

# Invertebrate Taxonomy



*Invertebrate Taxonomy*  
CSIRO Publishing  
PO Box 1139 (150 Oxford St)  
Collingwood, Vic. 3066, Australia

Telephone: +61 3 9662 7629  
Fax: +61 3 9662 7611  
Email: [it@publish.csiro.au](mailto:it@publish.csiro.au)

Published by CSIRO Publishing  
for CSIRO and the Australian Academy of Science

. b i h . c i o . a / o a / i

**A phylogenetic analysis of New Zealand giant and tree weta  
(Orthoptera : Anostomatidae : *Deinacrida*)**

*Abstract.* A phylogenetic analysis of New Zealand weta from the species were studied using 27 genetic characters (allozyme and cy combined data set produced a phylogenetic hypothesis with twelve of habitats and life styles exhibited by the eleven *Deinacrida* Wh them from the seven *Hemideina* Walker species. Six of the *Hemid respect to *H. broughi**



**Table 2. Collection details for the 17 species of New Zealand Anostomatidae (*Deinacrida* and *Hemideina*) used in the genetic analysis**

Species	Abbreviation	Location		Region	Latitude	Longitude	<i>n</i>
<i>D. heteracantha</i>	<i>D. het</i>	Little Barrier Island	Hauraki Gulf	Auckland	36° 13′	175° 05′	3
<i>D. fallai</i>	<i>D. fal</i>	Tawhiti Rahi Island	Poor Knight Islands	Northland	35° 27′	174° 44′	3
<i>D. mahoenui</i>	<i>D. mah</i>	Mahoenui	Te Kuiti	Waikato	38° 35′	174° 50′	3
<i>D. elegans</i>	<i>D. ele</i>	Hapuku River	Seaward Kaikoura Range	Kaikoura	42° 22′	173° 26′	2
<i>D. elegans</i>	<i>D. ele</i>	Woolshed Creek	Mt Somers	Mid Canterbury	43° 37′	171° 19′	3
<i>D. rugosa</i>	<i>D. rug</i>	Stephens Island		Cook Strait	40° 40′	174° 00′	3
<i>D. rugosa</i>	<i>D. rug</i>	Mana Island		Cook Strait	41° 05′	174° 00′	1
<i>D. parva</i>	<i>D. par</i>	Long Creek	Hapuku River	Kaikoura	42° 19′	173° 41′	2
<i>D. pluvialis</i>	<i>D. plu</i>	Prices Basin	Whitcome catchment	Westland	43° 08′	170° 57′	4
<i>D. pluvialis</i>	<i>D. plu</i>	Head Basin	West Matukituki River	West Otago	44° 25′	168° 42′	7
<i>D. talpa</i>	<i>D. tal</i>	Mt Faraday	Paparoa Range	Westland	42° 02′	171° 34′	3
<i>D. connectens</i>	<i>D. con</i>	see Morgan-Richards & Gibbs 1996					60
<i>D. tibiospina</i>	<i>D. tib</i>	Flora hut	Mt Arthur	North west Nelson	41° 12′	172° 44′	1
<i>H. broughi</i>	<i>H. bro</i>	Flora Saddle	Mt Arthur	North-west Nelson	41° 12′	172° 44′	2
<i>H. femorata</i>	<i>H. fem</i>	Flag Peak	Banks Peninsula	Canterbury	43° 51′	172° 59′	4
<i>H. femorata</i>	<i>H. fem</i>	Kowhai Bush	Kaikoura	Kaikoura	42° 23′	173° 36′	5
<i>H. maori</i>	<i>H. mao</i>	Mt Percival	Hanmer Range	North Canterbury	42° 29′	172° 56′	1
<i>H. maori</i>	<i>H. mao</i>	Maukuratawhai	Clarence Valley	Canterbury	42° 26′	172° 51′	1
<i>H. maori</i>	<i>H. mao</i>	Foggy Peak	Torlesse Range	Canterbury	43° 17′	171° 45′	3
<i>H. maori</i>	<i>H. mao</i>	Woolshed/Morgan Streams	Mt Somers	Mid Canterbury	43° 35′	171° 19′	8
<i>H. maori</i>	<i>H. mao</i>	Hooker River	Hermitage	Mount Cook	43° 44′	170° 07′	2
<i>H. maori</i>	<i>H. mao</i>	Harwick Island	Lake Wanaka	Otago Lakes	44° 33′	169° 05′	2
<i>H. maori</i>	<i>H. mao</i>	Crescent Island	Lake Wanaka	Otago Lakes	44° 37′	169° 04′	1
<i>H. maori</i>	<i>H. mao</i>	Rock & Pillar	Rock and Pillar Range	Otago	45° 28′	170° 00′	4

