Trans-equatorial range of a land bird lineage (Aves: Rallidae) from tropical forests to subantarctic grasslands

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Despite the capacity for dispersal, range size varies considerably among birds species. Many species have restricted geographic spread, whilst others routinely travel long distances to reach preferred habitat. □ese alternatives are well

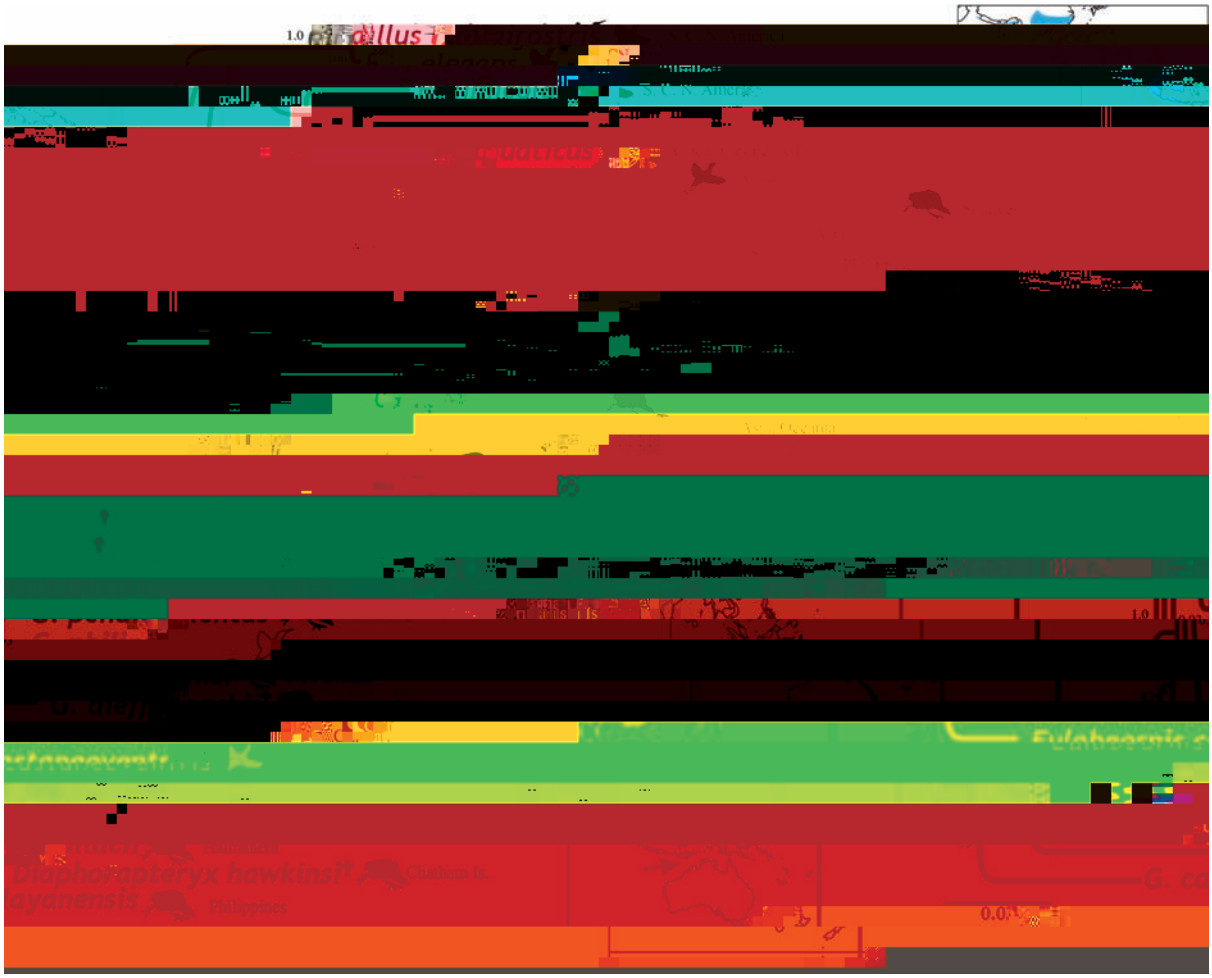

Figure 1. Bayesian phylogenetic inference of the 'Rallus' clade based on concatenated gene analysis. Posterior probabilities over 0.90 and

Garcia-R et al. 2014) for the 'Rallus' clade that includes Lewinia (Supplementary material Appendix 1, Table A3). Each of 30 ingroup species was represented by data from one individual with an outgroup comprising Rallina fasciata and Rallina tricolor. Bayesian and maximum likelihood hypotheses were inferred using MrBayes and RAxML, respectively. MrBayes was implemented in Geneious ver. 6.0.5 using a general time reversible model with gamma distribution (GTR + Γ), 10 million generations and 10% burn-in. A burn-in of 10% gave optimal results, and we obtained effective sample sizes (ESS) > 200 for 98% of the parameters. Convergence and diagnostics of the Markov process were visualized using Tracer ver. 1.6. (<http://tree.bio.ed.ac.uk/software/tracer/>). ML analysis used a GTR + Γ model implemented in RAxML via the Cipres portal (Miller et al. 2010). The model was estimated in ModelTest ver. 3.7 using the Akaike information criterion (Posada and Crandall 1998).

