Table 1 Sample locations of the [illegible] used in this study and the sample sizes

Population	Species	Locality	Region[1]	Longitude & Latitude	Sample size
1	*H. crassidens*	Harihari	WD	170°27′ 43°03′	3
2	*H. crassidens*	Hokitika	WD	171°00′ 42°46′	1
3	*H. crassidens*[2]	Mt Arthur	NN	172°46′ 41°12′	4
4	*H. crassidens*	Picton	SD	174°01′ 41°18′	2
5	*H. crassidens*	Maud Island	SD	173°54′ 41°02	4
6	*H. crassidens*	Wellington	WN	174°48′ 41°15′	25
7	*H. crassidens*	Paremata	WN	174°53′ 41°06′	4
8	*H. crassidens*	Kapiti Island	WN	174°56′ 40°51′	5
9	*H. crassidens*	Lake Pounui	WA	175°07′ 41°21′	3
10	*H. crassidens*[2]	Mt Holdsworth	WA	175°29′ 40°54′	4
11	*H. crassidens*	Mangaweka	RI	175°48′ 39°49′	1
12	*H. crassidens*	Mt Taranaki	TK	174°06′ 39°16′	8

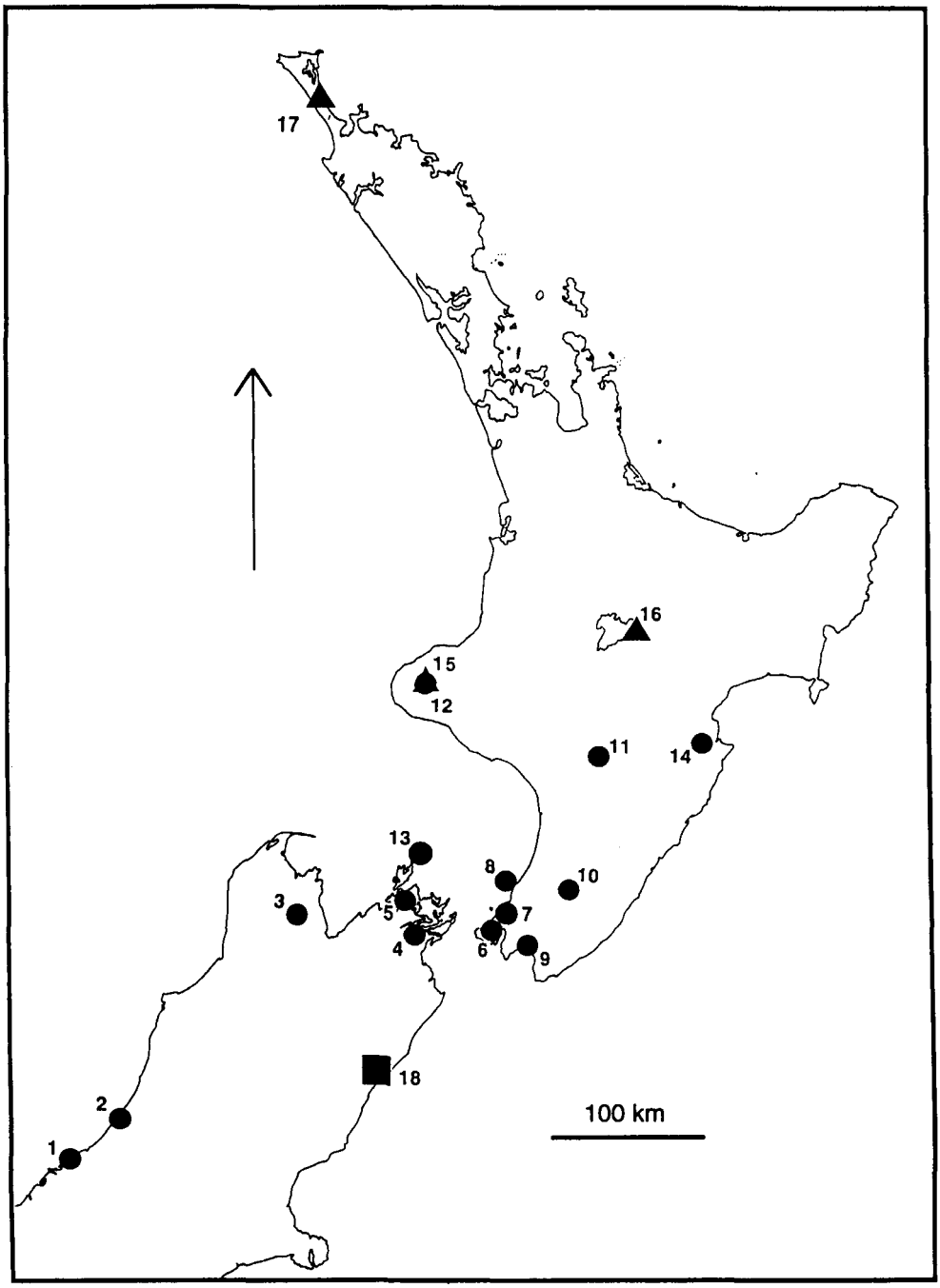

Fig. 1 – New Zealand localities where tree weta were collected for this study. Two species were

Weta were killed using ether and immediately dissected. Tissue from the malpighian tubules and femur muscles was removed, blended with an equal quantity of distilled water, and stored at –80°C until required for electrophoresis. All specimens were stored in ethanol

Starch gel electrophoresis techniques followed those of Allendorf et al. (1977). Tissue was transferred by a filter paper wick to a 12.5% horizontal starch gel. Direct current was applied

Table 3 – Allele frequencies and unbiased estimates of average heterozygosity, H (Nei, 1978), for 18 populations of tree weta, (populations as in table 1)

