A matter of time: Temporal variation in the introduction history and population genetic structuring of an invasive lizard

Hannah MOULE1, Kirilee CHAPLIN1,2, Rebecca D. BRAY1,5, Kimberly A. MILLER1, Michael B. THOMPSON3, David G. CHAPPLE1,2,*

1 School of Biological Sciences, Monash University, Clayton, Victoria 3800, Australia
2 Department of Sciences, Museum Victoria, Victoria 3001, Australia
3 School of Biological Sciences, University of Sydney, Sydney, NSW 2006, Australia
4 Allan Wilson Centre for Molecular Ecology and Evolution, School of Biological Sciences, Victoria University of Wellington, Wellington 6140, New Zealand

Abstract Invasive species are considered one of the greatest threats to native ecosystems, second only to habitat loss and fragmentation. Despite this, the temporal dynamics of invasions are poorly understood, with most studies focusing on a single time point, providing us with only a snapshot of the biology and genetics of the invader. We investigated the invasion of Lord Howe Island by the delicate skink Lampropholis delicata and assessed the introduction history and genetic structure of this species over a 5-year period. Using genetic data taken from 2007, and again in 2011/12, we examined changes in the population genetic structure (whether new haplotypes had been introduced to the island, and shifts in haplotype frequencies) of the species on the island between these two time points. No new haplotypes were introduced to the island between 2007 and 2011/12; however, significant shifts in haplotype frequencies across the island were detected. We conclude that the delicate skink is expanding its range into the southern regions of the island and that the haplotype frequencies on Lord Howe Island are still in a state of highly dynamic flux. Our study highlights the importance of considering invasions as dynamic and studying them in such a way that enable us to better manage their impacts [Current Zoology 61 (3): 456–464, 2015].

Keywords Biological invasion, Genetic admixture, Lampropholis delicata, Lord Howe Island, Population genetics, Unintentional introduction

Invasive species have the potential to have severe impacts on native biodiversity and are considered alongside climate change and habitat destruction and fragmentation as the leading threats to global biodiversity (Vitousek et al., 1997; Cooling et al., 2012; Bohm et al., 2013). Invasive species are those that have been introduced to non-native regions, established and then spread across the landscape (Blackburn et al., 2011; Chapple et al., 2012; Lockwood et al., 2013). During this process, invasive species may cost local economies upwards of US $125 billion per year and impose stresses on native ecosystems, severely impacting native biodiversity through competition for food and habitat and displacement of local species (Sakai et al., 2001; Pimentel et al., 2001, 2005; Allendorf and Lundquist, 2003). In this globalised world, with faster and more frequent methods of travel it has become increasingly easy for invasive species to spread from multiple regions of their source range to almost any other region throughout the world (Hulme, 2009; Chapple et al., 2013a). As a result of the myriad of transport methods available to these would be invaders, such as cargo holds on planes and ballast water in boats, for inadvertent introductions it is often difficult to establish the source population and transport pathway of a stowaway or newly established population when it is detected in a non-native region (Hulme, 2009; Lockwood et al., 2013). This uncertainty of the introduction history and pathway of invaders reduces our ability to understand how invasive species spread and ultimately hinders our capacity to control or mitigate their ecological or economic impacts (Handley et al., 2011).

Species invasions are inherently dynamic. For instance, most invaders go through a ‘lag’ phase following their initial colonisation of a new region where population size remains low, before a rapid increase in num-
bers (Mack et al., 2000; Lockwood et al., 2013). Conversely, there are numerous instances of well-established invaders experiencing sudden population crashes (reviewed in Simberloff and Gibbons, 2004). For example, the invasive Argentine ant *Linepithema humile* experienced a range-wide population crash in New Zealand, with the local extinction of ~40% of the established populations (Cooling et al., 2012). In addition, in prolific invaders, high propagule pressure may increase population size and, if the propagules are coming from multiple source locations, result in genetic admixture or intraspecific hybridisation that acts to supplement or enhance levels of genetic variation within invasive populations (Kolbe et al., 2004; Roman and Darling, 2007; Dlugosch and Parker, 2008; Simberloff, 2009; Rius and Darling, 2014). However, this acknowledged temporal component of biological invasions has been neglected in many studies that use molecular approaches to infer the introduction pathways and history of invaders. For instance, a brief review of the literature revealed only one of 59 studies that have used mtDNA markers to determine the source populations or introduction history of successful invaders have included a temporal component (Online Supplementary Materials Table S1).

Here we investigate whether there have been additional successful introductions, or shifts in the population genetic structuring, of the invasive delicate skink *Lampropholis delicata* on Lord Howe Island (LHI) over the past 5 years. The delicate skink is a small-sized lizard (maximum adult snout-vent length 55 mm; Wilson and Swan, 2013; Cogger, 2014) that is native to eastern mainland Australia. It is a prolific invader that is adept at reaching non-native regions via human-assisted dispersal (Chapple et al., 2011a, 2013a; Cromie and Chapple, 2012) and has successfully established and spread throughout the Hawaiian Islands, New Zealand and Lord Howe Island (Chapple et al., 2013b; Tingley et al., 2015). The delicate skink was first accidentally introduced to LHI in the 1980s in freight and cargo, but has since established and spread across the island (Lever, 2003; Hutchinson et al., 2005; Schulz, 2009; Chapple et al., 2013b, 2014). A previous molecular study, based on samples collected across the island in 2007, identified seven mtDNA haplotypes in the invasive delicate skink population on LHI, from four different native range source regions; i) Brisbane, Queensland (QLD), ii) North-eastern inland New South Wales (NSW), iii) Coffs Harbour/Yamba, NSW and iv) Sydney, NSW. Importantly, substantial fine scale genetic structure (two mitochondrial genes: ND2 & ND4) was evident across LHI, with up to 8.3% sequence divergence among mtDNA haplotypes and distinct differences in the distribution of particular haplotypes across the small island (approx 11 km long and 2 km wide; Chapple et al., 2013b) (Fig. 1, 2). Intraspecific hybridisation is occurring on LHI among the delicate skinks from each genetically divergent source region (as evidence from mtDNA sequence data and microsatellite markers), and the species has continued to spread into the mountainous southern regions of the island (Chaplin, 2013; Chapple et al., 2014; Fig. 1).

We use samples collected from across the entire island in 2011/2012 to examine whether there have been additional successful introductions from new native range source regions over the past five years. In addition, we assess whether the population genetic structuring of mtDNA haplotypes across the island has remained stable since 2007, and whether the recent southern spread of the delicate skink on LHI has been driven by new introductions, or the dispersal of existing, established populations.

## 1 Materials and Methods

### 1.1 Sample collection

*Lampropholis delicata* individuals were caught from across LHI between February 2011 and December 2012 as part of a broader study of the ecology of the lizards of LHI (our unpublished data). Tissue samples (tail tips) were taken from a total of 365 individuals (Table 1, Online Supplementary Materials Table S2) in order to assess whether the distribution and relative abundance of mitochondrial haplotypes across the island had changed since 2007 (Chapple et al., 2013a). This was...
done by re-sampling previous sites assessed in 2007, and including a new site at the southern end of LHI to increase the area of the island sampled.

We recognised three different regions of LHI (Northern, Central, Southern) based upon habitat, topography and the degree of human inhabitation (Fig. 2; Table 1). The Northern region is characterised by moderate hills (up to ~200 m asl) and predominately original vegetation, the Central region by low-lying flat areas and the Southern region by coastal vegetation and a recent increase in human habitation.

Fig. 2  Population genetic structure (ND2/ND4 mtDNA haplotypes) of the delicate skink on Lord Howe Island in A) 2007, and B) 2011–2012. The pie charts indicate the haplotype frequencies at each sampling location (N1–N3, C1–C3, S1–S4) and region of the island (Northern, Central, Southern). Sample sizes are provided in Table 1. The maximum sequence divergence among the haplotypes present at each location/region is indicated. OSB = Old Settlement Beach. The asterisk indicates that no samples were collected from the site at that time point.

