. *GigaScience*. 3(1) 2.

Davies, N., Field, D., Amaral-Zettler, L., Bica, M., Bourlat, S., Coddington, J., Deck, J., Drummond, A., ... & Stones-Havas, S. (2014). Report of the 14th Genomic Standards Consortium Meeting, Oxford, UK, September 17-21, 2012. *Standards in Genomic Sciences*. 9(3).

Cox, M.P., Dong, T., Shen, G., Dalvi, Y., Scott, D.B. & Ganley, A.R.D. (2014). An Interspecific Fungal Hybrid Reveals Cross-Kingdom Rules for Allopolyploid Gene Expression Patterns. *PLoS Genetics*. 10:e1004180.

Grosser, S. and Waters, J. M. (2014). Development and characterisation of 20 novel microsatellite markers for the little blue penguin (*Eudyptula minor*) using next-generation sequencing. *Conservation Genetics Resources*. 1-3.

Grueter, C.E., Wallis, G.P. & Jamieson, I.G. (2014). Episodic positive selection in the evolution of avian Toll-like receptor innate immunity genes. *PLoS One*. 9(3): e89632.

Hammerschmidt, K., Rose, C., Kerr, B. & Rainey, P. B. (2014). Life cycles, fitness decoupling and the evolution of multicellularity. *Nature*. 515, 75-79. DOI: 10.1038/nature13884.

Hernandez, S; Duffy, C; Francis, M P & Ritchie, P A. (2014). Evidence for multiple paternity in the school shark *Galeorhinus galeus* found in New Zealand waters. *Journal of Fish Biology*. 85(5):1739-1745

Joly, S., Bryant, D. & Lockhart, P.J. (2015). Flexible methods for estimating genetic distances from single nucleotide polymorphisms. *Methods in Ecology and Evolution*. doi: 10.1111/2041-210X.12343

Nussey, D.H., Baird, D., Barrett, E., Boner, W., Fairlie, J., Gemmill, N., Hartmann, N., Horn, T., Hausmann, M., Olsson, M., Turbill, C., Verhulst, S., Zahn, S. & Monaghan, P. (2014). Measuring telomere length and telomere dynamics in evolutionary biology and ecology. *Methods in Ecology and Evolution*. 5 (4), 299-310.

Johnson, S.L., Villarreal, P.R., Rosengrave, P., Carne, A., Kleffmann, T., Lokman, P. M., & Gemmill, N.J. (2014). Proteomic analysis of Chinook salmon (*Oncorhynchus tshawytscha*) ovarian fluid. *PLoS One*. doi: 10.1371/journal.pone.0104155.

Knafler, G.J., Fidler, A., Jamieson, I.G. & Robertson, B.C. (2014). Evidence for multiple MHC class II β loci in New Zealand's critically endangered kakapo, *Strigops habroptilus*. *Immunogenetics*. 66:115–121.

Knafler, G. and Jamieson, I.G. (2014). Primers for the amplification of major histocompatibility complex class I and II loci in the recovering red-crowned parakeet. *Conservation Genetics Resources*. 6: 37–39.

Liu, Y., Rainey, P. B. & Zhang, X.-X. (2014). Mini-Tn7 vectors for studying post-transcriptional gene expression in *Pseudomonas*. *Journal of Microbiological Methods*. doi: 10.1016/j.mimet.2014.10.015.

Marshall, B.A.; Fenwick, M.C. & Ritchie, P.A. (2014). New Zealand Recent Hyriidae (Mollusca: Bivalvia: Unionida). *Molluscan Research*. 34(3): 181-200.

Misof, B., et al. including Buckley, T.R. author 23 of 101 authors. (2014). Phylogenomics resolves the timing and pattern of insect evolution. *Science*. 346: 763-767.

Ross, H.A. (2014). The incidence of species-level paraphyly in animals: A re-assessment. *Molecular Phylogenetics and Evolution*. 76:10–17. doi: 10.1016/j.ympev.2014.02.021.

Taylor M.W., Tsai P., Anfang N., Ross H.A. & Goddard, M.R. (2014). Pyrosequencing reveals regional differences in fruit-associated fungal communities: Vine fungi biogeography by pyrosequencing. *Environmental Microbiology*. 16:2848–2858.

Vrancken, B., Rambaut, A., Suchard, M. A., Drummond, A., Baele, G., Derdelinckx, I., ... & Lemey, P. (2014). The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. *PLoS computational biology*. 10(4), e1003505.

