

Dr Nicholas J Clark

Lecturer - University of Queensland, School of Veterinary Science
Gatton, Queensland, Australia – n.clark@uq.edu.au
[Github](#) - [Google Scholar](#) - [ResearchGate](#)

Publication track record

2019

[28] Fountain-Jones, NM, **Clark, NJ**, Kinsley, AC, Carstensen, M, Johnson, TJ, Forester, J, Miller, E, Moore, S, Wolf, TM and Craft, ME. Microbial associations and spatial proximity predict North American moose (*Alces alces*) gastrointestinal community composition. *Journal of Animal Ecology* DOI: <https://doi.org/10.1111/1365-2656.13154>.

[27] Peel, AJ, Wells, K, Giles, J, Boyd, V, Burroughs, A, Edson, D, Crameri, G, Baker, ML, Field, H, Wang, LF, McCallum, H, Plowright, RK and **Clark, NJ**. Synchronous shedding of multiple bat paramyxoviruses coincides with peak periods of Hendra virus spillover. *Emerging Microbes & Infections* 8:1314-1323.

[26] Fecchio, A, Bell, JA, Bosholn, M, Vaughan, JA, Tkach, VV, Lutz, HL, Cueto, VR, Gorosito, CA, González-Acuña, D, Stromlund, C, Kvasager, D, Comiche, KJM, Kirchgatter, K, Pinho, JB, Berv, J, Anciães, M, Fontana, CS, Zyskowski, K, Sampaio, S, Dispoto, JH, Galen, SC, Weckstein, JD, and **Clark, NJ**. An inverse latitudinal gradient in infection probability and phylogenetic diversity for Leucocytozoon blood parasites in New World birds. *Journal of Animal Ecology* DOI: 10.1111/1365-2656.13117.

[25] **Clark, NJ**, Umulisa, I, Ruberanziza, E, Owada, K, Colley, DG, Ortu, G, Campbell, CH, Emmanuel, R, Lancaster, W, Mbonigaba, JB, Mbituyumuremyi, A, Fenwick, A, Soares Magalhães, RJ and Turate, I. Mapping *Schistosoma mansoni* endemicity in Rwanda: a critical assessment of geographical disparities arising from Circulating Cathodic Antigen versus Kato-Katz diagnostics. *PLoS Neglected Tropical Diseases* DOI: <https://doi.org/10.1371/journal.pntd.0007723>

[24] Ruberanziza, E, Owada, K, **Clark, NJ**, Umulisa, I, Ortu, G, Lancaster, W, Munyaneza, T, Mbituyumuremyi, A, Bayisenge, U, Fenwick, A, Soares Magalhães, RJ. Mapping soil-transmitted helminth parasite infection in Rwanda: estimating endemicity and identifying at-risk populations. *Tropical Medicine and Infectious Disease* (accepted 12/06/19)

[23] Proboste, T, Corvalan, P, **Clark, NJ**, Beyer, HL, Goldizen, AW and Seddon, JM. Commensal bacterial sharing is not predicted by host social association in kangaroos: implications for disease transmission networks. *Journal of Animal Ecology* (accepted 12/06/19; IF: 4.474)

[22] Wells, K, and **Clark, NJ**. Host specificity in variable environments. *Trends in Parasitology* DOI: 10.1016/j.pt.2019.04.001 (IF: 7.929) [UQ media release](#)

[21] Lawrence, AL, Webb, CE, **Clark, NJ**, Halajian, A, Mihalca, A, Miret, J, D'Amico, G, Brown, G, Kumsa, B, Modry, D, and Šlapeta, J. Out-of-Africa origins and global climatic distribution of the common cat flea, *Ctenocephalides felis*: the hitchhiker's guide to world domination. *International Journal for Parasitology* DOI: 10.1016/j.ijpara.2019.01.001 (IF: 3.730) [The Conversation](#)

[20] Fecchio, A, Wells, K, Bell, JA, Tkach, VV, Lutz, HL, Weckstein, JD, Clegg, SM, and **Clark, NJ**. Climate variation influences host specificity in avian malaria parasites. *Ecology Letters* 22 547-557 (IF: 9.137)

2018

[19] Wells, K, Gibson, D, and **Clark, NJ**. Global patterns in helminth host specificity: phylogenetic and functional diversity of regional host species pools matter. *Ecography* DOI: 10.1111/ecog.03886 (IF: 4.520) [UQ media release](#)

[18] **Clark, NJ** and Soares Magalhães, RJ. Airborne geographical dispersal of Q Fever from livestock holdings to human communities: a systematic review and critical appraisal of evidence. *BMC Infectious Diseases* DOI: 10.1186/s12879-018-3135-4 (IF: 2.678)