Table 1  Locality, region of island, sample code and haplotype for the samples of Lampropholis delicata

| Region      | Site Number | Site Name                     | Number of Samples | Haplotypes | Number of Samples | Haplotypes |
|-------------|-------------|-------------------------------|-------------------|------------|-------------------|------------|
| Northern    | N1          | North Bay Area                | 10                | LHI2       | 27                | LHI2       |
|             | N2          | Max Nichols Track, Point Dawson | 10              | LHI2, LHI3 | 24                | LHI2, LHI3 |
|             | N3          | Old Settlement Beach Area     | 32                | LHI2, LHI3 | 2                 | LHI2       |
| Central     | C1          | LHI Settlement Area           | 45                | LHI1, LHI3, LHI4, LHI5, LHI7 | 47          | LHI1, LHI2, LHI3, LHI4, LHI5, LHI7 |
|             | C2          | Track to Transit Hill         | 8                 | LHI7       | –                 | –          |
|             | C3          | Windy Point                   | –                 | –          | 25                | LHI4, LHI5, LHI7 |
| Southern    | S1          | Recycling Centre/ Cobby’s Corner | 9               | LHI2, LHI4, LHI7 | 23          | LHI1, LHI2, LHI3, LHI4, LHI5 |
|             | S2          | Kings’/Salmon Beach           | 8                 | LHI2, LHI7 | 49                | LHI2, LHI4, LHI6, LHI7 |
|             | S3          | Smoking Tree Ridge Area       | 18                | LHI6, LHI7 | 20                | LHI6, LHI7 |
|             | S4          | Goathouse Cave                | –                 | –          | 8                 | LHI6, LHI7 |

The location of each sampling site is presented in Fig. 2.
tion. The Central region is a lowland area (maximum ~120 m asl) with cleared or modified habitats that encompass the majority of human settlements on LHI. The Southern region is a topographically diverse area of original vegetation that ranges from seas level to the peaks of Mt Lidgbird (777 m asl) and Mt Gower (875 m asl). Three or four sampling sites (N1-N3, C1-C3, S1-S4) were located within each region (Table 1, Fig. 2)

1.2 DNA extraction, amplification and sequencing

Total genomic DNA was extracted from these tail-tip samples using a Qiagen DNeasy Extraction Kit (Qiagen, Hilden, Germany). Two mitochondrial genes, ND2 (approximately 600 bp) and ND4 (approximately 700 bp) were amplified and sequenced for each sample using the primers presented in Table 2. PCR was performed as outlined in Chapple et al. (2013a). PCR products were purified using Exo-SAP IT (USB Corporation, Cleveland, Ohio USA) and the purified product was sequenced using a BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems) and then analysed on an ABI 3730XL capillary sequencer. Sequence data was edited using Geneious v5.4 ((Drummond et al., 2011), and aligned using default parameters of CLUSTAL W (Thompson et al., 1994), executed in MEGA5 (Tamura et al., 2011). The haplotypes present in 2011/12 sampling range across LHI were identified using DNAsp v5.10 (Librado and Rozas, 2009). Tamura-Nei corrected genetic distances among introduced haplotypes were calculated in MEGA5.

The distribution and relative frequency of haplotypes across LHI was determined using haplotype frequency data computed in DNAsp v5.10. Comparisons of the haplotype frequencies and distributions were completed for the northern, central and southern areas of the island, between 2007 and 2011–2012 data. Specific sites were also compared between 2007 and 2011–2012 using mitochondrial genes, ND2 and ND4 on 2007, respectively. There was a significant increase in haplotype frequencies in the central region between 2007 and 2011/12, with an increase of one Yamba-Coffs Harbour haplotype and the decrease of another (Table 3, 4). In 2007, the southern region contained haplotypes from all four source regions and in 2011–2012 these same haplotypes were present with two additional haplotypes from the Yamba-Coffs harbour region also detected (Tables 1, 3; Fig. 2). Between the two time points there was a significant increase of the Brisbane haplotype in the Southern region of LHI (Table 3, 4).

Samples were obtained from both time points for seven of the ten sites (all except C2, C3 and S4), allowing comparison of the haplotype presence and frequency between the two time points and specific collecting sites on LHI (Table 1, Online Supplementary Materials Table S2). There were no additional haplotypes, or loss of haplotypes, found at sites N1, N2 or S3 (Table 1, Fig. 2). Despite this, the frequency of Yamba Coffs Harbour haplotype LHI2 at site N2 increased over time, whilst the frequency of LHI3 remained stable (Table 1, 3, 4; Fig. 2). However, there were changes to the haplotypes present at the other four sites across LHI between 2007 and 2011/12. In 2007, haplotypes LHI2 and LHI3 identified on LHI during 2011–2012. These haplotypes were the same as those previously detected on LHI in 2007 (Chapple et al., 2013a). The fine scale genetic structure present in native range populations of the delicate skink is such that nearly each population has its own specific haplotype (Chapple et al., 2011b). Thus, the lack of new haplotypes found across the whole island indicates that there appear to have been no additional successful introductions to LHI from the native-range between 2007 and 2011/12.

However, at the regional scale there were some changes in the distribution of haplotypes on LHI. The frequency of the haplotype LHI3 decreased in the northern region between 2007 and 2011, whilst the frequency of haplotype LHI2 showed no significant change (Tables 1, 3, 4; Fig. 2). For the central region, there were five haplotypes in 2007 (representing each of the four native-range sources regions), with an additional haplotype from the Yamba-Coffs harbour region detected in 2011/12 (Tables 1, 3, 4; Fig. 2). There was also a significant shift in haplotype frequencies in the central region between 2007 and 2011/12, with an increase of one Yamba-Coffs Harbour haplotype and the decrease of another (Table 3, 4). In 2007, the southern region contained haplotypes from all four source regions and in 2011–2012 these same haplotypes were present with two additional haplotypes from the Yamba-Coffs harbour region also detected (Tables 1, 3; Fig. 2). Between the two time points there was a significant increase of the Brisbane haplotype in the Southern region of LHI (Table 3, 4).

Table 2 Primers used in this study, where values in the ‘5’ position refer to the position of the 5’ position in the complete Eumeces egregius mtDNA sequence (Chapple et al., 2009)

| MtDNA Region | Primer name | 5’-3’ Sequence | 5’ Position | Source |
|--------------|-------------|----------------|-------------|--------|
| ND2          | L4437       | AAGCTTTTGGGCCCATACC | 3833 | Macey et al., 1997 |
| ND2r102      |             | GCAATTTTACGCGAATGAGACCAT | 4432 | Sadler et al., 2004 |
| ND4          | ND41        | TGACTACAAAAGCTCATGTAAGAC | 10,771 | Forstner et al., 1995 |
| tRNA-Leu     |             | TACCTTTACTTGGATTTGCACCA | 11,691 | Forstner et al., 1995 |
Table 3  Chi-square analysis results of sites and regions compared across both time points

| Population | \( \chi^2 \) | Degrees of Freedom | \( P \)-value |
|------------|---------------|--------------------|--------------|
| Northern   | 0.0184        | 1                  | 0.892        |
| Central    | 50.2214       | 20                 | <0.001       |
| Southern   | 16.875        | 18                 | 0.5317       |
| N2         | 1.9753        | 1                  | 0.1599       |
| N3         | 0             | 1                  | 1            |
| C1         | 50.3905       | 20                 | <0.001       |
| S1         | 4.9793        | 8                  | 0.7598       |
| S2         | 1.5503        | 3                  | 0.6707       |
| S3         | 0.8654        | 1                  | 0.3522       |

