Evidence for mega-landslides as drivers of island colonisation

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Evidence for mega-landslides as drivers of island colonisation

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Abstract

Aim: How non-dispersive taxa colonise islands is generalised as being by wind, or rafting, with the implicit assumption that such events involve one (wind) or a few (rafting) individuals. However, because of the evolutionary timescale for colonisation events, the fit of individual species to a conceptual model of wind or rafting is difficult to assess. Here we describe an alternative testable geological model for inter-island colonisation that can result in larger effective founding population sizes than traditionally accepted colonisation mechanisms. We then test for the fit of genetic data to this model using weevils from the *Laparocerus tessellatus* species complex.

Location: Canary Islands.

Methods: Using a combination of geological data for the Canary Islands, and mtDNA data from a weevil radiation within the Canary Islands, we test three species-level predictions for mega-landslides as drivers of oceanic rafting between islands and subsequent speciation: (i) colonisation should involve multiple female lineages: (ii) founding lineages should have a common geographic origin, consistent with a mega-landslide event, and: (iii) colonisation direction should be consistent with ocean currents.

Results: Both individual-level and population-level analyses support a mega-landslide event as the driver of colonisation from the island of Tenerife to La Palma. At least four female lineages colonised La Palma from Tenerife, with the geographic range of ancestral sequences to these four lineages describing the limits of the La Orotava mega-landslide in Tenerife.

Main conclusions: In the context of island biogeographic theory, mega-landslides may be an important driver of colonisation, and subsequent lineage diversification. They provide a framework for hypothesis testing using genetic data from species, or closely related species, with ranges that encompass landslides and potential areas of colonisation.

Key words: biogeography, invertebrate, dispersal, phylogeography, equilibrium theory, rafting

Introduction

Our understanding of speciation within oceanic archipelagos has advanced considerably in recent decades (Warren *et al.*, 2015), in large part as a consequence of continued efforts to analyse phylogenetic data from a diversity of taxa with geographical, ecological and geological data. In contrast, there has been little investigation of the mechanisms promoting dispersal among islands within an archipelago, a process that underpins island biogeographic theory (MacArthur & Wilson, 1963, 1967). Dispersal from one island to another must be either airborne or waterborne. For invertebrate taxa, which typically comprise the dominant component of species richness on oceanic islands, airborne colonisation may involve secondary transport by birds, or wind. Secondary transport by birds is likely important for ectoparasitic invertebrate taxa, or non-ectoparasitic taxa transported through ingestion (e.g. Wada *et al.*, 2011). However, transport by ingestion is unlikely to account for more than a very small proportion of invertebrate species, and likely limited to those that feed within seeds (Gillespie *et al.*, 2012). Windborne colonisation should be important for flighted invertebrates, but less consequential for flightless invertebrates. Unless windborne colonisation involves a gravid female, a female with stored sperm, or a parthenogenetic individual, colonisation would not be followed by establishment, as it is unlikely that wind-transported individuals would arrive within the geographic proximity of each other required for subsequent mating. Even allowing for the colonisation of a multiply mated female, successful establishment of a windborne colonist could be challenging due to low genetic variation and inbreeding, although this is not always the case (e.g., see Edelaar *et al.*, 2015). In contrast to windborne dispersal, colonisation by oceanic rafting may result in multiple individuals arriving, but is expected to involve a limited number of individuals of coastal or riverine affinity (Gillespie *et al.*, 2012). Thus, the conceptual model of colonisation by wind or rafting is expected to result in extreme founder events, something seen as a potential driver of insular speciation (Carson & Kaneshiro, 1976; Templeton, 1980, 2008). It is also expected to be mostly relevant for flighted species, or flightless species with coastal distributions, or with freshwater connections to the coast. Colonisation by non-coastal flightless species is harder to explain.

In their consideration of long distance dispersal (i.e. from continents to archipelagos), Gillespie *et al.* (2012) point out that the ability of organisms to disperse by oceanic drift, or rafting on flotsam, is a function of the interaction of four variables: (i) ocean dynamics, (ii) survival *en*

route, (iii) geomorphology and (iv) proximity to the ocean, given that rafts are initiated from areas proximate to oceans. With regard to ocean dynamics, although they may vary through geological time, they are idiosyncratic in nature and island or archipelago specific. However, the remaining three points suggest oceanic drift or rafting may be very consequential at the inter-island scale. Regarding point (ii), the comparatively short distances between islands must greatly increase survival probability, compared to the long distances that typically characterise continental source areas and isolated oceanic archipelagos. With regard to points (iii) and (iv), oceanic island geomorphology provides for periodic, expected and large-scale deposition of biota into the ocean, spanning large altitudinal ranges, through mega-landslide events. This has the potential to promote the synchronous rafting of individuals sampled across broad geographic areas, something that could result in much larger effective founding population sizes than traditionally accepted colonisation mechanisms.

