

Limited rodent-associated leptospirosis transmission in Hawke's Bay post-flooding

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Introduction

Aotearoa (New Zealand) was affected by flooding in early 2023 due to a series of extreme weather events, including Cyclone Hale, Auckland Anniversary Weekend floods and Cyclone Gabrielle (NIWA 2023). Following these events, human leptospirosis cases spiked, contributing to a 41% increase in cases in 2023 compared to 2022, with the largest increase seen in Hawke's Bay (ESR 2024). Internationally, post-flood leptospirosis outbreaks have been linked to rodents (Diaz 2015; Socolovschi *et al.* 2011), however, limited evidence of this exists in Aotearoa. We hypothesized that the increase in human leptospirosis cases was associated with rodents post-flooding. This study investigated this link by strain-typing *Leptospira* from human and rodent samples collected before and after the floods in Aotearoa.

Methods

A total of 209 human samples were collected nationwide, consisting of gDNA from patients tested for *Leptospira* at human diagnostic laboratories and a research laboratory (^mEpiLab). Of these, 107 were collected pre-floods (2 April 2016 to 20 April 2022) and 102 post-floods (1 January to 31 December 2023).

A total of 280 rodent kidneys from *Rattus exulans* (kiore, n=33), *Rattus norvegicus* (Norway rat, n=25), *Rattus rattus*, (ship rat, n=86) and *Mus musculus* (house mouse, n=136) were collected from rural Hawke's Bay, Mahia Peninsula, Christchurch, Southwest Chatham Island and Whangarei. Of these, 193 were collected pre-floods (19 April 2019 to 16 May 2022) and 87 post-floods (28 April 2023 to 16 May 2023). Rodent kidneys were used for gDNA extraction with the QIAamp DNA Mini Kit before testing.

Both human and rodent gDNA were first screened with a *lipL32* PCR that is specific for pathogenic *Leptospira* (Stoddard *et al.* 2009). Samples positive to the screening PCR were subjected to a *glmU* PCR (Wilkinson *et al.* 2021), and *glmU* positive amplicons were subjected to Sanger sequencing and typed relative to reference sequences of *Leptospira* serovars/strains endemic to Aotearoa (Wilkinson *et al.* 2023).

Leptospira genotypes in humans were compared pre- and post-floods in Aotearoa, and in Hawke's Bay, the region most severely affected by floods in 2023. *Leptospira* genotypes in rodents were also compared pre- and post-floods in Aotearoa. Additionally, post-floods genotypes in humans and mice from Hawke's Bay were compared. All the comparisons were conducted using the Proportional similarity index (PSI).

Results

A total of 90 *Leptospira* PCR positive samples were genotyped from humans (35 pre-flood and 55 post-flood) and 53 from rodents (34 pre-flood and 19 post-flood). Human genotypes included Hardjo (four pre- and five post-flood), Pomona (six pre- and 22 post-flood), Ballum (13 pre- and 19 post-flood), Pacifica (three pre- and two post-flood), Balcanica NZ (one post-flood), Australis (one pre-flood) and Copenhageni (eight pre- and six post-flood). Rodent genotypes included Ballum from mice (27 pre- and 18 post-flood), Norway rats (one pre-flood) and ship rats (1 post-flood) while Copenhageni was detected in Norway rats (six pre-flood). Due to limited

rodent samples from all species, only serovars genotyped from mice were compared pre- and post-floods. All genotyped mice samples were from rural Hawke's Bay.

Comparison of *Leptospira* genotypes in humans pre- and post-floods in New Zealand showed a moderately similar distribution (PSI 0.75, 95% CI: 0.54-0.86), with serovar Pomona showing a statistically significant increase in percentage post-floods ($p=0.04$). This suggests that the rise in human cases post-floods was driven by an increase in Pomona infections. In Hawke's Bay, a dissimilar distribution of *Leptospira* genotypes in humans pre- and post-floods was observed (PSI 0.48, 95% CI: 0.08-0.75), with Pomona (77%, 10/13) being the most common genotyped serovar post-floods, suggesting the increase in Pomona cases in New Zealand was due to increase in Pomona cases in Hawke's Bay. An extremely dissimilar distribution of *Leptospira* genotypes between humans and mice was observed post-floods in Hawke's Bay (PSI 0.08, 95% CI: 0-0.23), suggesting mice were not the primary source of increased human leptospirosis cases in this region.

Conclusions

Our findings did not support the hypothesis that the rise in human leptospirosis cases following floods in Aotearoa was rodent-associated. The serovar identified in rodents was primarily Ballum, followed by Copenhageni, while the increase in human cases was largely due to Pomona. Previous research on host-serovar associations in New Zealand indicate that Pomona is a dry-stock associated serovar (Wilkinson *et al.* 2023), suggesting that unvaccinated dry stock (cattle, sheep, and deer) were likely responsible for the increase in human cases. This study highlights the need to enhance vaccination coverage among dry stock as a critical measure to reduce the risk of future leptospirosis outbreaks following floods in farming regions.

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