Table 4  GLM results of haplotype frequency changes of sites and regions compared from 2007 to 2011

| Region/Site | Haplotype | \( P \)-value | Change Observed |
|-------------|-----------|---------------|-----------------|
| Northern    | LHI2      | 0.298         | Nil             |
|             | LHI3      | 0.0461*       | Decrease        |
| Central     | LHI1      | 0.292         | Nil             |
|             | LHI2      | 1             | Nil             |
|             | LHI3      | 0.034*        | Decrease        |
|             | LHI4      | 0.034*        | Increase        |
|             | LHI5      | 0.208         | Nil             |
|             | LHI7      | 1.473         | Nil             |
| Southern    | LHI1      | 1             | Nil             |
|             | LHI2      | 0.0994        | Nil             |
|             | LHI3      | 1             | Nil             |
|             | LHI4      | 0.0239*       | Increase        |
|             | LHI5      | 1             | Nil             |
|             | LHI6      | 0.695         | Nil             |
|             | LHI7      | 1.09e-5*      | Increase        |
| N1          | NA        | NA            | NA              |
| N2          | LHI2      | 0.0239*       | Increase        |
|             | LHI3      | 0.571         | Nil             |
| N3          | LHI2      | 0.00117*      | Decrease        |
|             | LHI3      | 1             | Nil             |
| C1          | LHI1      | 0.292         | Nil             |
|             | LHI2      | 1             | Nil             |
|             | LHI3      | 0.42349       | Nil             |
|             | LHI4      | 0.0482*       | Increase        |
|             | LHI5      | 1             | Nil             |
|             | LHI7      | 0.416         | Nil             |
| S1          | LHI1      | 1             | Nil             |
|             | LHI2      | 0.142         | Nil             |
|             | LHI3      | 1             | Nil             |
|             | LHI4      | 0.35          | Nil             |
|             | LHI5      | 1             | Nil             |
|             | LHI7      | 1             | Nil             |
| S2          | LHI2      | 0.423         | Nil             |
|             | LHI4      | 1             | Nil             |
|             | LHI6      | 1             | Nil             |
|             | LHI7      | 0.00032*      | Increase        |
| S3          | LHI6      | 0.1           | Nil             |
|             | LHI7      | 0.0578        | Nil             |

were present at site N3, but in 2011/12 only haplotype LHI2 was detected, resulting in a significant shift in haplotype frequencies (Tables 1, 3, 4; Fig. 2). At C1, five haplotypes were detected in 2007, and an additional haplotype was detected in 2011/12 (Table 1; Fig. 2). This was accompanied by a significant shift in haplotype frequencies, with the Brisbane haplotype increasing over time in frequency (Table 3, 4). Site S1 had three haplotypes in 2007; however, one of these haplotypes was not detected again in 2011/12, but three additional others were (Tables 1, 3, 4; Fig. 2). In 2007, site S2 contained two haplotypes, and in 2011/12 two additional haplotypes were also detected, accompanied by a significant increase in the frequency of the Sydney haplotype (LHI7) (Tables 1, 3, 4; Fig. 2).

3 Discussion

While no new delicate skink haplotypes appear to have successfully established on LHI between 2007 and 2011/12, there were shifts, both at the regional and site level, in the genetic structure of the species across the island between the two time points. The spread of the species over last five years through the mountainous southern region of the island (summit of Mt Lidgbird [~770 m asl], mid-elevation regions [~500–600 m asl] of Mt Gower; Chapple et al., 2014) has occurred as the result of existing, established genetic lineages that originate from the Border Ranges (LHI6) and Sydney (LHI7) regions of the native range. Our main findings are consistent with the temporal variation in genetic structuring observed in an invasive fruit fly Ceratitis capitata in Florida, albeit over a shorter timeframe, where no new mtDNA haplotypes were observed over time (1997 vs 1998), with the existing haplotypes spreading across the introduced range (Silva et al., 2003).

The delicate skink has reached LHI from all of the major sea (Coffs Harbour-Yamba) and air ports (Brisbane, Sydney) that supplied the island in 2007 (Chapple et al., 2013a). However, the home port of the supply ship that services LHI (the MV Island Trader) was recently shifted to Port Macquarie. Yet, although there are
also direct flights to LHI from Port Macquarie during the summer months, we did not detect any haplotypes from this native range region on the island during our sampling in 2011/12. This might indicate that delicate skinks have not yet been stowaways in freight and cargo from this new location, or that they are yet to successfully establish via this trade route. However, it is highly likely that a new introduction could occur from Port Macquarie, because propagule pressure of the delicate skink in the Pacific region is high (i.e. 10+ separate, successful introductions from the species native range to Hawaii, New Zealand and LHI, and multiple instances of long-distance jump dispersal within the New Zealand and the Hawaiian Islands; Chapple et al., 2013a,b). Propagule pressure is considered important in the successful introduction of an invasive species. For instance, in a study on 133 invasive bird species, it was found that introductions with less than ten individuals had only a 6% establishment success, whilst introductions of > 100 individuals had a 83% establishment success (Lockwood et al., 2007). Alternatively, the failure to detect a delicate skink haplotype from the Port Macquarie region could be due to a lag phase (Mack, 1985; Lockwood et al., 2013) and the time taken for a new haplotype to attain a sufficient abundance on LHI to be detected. Another explanation for the lack of detection could be that new haplotypes do not confer a fitness advantage compared to the current haplotypes. In addition, some haplotypes may not be able to spread throughout a high density population, such as those found in the inhabited central region of LHI (Fisher, 1937).

There were no new haplotypes detected in the northern region of the island in 2011/12, which could be due to the high population density of the delicate skink preventing the movement of individuals from other regions of the island, with different haplotypes, into the northern region. The northern region of the island was the first colonised by the delicate skink (Lever, 2003; Hutchinson et al., 2005), so complete niche filling by the lizards may have occurred. Such niche filling has been found in the invasion of a plant *Ambrosia artemisiifolia* in Austria, where the establishment of a population in a suitable niche, prevented subsequent introductions of the same species from entering the same, filled niche (Dullinger et al., 2009). Alternatively, mate recognition might play a role. For instance, delicate skinks stemming from the Yamba-Coffs harbour region may avoid mating with lizards from other source populations, instead preferring to mate with males from their “local” source population. The preference of females to mate with males from local populations has been demonstrated in many taxa including snails (Rupp and Woolhouse, 1999), salamanders (Tilley et al., 1990) and rodents (Pillay et al., 1995; Pillay, 2000). In populations of an Australian tropical skink *Lampropholis coggeri*, it was found that chemoreception may play a role in mate recognition between populations. Skinks were found to mate more with skinks from their own population, and tongue flicking (an important part of mating behaviour) occurred more when individuals were presented with scent from the same population (Scott et al., 2015). Such mate choice systems may also be present in the population of delicate skink on LHI, preventing the spread of non-Yamba-Coffs harbour haplotypes into the northern region of the island. Microsatellite markers have been developed for *L. delicata* (Chapple and Thompson, 2009), and we plan to investigate mate preferences on LHI in the future.

The detection of additional haplotype (LHI2) at site C1, which has significantly altered the haplotype frequencies seen at this site and in the central region, is not surprising because the central region of the island is where boats and planes unload cargo, and stowaways generally are first introduced to the island here. Consequently it is likely (e.g. Sakai et al., 2001; Lockwood et al., 2005) that this is where the population of *L. delicata* would have first established. Hence, the detection of six of the seven source haplotypes in this region is to be expected. The lack of detection of LHI6 in the central region, even though it is found in the southern region of the island could simply be due to small sampling numbers and lag effects (Mack et al., 2000), or because it arrived via an air route (the airport represents the boundary between the central and southern regions; Fig. 2) before migrating southwards. Because the central region of the island now contains nearly all the haplotypes available we would expect to see the spread of previously undetected haplotypes into the sparsely populated southern region of the island, which contained only four haplotypes in 2007. The accepted chronology of the delicate skink introduction to LHI suggests that spread of the species is mostly likely to have been driven by established populations from the central region of the island (e.g. Sakai et al., 2001; Allendorf and Lundquist, 2003; Lockwood et al., 2005).

For instance, in the introduction of the brown anole *Anolis sagrei* to Florida, the species first established in the Florida Keys but then, after a lag period of half a century, rapidly expanded across northern Florida due to
expansion from the southern Keys and additional introductions into peninsular Florida (Kolbe et al., 2004).

The increase or decrease in frequency of certain haplotypes across the island, even where no addition or loss of haplotype was recorded, also yield some interesting preliminary results into the fitness advantage of certain genetic haplotypes (Fisher, 1937). Hence the increase in the frequency of the Yamba-Coffs Harbour haplotype (LHI3) in both the Northern and Central region, as well as the increase of the Brisbane haplotype (LHI4) in the Central and Southern region, and the Sydney haplotype (LHI7) in the Southern region, could indicate that these haplotypes confer a fitness advantage above the other haplotypes on LHI. Alternatively, these changes in haplotype frequency may be due to genetic drift, particularly as small population size is often characteristic of recent introductions (Wares et al., 2005). Thus, further investigation is required to investigate whether there is any relative advantage of each introduced delicate skink haplotype on LHI.