Biotic consequences of volcanic flank collapse

When volcanic edifices reach high altitudes from the ocean floor they are prone to suffer flank collapses for several reasons, principally gravitational instability, volcanic or tectonic seismicity, and dyke injections (McGuire, 2003). Areas in excess of hundreds of km² can be affected, with flank collapse triggering substantial down slope movement of terrain, movements that can occur in only a few minutes at calculated velocities exceeding 100 km/h (Siebert, 1984). These mega-landslide events can generate ocean floor deposits of hundreds of km², measuring hundreds of km in length, involving volumes in the order of thousands of km³ (Canals *et al.*, 2000). Such mega-landslides are not infrequent events, as revealed by terrestrial geological studies, sonar, three-dimensional bathymetry, offshore seismic analysis, and even historical records (e.g. Ward & Day, 2003). There is both inland and sea floor evidence for numerous mega-landslides in the Hawaiian Islands (e.g. Moore *et al.*, 1994), Canary Islands (e.g. Carracedo *et al.*, 2009), Réunion (e.g. Oehler *et al.*, 2004), French Polynesian Islands (e.g. Clément *et al.*, 2002), Tristan da Cunha Island (e.g. Holcomb & Searle, 1991), Cape Verde Islands (e.g. Masson *et al.*, 2008) and the Lesser Antilles Islands (e.g. Samper *et al.*, 2008), among others. The most detailed long-term data on flank collapses within an archipelago comes from a 17 Myr (million years) record for the Canary Islands. Hunt *et al.* (2014) reveal that the mean recurrence of landslides across the Canary Islands over the

last 17 Myr is 135 kyr (thousand years), with the last 7 Myr characterised by a similar mean recurrence of 135 kyr.

Within the Canary Islands the biggest recorded mega-landslides occurred on the island of Tenerife, with 11 documented events that affected vast areas of the island, in some cases from more than 2000 macsl (metres above current sea level) to the coast, resulting in the transfer of enormous debris deposits to the seafloor (Fig. 1, Table S1.1 in Appendix S1 in Supporting Information). While many landslides have been overwritten by subsequent lava deposits, the Orotava and Güímar valleys present clear evidence, with flat floors flanked by steep scarps defining most of their perimeter (Masson *et al.*, 2002). The within island evolutionary significance of such landslides is well understood, as they have produced important habitat discontinuities implicated in divergent evolution between populations on opposing flanks (e.g. Brown *et al.*, 2006; Macías-Hernández *et al.*, 2013; Mairal *et al.*, 2015), the biogeographic relevance of which has also been recognised (Whittaker *et al.*, 2008). What is less understood is the fate of the vast biomass that was deposited into the ocean.

The landslide of La Orotava was initiated at sea level, followed by the rapid downslope movement of higher altitude terrains up to several hundred meters deep. During the subaerial phase of this process, maximum terrain destruction occurs at depth, with limited transformation of the surface, meaning that surface organic material likely remains relatively intact prior to entering the ocean. An obvious consequence of this dynamic would be the flotation of organic matter, derived from more than 100 km² of diverse habitat, from the coastline to altitudes exceeding 2000 macsl (Fig. 2). Oceanic rafting on this scale, with favourable ocean currents, could potentially favour the synchronous transport of many individuals to neighbouring islands, providing a suitable scenario for testable predictions.

Predictions for colonisation from a mega-landslide

Three testable predictions can be made for the colonisation of an invertebrate species originating from a mega-landslide. The first is that colonisation should have involved multiple female lineages. The second is that founding lineages should share a common geographic origin that is spatially consistent with a mega-landslide event. The third is that colonisation direction should be consistent with ocean currents. Here we evaluate evidence for these predictions using mtDNA

