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of pairwise differences, might be mistaken for are four distinct process mtDNA sequence differen we examine one case in among competing hypot w (*Hemideina c*

1. Introduction

S E A (. 32 000 28 000 ; 38 41). D , , 23 . B , , , 42 44 .

Hemideina crassidens (; E ; A),

2.2. Morphological variation

52 53 H. crassidens Hemideina thoracica ( ) ( ) (0.5)

2.3. mtDNA analysis

D A 800. D A 44 . D A b (cytb), A AD 1 (ND1) , E E S . 8.1.4 (:// , 54). (π) 55 , D A E E S . $N = \pi/4u$ 13 . : Drosophila 6.2×10^{-8} 56 ; Daphnia 1.5×10^{-7} 57 Nematode 7.6×10^{-8} 58

2.5. Whole mtDNA selection

, 2 2 2DA (2 3), 2 2 2 K_A/K_S 2 2 2 2DA . 2 - 2 2 2 , , C 2 67 . 2 - 222 (K_A) 2 222 (K_S) 2 2 2 2 - ; 2 1 2 2 , 2 2 1 2 2 2 1 2 ( ) 2 . C 2 2 2 DA 2 . 2 DA 2 (*H. crassidens* 2 (2) *H. crassidens* 3 (2)) 2 2 , - 2 2 (S 2000) 2 . 2 2 2 2 2 68 . DA

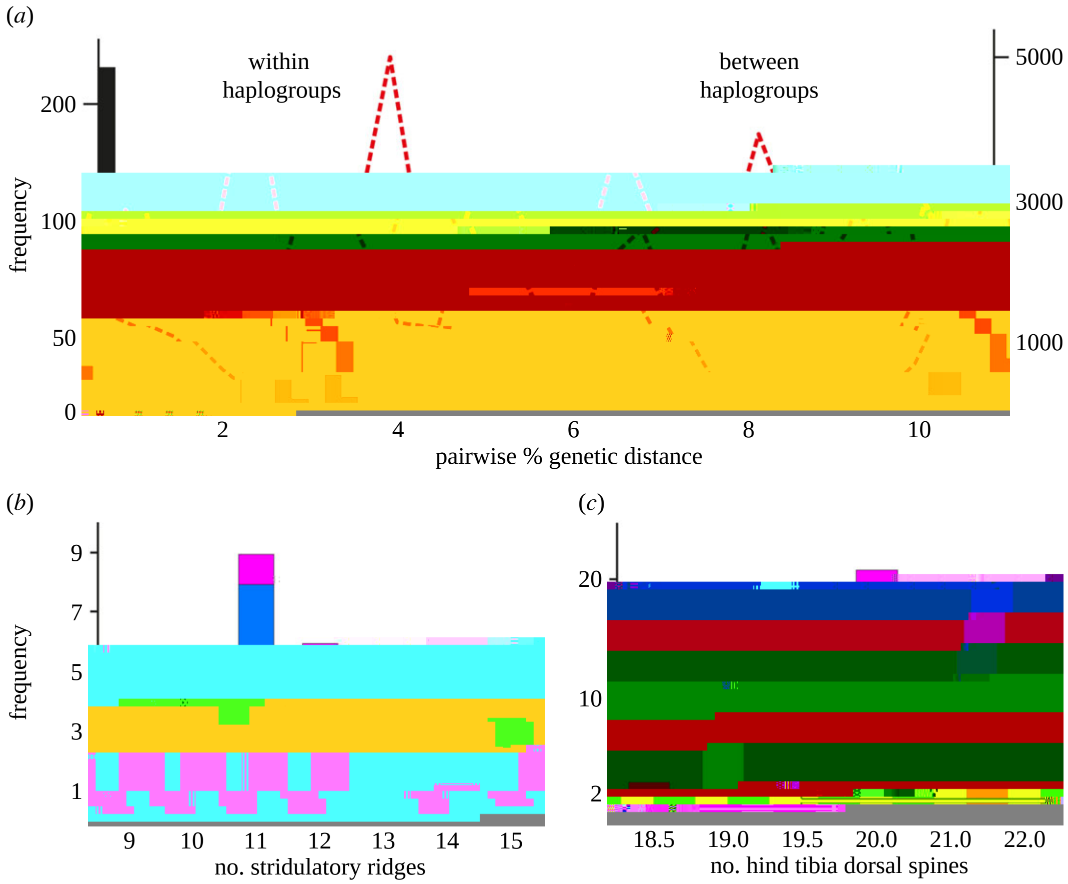

Figure 3. The non-recombining mtDNA has a bimodal frequency distribution of pairwise differences generated by the coalescent process in a large population, for whole *H. crassidens* species dataset (dotted red line), and Rangiwahia population sample (black fill) (*a*).