The delicate skink is still spreading south throughout the island, with individuals now observed as far south as Mount Lidgbird on the island (Chapple et al., 2014). Interestingly, as the delicate skink spreads south more haplotypes were detected in the region. In 2007, haplotypes LHI2, 4, 6 and 7 were detected in the area whilst in 2011/12 the additional haplotypes 1, 3 and 5 were also detected though not in such numbers as to significantly influence the haplotype frequencies in the region or at specific sites. Spread of lizards through the mountainous southern areas of LHI is not surprising because the lizards are found in high elevations in mainland Australia and have been found in Hawaii at elevations of up to 1,000 m (Baker, 1979). It is likely that the delicate skink will spread to Mount Gower, because it is a moist rainforest habitat and the delicate skink is a moist adapted species that can be found in rainforests in mainland Australia (Wilson and Swan, 2013; Cogger, 2014). Currently all seven haplotypes are found in the southern regions, but are not yet found at all sites. However, given that this region has not yet reached high population densities of lizards it is likely that more haplotypes will spread to all the southern sites.

In conclusion, our temporal study of the delicate skink invasion of LHI highlights that biological invasions can be dynamic. We detected significant shifts in the distribution and frequency of introduced delicate skink haplotypes on LHI over the 5-year time frame. Future studies of biological invasions should include temporal aspects because they will allow better understanding of invasions and could lead to better measures to mitigate and control such species in the future.

Acknowledgments We thank H. Bower, S. Bower, G. Cromie, J. Hale, C. Haselden, D. Kelly, F. Lyndon-Gee, M. Michelangelo, L. Plenderleith, and M. Pepper for assisting with fieldwork on LHI. We thank C. Johnstone for providing statistical advice. Our research was conducted with animal ethics approvals from Monash University (BSCI/2010/15, BSCI/2011/23, BSCI/2012/12), and in accordance with New South Wales scientific research permits (S12249, S13015, SL100264, SL100564, SL101030). The research was completed with the approval and assistance of the LHI Board. The research was funded by the Australian Research Council (grant to DGC; DP0771913), the National Geographic Society (grants to DGC; MBT and RDB; CRE 8085-06, CRE 8952-11), the Hermon Slade Foundation (grant to DGC and MBT; HSF09-02), a Holsworth Wildlife Research Endowment- ANZ Trustees Foundation (to RDB), and Monash University (School of Biological Sciences Small Grant, Science Faculty Early Career Researcher Grant; to DGC).

References

Allendorf WF, Lundquist LL, 2003. Introduction: Population biology, evolution, and control of invasive species. Conservation Biology 17: 24–30.

Baker JK, 1979. The rainbow skink Lamprophis delicata in Hawaii. Pacific Science 33: 207–212.

Blackburn TM, Pysek P, Bacher S, Carlton JT, Duncan RP et al., 2011. A proposed unified framework for biological invasions. Trends in Ecology and Evolution 26: 333–339.

Bohm M, Collen B, Baillie JEM, Bowles P, Chanson J et al., 2013. The conservation status of the world’s reptiles. Biological Conservation 157: 372–385.

Chapple DG, Birkett A, Miller KA, Daugherty CH, Gleeson DM, 2012. Phylogeography of the endangered Otago skink Oligosoma otagense: Population structure, hybridisation and genetic diversity in captive populations. PLoS ONE 7: e34599.

Chapple DG, Simmonds SM, Wong BBM, 2011a. Know when to run, know when to hide: Can behavioral differences explain the divergent invasion success of two sympatric lizards? Ecology and Evolution 1: 278–289.

Chapple DG, Hoskin CJ, Chapple SNJ, Thompson MB, 2011b. Phylogeographic divergence in the widespread delicate skink Lamprophis delicata corresponds to dry habitat barriers in eastern Australia. BMC Evolutionary Biology 11: 191

Chapple DG, Whitaker AH, Chapple SNJ, Miller KA, Thompson MB, 2013a. Biosecurity interceptions of an invasive lizard: Origin of stowaways and human-assisted spread within New Zealand. Evolutionary Applications 6: 324–339.

Chapple DG, Miller KA, Kraus F, Thompson MB, 2013b. Divergent introduction histories among invasive populations of

Current Zoology
Vol. 61  No. 3
the delicate skink Lampropholis delicata: Has the importance of genetic admixture in the success of biological invasions been overemphasised? Diversity and Distributions 19: 134–146.

Chapple DG, Miller KA, Chaplin K, Barnett L, Thompson MB et al., 2014. Biology of the invasive delicate skink Lampropholis delicata on Lord Howe Island. Australian Journal of Zoology 62: 498–506.

Chapple DG, Ritchie PA, Daugherty CH, 2009. Origin, diversification, and systematics of the New Zealand skink fauna (Reptilia: Scincidae). Molecular Phylogenetics and Evolution 52: 470–487.

Chapple DG, Simmonds SM, Wong BBM, 2012. Can behavioral and personality traits influence the success of unintentional species introductions? Trends in Ecology & Evolution 27: 57–64.

Chapple DG, Thompson MB, 2009. Isolation and characterization of microsatellite loci from the invasive delicate skink Lampropholis delicata with cross-amplification in other Australian Eungongylus group species. Conservation Genetics Resources 1: 55–58.

Cogger HG, 2014. Reptiles and Amphibians of Australia. 7th edn. Melbourne, Australia: CSIRO Publishing.

Cooling M, Hartley S, Sim DA, Lester PJ, 2012. The widespread collapse of an invasive species: Argentine ants Linepithema humile in New Zealand. Biology Letters 8: 430–433.

Cromie GL, Chapple DG, 2012. Impact of tail loss on the behaviour and locomotor performance of two sympatric Lampropholis skink species. PLoS ONE 7: e34732.

Dlugosch KM, Parker IM, 2008. Founding events in species pathways in an era of globalization. Journal of Applied Molecular Phylogenetic Evolution 4: 93–102.

Dyer AL, Pillay N, Willan K, Meester J, 2007. Does the level of genetic diversity affect the potential success of new introductions of exotic species? In: White J ed. Studies on Plant Demography: A Festschrift for John L. Harper. London: Academic, 127–142.

Dyer AL, Pillay N, Simberloff D, Lonsdale WM, Evans H, Clout M, 2000. Biotic invasions: Causes, epidemiology, global consequences, and control. Ecological Applications 10: 689–710.

Forstner MRJ, Davis SK, Arevalo E, 1995. Support for the hypothesis of Anguimorph ancestry for the suborder Serpentes from molecular phylogenetic analysis of mitochondrial DNA sequences. Molecular Phylogenetic Evolution 4: 93–102.

Handley LJ, Estoup A, Evans DM, Thomas CE, Lombaert E et al., 2011. Geneious v5.4, available from http://geneious.com/. Dallinger S, Kleinbauer I, Peterseil J, Smolik M, Essl F, 2009. Niche based distribution modelling of an invasive alien plant: Effects of population status, propagule pressure and invasion history. Biological Invasions 11: 2401–2414.

Fisher RA, 1937. The wave of advance of advantageous genes. Annals of Eugenics 7: 355–369.

Forstner MRJ, Davis SK, Arevalo E, 1995. Support for the hypothesis of Anguimorph ancestry for the suborder Serpentes from phylogenetic analysis of mitochondrial DNA sequences. Molecular Phylogenetic Evolution 4: 93–102.

Hulme PE, 2009. Trade, transport and trouble: Managing invasive species introductions? Trends in Ecology & Evolution 24: 233–242.

Hurni PE. 2009. Trade, transport and trouble: Managing invasive species pathways in an era of globalization. Journal of Applied Ecology 46: 10–18.

Hutchinson MN, Thompson MB, Stewart JR, 2005. Lampropholis delicata (Delicate skink, Rainbow skink): Introduction. Herpetological Review 36: 450–451.

Kolbe JJ, Glor RE, Schettino LR, Lara AC, Larson A et al., 2004. Genetic variation increases during biological invasion by a Cuban lizard. Nature 431: 177–181.

Lever C, 2003. Naturalized Reptiles and Amphibians of the World, Oxford: Oxford University Press.

Librado P, Rozas J, 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. Bioinformatics 25: 1451–1452.

Lockwood JL, Cassey P, Blackburn T, 2005. The role of propagule pressure in explaining species invasions. Trends in Ecology and Evolution 20: 223–228.