Yildirim, Y., Patel, S., Millar, C. D. & Rainey, P. B. (2014). Microsatellite development for a tetrodotoxin-containing sea slug (*Pleurobranchaea maculata*). *Biochemical Systematics and Ecology*. doi: 10.1016/j.bse.2014.04.001.

Zhang, X.-X., Ritchie, S., Rainey, P. B. (2014). Urocanate as a potential signaling molecule for bacterial recognition of eukaryotic hosts. *Cell and Molecular Life Sciences*. 71, 541-547. doi: 10.1007/s00018-013-1527-6.

1C. Analytic and predictive modeling in ecology and evolution

Botero, C.A., Gardner, B, Kirby, K.R., Bulbulia, J., Gavin, M.C. and Gray, R.D. (2014). The ecology of religious beliefs. *Proceedings of the National Academy of Sciences*. Published ahead of print November 10, doi:10.1073/pnas.1408701111.

Collins, C.J, Rawlence, N. J., Prost, S, Anderson, C. N. K., Knapp, M., Scofield, R. P., Robertson, B.C., Smith, I., Matisoo-Smith, E. A., Chilvers, B. L. & Waters, J. M. (2014). Extinction and recolonization of coastal megafauna following human arrival in New Zealand. *Proceedings of the Royal Society B*. 281: 20140097.

De Monte, S. and Rainey, P. B. (2014). Nascent multicellular organisms and the evolution of individuality. *Journal of Biosciences*. 39, 237-248. DOI: 10.1007/s12038-014-9420-5.

Fischer, M., Galla, M., Herbst, L. & Steel, M. (2014). The most parsimonious tree for random data. *Molecular Phylogenetics and Evolution*. 80: 165--168.

- Frost C.M., Didham R.K., Rand T.A., Peralta G. & Tylianakis J.M. (2014). Community-level net spillover of natural enemies from managed to natural forest. *Ecology*. 96:193–202.
- Gascuel, O. and Steel, M. (2014). Predicting the ancestral character changes in a tree is typically easier than predicting the root state. *Systematic Biology*. 63(3): 421-435.
- Gavryushkina, A., Welch, D., Stadler, T., & Drummond, A. (2014). Bayesian inference of sampled ancestor trees for epidemiology and fossil calibration. *PLoS Computational Biology*. doi: 10.1371/journal.pcbi.1003919.
- Grange, Z., van Andel, M., French, N. & Gartrell, B. (2014). Network analysis of translocated Takahe populations to identify disease surveillance targets. *Conservation Biology*. 28, 518-528.
- Herman, J.J., Spencer, H.G., Donohue, K. & Sultan, S.E. (2014). How stable ‘should’ epigenetic modifications be? Insights from adaptive plasticity and bet-hedging. *Evolution*. 68: 632-643.
- Hordijk, W., Wills, P. & Steel, M. (2014). Autocatalytic Sets and Biological Specificity. *Bulletin of Mathematical Biology*. 76(1): 201-224
- Huber, K. T., Moulton, V., Semple, C., & Wu, T. (2014). Representing partitions on trees. *SIAM Journal on Discrete Mathematics*. 28, 1152-1172.
- Kühnert, D., Stadler, T., Vaughan, T. G., & Drummond, A. J. (2014). Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth–death SIR model. *Journal of The Royal Society Interface*. 11(94), 20131106.
- Lansing, J.S., Cheong, S.A., Chew, L.Y., Cox, M.P., Ho, M.-H.R. & Arthawiguna, W.A. (2014). Regime shifts in Balinese *subaks*. *Current Anthropology*. 55:232-239.
- Mossel, E. & Steel, M. (2014). Majority rule has transition ratio 4 on Yule trees under a 2-state symmetric model. *Journal of Theoretical Biology*. 360: 315-318.
- Peralta G., Frost C.M., Rand T.A., Didham R.K., Varsani A. & Tylianakis J.M. (2014). Phylogenetic diversity and coevolutionary signals among trophic levels change across a habitat edge. *Journal of Animal Ecology*. doi: 10.1111/1365-2656.12296.
- Peralta G., Frost C.M., Rand T.A., Didham R.K. & Tylianakis J.M. (2014). Complementarity and redundancy of interactions enhance attack rates and spatial stability in host-parasitoid food webs. *Ecology*. 95, 1888-1896.
- Rainey, P. B. and De Monte, S. (2014). Resolving conflicts during the transition to multicellular life. *Annual Review of Ecology Evolution and Systematics*. doi: 10.1146/annurev-ecolsys-120213-091740.
- Rainey, P. B., Desprat, N., Driscoll, W. W. & Zhang, X.-X. (2014). Microbes are not bound by sociobiology: response to Kümmerli and Ross-Gillespie (2013). *Evolution*. doi: 10.1111/evo.12508.

