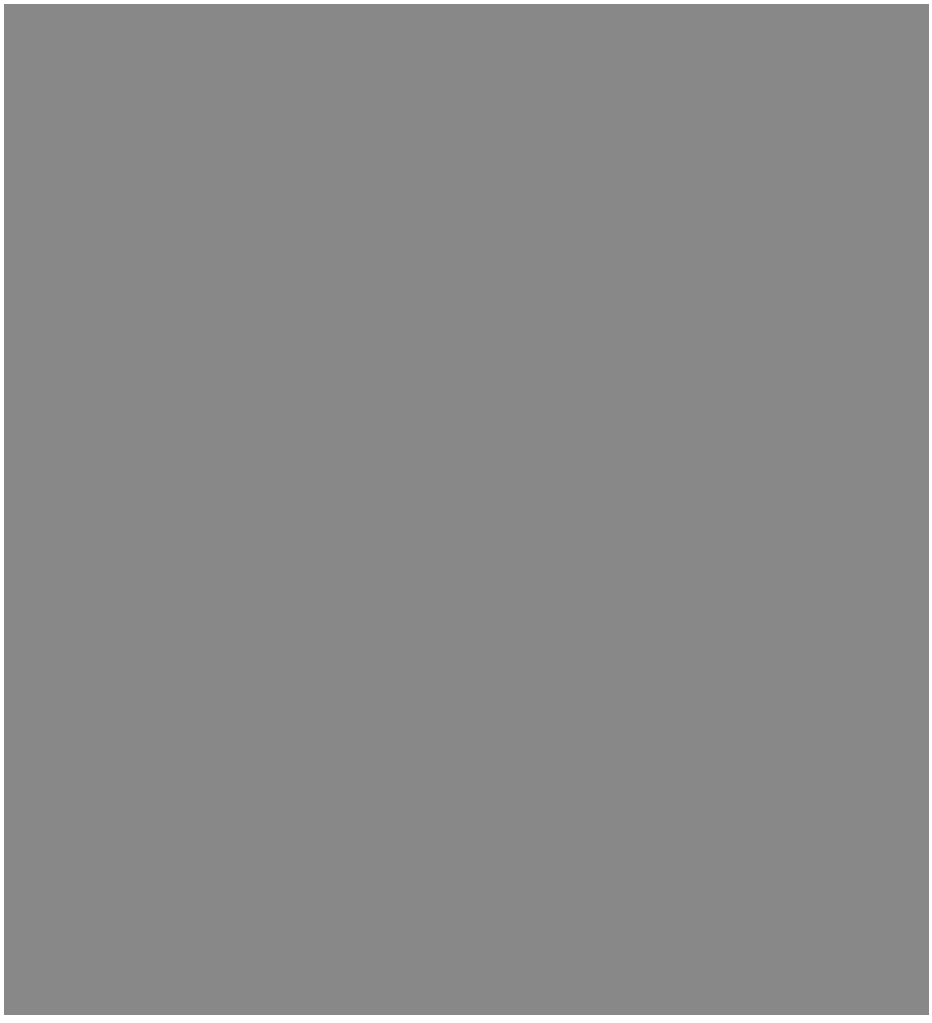


insular (e.g., Lamichhaney et al., 2015) and landscape (e.g., Prugh, Hodges, Sinclair, & Brasharesa, 2008) systems present assemblages with many and varied characteristics that challenge unifying explanation. However, the dual treatment of islands as habitat patches subject to a colonization lottery, and as evolutionary laboratories reflects the importance of gene flow in all situations. Here we examine the correlation between population genetic structure of a flightless bird and other endemic avifauna, and a narrow seaway that divides continental islands (Cowie & Holland, 2006). Does this geologically young feature indicate a significant barrier to gene flow allowing the accumulation of neutral genetic differences or does it represent a recent and ephemeral separation of populations?