Lockwood JL, Hoopes MF, Marchetti MP, 2013. Invasion Ecology. Oxford: Wiley-Blackwell.

Macey JR, Larson A, Ananjeva NB, Fang ZL, Papenfuss TJ, 1997. Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Molecular Biology Evolution 14: 91–104.

Mack RN, 1985. Invading plants: Their potential contribution to population biology. In: White J ed. Studies on Plant Demography: A Festschrift for John L. Harper. London: Academic, 127–142.

Mack RN, Simberloff D, Lonsdale WM, Evans H, Clout M, 2000. Biotic invasions: Causes, epidemiology, global consequences, and control. Ecological Applications 10: 689–710.

Pilef N, 2000. Female mate preference and reproductive isolation in populations of the striped mouse Rhabdomys pumilio. Behaviour 137: 1431–1441.

Pilef N, Willan K, Meester J, 1995. Evidence of pre-mating reproductive isolation in two allopatric populations of the vleirat Otomys irrata. Ethology 100: 61–71.

Pimentel D, McNair S, Janecka J, Wightman AH, Simmons C et al., 2001. Economic and environmental threats of alien plant, animal and microbe invasions. Agriculture, Ecosystems and Environment 84: 1–20.

Pimentel D, Zuniga R, Morrison D, 2005. Update on the environmental and economic costs associated with alien-invasive species in the United States. Ecological Economics 52: 273–288.

Rius M, Darling J, 2014. How important is intraspecific genetic admixture to the success of colonising populations? Trends in Ecology and Evolution 28: 233–242.

Roman J, Darling JA, 2007. Paradox lost: Genetic diversity and the success of aquatic invasions. Trends in Ecology and Evolution 22: 454–464.

Rupp JC, Woolhouse MEJ, 1999. Impact of geographical origin on mating behaviour in two species of Biomphalaria (Planorbidae: Gastropoda). Animal Behaviour 58: 1247–1251.

Sadlier RA, Smith SA, Bauer AM, Whitaker AH, 2004. A new genus and species of live-bearing scincid lizard (Reptilia: Scincidae). New Caledonia Journal of Herpetology 38: 320–330.

Sakai AK, Allendroff FW, Holt JS, Lodge DM, Molofsky J et al., 2001. The population biology of invasive species. Annual Review of Ecology and Systematics 32: 305–332.

Schulz M, 2009. Notes on the delicate skink Lampropholis delicata occurring on Lord Howe Island. Herpetofauna 39: 48–52.

Scott ML., Llewelyn J, Higgie M, Hoskin CJ, Pike K et al., 2015. Chemoreception and mating behaviour of a tropical Australian skink. Acta Ethologica, doi: 10.1007/s10211-015-0213-0.

Silva JG, Meiner MD, McPherson BA, Steck GJ, Sheppard WS, 2003. Recent Mediterranean fruit fly (Diptera: Tephritidae) infestations in Florida. A genetic perspective. Journal of Economic Entomology 96: 1711–1718.

Simberloff D, 2009. The role of propagule pressure in biological invasions. Annual Review of Ecology, Evolution and Systematics 40: 81–102.
Simberloff D, Gibbons L, 2004. Now you see them, now you don't: Population crashes of established introduced species. Biological Invasions 6: 161–172.

Tamura K, Peterson D, Peterson N, Stecher G, Nei M et al., 2011. MEGA5: Molecular evolutionary genetics analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony methods. Molecular Biology and Evolution 28: 2731–2739.

Thompson JD, Higgins DG, Gibson TJ, 1994. Clustal W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22: 4673–4680.

Tilley SG, Verrell PA, Arnold SJ, 1990. Correspondence between sexual isolation and allozyme differentiation: A test in the salamander Desmognathus ochrophaeus. Proceedings. Natl. Acad. Sci.USA 87: 2715–2719.

Tingley R, Thompson MB, Hartley S, Chapple DG, 2015. Patterns of niche filling and expansion across the invaded ranges of an Australian lizard. Ecography doi: 10.1111/ecog.01576

Vitousek PM, D’Antonio CM, Loope LL, Rejmanek M, Westbrooks R, 1997. Introduced species: A significant component of human-caused global change. New Zealand Journal of Ecology 21: 1–16.

Wares JP, Hughes AR, Grosberg RK, 2005. Mechanisms that drive evolutionary change: Insights from species introductions and invasions. In: Sax DF, Stachowicz JJ, Gaines SD ed. Species Invasions: Insights into Ecology, Evolution and Biogeography. Sunderland: Sinauer Associates, 229–257.

Wilson S, Swan G, 2013. Complete Guide to Reptiles of Australia. 4th edn. Sydney: Reed New Holland.
### Online Supplementary Materials

**Table S1** Table of papers reviewed to determine if temporal components were included in studies of invasive species mitochondrial DNA, including title, author, publication year and journal information of study