Smith, A.N.H., Anderson, M.J., Millar, R.B. & Willis, T.J. (2014). Effects of marine reserves in the context of spatial and temporal variation: an analysis using Bayesian zero-inflated mixed models. *Marine Ecology Progress Series*. 499: 203-216.

Smith, J., Steel, M. & Hordijk, W. (2014). Autocatalytic sets in a partitioned biochemical network. *Journal of Systems Chemistry*. 5: 2

Sober, E. & Steel, M. (2014). Time and knowability in evolutionary processes. *Philosophy of Science*. 81(4): 558—579.

Terlizzi, A., Anderson, M.J., Bevilacqua, S. & Ugland, K.I. (2014). Species-accumulation curves and taxonomic surrogates: an integrated approach for estimation of regional species richness. *Diversity and Distributions*. 20: 356-368.

Tylianakis J.M. and Coux C. (2014). Tipping points in ecological networks. *Trends in Plant Science*. doi: 10.1016/j.tplants.2014.03.006.

Tylianakis J.M. and Binzer A. (2014). Effects of global environmental changes on parasitoid-host food webs and biological control. *Biological Control*. doi: 10.1016/j.biocontrol.2013.10.003.

Vaughan, T. G., Kühnert, D., Poppinga, A., Welch, D., & Drummond, A. J. (2014). Efficient Bayesian inference under the structured coalescent. *Bioinformatics*. doi: 10.1093/bioinformatics/btu201.

2. Biodiversity & Human Impacts

Jaeger, S. R., Reinbach, H. C., Roigard, C. M., McRae, J. F., Pineau, B., Chheang, S. L., Beresford, M. K., Rouse, S. A., Jin, D., Paisley, A. G., Jia, Y. & Newcomb, R. D. (2014). Sensory characterisation of food and beverage stimuli containing β -ionone and differences between individuals by genotype for rs6591536. *Food Research International*. 62: 205-214.

2A. Biodiversity knowledge and strategy for New Zealand

Anderson, L., Cree, A., Towns, D.R. & Nelson, N.J. (2014). Modulation of corticosterone secretion in tuatara (*Sphenodon punctatus*): Evidence of a dampened stress response in gravid females. *General and Comparative Endocrinology*. 201: 45-52.

Bell, J.J., Smith, D., Hannan, D., Haris, A., & Thomas, L. (2014). Isolation and characterisation of twelve polymorphic microsatellite markers for *Xestospongia* spp. And their use for confirming species identity. *Conservation Genetics Resources*. 6(1): 105-106.

Bryant, D. (2014). Statistical flaws undermine pre-Columbian chicken debate. *PNAS* (letter to editor). doi: 10.1073/pnas.1410797111.

Buckley, T.R., White, D.J., Howitt, V., Winstanley, T., Ramon-Laca, A. & Gleeson, D. (2014). Nuclear and mitochondrial DNA variation within threatened species and subspecies of the giant New Zealand land snail genus *Powelliphanta*: implications for classification and conservation. *Journal of Molluscan Studies*. 80: 291-302.

Chambers, G., Curtis, C., Millar, C., Huynen, L. & Lambert, D. (2014). DNA fingerprinting in zoology: Past, present, future. *Investigative Genetics*. 5: 3.

Cheeseman, J., Millar, C., Greggers, U., Lehmann, K., Pawley, M., Gallistelf, C., Guy, R., Warman, G. & Menzel, R. (2014). Reply to Cheung et al.: The cognitive map hypothesis remains the best interpretation of the data in honeybee navigation. *Proceedings of the National Academy of Science*. 111, E4398-E4398.

Cheeseman, J., Millar, C., Greggers, U., Lehmann, K., Pawley, M., Gallistel, C., Warman, G. & Menzel, R. (2014). Way-finding in displaced clock-shifted bees proves bees use a cognitive map. *Proceedings of the National Academy of Science*. 111: 8949–8954.

Courchamp, F., Hoffman, B. D., Russell, J. C., Leclerc, C. & Bellard, C. (2014). Climate change, sea-level rise and conservation: keeping island biodiversity afloat. *Trends in Ecology and Evolution*. 29 (3), 127-130.

