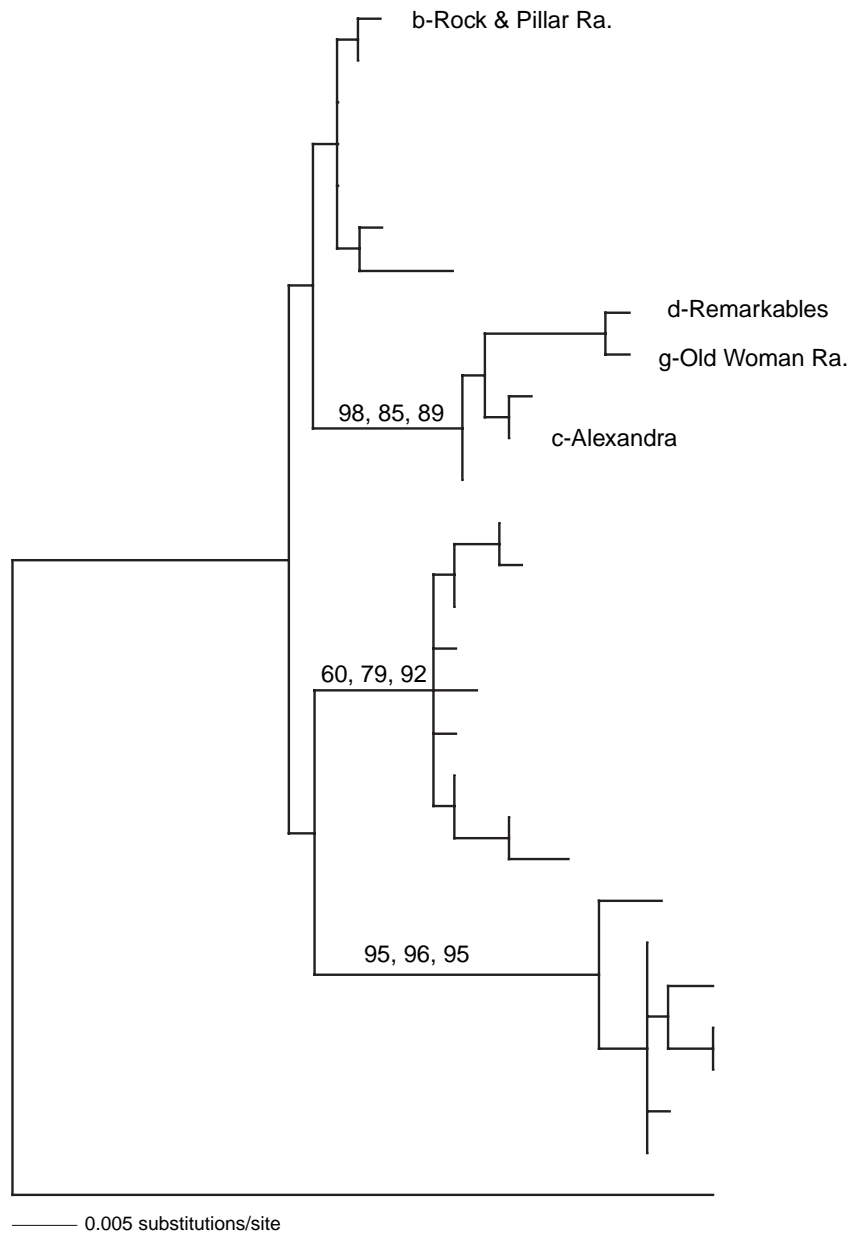2004; but see Funk and Omland, 2003). While there is often a good match between recognized (or recognizable) morphological/behavioral distinctions that form the basis of traditional

recorded locally below 1000 m where suitable native grassland habitat is present (Bigelow, 1967). Whether all or any individuals found at lower altitudes are resident or are seasonal altitude migrants is not known. A related species, S. campestris (Hutton) has a wide range in South Island. It is broadly sympatric with S. australis but these species exhibit some degree of altitudinal separation with S. campestris tending to lower altitudes. Morris (2002) distinguishes two species complexes within Sigaus; the S. campestris group that have a sinuous caudal margin on the pronotum (S. campestris, S. minutus, S. childi) and the S. australis group that have a smooth margin to the pronotum (S. australis, S. obelisci and several undescribed species). Sigaus obelisci is restricted to one mountain range (Old Man Ra.) in the southern part of the S. australis distribution. Two recently described species S. homorensis Morris and S. takahe Morris have narrow geographic ranges in the

and Morgan-

comprising S. villosus, S. campestris and S. minutus. Bootstrap resampling indicated strong support for a phylogenetic pattern that places S. childi within the S. australis complex rather than

b-Rock & Pillar Ra.

d-Remarkables

g-Old Woman Ra.

98, 85, 89

c-Alexandra

60, 79, 92

95, 96, 95

—— 0.005 substitutions/site

(three SSCP; two sequenced) from Mt Sutton failed to group with other sequences indicating the presence of additional significant diversity. All analyses are consistent in revealing the polyphyly of S. australis haplotypes with respect to those from S. obelisci, S. homorensis, Sigaus species A and S. childi (Fig. 3, 4).