| Authors                                      | Paper Title                                                                                                                                       | Year Published | Temporal Component Included? | Journal, Volume, Page Number                  |
|----------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|----------------|-------------------------------|-----------------------------------------------|
| Turon X, Tarjuelo I, Duran S, Pascual M      | Characterising invasion processes with genetic data: An Atlantic clade of Clavelina leodiiformis (Ascidiaeae) introduced into Mediterranean harbours. | 2003           | No                            | Hydrobiologia 503: 29–35.                     |
| Castilla JC, Collins AG, Meyer CP, Guinea R, Lindberg DR | Recent introduction of the dominant tunicate Pyura praespatialis (Urochordata, Pyuridae) to Antofagasta, Chile.                                              | 2002           | No                            | Molecular Ecology 11: 1579–584.                |
| López-Legentil S, Turon X, Planes S          | Genetic structure of the star sea squirt Botryllus schlosseri introduced in southern European harbours.                                            | 2006           | No                            | Molecular Ecology 15: 3957–3967.               |
| May GE, Gelenbiuk GW, Panov VE, Olrova MI, Lee CE | Molar ecology of zebra mussel invasions.                                                                                                           | 2006           | No                            | Molecular Ecology: 15 1021–031.                |
| Therriault TW, Grigorovich IA, Cristescu ME Ketelaars HAM, Viljanen M et al. | Taxonomic resolution of the genus Bythotrephes Leydig using molecular markers and re-evaluation of its global distribution. | 2002           | No                            | Diversity and Distributions: 8 67–84.         |
| Cristescu MFA, Hebert PDI, Witt JDS, Maciascau HJ, Grigorovich IA | An invasion history for Cerconpaganus penguic based on mitochondrial gene sequences.                                                                 | 2001           | No                            | Linnology and Oceanography: 46: 224–229.      |
| Martel C, Viard F, Bourgue E, Garcia-Meunier P | Invasions by the marine gastropod Octinerebrius inernatus in France 1. Scenario for the source of introduction.                                   | 2004           | No                            | Journal of Experimental Marine Biology and Ecology: 305: 155–170. |
| Facon B, Pointier JP, Glaubrecht M, Poux C, Jancz F et al. | A molecular phylogeography approach to biological invasions of the New World by parthenogenetic Thaoid snails.                                 | 2003           | No                            | Molecular Ecology 12: 3027–3039.              |
| Genné MJ, Michel E, Erpenbeck D, De Voogd N, Witte F et al. | Camouflaged invasion of Lake Milawi by an Oriental gastropod.                                                                                   | 2004           | No                            | Molecular Ecology 13: 2135–2141.              |
| Cristescu MFA, Witt JDS, Grigorovich IA, Hebert PDI, Maciascau HJ | Dispersal of the Pontos-Caspian amphipod Echinogammarus ischnus: Invasion waves from the Paleocene to the present.                          | 2004           | No                            | Heredity 92: 197–203.                        |
| Kelly DW, Muirhead JR, Heath DD, Maciascau HJ | Contrasting patterns in genetic diversity following multiple invasions of fresh and brackish waters.                                            | 2006           | No                            | Molecular Ecology 15: 3641–3653.              |
| Gopurenko D, Hughes JM, Bellchambers L        | Colouration o' the south-west Australian coastline by mud crabs: Evidence for a recent range expansion or human-induced translocation?           | 2003           | No                            | Marine and Freshwater Research 54: 833–840.   |
| Peterson C                                   | Range expansion in the northeast: Pacific by an estuary mud crab: A molecular study.                                                            | 2006           | No                            | Biological Invasions 8: 565–567.              |
| Zardus JD, Hadfield MG                       | Multiple origins and incursions of the Atlantic barnacle Chthamalus proteus in the Pacific                                                    | 2005           | No                            | Molecular Ecology 14: 3719–3733.              |
| Bastrop R, Jurs K, Sturmbauer C               | Cryptic species in a marine polychaete and their independent introduction from North America to Europe.                                            | 1998           | No                            | Molecular Biology and Evolution 15: 97–103.    |
| Holland BS, Davson MN, Crow GL, Holmann DK    | Global phylogeography of Cassiopea (Scyphozoa: Rhizostomeae): Molecular evidence for cryptic species and multiple invasions of the Hawaiian islands. | 2004           | No                            | Marine Biology 145: 1119–1128.              |
| Authors                          | Paper Title                                                                                                                                                                                                                                                                                                                                 | Year Published | Temporal Component Included? | Journal, Volume, Page Number          |
|---------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|------------------------------|---------------------------------------|
| Grapputo A, Borsan S, Lindstrom L, Lyytinen A, Mappes J | The voyage of an invasive species across continents: Genetic diversity of North American and European Colorado potato beetle populations.                                                                                                                                          | 2005           | No                          | Molecular Ecology 14: 4207–4219.       |
| Cognato AJ, Sun JH, Anducho-Reyes MA, Owen DR.            | Genetic variation and origin of red turpentine beetle (*Dendroctonus valens* LeConte) introduced to the People's Republic of China.                                                                                                                                               | 2005           | No                          | Agricultural and Forest Entomology 7: 87–94. |
| Evans JD, Petit JS, Shimunaka H | Mitochondrial DNA relationships in an emergent pest of honey bees: *Aethina tumida* (Coleoptera: Nitidulidae) from the United States and Africa.                                                                                                                                   | 2000           | No                          | Annals of the Entomological Society of America 93: 415–420. |
| Lafflin RD, Dowdall LM, Sperling FAH | Population structure of the cabbage seedpod weevil *Ceutorhynchus obstrictus* (Marsham) (Coleoptera: Curculionidae): Origins of North American introductions.                                                                                                                  | 2005           | No                          | Environmental Entomology 34: 504–510.   |
| Fonseca DM, Campbell S, Crans WJ, Mogi M, Miyagi I et al. | *Aedes* (*Finlaya*) *japonicus* (Diptera: Culicidae), a newly recognized mosquito in the United States: Analyses of genetic variation in the United States and putative source populations.                                                                 | 2001           | No                          | Journal of Medical Entomology 38: 135–146 |
| Johnson AJ, Schemerhorn BJ, Shulke RH | A first assessment of mitochondrial DNA variation and geographic distribution of haplotypes in hessian fly (Diptera: Cecidomyiidae).                                                                                                               | 2004           | No                          | Annals of the Entomological Society of America 97: 940–948. |
| Nardi F, Carapelli A, Dallai R, Roderick GK, Frati F | Population structure and colonization history of the olive fly *Bactrocera oleae* (Diptera, Tephritidae).                                                                                                                                                                   | 2005           | No                          | Molecular Ecology 14: 2729–2738.       |
| Scheffer SJ                | Molecular evidence of cryptic species within the *Liromyza huidobrensis* (Diptera: Agromyzidae)                                                                                                                                                                                          | 2000           | No                          | Journal of Economic Entomology 93: 1146–1151. |
| Scheffer SJ, Lewis ML           | Mitochondrial phylogeography of the vegetable pest *Liromyza trifolii* (Diptera: Agromyzidae): diverged clades and invasive populations                                                                                                                                                   | 2006           | No                          | Annals of the Entomological Society of America 99: 991–998. |
| Silva JG, Meixner MD, McPherson BA, Steck GJ, Sheppar WS | Recent mediterranean fruit fly (Diptera: Tephritidae) infestations in Florida: A genetic perspective.                                                                                                                                                                                   | 2003           | Yes                         | Journal of Economic Entomology 96: 1711–1718. |
| Downie DA                     | Locating the sources of an invasive pest, grape phylloxera, using a mitochondrial DNA genealogy.                                                                                                                                                                                       | 2002           | No                          | Molecular Ecology 11: 2013–2026        |
| Gwiazdowski RA, Van Driesche RG, Desteyes RS et al. | Possible geographic origin of beech scale *Cryptococcus fagisuga* (Hemiptera: Eriococcidae), an invasive pest in North America.                                                                                                                                                   | 2006           | No                          | Biological Control 39: 9–18.           |
| Havill NP, Montgomery ME, Yu G, Shiyake S, Caccone A | Mitochondrial DNA from Hemlock Woolly adelgid (Hemiptera: Adelgidae) suggests cryptic speciation and pinpoints the source of the introduction to eastern North America.                                                                                                                | 2006           | No                          | Annals of the Entomological Society of America 99: 195–203 |
| Hufbauer RA, Bogdanowicz SM, Harrison RG | The population genetics of a biological control introduction: Mitochondrial DNA and microsatellite variation in native and introduced populations of *Aphidius ervi*, a parasitoid wasp.                                                                                     | 2004           | No                          | Molecular Ecology 13: 337–348.         |
| Scheffer SJ, Grissell EE            | Tracing the geographical origin of *Hegastigma transvaalensi* (Hymenoptera: Torymidae): An African wasp feeding on a South American plant in North America.                                                                                                                     | 2003           | No                          | Molecular Ecology 12: 415–421.         |
| Steiner FM, Schlick-Steiner BC, Trager JC, Modr K, Sanetra M et al. | *Tetramorium tsushimae*, a new invasive ant in North America.                                                                                                                                                                                                              | 2006           | No                          | Biological Invasions 8: 117–123        |
| Authors | Paper Title | Year Published | Temporal Component Included? | Journal, Volume, Page Number |
|---------|-------------|----------------|-----------------------------|------------------------------|
| Tsutsui ND, Suarez AV, Holway DA, Case TJ | Relationships among native and introduced populations of the Argentine ant Linepithema humile and the source of introduced populations. | 2001 | No | Molecular Ecology 10: 2151–61. |
| Austin JW, Szalanski AL, Scheffrahn RH, Messenger MT, McKern JA et al. | Genetic evidence for two introductions of the Formosan subterranean termite Coptotermes formosanus (Isoptera: Rhinotermitidae) to the United States. | 2006 | No | Florida Entomologist 89: 183–193. |
| Gomi T, Muraji M, Takeda M | Mitochondrial DNA analysis of the introduced fall webworm, showing its shift in lifecycle in Japan. | 2004 | No | Entomological Science 7: 133–188. |
| Collins TM, Trexler JC, Nico LG, Rawlings TA | Genetic diversity in a morphologically conservative invasive xaxon: Multiple introductions of swamp eels to the southeastern United States. | 2002 | No | Conservation Biology 16: 1024–1035. |
| Moyer GR, Osborne M, Turner TF | Genetic and ecological dynamics of species replacement in an arid-land river system. | 2005 | No | Molecular Ecology 14: 1263–1273 |
| Lindholm AK, Breden F, Alexander HJ, Cha WK, Thakurta SG et al. | Invasion success and genetic diversity of introduced populations of guppies Poecilia reticulata in Australia. | 2005 | No | Molecular Ecology 14: 3671–3682. |
| Azzurro E, Golani D, Bucciarelli G, Berardi, G | Genetics of the early stages of invasion of Lessepsian rabbitfish Siganus luridus. | 2006 | No | Journal of Experimental Marine Biology and Ecology 333: 190–201. |
| Dougherty JD, Moore WS, Ram JL | Mitochondrial DNA analysis of round goby Neogobius melanostomus and tubercle goby Proterorhinus marmoratus in the Great Lakes basin. | 1996 | No | Canadian Journal of Fisheries and Aquatic Sciences 53: 474–480. |
| Slade RW, Moritz C | Phylogeography of Bufo marinus from its natural and introduced ranges. | 1998 | No | Proceedings of the Royal Society B: Biological Sciences 265: 769–777. |
| Muñoz-Fuentes V, Green AJ, Sorenson MD, Negro JJ, Villa, C | The ruddy duck Oxyura jamaicensis in Europe: Natural colonization or human introduction? | 2006 | No | Molecular Ecology 15: 1441–1453. |
| Le Page SL, Livermore RA, Cooper DW, Taylor AC | Genetic analysis of a documented population bottleneck: Introduced Bennett’s wallabies Macropus rufigrises rufigrises in New Zealand. | 2000 | No | Molecular Ecology 9: 753–763. |
| Eldridge MDB, Browning TL, Close RL | Provenance of a New Zealand brush-tailed rock-wallaby Petrogale penicillata population determined by mitochondrial DNA sequence analysis. | 2001 | No | Molecular Ecology 10: 2561–2567. |
| Hingston M, Goodman SM, Ganzhorn JU, Sommer S | Reconstruction of the colonization of southern Madagascar by introduced Rattus rattus. | 2005 | No | Journal of Biogeography 32: 1549–1559. |
| Libois RM, Michelau Jr, Ramalhinho MG, Mauroits C, Sara M | On the origin and systematics of the northern African wood mouse Apodemus syrians: A comparative study of mtDNA restriction patterns. | 2001 | No | Canadian Journal of Zoology 79: 1503–1511. |
| Kolbe JI, Glor RE, Schettino LRG et al. | Genetic variation increases during biological invasion by a Cuban lizard. | 2004 | No | Nature 431: 177–81. |
| Oliverio M, Burke R, Bologna MA, Wirz A, Mariotti P | Molecular characterization of native (Italy) and introduced (JSA) Podarcis sicula populations (Reptilia, Lacertidae). | 2001 | No | Italian Journal of Zoology 68: 121–124. |
| Gooldby JA, De Barro PJ, Makinson JR Pemberton RW, Hartley DM et al. | Matching the origin of an invasive weed for selection of a herbivore haplotype for a biological control programme. | 2006 | No | Molecular Ecology 15: 287–297. |
Table S2  Delicate skinks *Lamprophis delicata* sampled from Lord Howe Island at different sites across two different time points (2007 & 2011/12), with GenBank Accession Numbers provided for mtDNA markers used in this study