Corkery, I., Bell, B.D. & Nelson, N.J. (2014). Investigating kleptothermy: a reptile-seabird association with thermal benefits. *Physiological and Biochemical Zoology*. 87(2): 216-221.

Cumming, R.A., Nikula, R., Spencer, H. G. & Waters, J. M. (2014). Transoceanic genetic similarities of kelp-associated sea slug populations: long-distance dispersal via rafting? *Journal of Biogeography*. 41: 2357-2370.

Dennis, A.B., Dunning, L.T., Dennis, C.J., Sinclair, B.J. & Buckley, T.R. (2014). Overwintering in New Zealand stick insects. *New Zealand Entomologist*. 37: 35-44.

Dunning, L.T., Dennis, A.B., Sinclair, B.J., Newcomb, R.D. & Buckley, T.R. (2014). Divergent transcriptional responses to low temperature among populations of alpine and lowland species of New Zealand stick insects (*Micrarchus*). *Molecular Ecology*. 23, 2712-2726.

Fraser, C.I., Banks, S. C. & Waters, J. M. (2014). Priority effects can lead to underestimation of dispersal and invasion potential. *Biological Invasions*. doi: 10.1007/s10530-014-0714-1.

Garden, C.J., Currie, K., Fraser, C. I. & Waters, J. M. (2014). Rafting dispersal constrained by an oceanographic boundary. *Marine Ecology Progress Series*. 501: 297-302.

Geary, A.F., Corin, S.E. & Nelson, N.J. (2014). Breeding parameters of the Sooty Shearwater (*Ardenna grisea*) on Long Island, New Zealand. *Emu – Austral Ornithology*. 114: 74-79.

Gillum, J.E., Jimenez, L., White, D.J., Goldstien, S.J. & Gemmell, N.J. (2014). Development and application of a quantitative real-time PCR assay for the globally invasive tunicate *Styela clava*. *Management of Biological Invasions*. 5 (2): 133-142.

Grange, Z.L., van Anandel, M., French, N.P. & B.D. Gartrell. (2014). Network analysis of translocated takahe populations to identify disease surveillance targets. *Conservation Biology*. 28(2): 518-528.

Grayson, K.L., Mitchell, N.J., Monks, J.M., Keall, S.N., Wilson, J.N. & Nelson, N.J. (2014). Sex ratio bias drives conditions for extinction in an isolated tuatara (*Sphenodon punctatus*) population. *PLOS One*. 9(4). doi: pone.0094214.

Grayson, K.L., Mitchell, N.J. & Nelson, N.J. (2014). A threat to NZ's tuatara heats up. *American Scientist*. 102: 350-357. (Feature article).

Hannan, D.A., Bell, J.J., Gardner, J.P.A. & Ritchie, P.A. (2014). Characterisation of novel microsatellite markers for the surf clams *Paphies subtriangulta* and *P. australis* (Bivalvia: Mesodesmatidae). *Conservation Genetics Resources*. 6: 315-317.

Ismar, S., Daniel, C., Igic, B., Morrison-Whittle, P., Ballard, G., Millar, C., Fidler, A., McGraw, K., Wakamatsu, K., Stephenson, B., Cassey, P., Dearborn, D. & Haube, M. (2014). Sexual plumage dichromatism in a size-monomorphic seabird. *The Wilson Journal of Ornithology*. 126: 417-428.

Hagstrom, A. K., Albre, J., Lofstedt, C. & Newcomb, R. D. (2014). A novel fatty acyl desaturase from the pheromone glands of *Ctenopseustis obliquana* and *C. herana* with specific Z5-desaturase activity on myristic acid. *Journal of Chemical Ecology*. 40: 63-70.

Huynen, L., Suzuki, T., Ogura, T., Watanabe, Y., Millar, C., Hofreiter, M., Smith C., Mirmoeini, S. & Lambert, D. (2014). Reconstruction and in vivo analysis of the extinct *tbx5* gene from ancient wingless moa (Aves: Dinornithiformes). *BMC Evolutionary Biology*. 14: 75.

Huynen, L., Millar C. & Lambert, D. (2014). New Zealand's extinct moa: How many species were there? *Barcoding Bulletin*. 5: 8-9.

Huynen, L., Gill, B., Doyle, A., Millar, C. & Lambert, D. (2014). Identification, classification, and growth of moa chicks (Aves: Dinornithiformes) from the genus *Euryapteryx*. *PLoS One*. 9: e99929.