sequence data for a complex of flightless beetle species on the Canary Islands. Among the more than 128 species within the weevil genus *Laparocerus* in the Canary Islands, the *L. tessellatus* complex comprises 11 taxonomically described species, each being a single island endemic. A recent molecular genetic analysis of the complex (Faria *et al.*, 2016) sampled nine species (two new species were subsequently described by Machado, 2016) revealed complex relationships among individual-level patterns of nuclear and mtDNA sequence relatedness, and taxonomy (see Faria *et al.*, 2016 for details). Of relevance to the above-mentioned predictions, it was revealed that the single species from the island of La Palma was founded by individuals of related species from the islands of Tenerife and Gran Canaria (Faria *et al.*, 2016). In the case of Tenerife, two founding mtDNA haplotypes to La Palma were inferred from sequences sampled from several localities above the steep scarps defining the perimeter of the Orotava valley. This provides a minimum estimate of two colonising female lineages, and is suggestive of a possible role for the La Orotava mega-landslide. We evaluate this hypothesis by sampling the *L. tessellatus* complex to specifically test the prediction of multiple founding female lineages to La Palma from the region of the Orotava valley. We use DNA sequence data from the mitochondrial genome, as its characteristic female inheritance and absence of recombination allows for robust inferences of the minimum number of founding female lineages through the reconstruction of coalescent ancestry.

Materials and Methods

Sampling and laboratory procedures

We increased previous geographic sampling for the *L. tessellatus* complex (Faria *et al.*, 2016) by visiting collecting localities for species of the *L. tessellatus* complex within the collection of AM, and several other new localities. From two to five individuals were sequenced from each locality on the island of Gran Canaria. As our focus is on the mtDNA relatedness between La Palma and Tenerife, we took an iterative approach to sequencing. Two individuals from each sampling locality were sequenced in the first instance for the mtDNA COII gene region for joint analysis with published data (Faria *et al.*, 2016). Localities in Tenerife yielding mtDNA sequences closely related to La Palma were then sequenced for a further three individuals (unless limited by sample

numbers). Similarly, all localities in La Palma with mtDNA sequences closely related to sequences from Tenerife were sequenced for a further three individuals. Total genomic DNA was extracted from the two hind legs using a Chelex extraction protocol (Casquet *et al.*, 2012). The mitochondrial COII gene was amplified using previously described conditions (Faria *et al.*, 2016) and sequenced using the Sanger DNA sequencing service of Macrogen (www.macrogen.com). Sequences were edited with Geneious R8 8.0.3 (<http://geneious.com>, Kearse *et al.*, 2012), aligned using MEGA 6.06 (Tamura *et al.*, 2013), and unique haplotypes were collapsed Fabox 1.41 (Villesen, 2007).

Haplotype network and Bayesian phylogenetic tree construction

Statistical parsimony was used to infer a haplotype network using PopART (Leigh & Bryant, 2015). Predictions from coalescent theory, related to the frequency and geographical distribution of haplotypes, are often applied to resolve reticulations within haplotype networks (Posada & Crandall, 2001). However, the strong geographic structuring of mtDNA variation within the *L. tessellatus* complex (Faria *et al.*, 2016) precludes the use of probability-based predictions derived from coalescent theory to solve reticulations (Posada & Crandall, 2001). We therefore used an alternative probability-based approach where, for each reticulation, we evaluated alternative solutions under an appropriate model of DNA sequence evolution. This was achieved by constructing a Bayesian tree from the sequence data with MrBayes v3.2.5 (Ronquist, 2012) under a general time reversible model of sequence evolution with a gamma correction (GTR+G) without modelling invariant sites (I), as in Faria *et al.* (2016). Four analyses were each run for 100 million generations using 4 MCMC (Markov chain Monte Carlo) chains, starting from a random tree, and sampling trees every 1000 generations. For both the network and Bayesian analyses a sequence from the closely related species *L. vicinus* was used as an outgroup. Stationarity and convergence of the chains were determined by graphical inspection of the values of the log-likelihoods of the four MCMC analyses; confirmation that the average standard deviation of split frequencies was below 0.01 at the completion of the analysis; and verification that effective sample size (ESS) values were above 200 using the log files in Tracer 1.6 (Rambaut, 2016). A burn-in of 25% was removed from each run, and the remaining trees were used to construct a majority-rule consensus tree.

213 *Minimum estimation of founding female lineages*

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215 We used a rooted haplotype network of geographically referenced mtDNA sequences, to infer the
216 dispersal history of maternal lineages (e.g. Emerson *et al.*, 2006). The rooted mtDNA haplotype
217 network was used to estimate the minimum number of mtDNA haplotypes that are, or have been,
218 shared between islands, with the direction of dispersal inferred from the order of geographic state
219 change from the root of the network (Fig. 3). This provides a minimum estimate of the number of
220 female lineages that have dispersed between islands. One or more geographic states (islands) can
221 be assigned to each sampled haplotype, and on the basis of these known states, one can infer the
222 geographic states of missing (extinct or unsampled) haplotypes within the network. We inferred
223 haplotype sharing (female dispersal) either (i) directly, when a sampled haplotype had two
224 geographic states (Fig. 3A), or (ii) indirectly, when the geographic state changed between an
225 ancestral and descendent haplotype (Fig. 3B-F).