| Pop. | Site Name                  | Sample Code | Time point | Haplotype | GenBank Accession Number |
|------|----------------------------|-------------|------------|-----------|--------------------------|
| N1   | Northern: North Bay Area   | LDL82       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL83       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL104      | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL105      | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL98       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL99       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL100      | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL101      | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL102      | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL103      | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL144      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL145      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL151      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL429      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL430      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL502      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL503      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL505      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL516      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL531      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL533      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL557      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL559      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL560      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL561      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL562      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL563      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL564      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL431      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL529      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL532      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL501      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL504      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL530      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL555      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL556      | 2011/12    | LHI2      | JF915800 JF915814       |
|      |                            | LDL558      | 2011/12    | LHI2      | JF915800 JF915814       |
| N2   | Northern: Max Nichols Track, Dawson Pt Ridge | LDL88 | 2007 | LHI2 | JF915800 JF915814 |
|      |                            | LDL89       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL90       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL91       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL92       | 2007       | LHI2      | JF915800 JF915814       |
|      |                            | LDL93       | 2007       | LHI3      | JF915803 JF915817       |
|      |                            | LDL94       | 2007       | LHI2      | JF915800 JF915814       |
| Pop.   | Site Name      | Sample Code | Time point | Haplotype | GenBank Accession Number |
|--------|----------------|-------------|------------|-----------|--------------------------|
| LDL95  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL96  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL97  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL627 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL628 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL629 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL630 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL631 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL632 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL633 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL634 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL635 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL636 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL637 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL638 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL639 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL640 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL641 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL642 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL643 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL644 |                |             | 2011/12    | LHI3      | JF915803 JF915817        |
| LDL645 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL646 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL647 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL648 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL649 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL650 |                |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL20  |                |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL21  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL22  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL23  |                |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL24  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL25  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL26  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL27  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL28  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL29  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL30  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL31  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL32  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL33  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL34  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL35  |                |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL36  |                |             | 2007       | LHI2      | JF915800 JF915814        |
### Continued Table S2

| Pop. | Site Name | Sample Code | Time point | Haplotype | GenBank Accession Number |
|------|-----------|-------------|------------|-----------|--------------------------|
| LDL37|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL38|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL39|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL40|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL41|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL42|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL43|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL44|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL45|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL46|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL47|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL48|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL49|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL50|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL51|           |             | 2007       | LHI2      | JF915800 JF915814        |
| LDL141|          |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL142|          |             | 2011/12    | LHI2      | JF915800 JF915814        |
| LDL68|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL69|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL70|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL71|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL72|           |             | 2007       | LHI3      | JF915803 JF915817        |
| LDL73|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL74|           |             | 2007       | LHI7      | JF915799 JF915813        |
| LDL75|           |             | 2007       | LHI4      | JF915801 JF915815        |
| LDL76|           |             | 2007       | LHI7      | JF915799 JF915813        |
| LDL77|           |             | 2007       | LHI7      | JF915799 JF915813        |
| LDL01|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL02|           |             | 2007       | LHI5      | JF915791 JF915805        |
| LDL03|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL04|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL05|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL06|           |             | 2007       | LHI5      | JF915791 JF915805        |
| LDL07|           |             | 2007       | LHI1      | JF915798 JF915812        |
| LDL84|           |             | 2007       | LHI4      | JF915801 JF915815        |