Table 1. Genetic diversity within a single population sample of the tree wētā *H. crassidens* for five nuclear markers. (Sample is divided using the two distinct mtDNA haplogroups observed. The number of alleles per locus is indicated along with (number) of alleles restricted to each mtDNA haplogroup. *n* = sample size.)

	nuclear loci					
MtDNA	*n*	*Sflag*	*HR12*	*HR35*	*HR43*	*HM04*
haplogroup 2	23	2	2	12 (6)	3 (1)	3 (1)
haplogroup 3	6	2	2	6	2	3 (1)

Table 2. Assignment of wētā individuals to clusters based on mtDNA haplogroup is not concordant with cluster assignment based on Bayesian modelling using principal components of phenotypic and genotypic variation. (Alternative assignments indicated by italics.)

			mtDNA	assigned cluster	
wētā ID	sex	age	haplogroup	PC 1 and 2	PC 1–5
Hc-Ran-618	female	juvenile	*2*	*2*	1
Hc-Ran-624	female	adult	*2*	*2*	1
Hc-Ran-619	male	adult	*2*	1	1
Hc-Ran-620	female	adult	*2*	*2*	1
Hc-Ran-1308	female	adult	*2*	1	*2*
Hc-Ran-1310	male	juvenile	*2*	1	1
Hc-Ran-1311	female	juvenile	*2*	1	1
Hc-Ran-1312	female	juvenile	*2*	1	1
Hc-Ran-1328	female	adult	*2*	1	1
Hc-Ran-1315	female	adult	*2*	*2*	1
Hc-Ran-622	female	adult	*2*	*2*	1
Hc-Ran-1316	male	juvenile	*2*	3	*2*
Hc-Ran-1317	male	juvenile	*2*	1	1
Hc-Ran-1318	male	juvenile	*2*	1	1
Hc-Ran-1319	male	juvenile	*2*	1	1
Hc-Ran-1320	female	juvenile	*2*	1	1
Hc-Ran-1321	female	juvenile	*2*	1	1
Hc-Ran-1322	female	juvenile	*2*	1	*2*
Hc-Ran-1323	male	juvenile	*2*	1	*2*
Hc-Ran-1324	female	juvenile	*2*	1	1
Hc-Ran-1325	female	juvenile	*2*	1	*2*
Hc-Ran-1326	male	juvenile	*2*	1	1
Hc-Ran-1327	male	juvenile	*2*	1	1

barcode gaps, haplowebs and GMYC. *Syst. Biol.* **64**, 900–908. (doi:10.1093/sysbio/syu130)

19. Fujisawa T, Barraclough TG. 2013 Delimiting species using single-locus data and the generalized mixed yule coalescent approach: a revised method and evaluation on simulated data sets. *Syst. Biol.* **62**, 707–724. (doi:10.1093/sysbio/syt033)
20. Nekrutenko A, Makova KD, Li W. 2002 The KA/KS ratio test for assessing the protein-coding potential of genomic regions: an empirical and simulation study. *Genome Res.* **12**, 198–202. (doi:10.1101/gr.200901)
21. Bickford D, Lohman DJ, Sodhi NS, Ng PKL, Meier R, Winker K, Ingram KK, Das I. 2007 Cryptic species as a window on diversity and conservation. *Trends Ecol. Evol.* **22**, 148–155. (doi:10.1016/j.tree.2006.11.004)
22. Mallet J. 2008 Hybridization, ecological races and the nature of species: empirical evidence for the ease of speciation. *Phil. Trans. R. Soc. B* **363**, 2971–2986. (doi:10.1098/rstb.2008.0081)
23. Excoffier L, Foll M, Petit RJ. 2009 Genetic consequences of range expansions. *Annu. Rev. Ecol. Evol. Syst.* **40**, 481–501. (doi:10.1146/annurev.ecolsys.39.110707.173414)
24. Baird SJE. 2015 Exploring linkage disequilibrium. *Mol. Ecol. Resour.*