227 *Analyses of population structure*

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229 We defined three geographic regions based upon the relatedness of mtDNA haplotypes between
230 La Palma and Tenerife. The first region consists of all sites on La Palma sampled for mtDNA
231 lineages derived from Tenerife. The second region is a polygon describing the minimum geographic
232 range of mtDNA haplotypes and their descendants from Tenerife that are ancestral to La Palma
233 haplotypes. To construct the polygon we applied an iterative approach, using the minimum convex
234 polygon method (Mohr, 1947). In a first iteration a polygon describing the geographic range of this
235 group of haplotypes was constructed. Subsequent iterations removed haplotypes from
236 populations at the periphery of the polygon if they were also present within interior population,
237 until no more haplotypes could be removed. The third region comprises the remaining sampling
238 sites on Tenerife that fall outside the polygon.

239 To test whether the distribution of mtDNA genetic diversity reveals a phylogeographic
240 pattern within the *L. tessellatus* complex distributed across the three regions, genetic
241 differentiation among populations was estimated using both F_{ST} (genetic distance among
242 haplotypes is unweighted) and N_{ST} (genetic distance among haplotypes is weighted). When
243 mutation rate exceeds dispersal rate, haplotypes within regions will be more closely related than

haplotypes compared among regions (Pons & Petit, 1996). Under these conditions N_{ST} will exceed F_{ST} , indicating a greater role of mutation and the phylogeographic structuring of genetic variation over evolutionary time scales, compared to the structuring of genetic variation by gene flow and genetic drift over ecological time scales. To test whether N_{ST} was significantly higher than F_{ST} , a randomization procedure permuting haplotype assignation in the matrix of genetic distances among haplotypes was performed and repeated 10,000 times in SPaGeDi 1.4b (Hardy & Vekemans, 2002).

Results

Haplotype network and Bayesian phylogenetic tree

Forty-seven sites were sampled in Tenerife, 32 in La Palma, and 21 in Gran Canaria (Fig. 4, Table S2.2 in Appendix S2). A total of 255 new individuals were sequenced, yielding 394 DNA sequences together with previously published sequences (Faria *et al.*, 2016). DNA sequences were collapsed to 195 unique haplotypes, characterised by 164 polymorphic sites across 633 bp, 127 of which were parsimony informative. A single haplotype network was obtained from the statistical parsimony analysis, with a total of 44 reticulations, of which all but two were solved with the Bayesian phylogenetic reconstruction (Fig. S2.1 in Appendix S2). The resolved network (Fig. 5) thus presents comparable geographic clusters of sequences, branching relationships among them, and root location, as those obtained in the Bayesian phylogenetic analysis (Fig. S2.1 in Appendix S2).

Number and origin of founding female lineages from Tenerife to La Palma

The rooted haplotype network reveals that the mtDNA variation of the *L. tessellatus* complex across the four islands has involved the establishment of at least 11 female lineages by inter-island colonisation (Fig. 5). Our sampling reveals a total of six colonising haplotypes to the island of La Palma, doubling a previous estimate (Faria *et al.*, 2016), of which two are derived from Gran Canaria, with the remaining four derived from Tenerife. Twenty mtDNA haplotypes from Tenerife were identified either as ancestral to La Palma (2), or derived from ancestral haplotypes (18) by no

more than 4 mutations (Fig. 5) and were sampled from 18 of the 47 sampling sites. For ease of understanding we refer to these as TF-LP haplotypes. The mean divergence between the 18 derived TF-LP haplotypes and the most closely related sampled or unsampled ancestral haplotype was 1 mutation. A polygon describing the minimum geographic range of the 20 TF-LP haplotypes was arrived at after 4 iterations, and included a total of 18 sampling sites, 14 of which contain TF-LP haplotypes, which broadly describes the Orotava valley (Fig. 4). All but two of the 18 sites are above the steep escarpments or within the Orotava valley, with the remaining two sites on the geographically proximate southern slope of the Güímar valley. The 18 sampling sites within the polygon were sampled for a total of 80 individuals, of which 49 presented a TF-LP haplotype, with the remaining 31 presenting one of the 18 other haplotypes sampled within this region. The remaining 29 Tenerife sampling sites outside the polygon were sampled for a total of 89 individuals and 39 haplotypes.