**Table 3. Character matrix for 21 species of weta, 25 morphological characters and 27 genetic characters**

	<i>D. het</i>	<i>D. fal</i>	<i>D. mah</i>	<i>D. ele</i>	<i>D. rug</i>	<i>D. par</i>	<i>D. plu</i>	<i>D. tal</i>	<i>D. con</i>	<i>D. tib</i>	<i>D. car</i>	<i>H. bro</i>	<i>H. fem</i>	<i>H. mar</i>	<i>H. ric</i>	<i>H. tho</i>	<i>H. tre</i>	<i>H. cra</i>	<i>Motu</i>	<i>andrus 1</i>	<i>andrus 2</i>
<b>Genetic characters</b>																					
<i>Ak</i>	1	1	1	0	1		1	1	1	1		0	1	0	0	0	0	0			
<i>Got-1</i>	2	2	2	2	2		0	0	0	0&1		0	0	0	0	0	0	0			
<i>Got-2</i>	1&2	2	2	2	2		3	0	0	?		0	1	1&2	1	0	0	0			
<i>Gp</i>	2	2	2	0	0		0	0	0	0		0	0	0	0	0&1	0	0			
<i>Gpi</i>	3	3	3	3	3		3&4	3	3	3		2	0	0	0	0	0	1			
<i>Hk-1</i>	4	6	6	6	2		6	6	4	?		3	1	2	2	0	0	0			
<i>Hk-2</i>	1	1	1	1	2		5	5	4	?		1	1	1&2&3	2&3	0	0	0			
<i>Icd-1</i>	6	6	6	6	3		0	5	0	4		0	1	3	2	0	0	0			
<i>Icd-2</i>	7	7	2	7	0		5	6	0	0		3	0	0&3&4	0	2	0	0		0&1	
<i>Ldh-1</i>	3	3&6	3	6	0&3		2	2	2	2		5	1	1	0&1	0	0	0		0&1&2&3&4	
<i>Ldh-2</i>	?	?	?	2	3		2	2	2	2		1	1	1	1	0	0	0		1	
<i>Mdh-1</i>	0	0	3	0	0		0	0	0&4	0&3		1	0	2&3	2	0	0	0		0&1	
<i>Mdh-2</i>	1	1	1	4&7	2		5&6&7&8	2	4&5&6&7	5		6	2&4	4&5	5	3	1	0		0&1&2	
<i>Mdh-3</i>	2	2	2	1	1		1	1	1	1		1	0	0	0	0	0	0		0	
<i>Me-1</i>	0	0	0	1	0		1	1	1&2	?		0	0	0	0	0	0	0		0	
<i>Me-2</i>	0	0	0	4	1		1&4	5	1&4	?		4	1&2&3	1	1	0	0	0		0	
<i>Me-3</i>	?	0	?	?	0		0	0	?	?		?	0	1	1	0	0	0		0	
<i>Mnr</i>	0	0	0	0	0		0	0	2	?		0	0	0	0	0&1	0	0		0	
<i>Pep-1</i>	0	0	0	0	0		0	0	2	0		0	1	1	1	1	1	1		1	
<i>Pep-2</i>	0	0	0	1	1		3	3	0	1		2	0	1	1	1	1	1		1	
<i>Pep-3</i>	1	0&1	1	1	0		1	1	1	1		1	0	0	0	1	1	1		1	
<i>Pep-4</i>	0	0	0	0	0		1	1	0	0		0	0	0	0	0	0	0		0	
<i>Pgd-1</i>	0	0	0	0&3	0		2	2	1&2&3&5	?		4	2	0&3	0&3	0	0&1	0		0	
<i>Pgm-1</i>	4	4	4	4	4		4	4	3&4	4		4	1&4	3	3	1&3&4	2	0		0&1	
<i>Pgm-2</i>	4	4	4	5	4		0	0	1	?		3	0	0	0	1&2&3	0	0		0&1	
<i>2n*</i>																					

Character codes are given in the text. Stridulatory characters (1–14) are weighted so that in total they equal a single character. All characters are unordered except those marked \*. 2n = diploid number, NF = number of major chromosome arms.

3. *Male megacephaly*: (0) absent; (1) present
4. *Head vertex texture*: (0) smooth; (1) sculptured/punctures
5. *Mandibular 'crest'*: (0) absent; (1) present
6. *Pronotum texture*: (0) smooth/shiny; (1) rugose

loci. Support for the bipartitions within the tree were explored with the use of bootstrapping and Bremer indices (Bremer 1988, 1994). Bremer indices were calculated using inverse-constraints in separate heuristic searches and bootstrapping was performed with 1000 replicates.

Outgroup analysis was not possible with the allozyme data set due to the degree of divergence of the taxa available as outgroups. An undescribed *Hemiandrus* species from Poor Knights Islands, and two New Zealand tusked weta (*Motuweta isolata* Johns, *Anisoura nicobarica*



*D. pluvialis* Gibbs, *D. connectens*

*Combined*

The combined data set, with 50 parsimonously informative characters, resulted in a single shortest tree of 255 steps ( $CI = 0.738$ ,  $RI = 0.739$ ). Although only five nodes had good support in either the morphological or genetic trees, twelve nodes with bootstrap values above 70 were recovered from





