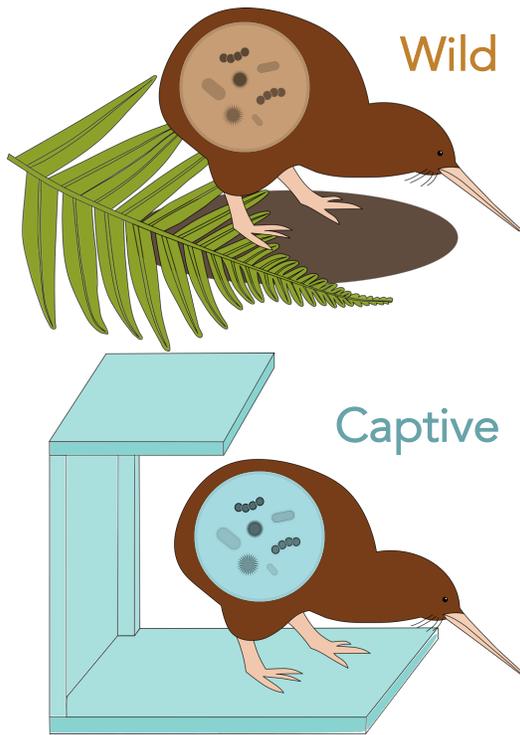


Exploring Brown Kiwi (*Apteryx mantelli*) gut microbiome to identify disease vulnerability

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Brown Kiwi (*Apteryx mantelli*), a flightless bird endemic to New Zealand, is vulnerable to extinction in the wild. Captive-rearing facilitated through programs such as Operation Nest Egg (ONE), has undoubtedly increased population size. However, the health effects due to the modification of the gut microbiome have been largely overlooked. The conditions of captivity, including sterile built environments, medical treatment of diseases, artificial diets, and close interactions with humans may be altering their gut microbiomes. This microbial community have been recognized as a key player in host health via digestion, immune function, and pathogen defense. Coccidiosis, deemed the most important disease in captive kiwi, is caused by protozoan *Eimeria spp.* that disseminates through consumption of oocysts in faeces. Disease prevention methods are limited and often resort to administering of antiprotozoal agents after infection.

Captivity has been seen as an important factor in altering the gut microbiome in a number of animal hosts, however, this has not been explored in the Brown Kiwi. This emphasizes the need to investigate the relationship between captivity, coccidia, and gut microbial communities. We sought to characterize the gut bacteria and fungi of captive and wild kiwi. We tested the hypothesis that (1) captivity status and (2) history of coccidiosis would change diversity and composition of the gut microbiome.

Our preliminary findings suggest captivity influences the diversity and composition of microbial communities in the Brown Kiwi (Figure 1). Each point represents a faecal sample and its associated bacterial community. There is a stark difference between treatments, prompting further investigation into these discrepancies.

Overall, this data will increase our understanding of kiwi and how its gut microbiome forms and changes with captivity and disease.

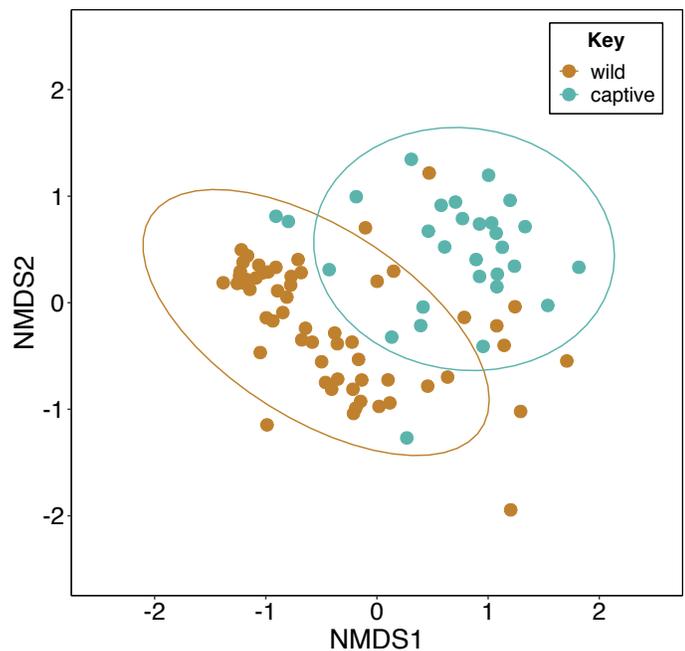


Figure 1: Captivity shifts the Brown Kiwi gut bacterial composition. NMDS plot shows samples clustering by captivity status with little overlap between the groups. Ellipses denote 95% confidence level.