Masuda, B.M., Fisher, P. & Jamieson, I.G. (2014). Anti-coagulant rodenticide brodifacoum detected in dead nestlings of an insectivorous passerine. *New Zealand Journal of Ecology*. 38(1): 110-115.

Middleton, D.M.R.L., La Flamme, A.C., Gartrell, B.D. & Nelson, N.J. (2014). Reptile reservoirs and seasonal variation in the environmental presence of *Salmonella* in an island ecosystem, Stephens Island, New Zealand. *Journal of Wildlife Diseases*. 50(3): 655-659.

Murienne, J., Daniels, S.R., Buckley, T.R., Mayer, G. and Giribet, G. (2014). A living fossil tale of Pangean biogeography. *Proceedings of the Royal Society B*. 281: 20132648.

Painting, C.J., Buckley, T.R. & Holwell, G.I. (2014). Male-biased sexual size dimorphism and sex ratio in the New Zealand Giraffe Weevil, *Lasiornychus barbicornis* (Fabricius) (Coleoptera: Brentidae). *Austral Entomology*. 53: 317-327.

Parks, M., Subramanian, S., Baroni, C., Salvatore, M., Zhang, G., Millar, C. & Lambert, D. (2014). Ancient population genomics and the study of evolution. *Philosophical Transactions of the Royal Society B*. doi: 10.1098/rstb.2013.0381.

Patel, S., Thompson, K., Williams, L., Tsai, P., Constantine R. & Millar, C. (2014). Mining microsatellites for Gray's beaked whale from second-generation sequencing data. *Conservation Genetics Resources*. 6: 657-659.

Rader R., Bartomeus I., Tylianakis J.M. & Laliberté, E. (2014). The winners and losers of land-use intensification: pollinator community disassembly is non-random and alters functional diversity. *Diversity and Distributions*. doi: 10.1111/ddi.12221.

Rawlence, N.J., Kennedy, M., Waters, J. M. & Scofield, R. P. (2014). Morphological and ancient DNA analyses reveal inaccurate labels on two of Buller's bird specimens. *Journal of the Royal Society of New Zealand*. doi: 10.1080/03036758.2014.972962.

Russell, J. C. (2014). A comparison of attitudes towards introduced wildlife in New Zealand in 1994 and 2012. *Journal of the Royal Society of New Zealand*. doi: 10.1080/03036758.2014.944192.

Smith, H.L., Anderson, M.J., Gillanders, B.M. & Connell, S.D. (2014). Longitudinal variation and effects of habitat on biodiversity of Australasian temperate reef fishes. *Journal of Biogeography*. 41: 2128-2139.

Steinwender, B., Thrimawithan, A, H., Crowhurst, R. & Newcomb, R. D. (2014) Pheromone receptor evolution in the cryptic leafroller species, *Ctenopseustis obliquana* and *C. herana*. *Journal of Molecular Evolution*. 80: 42-56.

Taylor, H.R., Nelson, N.J. & Ramstad, K.M. (2014). Chick Timer™ software proves an accurate disturbance-minimizing tool for monitoring hatching success in little spotted kiwi (*Apteryx owenii*). *New Zealand Journal of Zoology*. 41(2): 139-146.

Teske, P.R., Sandoval-Castillo, J., Waters, J. M. & Beheregaray, L. B. (2014). Can novel genetic analyses help to identify low-dispersal marine invasive species? *Ecology and Evolution*. 4: 2848-2866.

Thompson, K., Patel, S., Williams, L., Tsai, P., Constantine, R. & Millar, C. (2014). High coverage of the complete mitochondrial genome of the Gray's beaked whale, *Mesoplodon grayi*, using Illumina next generation sequencing. *Mitochondrial DNA*. doi: 10.3109/19401736.2013.878908.

Thompson, K., Ruggiero, K., Millar, C., Constantine, R. & van Helden, A. (2014). Large-scale multivariate analysis reveals sexual dimorphism and geographic differences in the Gray's beaked whale. *Journal of Zoology*. 294: 13–21.

Waters, J.M., Condie, S. & Beheregaray, L. (2014). Does coastal topography constrain marine biogeography at an oceanographic interface? *Marine and Freshwater Research*. 65: 969-977.

