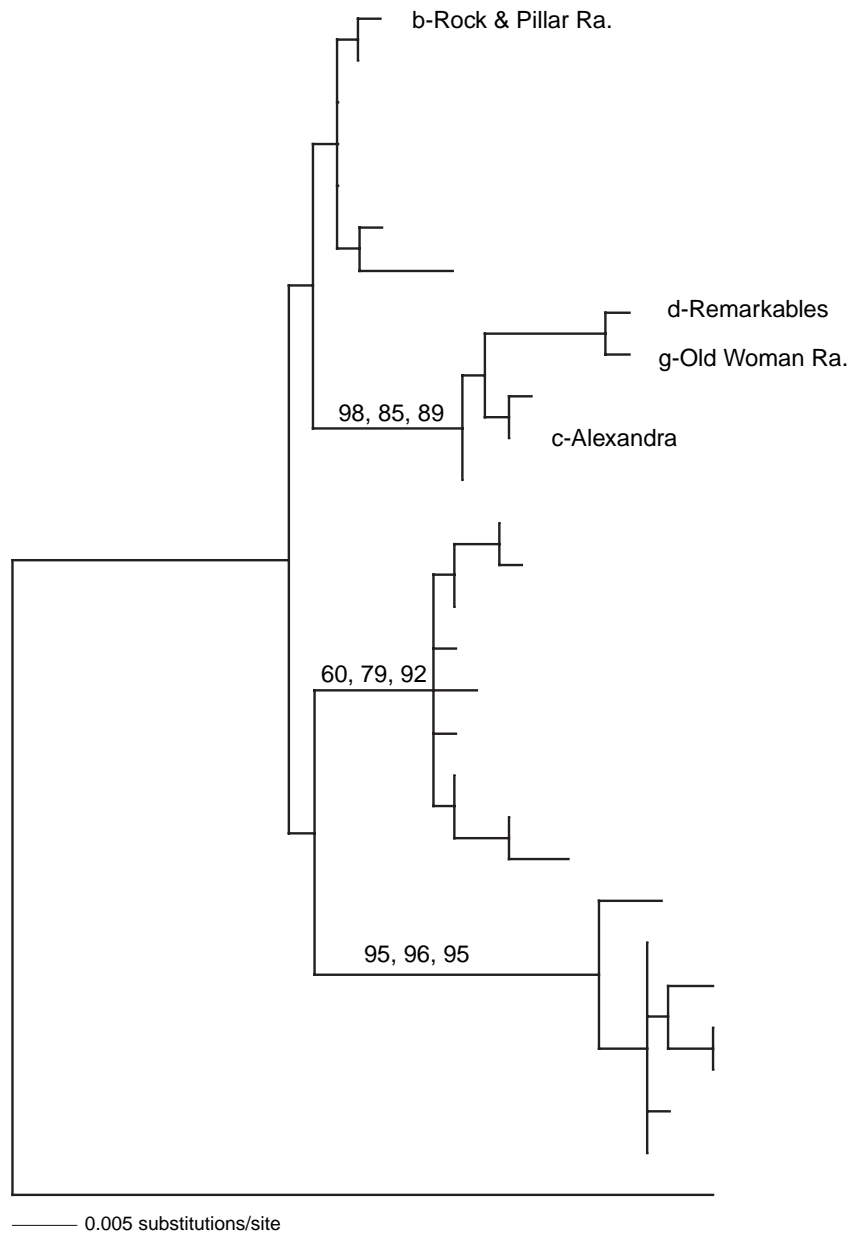


2004; but see Funk and Omland, 2003). While there is often a good match between recognized (or recognizable) morphological/behavioral distinctions that form the basis of traditional

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

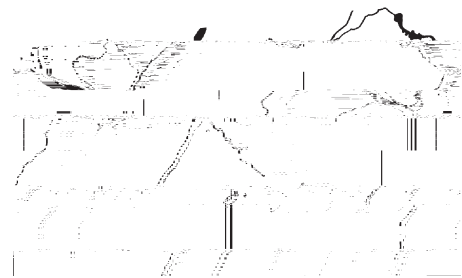
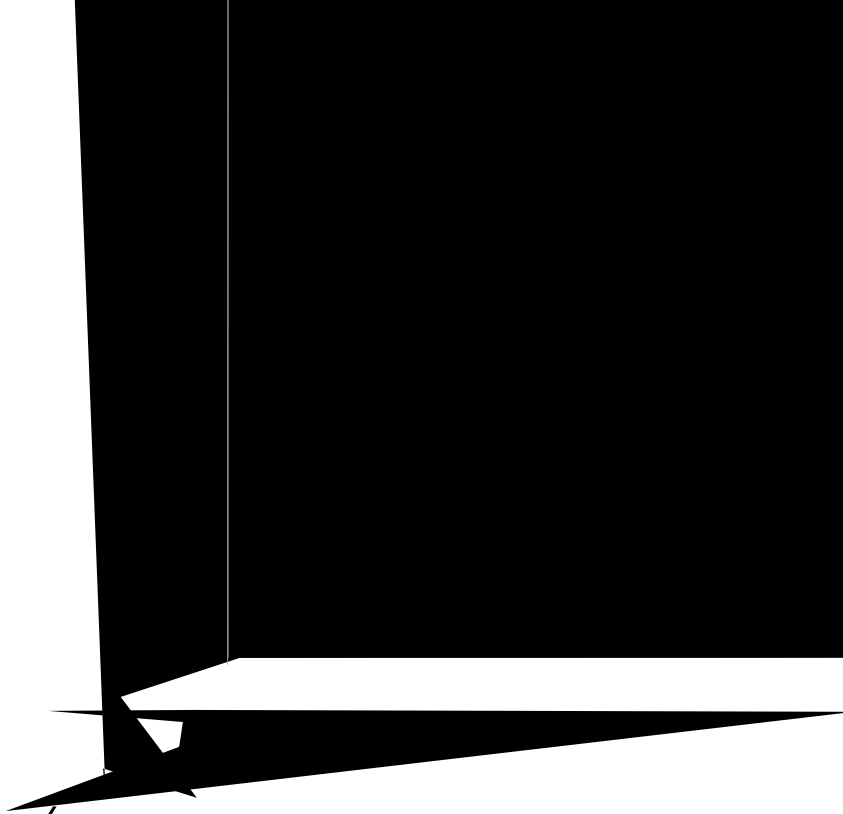


(three SSCP; two sequenced) from Mt Sutton failed to group with other sequences indicating the presence of additional significant diversity. All analyses are

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 genetic 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 endemism 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 *Siga* 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

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

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