[17] **Clark, NJ**, Wells, K, Lindberg, O. MRFCov: Markov Random Fields with additional covariates. R package version 1.0, <https://github.com/nicholasjclark/MRFCov>

[16] **Clark, NJ**, Wells, K, and Lindberg, O. Unravelling changing interspecific interactions across environmental gradients using Markov random fields. *Ecology* DOI: 10.1002/ecy.2221 (IF: 4.809) [UQ media release](#)

[15] **Clark, NJ**. Phylogenetic uniqueness, not latitude, explains the diversity of avian blood parasite communities worldwide. *Global Ecology and Biogeography* DOI: 10.1111/geb.12741 (IF: 6.045)

[14] Wells, L, Gibson, DI, **Clark, NJ**, Ribas, A, Morand, S, McCallum, H. Global spread of helminth parasites at the human – domestic animal – wildlife interface. *Global Change Biology* DOI: 10.1111/gcb.14064 (IF: 8.502)

[13] **Clark, NJ**, Seddon, JM, Kyaw-Tanner, M, Al-Alawneh, J, Harper, G, McDonagh, P, and Meers, J. Emergence of canine parvovirus subtype 2b (CPV-2b) infections in Australian dogs. *Infection, Genetics and Evolution* DOI: 10.1016/j.meegid.2017.12.013 (IF: 2.885) [UQ media release](#)

[12] **Clark, NJ**, Seddon, JM, Šlapeta, J, and Wells, K. Parasite spread at the domestic animal - wildlife interface: anthropogenic habitat use, phylogeny and body mass drive risk of cat and dog flea (*Ctenocephalides* spp.) infestation in wild mammals. *Parasites & Vectors* 11:8 (IF: 3.035) [UQ media release](#)

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[11] **Clark, NJ**, Clegg, SM, Sam, K, Goulding, W, Koane, B and Wells, K. Climate, host phylogeny and the connectivity of host communities govern regional parasite assembly. *Diversity and Distributions* DOI: 10.1111/ddi.12661 (IF: 4.391)

[10] **Clark, NJ** and Clegg, SM. Integrating phylogenetic and ecological distances reveals new insights into parasite host specificity. *Molecular Ecology* 26(11), 3074-3086 (IF: 6.086)

[9] McKee, J, **Clark, NJ**, Shapter, F and Simmons, G. A new look at the origins of Gibbon Ape Leukemia Virus. *Virus Genes* 53(2), 165-172 (IF: 1.431)

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[8] **Clark, NJ**, Wells, K, Dimitrov, D and Clegg, SM. Co-infections and environmental conditions drive the distributions of blood parasites in wild birds. *Journal of Animal Ecology* 85(6), 1461-1470 (IF: 4.474)

[7] Aharon-Rotman, Y, Buchanan, KL, **Clark, NJ**, Klaassen, M and Buttemer, WA. Why fly the extra mile? Using stress biomarkers to assess wintering habitat quality in migratory shorebirds. *Oecologia* 182(2), 385-395 (IF: 3.130)

[6] Goulding, W, Adlard, RD, Clegg, SM and **Clark, NJ**. Molecular and morphological description of *Haemoproteus (Parahaemoproteus) bukaka* (species nova), a haemosporidian associated with the strictly Australo-Papuan host Subfamily Cracticinae. *Parasitology Research* 115, 3387-3400 (IF: 2.329)

[5] **Clark, NJ**, Clegg, SM and Klaassen, M. Migration strategy and pathogen risk: non-breeding distribution drives malaria prevalence in migratory waders. *Oikos* 125(9), 1358-1368 (IF: 4.030)

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[4] **Clark, NJ**, Ishtiaq, F, Olsson-Pons, S and Clegg, SM. Specialist enemies, generalist weapons and the potential spread of exotic pathogens: malaria parasites in a highly invasive bird. *International Journal for Parasitology* 45(14), 891-899 (IF: 3.730)

[3] Olsson-Pons, S, **Clark, NJ**, Ishtiaq, F and Clegg, SM. Differences in host species relationships and biogeographical influences produce contrasting patterns of prevalence, community composition and genetic structure in two genera of avian malaria parasites in southern Melanesia. *Journal of Animal Ecology* 84(4), 985-998 (IF: 4.474)

[2] **Clark, NJ**, Adlard, RD and Clegg, SM. Molecular and morphological characterization of *Haemoproteus (Parahaemoproteus) ptilotis*, a parasite infecting Australian honeyeaters (Meliphagidae), with remarks on prevalence and potential cryptic speciation. *Parasitology Research* 114(5), 1921-1928 (IF: 2.329)

[1] **Clark, NJ** and Clegg, SM. The influence of vagrant hosts and weather patterns on the colonisation and persistence of blood parasites in an island bird. *Journal of Biogeography* 42(4), 641-651 (IF: 4.248)