2B. Tracing the origins and histories of the peoples and biota of New Zealand and the Pacific

Collins, C.J., Rawlence, N.J., Prost, S., Anderson, C., Knapp, M., Scofield, R. P., Robertson, B.C., Smith, I., Matisoo-Smith, E.A., Chilvers, B.L. & Waters, J.M. (2014). Extinction and recolonization of coastal megafauna following human arrival in New Zealand. *Proceedings of the Royal Society B*. doi: org/10.1098/rspb.2014.0097.

Gosling, A., Matisoo-Smith, E., & Merriman, T. (2014). Hyperuricaemia in the Pacific: Why the elevated serum urate levels? *Rheumatology International*. 34: 743-757. doi: 10.1007/s00296-013-2922-x.

Kushnick, G., Gray, R. D., & Jordan, F. M. (2014). The sequential evolution of land tenure norms. *Evolution and Human Behavior*. 35(4), 309-318. doi: 10.1016/j.evolhumbehav.2014.03.001

Logan, C.J., Jelbert, S. A., Breen, A. J., Gray, R. D. & Taylor, A. H. (2014). Modifications to the Aesop's Fable Paradigm Change New Caledonian Crow Performances. *PLoS ONE*. 9(7): e103049. doi:10.1371/journal.pone.0103049.

Paterson, A. M., Wallis, G. P., Kennedy, M. & Gray, R. D. (2014). Behavioural evolution in penguins does not reflect phylogeny. *Cladistics*. 30 (3), 243-259.

Rawlence, N.J., Till, C.E., Scofield, R. P., Tennyson, A.J.D., Lallas, C., Loh, G., Matisoo-Smith, L., Waters, J.M., Spencer, H. G. & Kennedy, M. (2014). Strong phylogeographic structure in a philopatric seabird, the Stewart Island Shag (*Leucocarbo chalconotus*). *PLoS One*. 9: e90769.

Robins, J.H., Tintinger, V., Aplin, K., Hingston, M., Matisoo-Smith, E., Penny, D. & Lavery, S. (2014). Phylogenetic species identification in *Rattus* highlights rapid radiation and morphological similarity of New Guinean species. *PLoS One*. 9(5): e98002. doi:10.1371/journal.pone.0098002.

Storey, A. and Matisoo-Smith, E. (2014). No evidence against Polynesian dispersal of chickens to pre-Columbian South America. *Proceedings of the National Academy of Sciences, USA*. 111(35):e3583.

Taylor, A.H. and Gray, R.D. (2014). Is there a link between the crafting of tools and the evolution of cognition? *WIREs Cognitive Science*. 5 (6). doi: 10.1002/wcs.1322.

Taylor A.H., Cheke, L. G., Waismeyer, A., Meltzoff, A. N., Miller, R., Gopnik, A., Clayton, N. S. & Gray, R. D. (2014). Of babies and birds: complex tool behaviours are not sufficient for the evolution of the ability to create a novel causal intervention. *The Royal Society Proceedings B*. 282 (1803). doi: 10.1098/rspb.2014.0837.

2C. Genetic studies on human and wildlife health in a changing environment

McRae, K. M., McEwan, J. C., Dodds, K. G. & Gemmell, N. J. (2014). Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. *BMC Genomics*. 15 (1), 637.

Ritchie, S. R., Thomas, M. G. & Rainey, P. B. (2014). Genetic structure of *Staphylococcus aureus* from the Southwest Pacific. *PLoS One*. doi: 10.1371/journal.pone.0100300.

Schardl, C.L., Young, C. A., Moore, N., Krom, N. D., Dupont, P.-Y., Pan, J., Florea, S., Webb, J. S., Jaromczyk, J., Jaromczyk, J. W., Cox, M. P. & Farman, M. L. (2014). Genomes of plant-associated Clavicipitaceae. In F. Martin (ed.), *Advances in Botanical Research*. 70, 291-327.

Whiteson, K. L., Bailey, B., Bergkessel, M., Conrad, D., Delhaes, L., Felts, B., Harris, J. K., Hunter, R., Lim Y.-W., Maughan, H., Quinn, R., Salamon, P., Sullivan, J., Wagner, B. D. & Rainey, P. B. (2014). The upper respiratory tract as a microbial source for pulmonary infections in cystic fibrosis: parallels from island biogeography. *American Journal of Respiratory and Critical Care Medicine*. 189, 1309-1315.

Yıldırım, Y., Patel, S., Millar, C. & Rainey, P. (2014). Microsatellite development for a tetrodotoxin-containing sea slug species, *Pleurobranchaea maculata*. *Biochemical Systematics and Ecology*. 55: 342–345.