Lewinia sequences obtained for phylogeographic analysis were edited and aligned using the MAFFT aligner implemented in Geneious ver. 6.05 (Drummond et al. 2012) and checked by eye. Nucleotide and inferred amino acid sequences of cyt b were checked to verify the absence of indels and stop codons. Sequence ambiguities at heterozygous sites in βfib-7 were resolved using PHASE implemented in DnaSP ver. 5.0 (Librado and Rozas 2009). We calculated maximum pairwise divergence (p-distances) of concatenated mitochondrial loci (cyt b

Table 1. Mean ($\bar{x}$), standard deviation (SD) and coefficient of variation (CV) of linear measurements (mm) and weight (g) of *Lewinia mirifica*, *L. pectoralis* and *L. muelleri*. Mean, standard deviation and coefficient of variation in *L. pectoralis* were calculated using data available for all subspecies (Supplementary material Appendix 1, Table A4). p-values indicate support for difference between means of each taxon where ** = < 0.001; * = 0.01 < p < 0.05; ns = no significant.

	L. muelleri (A)				*L. pectoralis* (B)				*L. mirifica* (C)				A-B	A-C	B-C	
	n	$\bar{x}$	SD	CV	n	$\bar{x}$	SD	CV	n	$\bar{x}$	SD	CV	p	p	p	Overall CV
Bill	9	27.78	4.35	0.16	45	34.3	2.14	0.06	10	27.2	1.71	0.06	**	ns	**	0.09
Tail	8	34.35	4.94	0.14	41	39.24	3.1	0.08	9	44.6	2.13	0.05	**	**	**	0.09
Weight	9	80.8	14.91	0.18	2	68	14.14	0.21	9	62.9	6.18	0.10	ns	*	ns	0.17
Tarsus	11	28.69	1.3	0.05	55	30.8	1.87	0.06	17	29	0.76	0.03	**	ns	**	0.04
Toe	11	31.17	1.78	0.06	10	36.18	2.52	0.07	7	35.71	1.8	0.05	**	**	ns	0.06
Wing	8	80.12	3.76	0.05	82	100.11	4.21	0.04	16	108.9	4.03	0.04	**	**	**	0.04
Culmen	2	26.5	2.12	0.08	76	34.18	3.19	0.09	7	25.43	0.98	0.04	**	ns	**	0.07

the broad 'Rallus' clade. Closely related with this group are two flightless insular endemic species found in the western Pacific (Aramidopsis plateni) and Indian (Dryolimnas cuvieri) Oceans. Also, in this subclade is the widespread volant species Crex crex that occurs in Europe, Asia and Africa but is only a rare vagrant in Oceania and Australasia. Members of Gallirallus and other monotypic genera form the sister group (Fig. 1).

For phylogeographic analysis the complete alignment of three gene fragments contained 2089 bp, comprising 892 bp of cyt b, 596 bp of CR and 601 bp of βfib-7. No premature stop codons were detected in the protein-coding cyt b gene. The sampled Lewinia did not share mtDNA haplotypes between locations (Fig. 2B), except for the L. pectoralis sampled from Victoria and New South Wales on the Australian mainland. The network of βfib-7 sequences revealed a pattern of incomplete lineage sorting among the three taxa (Fig. 2B). Maximum uncorrected pairwise genetic distances among these species using concatenated mitochondrial genes was highest between L. mirifica and L. muelleri (0.01 ± 0.003), less between L. mirifica and L. pectoralis (0.008 ± 0.002), and smallest between L. pectoralis and L. muelleri (0.006 ± 0.002). Pairwise distance between populations of L. pectoralis in Victoria and NSW was 0.002 (± 0.001). Concatenated sequences therefore differed by less than 1% within Lewinia.

Morphology

Despite limitations of sample size, variation in data collection methods and detailed information about specimens (e.g. sex and maturity stage), the available L. muelleri sample comprised birds that had on average the shortest

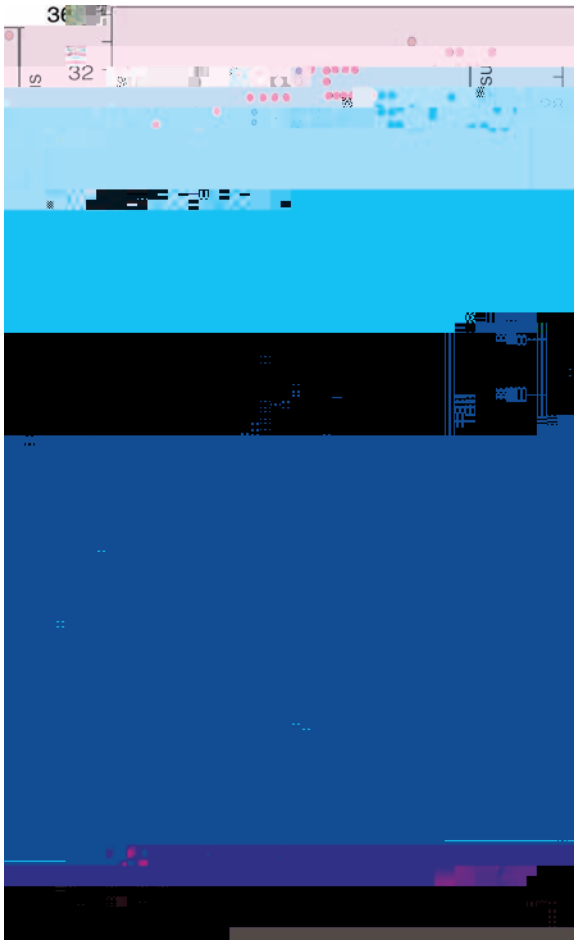

Figure 3. Shape differences of Lewinia species depicted by the interaction between wing and tarsus length, tail length and body weight. Yellow = L. muelleri, red = L. pectoralis and blue = L. mirifica.

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