Dispersal of individuals and establishment of populations allows species

2.4 |

Microsatellite PCRs for selected loci were multiplexed for genotyping according to size and fluorescent label (6-FAM or HEX), with allele sizes determined using an ABI3730 automated sequencer with an internal LIZ size standard (Applied Biosystems). Results were scored using GENEMAPPER® version 4.7 (Applied Biosystems), and data

Island (A). Mokoia Weka (n = 18) were polymorphic, but all those sampled from Kapiti (n = 23) carried just haplotype A. Haplotype F also occurred in the one sample from the extinct Whanganui population putatively collected in 1964. Unique CR haplotypes were obtained from a museum skin from Whangarei (S) and a bone from a prehuman deposit at Matira (T), again, part of the northern cluster (Figure 2).

The southern cluster included haplotypes found in Weka assigned by their location to the three other Weka subspecies; . _. ▮ r⌐ı , . _. / and . _. n / r. Haplotype I occurred in 22 putative . _. ▮ r⌐ı (West Coast South Island) and all 15 putative . _. n / r samples (from Chatham Island). Putative . _. / from the Bravo islets (n =

3.4

TABLE 5 Diversity and pairwise $_{ST}$ among microsatellite genotypes from regional samples of Weka (

Titī islands near Stewart Island hosting only . Both species of louse were found on a sample of 12 Weka from west coast South Island (near Hokitika and Westport) with the most similar numbers on a single Weka being 125 and 31 . (4 : 1) A Weka from Chatham Island had 125 and five , (25 : 1) and the lousiest host was among three Weka from near Opotiki (North Island), which carried 488 and 34 (14 : 1) (Table S4).

MtDNA COI sequences were obtained from 33 lice (25 and eight) including representatives of both genera from the same Weka individuals (GenBank MF539919–MF539926 and MF539915–MF539918 respectively). Alignments of 330 bp ( ) and 337 bp ( ) had 59 and 31 parsimony informative sites, respectively. Maximum genetic distances (Juke Cantor) among haplotypes were substantially higher in the sample of (0.2) than the (0.098). Nevertheless, minimum-spanning networks revealed two clusters of variation in and , each associated with sampling from North Island and South Island Weka hosts (Figure 6a). We also obtained homologous mtDNA COI sequences from specimens of the same louse genera living on congeneric rails in New Zealand. The Weka louse clades were confirmed as sister groups within both genera (Figure 6b).