Ak																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	–
(b)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00
Gpi																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	–	1.00	1.00	1.00	1.00
(b)	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00	–	–	–	–
Hk–1																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	–
(b)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00
Hk–2																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	–
(b)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00
Idh–2																		
(a)	1.00	1.00	1.00	1.00	1.00	0.98	0.75	1.00	0.67	1.00	1.00	1.00	1.00	1.00	–	–	–	1.00
(b)	–	–	–	–	–	0.02	0.25	–	0.33	–	–	–	–	–	–	–	–	–
(c)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00	0.25	1.00	–
(d)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.75	–	–
Ldh–1																		
(a)	–	–	–	–	–	0.18	–	0.70	0.25	0.33	–	0.80	–	–	–	–	–	–
(b)	0.25	–	–	–	–	0.74	0.13	0.20	–	0.67	–	0.10	–	1.00	1.00	1.00	1.00	–
(c)	0.75	1.00	1.00	1.00	0.75	0.06	0.87	0.10	0.25	–	–	–	0.98	–	–	–	–	1.00
(d)	–	–	–	–	0.25	–	–	–	–	–	1.00	–	0.02	–	–	–	–	–
(e)	–	–	–	–	–	0.02	–	–	0.50	–	–	0.10	–	–	–	–	–	–
Ldh–2																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	–	–	–	–	1.00

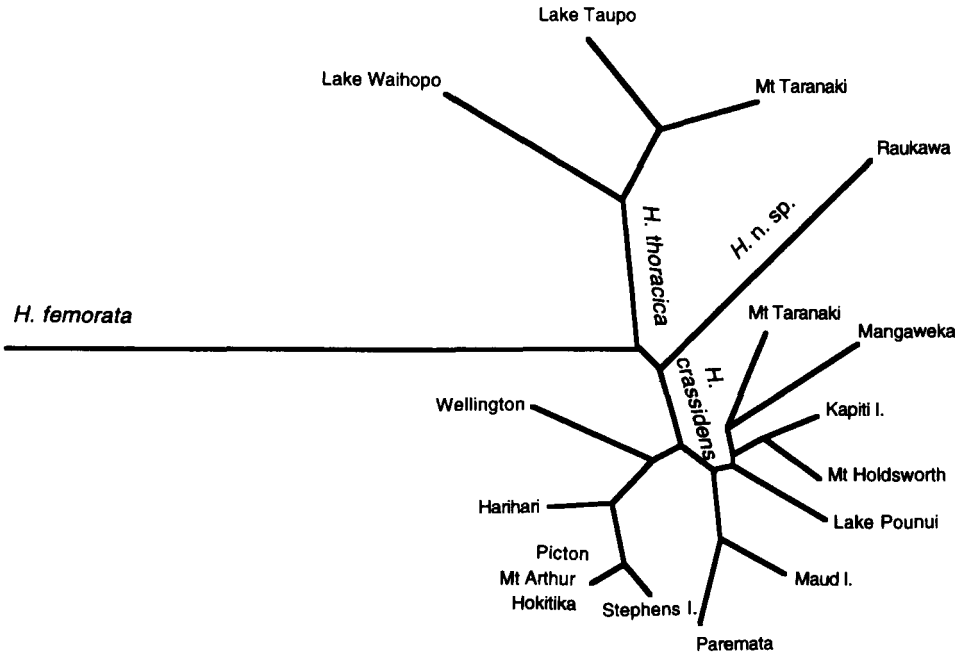

Fig. 2 – Neighbor-joining tree (Saitou and Nei 1987) using Cavalli-Sforza and Edwards (1967) arc distance from 26 loci for 18 populations of *Hemideina*. Branch lengths are proportional to genetic distances.

