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There are eight distinct chromosomal races of the New Zealand weta Hemideina thoracica. We used mtDNA sequence data to test the hypothesis that these races originated on islands during the early Pliocene (7–4 million years ago). Nine major mitochondrial lineages were identified from 65 cytochrome oxidase I sequences. Phylogenetic analysis of these lineages suggests that they arose at approximately the same time. The geographical distribution of some lineages coincides with areas that were islands during the Pliocene. Overall, hierarchical AMOVA analysis shows that chromosomal races

haploid maternally inherited markers with a smaller effective population size, giving the ability to detect recent barriers to gene flow where nuclear markers fail (Avise, 1992). Thus a survey of mitochondrial markers has the potential to reveal genetic differentiation and provide an historical biogeographic framework to the analysis of gene flow through contact zones.

Greater diversity of both allozyme and chromosome markers was found in the northern part of the range of H. thoracica and led to the suggestion that a chain of early Pliocene (7–4 million years (Ma) ago) islands in the north of New Zealand may have facilitated the fixation of chromosome rearrangements (Fleming, 1979; Morgan-Richards, 1997). The Pliocene archipelago has

across Pliocene Islands based on geological evidence (Fig. 1; Fleming, 1979; Stevens, 1981; Ballance & Williams, 1992).

Isolation by distance was tested using geographical distances between locations and pairwise K2P genetic distances. One representative of each haplotype from each location was used. Sample sizes range from 1 to 14 weta per location while numbers of haplotypes per location range 4

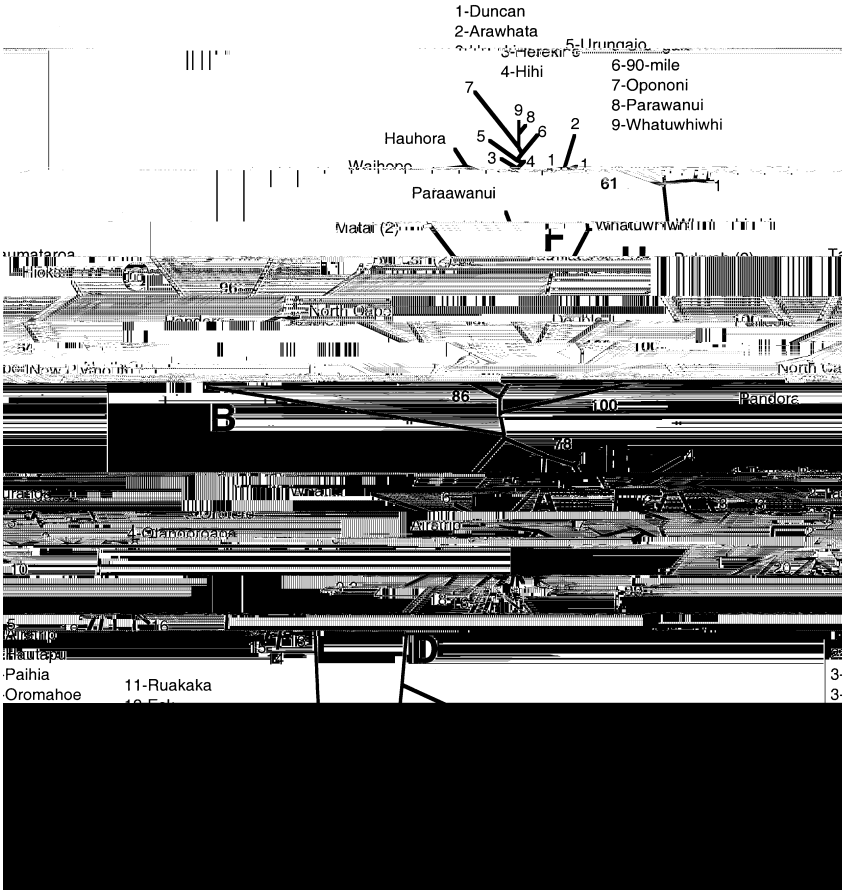

Fig. 3 Neighbour-Joining tree of HKY + I + Γ distances of COI from 65 Hemideina thoracica. Principal lineages are coded with a letter (A–I). Numbers on branches show percentage support from 2000 bootstrap replicates using MP and 4:1 tv:ts weighting.

Table 2 Average pairwise genetic distances (HKY + I + Γ) within and among the nine major mtDNA lineages in Hemideina thoracica

	A	B	C	D	E	F	G	H	I
A	0.030								
B	0.096								
C	0.082	0.090	0.030						
D	0.106	0.112	0.110	0.022					
E	0.066	0.096	0.057	0.072	0.013				
F	0.105	0.085	0.088	0.101	0.089	0.017			
G	0.086	0.975	0.081	0.104	0.075	0.069	0.001		
H	0.084	0.976	0.062	0.098	0.061	0.073	0.062	0.000	
I	0.106	0.134	0.095	0.139	0.099	0.125	0.119	0.102	0.022

major lineage observed. Average genetic distances (HKY + I + Γ) among the nine major lineages were all above 5% (Table 2).

Due to the computational time required for a data set of this size, a subset of sequences was chosen for further analysis. One member of each major mtDNA lineage (A–I) was randomly selected, plus an additional sequence for lineage A, C, D, F and I. For these 14 weta the 12S fragment previously used for SSCP was sequenced. A partition homogeneity test ($P = 0.140$) was performed before combining COI and 12S data. One hundred and five nucleotide sites were variable over these 840 bp. MP (weighting: tv:ts 4:1) gave a single tree with each major lineage well supported (>80% bootstrap support), but the highest inter-lineage bootstrap value was only 56% for A + B.

To test whether the sequences had evolved in a clock-like fashion we used the subset of 14 taxa. We

constrained the most likely tree found under ML to conform to a molecular clock and found using a χ^2 test that this did not differ significantly in likelihood scores. Neither the combined data set (COI and 12S) nor COI analysed separately differed significantly from a clock-like model.

P *al* *I*

genetic variation that was described by both the chromosomal races and the Pliocene island partitioning of the data. The distribution of lineages A, C and D also implies dispersal over longer distances from Pliocene refugia. The occurrence of lineage B on the

in contrast to many studies that have found evidence of extremely recent and rapid karyotype evolution. For example, in the shrew Sorex araneus mtDNA diversity suggests that chromosomal rearrangements have arisen within the last 1 Ma (Taberlet et al., 1994). In the house mouse (Mus domesticus) five chromosome races may have arisen on Madeira in 500 years (Britton-Davidian et al., 2000), and in an aphid (Sitobion) the rate of chromosome evolution exceeds the rate of microsatellite evolution (Sunnucks et al., 1996). The antiquity of the chromosome races of H. thoracica is more remarkable given that these populations have apparently survived as distinct units and yet remained as part of a single species for millions of years, especially when one considers the climate changes during the Pleistocene, and the continuity of land during glacial maxima.

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