**C1 Central: LHI Settlement Area**
Continued Table S2

| Pop.  | Site Name | Sample Code | Time point | Haplotype | GenBank Accession Number |
|-------|-----------|-------------|------------|-----------|--------------------------|
| LDL85 |           |             | 2007       | LH15      | JF915791 JF915805        |
| LDL86 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL87 |           |             | 2007       | LH14      | JF915801 JF915815        |
| LDL53 |           |             | 2007       | LH14      | JF915801 JF915815        |
| LDL54 |           |             | 2007       | LH14      | JF915801 JF915815        |
| LDL55 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL56 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL57 |           |             | 2007       | LH15      | JF915791 JF915805        |
| LDL58 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL59 |           |             | 2007       | LH11      | JF915798 JF915812        |
| LDL60 |           |             | 2007       | LH15      | JF915791 JF915805        |
| LDL61 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL62 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL63 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL64 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL65 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL66 |           |             | 2007       | LH14      | JF915801 JF915815        |
| LDL67 |           |             | 2007       | LH17      | JF915799 JF915813        |
| LDL143|           |             | 2011/12    | LH12      | JF915800 JF915814        |
| LDL601|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL602|           |             | 2011/12    | LH15      | JF915791 JF915805        |
| LDL603|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL604|           |             | 2011/12    | LH13      | JF915803 JF915817        |
| LDL605|           |             | 2011/12    | LH15      | JF915791 JF915805        |
| LDL606|           |             | 2011/12    | LH11      | JF915798 JF915812        |
| LDL607|           |             | 2011/12    | LH14      | JF915801 JF915815        |
| LDL608|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL609|           |             | 2011/12    | LH11      | JF915798 JF915812        |
| LDL610|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL611|           |             | 2011/12    | LH15      | JF915791 JF915805        |
| LDL612|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL614|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL615|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL616|           |             | 2011/12    | LH13      | JF915803 JF915817        |
| LDL617|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL621|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL622|           |             | 2011/12    | LH11      | JF915798 JF915812        |
| LDL623|           |             | 2011/12    | LH11      | JF915798 JF915812        |
| LDL624|           |             | 2011/12    | LH17      | JF915799 JF915813        |
| LDL625|           |             | 2011/12    | LH11      | JF915798 JF915812        |
| LDL626|           |             | 2011/12    | LH14      | JF915801 JF915815        |
| LDL540|           |             | 2011/12    | LH14      | JF915801 JF915815        |
| LDL541|           |             | 2011/12    | LH15      | JF915791 JF915805        |
| LDL542|           |             | 2011/12    | LH15      | JF915791 JF915805        |
| Pop.  | Site Name      | Sample Code | Time point | Haplotype | GenBank Accession Number |
|-------|----------------|-------------|------------|-----------|-------------------------|
| LDL548|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL549|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL550|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL565|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL573|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL574|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL575|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL576|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL577|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL578|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL579|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL581|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL582|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL583|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL584|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL585|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL586|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL587|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL588|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL618|                |             | 2011/12    | LHI4      | JF915801 JF915815       |
| LDL106| C2 Central: Track to Transit Hill |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL107|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL108|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL109|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL110|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL111|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL112|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL113|                |             | 2007       | LHI7      | JF915799 JF915813       |
| LDL257| C3 Central: Windy Point |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL258|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL279|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL332|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL333|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL334|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL417|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL418|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL432|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL437|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL459|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL518|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL521|                |             | 2011/12    | LHI5      | JF915791 JF915805       |
| LDL522|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL523|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL528|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL534|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| LDL539|                |             | 2011/12    | LHI7      | JF915799 JF915813       |
| Pop. | Site Name                  | Sample Code | Time point | Haplotype | GenBank Accession Number |
|------|----------------------------|-------------|------------|-----------|-------------------------|
| LDL553 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
| LDL554 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL571 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
| LDL572 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
| LDL589 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
| LDL590 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
| LDL591 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
| LDL17  | Southern: Recycling Centre/Cobby’s Corner | 2007     | LHI4       |           | JF915801 JF915815       |
| LDL18  |                           | 2007        | LHI4       |           | JF915801 JF915815       |
| LDL19  |                           | 2007        | LHI4       |           | JF915801 JF915815       |
| LDL52  |                           | 2007        | LHI2       |           | JF915800 JF915814       |
| LDL114 |                           | 2007        | LHI4       |           | JF915801 JF915815       |
| LDL115 |                           | 2007        | LHI4       |           | JF915801 JF915815       |
| LDL116 |                           | 2007        | LHI4       |           | JF915801 JF915815       |
| LDL117 |                           | 2007        | LHI7       |           | JF915799 JF915813       |
| LDL118 |                           | 2007        | LHI4       |           | JF915801 JF915815       |
| LDL362 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL368 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL369 |                           | 2011/12     | LHI3       |           | JF915803 JF915817       |
| LDL370 |                           | 2011/12     | LHI2       |           | JF915800 JF915814       |
| LDL371 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL372 |                           | 2011/12     | LHI2       |           | JF915800 JF915814       |
| LDL373 |                           | 2011/12     | LHI2       |           | JF915800 JF915814       |
| LDL374 |                           | 2011/12     | LHI3       |           | JF915803 JF915817       |
| LDL403 |                           | 2011/12     | LHI2       |           | JF915800 JF915814       |
| LDL404 |                           | 2011/12     | LHI2       |           | JF915800 JF915814       |
| LDL405 |                           | 2011/12     | LHI1       |           | JF915798 JF915812       |
| LDL406 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL419 |                           | 2011/12     | LHI5       |           | JF915791 JF915805       |
| LDL422 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL423 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL424 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL440 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL465 |                           | 2011/12     | LHI3       |           | JF915803 JF915817       |
| LDL466 |                           | 2011/12     | LHI1       |           | JF915798 JF915812       |
| LDL486 |                           | 2011/12     | LHI5       |           | JF915791 JF915805       |
| LDL487 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL488 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL493 |                           | 2011/12     | LHI4       |           | JF915801 JF915815       |
| LDL79  | Southern: King’s/ Salmon beach | 2007     | LHI7       |           | JF915799 JF915813       |
| LDL80  |                           | 2007        | LHI2       |           | JF915800 JF915814       |
| LDL81  |                           | 2007        | LHI2       |           | JF915800 JF915814       |
| LDL78  |                           | 2007        | LHI7       |           | JF915799 JF915813       |
| LDL119 |                           | 2007        | LHI7       |           | JF915799 JF915813       |
| LDL120 |                           | 2007        | LHI7       |           | JF915799 JF915813       |
| LDL139 |                           | 2007        | LHI7       |           | JF915799 JF915813       |
| LDL140 |                           | 2007        | LHI7       |           | JF915799 JF915813       |
| LDL349 |                           | 2011/12     | LHI6       |           | JF915802 JF915816       |
| LDL350 |                           | 2011/12     | LHI7       |           | JF915799 JF915813       |
### Continued Table S2

| Pop.   | Site Name | Sample Code | Time point | Haplotype | GenBank Accession Number |
|--------|-----------|-------------|------------|-----------|--------------------------|
| LDL351 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL407 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL408 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL409 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL410 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL411 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL421 |           |             | 2011/12    | LHI6      | JF915802, JF915816      |
| LDL427 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL428 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL455 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL456 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL457 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL463 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL469 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL470 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL471 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL472 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL485 |           |             | 2011/12    | LHI6      | JF915802, JF915816      |
| LDL497 |           |             | 2011/12    | LHI4      | JF915801, JF915815      |
| LDL498 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL499 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL500 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL451 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL452 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL453 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL454 |           |             | 2011/12    | LHI2      | JF915800, JF915814      |
| LDL458 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL464 |           |             | 2011/12    | LHI2      | JF915800, JF915814      |
| LDL473 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL474 |           |             | 2011/12    | LHI2      | JF915800, JF915814      |
| LDL475 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL476 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL477 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL478 |           |             | 2011/12    | LHI6      | JF915802, JF915816      |
| LDL479 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL480 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL481 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL482 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL483 |           |             | 2011/12    | LHI2      | JF915800, JF915814      |
| LDL484 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL489 |           |             | 2011/12    | LHI6      | JF915802, JF915816      |
| LDL490 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL491 |           |             | 2011/12    | LHI6      | JF915802, JF915816      |
| LDL492 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL494 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL495 |           |             | 2011/12    | LHI6      | JF915802, JF915816      |
| LDL496 |           |             | 2011/12    | LHI7      | JF915799, JF915813      |
| LDL121 |           |             | 2007       | LHI6      | JF915802, JF915816      |
| LDL122 |           |             | 2007       | LHI7      | JF915799, JF915813      |
| Pop. | Site Name       | Sample Code | Time point | Haplotype | GenBank Accession Number |
|------|----------------|-------------|------------|-----------|-------------------------|
| LDL123 |                | LDL123     | 2007       | LH6       | JF915802, JF915816      |
| LDL124 |                | LDL124     | 2007       | LH6       | JF915802, JF915816      |
| LDL125 |                | LDL125     | 2007       | LH6       | JF915802, JF915816      |
| LDL126 |                | LDL126     | 2007       | LH6       | JF915802, JF915816      |
| LDL127 |                | LDL127     | 2007       | LH7       | JF915799, JF915813      |
| LDL128 |                | LDL128     | 2007       | LH6       | JF915802, JF915816      |
| LDL129 |                | LDL129     | 2007       | LH7       | JF915799, JF915813      |
| LDL130 |                | LDL130     | 2007       | LH7       | JF915799, JF915813      |
| LDL131 |                | LDL131     | 2007       | LH7       | JF915799, JF915813      |
| LDL132 |                | LDL132     | 2007       | LH6       | JF915802, JF915816      |
| LDL133 |                | LDL133     | 2007       | LH6       | JF915802, JF915816      |
| LDL134 |                | LDL134     | 2007       | LH6       | JF915802, JF915816      |
| LDL135 |                | LDL135     | 2007       | LH6       | JF915802, JF915816      |
| LDL136 |                | LDL136     | 2007       | LH6       | JF915802, JF915816      |
| LDL137 |                | LDL137     | 2007       | LH6       | JF915802, JF915816      |
| LDL138 |                | LDL138     | 2007       | LH7       | JF915799, JF915813      |
| LDL687 |                | LDL687     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL688 |                | LDL688     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL689 |                | LDL689     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL690 |                | LDL690     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL691 |                | LDL691     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL692 |                | LDL692     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL693 |                | LDL693     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL694 |                | LDL694     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL695 |                | LDL695     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL696 |                | LDL696     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL697 |                | LDL697     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL698 |                | LDL698     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL699 |                | LDL699     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL700 |                | LDL700     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL701 |                | LDL701     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL702 |                | LDL702     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL703 |                | LDL703     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL704 |                | LDL704     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL705 |                | LDL705     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL706 |                | LDL706     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL707 |                | LDL707     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL708 |                | LDL708     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL709 |                | LDL709     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL710 |                | LDL710     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL711 |                | LDL711     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL712 |                | LDL712     | 2011/12    | LH6       | JF915802, JF915816      |
| LDL713 |                | LDL713     | 2011/12    | LH7       | JF915799, JF915813      |
| LDL714 |                | LDL714     | 2011/12    | LH7       | JF915799, JF915813      |