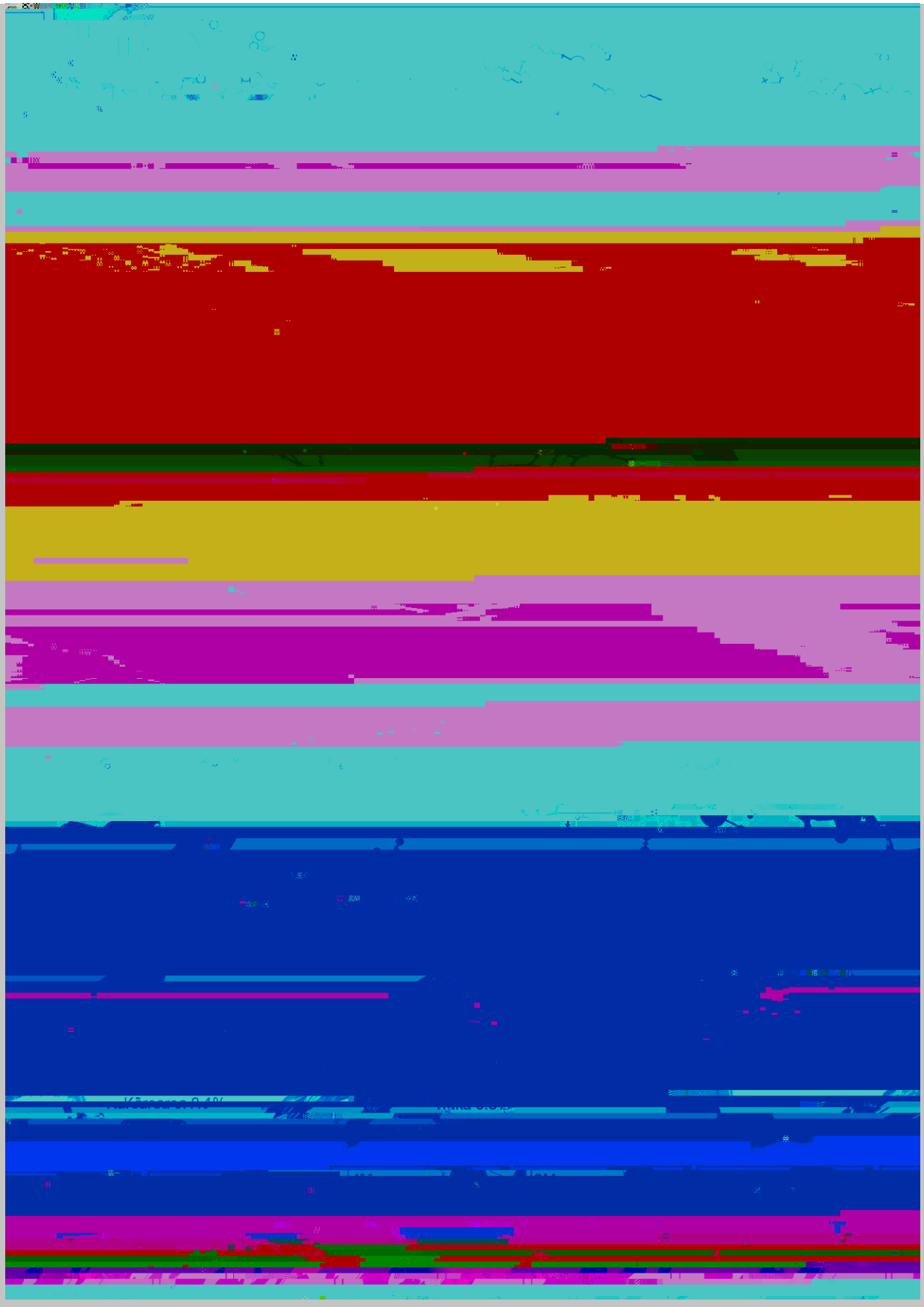
4 | DISCUSSION

4.1 | Concordance of genetic markers and Cook Strait

We found an overall signal in the genetic data from Weka for just two primary lineages among the extant populations (Figure 2), suggesting an accumulation of genetic differences during prolonged separation. These lineages are partitioned by the most prominent, and yet geologically young, geophysical feature in the New Zealand landscape; the Cook Strait seaway. MtDNA genetic diversity was lower among southern Weka, comprising three putative subspecies, than northern Weka (Table 1 and 2, Table S2). Associated with this were different inferences of demographic history. North Island Weka that have today the more restricted range gave a signal of recent population reduction, and novel haplotypes in extinct populations show diversity as well as range has been lost recently. In contrast, southern Weka appear to have experienced recent population expansion (Figure 3).

Corresponding north and south lineages were evident in the mtDNA variation of two independent Weka ectoparasites. Although feather lice are not attached permanently to their hosts or carried within their cells, the close association means that lice share many evolutionary features with host mitochondria. Multiple lice individuals live on each host and are transmitted primarily from parents to offspring (vertically). Rarer opportunity and priority effects limit horizontal transfer although this also requires close physical proximity and would therefore also retain a signal of host spatial distribution (Clayton et al., 2016). Feather louse lineages therefore represent

another is absent. The Weka species (= ▪ ▪ ▪) was first described by Sparrman (1786) as inhabiting southern New Zealand. As such the name



provided support in the laboratory. Images for Figure 7 are used under the Creative Commons licence: Kārearea - Robin Ducker; Kaka