Table 3 (contd)

	H. crassidens													*H. c.c.* n. sp		*H. thoracica*		*H. femorata*
locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Pep–3																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	–
(b)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00
Pgd–1																		
(a)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.87	1.00	1.00	1.00	0.25	1.00	0.50	1.00	–
(b)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.50	–	–
(c)	–	–	–	–	–	–	–	–	–	0.13	–	–	–	0.75	–	–	–	–
(d)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00
Pgm-1																		
(a)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00	1.00	0.75	0.25
(b)	1.00	1.00	1.00	1.00	–	1.00	–	–	–	–	–	–	1.00	–	–	–	0.25	0.75
(c)	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00	–	–	–	–
(d)	–	–	–	–	1.00	–	1.00	1.00	1.00	1.00	1.00	1.00	–	–	–	–	–	–
Pgm-2																		
(a)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00	1.00	–	1.00
(b)	0.50	–	–	–	–	1.00	–	0.17	0.50	0.50	1.00	1.00	–	–	–	–	–	–
(c)	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1.00	–
(d)	0.50	1.00	1.00	1.00	1.00	–	1.00	0.83	0.50	0.50	–	–	1.00	1.00	–	–	–	–
H																		
	0.058		0.00		0.033		0.029		0.078		0.00		0.013		0.00		0.016	
		0.00		0.00		0.023		0.032		0.052		0.015		0.019		0.045		0.018

Table 4 Pairwise genetic distances between 18 populations of two species of Cercopithecini (Sforza and Edwards's (1967) coordinates and chord distance based

Table 5 – Comparison of tree weta from Stephens Island with those from Wellington using three morphological characters using Student t-tests for separate populations (separate variances), P = probability that the mean of the two population samples do not differ significantly, $P > 0.05$ = not significant (n.s.).

Character	Comparison	(n)	Mean	Significance (P)
Number of stridulatory ridges	All adults	(41)	13.610	n.s.
	All juveniles	(14)	13.786	
	All females	(27)	13.296	n.s.
	All males	(28)	14.000	
	Wellington	(13)	12.769	0.038
	Stephens I.	(31)	14.548	
Hind-tibia	All adults	(40)	21.333	0.000
	Adult females	(18)	22.569	0.000
	Adult males	(18)	20.247	
	Wellington females	(9)	21.878	n.s.
	Stephens I. females	(9)	23.261	
	Wellington males	(4)	21.428	
	Stephens I. males	(14)	19.907	
Hind-tibia	All adults	(40)	2.103	n.s.

Allozyme variation is conservative, reflecting at most 30% of the underlying DNA variation (Lewontin 1974). Thus the data obtained in this study are conservative and almost certainly underestimate the level of divergence among study populations. We make our assessments below by analysing the level and pattern of divergence in allozyme variation, realising that no single species definition is sufficient to deal with every population.

Hemideina crassidens

Levels of population divergence among all populations now assigned to *H. crassidens* are

majority of samples are small, more than half of the clusters in the neighbor-joining tree (Fig. 2) group samples from geographically proximate locations together, a result which gives us confidence in this analysis. The Stephens Island population and those from Mt Holdsworth and Mt Arthur fit into the geographical structure of *H. crassidens.* All genetic variation in these populations is in the form of allele frequency differences. The parapatric populations of *H. crassidens* show in many cases less divergence from the Stephens Island tree weta than

that had genetic characters significantly different from those of all the other populations of *H.*

crassidens studied. It came from the most eastern collection site, and from initial searches it now appears to be isolated from other *H. crassidens* populations. The extent of the genetic differentiation of this weta from *H. crassidens* is equivalent to the differentiation separating *H. thoracica* and *H. crassidens*. The differentiation includes three fixed differences and unique alleles, which we believe warrant its recognition as a separate species under both the Evolutionary and Phylogenetic Species Concept. Despite apparent opportunity in the recent past for interbreeding with *H. crassidens*, this species has maintained a high level of genetic differentiation and therefore may also be a separate species under the Biological Species Concept. It is formally described by Morgan-Richards (in press).

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