The maximum COI distance between the ingroup and outgroup (S. villosus) sequences was 24% (ML—TrN + G). Genetic distances inferred from the 12S–16S data were, as expected, lower than those inferred from COI. For example, the ML distance using 12S

a maximum of 8.3% (P distance) or 15.9% (ML), with a mean of 7.4% (ML). Average genetics distances within haplogroups were (K2P/ML): haplogroup I 1.5%/1.7%, haplogroup II 1.6%/1.6%, haplogroup III 2.6%/3.4% and haplogroup IV 1.5%/1.6%. Most (92%) of pair-wise intraclade K2P genetic distances were smaller or equal to 3%, whereas most (98%) of interclade pair-wise distances were greater than 3% (Fig. 5). As indicated by phylogenetic analysis, genetic distances among pairs of

S. australis (typical morphotype) grasshoppers ranged across the spectrum with no evidence of a barcode ''gap'' necessary to distinguish between species (Hebert et al., 2004b) (Fig. 5).

Phylogeography versus taxonomy

Sigaus australis populations tend to have unique mtDNA haplotypes. The general pattern of low diversity

at sites inferred from SSCP haplotyping is confirmed by sequence data. Most locations had a single and usually unique haplotype, although three closely related haplotypes were evident in the Mt Dobson sample. In contrast, three haplotypes (n, o, j) at Mt St Bathans correspond to two haplogroups (II and IV), and five SSCP haplotypes (a, c, i, s, L) at Alexandra correspond to three haplogroups (II, III and IV) (Fig. 3).

Individuals that yielded haplogroup I DNA sequences came from the northern-most extent of the S. australis range in the central waist of South Island (Fig. 4). Central South Island is an area noted for low species endemicity associated with the New Zealand beech-gap (a region of distributional discontinuity for Nothofagus beech and many other taxa; Trewick and Wallis, 2001). Genetic distances (COI) between haplogroup I and other ingroup sequences were relatively high (mean ML 10.7%).

Each of the three southern haplogroups comprised sequences from individuals collected in geographically distinct (but parapatric) ranges that meet at Alexandra. Haplogroup III comprises putative haplotypes (in brackets) from S. australis (c, d, g) and S. obelisci (p) distributed from Alexandra westwards. Putative haplotype p was unique to, an

Spatial structure of Sigaus australis

   Molecular studies of alpine taxa often reveal a strong association between sequence similarity and spatial proximity. This reflects the isolation of habitats that are limited by altitude; sub⁄alpine taxa occupy geographically near-stationary habitats through time by tracking microclimate altitudinally as global climate changes. Such habitats are akin to oc/F1.01Tf(habita)TjETBT9.9

systematics (Rubino et al., 2006). Unfortunately, barcoding, which is a quasi-taxonomic enterprise, and molecular systematics, which looks at broader relationships, have been confused (e.g., DeSalle et al., 2005).

Neither DNA barcoding nor traditional taxonomy can satisfactorily describe the evolutionary history (and future) of the Sigaus grasshopper complex, but a combination of natural history and population genetics could. It is at this evolutionary coal face that taxonomy has always been most challenging. In most cases the problem is not merely one of the time needed to handle and process information (Hebert et al., 2003); underlying the

Hutton, F.W., 1897. The grasshoppers and locusts of New Zealand and the Kermadec Islands. Proc. N. Z. Inst. 30, 135–150.

Hutton, F.W., 1898. Notes on the New Zealand Acrididae. Proc. N. Z. Inst. 31, 44–50.

Jamieson, C.D., 1999a. A new species of Sigaus from Alexandra, New Zealand (Orthoptera: Acrididae). N. Z. J. Zool. 26, 43–48.

Juan, C., Oromi, P., Hewitt, G.M., 1995. Mitochondrial DNA phylogeny and sequential colonization of Canary Islands by darkling beetles of the genus Pimelia (Tenebrionidae). Proc. R. Soc. Lond., Ser. B. Biol. Sci. 162, 173–180.

Knowles, L.L., 2000. Tests of Pleistocene speciation in montane grasshoppers (genus Melanoplus) from the sky islands of western North America. Evolution 54, 1337–1348.

Lockhart, P.J., McLenachan, P.A.,

Trewick, S.A., Wallis, G.P., Morgan-Richards, M., 2000. Phylogeographic pattern correlates with Pliocene mountain building in the alpine scree weta (Orthoptera, Anostostomatidae). Mol. Ecol. 9, 657–666.

Trewick, S.A., Paterson, A.M., Campbell, H.J., 2007. Hello New Zealand. J. Biogeog. 34, 1–6.

Wagsta , S.J., Garnock-Jones, P.J., 1999. Whipcord Hebes — systematics, distribution, ecology and evolution. N. Z. J. Bot. 37, 17–39.

Wakeley, J., 2004. Coalescent Theory: an Introduction. Roberts & Company, Greenwood Village, CO, USA.

Wallis, G., 2001. Taxonomic Status of the Chafer Beetles Prodontria modesta and P. bicolorata. DOC Science Internal Series 10. Department of Conservation, Wellington, New Zealand.

Wallis, G.P., Trewick, S.A., 2001. Finding fault with vicariance: a critique of Heads (1998). Syst. Biol. 50, 602–609.

Wardle, P., 1963. Evolution and distribution of the New Zealand flora, as a ected by Quaternary climates. N. N.