

Exploring Brown Kiwi (*Apteryx mantelli*) gut microbiome to identify disease vulnerability

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Brown Kiwi (*Apteryx mantelli*), a flightless endemic bird from New Zealand, is vulnerable to extinction in the wild. Ongoing conservation efforts include Operation Nest Egg (ONE) project, or captive rearing, which has undoubtedly increased chick survival rate. However, both the stress of captivity and high density of chicks co-habiting puts them at risk for disease. For example, coccidiosis, deemed the most important disease in captive kiwi, is caused by protozoan *Eimeria spp.* that disseminates through consumption of oocysts in faeces [1]. Disease prevention methods are limited and often resort to administering of antiprotozoal agents after infection.

One potential yet overlooked avenue is the gut microbiome, which has been recognized both as a mediator and indicator of host health. This microbial community may contain key bacteria important for disease resistance. Recent studies in poultry have found that combining probiotics with coccidiosis vaccines enhances protection from the parasite [2]. However, before practical solutions can be implemented in kiwi management, a survey of gut bacterial membership in wild, captive, healthy, and infected kiwi is necessary.

Our main goal is to determine the relationship between gut microbial communities and parasite prevalence in wild and captive Brown Kiwi. Overall, this data will increase understanding of coccidia in kiwi and its gut microbiome.

References: [1] Morgan, K.J et al. 2013 Avian Pathol 42(2): 137-146. [2] Ritzi, MM et al. 2016. BMC Vet Res 47:111.

