Distribution of coccidia in kiwi.

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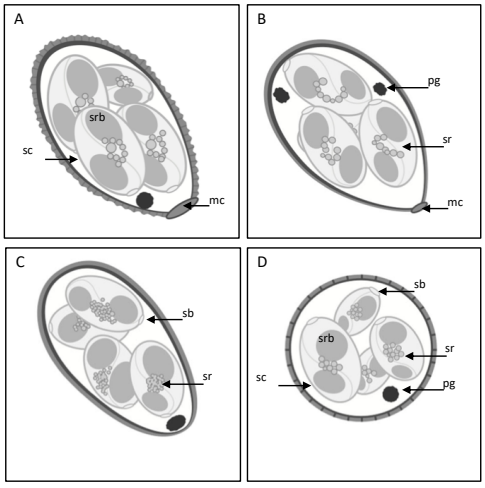
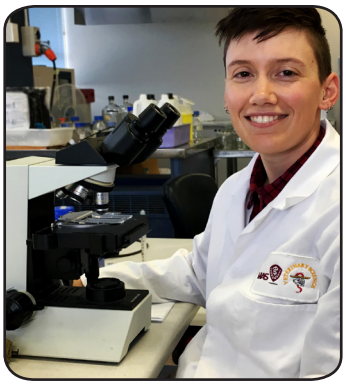
The success of kiwi (*Apteryx* spp.) population management depends on raising kiwi chicks in captivity until they are large enough to defend themselves against introduced mammal predators[1]. However, these captive facilities increase the density of very young kiwi, leading to increased transmission of coccidian parasites in birds that have not developed any immune response to these single-celled invaders. Exposure to high numbers of this parasite can lead to significant disease and mortality[2,3].

The main objective of my research is to characterise the species of coccidia in kiwi. Recent studies demonstrate a high diversity of these parasites (*Eimeria* spp.) in brown kiwi (*Apteryx mantelli*), but little is known of the species of coccidia affecting the other four species of kiwi[3]. Mixing kiwi species in Kiwi for Kiwi's Operation Nest Egg programme and in captive facilities represents a risk pathway for the transfer of coccidia between wild kiwi populations. Therefore, understanding the infection rates and loads, life cycles, as well as distribution of coccidia species has significant management implications.



Line drawings of sporulated oocysts for A) *Eimeria parauri*i; B) *E. apteryxii*; C) *E. mantelii*; D) *E. kiwii*. Polar granules (pg), micropyles (mc), steida bodies (sb), sporocysts (sc), sporocyst residuum (sr), and sporozoite refractile bodies (srb) are indicated. Interpreted from Morgan et al. (2017).

One of the major challenges with managing and studying coccidia in kiwi is an inability to differentiate the coccidial species from each other without sporulating oocysts (i.e. the infective stage) collected from fresh faecal samples[3]. Thus, little is known about which coccidia species can cause severe disease in a young kiwi or the distribution of each species of coccidia in the wild and among captive facilities. Thanks to funding via the Birds New Zealand Research Fund 2018, I am addressing this issue by using new sequencing techniques (i.e. Next Generation Sequencing) to develop a rapid genetic test that will be able to identify each species of coccidia from fresh, frozen, or preserved samples of faeces, tissue, and soil. This test will be used to identify key species of coccidia that cause severe disease in kiwi, enabling researchers, vets, and conservation managers to monitor and manage exposure. It will also be used to ensure wild populations are not exposed to new species of coccidia that could cause significant disease in a naive kiwi host species.



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2. Morgan, K. (2013). Coccidiosis in the kiwi (*Apteryx* spp): Aspects of the Pathology, Epidemiology and parasite biology. (Doctor of Philosophy), Massey University, Palmerston North, New Zealand.
3. Morgan, K. J., Pomroy, W. E., Howe, L., Alley, M. R., & Castro, I. (2017). Description of four new species of coccidia (Apicomplexa: Eimeriidae) from brown kiwi, *Apteryx mantelli*, in New Zealand. Parasitol Res, 116(5), 1433-1441. doi:10.1007/