The global N_{ST} of 0.34 is significantly higher ($P<0.001$) than the global F_{ST} of 0.03 ($P<0.001$), indicating the dominant role of geographic isolation and mutation over gene flow and genetic drift for the structuring of genetic variation across the three regions. All pairwise F_{ST} and N_{ST} comparisons are significantly different from zero and N_{ST} were consistently significantly higher than F_{ST} ($P<0.001$; Table 1). The two regions of Tenerife are the least differentiated from each other. La Palma is similarly differentiated from the Orotava valley and all other Tenerife sampling sites for F_{ST} (0.04 for both), but less differentiated from the polygon representing the Orotava valley for N_{ST} (0.38 from the Orotava valley and 0.45 from the rest of Tenerife). Thus, mtDNA variation in La Palma is less differentiated from mtDNA variation in the Orotava valley than it is from the rest of Tenerife, supporting the hypothesis that the Orotava valley is the source area for individuals that colonised La Palma.

Discussion

In support of predictions one and two, we find that multiple founding individuals to La Palma share a common geographic origin consistent with the mega-landslide event of the Orotava valley. Marine currents between Tenerife and La Palma provide support for prediction three. The Canary Current is estimated to have been relatively unchanged over the past 22 Myr, passing southward

along the northwest African coast, until reaching the Canary Islands, the geomorphology of which forces it to pass among the islands. Of particular relevance is the trade wind season which results in currents that flow to the south between islands, but also an offshore current that swings around the archipelago (Mittelstaedt, 1991), providing a connection between Tenerife and La Palma. The Canary Current has an estimated flow speed of $10\text{--}30\text{ cm}\cdot\text{s}^{-1}$ (Wooster *et al.*, 1976), suggesting that the offshore current would carry floating organic material deposited from the Orotava valley over the minimum distance of 120 km between the coast of La Orotava and the coast of La Palma in a period between 4 and 13 days.

Mega-landslide, or small raft?

Rafts of vegetation are recognised as an important mechanism for the arrival of species to oceanic islands from more distant continental source areas, and rafts of a similar nature are also likely to play a role in inter-island colonisation. However, as highlighted by Gillespie *et al.* (2012), such rafts will be initiated from areas proximate to oceans (e.g. coastal areas, or upriver), and are thus more relevant for flora and fauna of coastal or riverine affinity. The *L. tessellatus* complex in Tenerife is typical of altitudes between 764 macsl and 1424 macsl (first and third quartiles of species distribution records), and is rarely observed below an altitude of 300 macsl (see Appendix S3), meaning that transportation by rafts, in the classical sense of coastal or freshwater origin, is improbable. In contrast, a landslide event on the scale of that forming the Orotava Valley would yield rafting organic matter from higher altitudes (Fig. 2). There is little direct data on what would happen to this organic matter once it enters the sea, but an important insight comes from the eruption of Mount St. Helens in May 1980. The eruption itself was preceded, and probably in part promoted, by a mega-landslide that carried tens of thousands of trees into Spirit Lake, where a giant log raft formed and persisted for years (Coffin, 1983; see Appendix S3). The behaviour of the Mount St. Helens landslide highlights the potential for large scale oceanic rafting of organic material derived from a mega-landslide. For the Orotava landslide, the estimated surface area 136 km^2 (Table S1.1 in Appendix S1), would have contributed many millions of individual plants and invertebrates to floating organic matter.

Mega-landslides, tsunamis, and their consequences for island biogeography

Mega-landslides from volcanic island flank collapses are expected to directly deposit a large amount of organic material into the ocean (Fig. 2). An additional consequence of such landslide events is that they also trigger tsunamis when entering energetically into the sea (McGuire, 1996), and there are records of tsunamis from landslides in recent times (Evans *et al.*, 2006; Furukawa *et al.*, 2008 and references therein), as well as coastal deposits for more historical events (e.g. McMurtry *et al.*, 1999; McMurtry *et al.*, 2004b; Pérez-Torrado *et al.*, 2006; Coello *et al.*, 2014; Ramalho *et al.*, 2015). The resulting tsunami waves are propagated both offshore and onshore (Didenkulova *et al.*, 2010; Sue *et al.*, 2011), and can reach heights of hundreds of metres, as recorded by coastal deposits (e.g. McMurtry *et al.*, 2004b: 240–356 m; McMurtry *et al.*, 2004a: 400 m; Pérez-Torrado *et al.*, 2006: 188 m; Ramalho *et al.*, 2015: 270 m). Thus, tsunamis not only wash up the coasts of islands and mainland areas in their trajectory, but also the coast of the island suffering the landslide.

Given that there are both offshore and onshore tsunami waves propagating from a mega-landslide (Didenkulova *et al.*, 2010; Sue *et al.*, 2011), deposition of organic material into the ocean is also expected from (i) areas of the source island affected by the onshore tsunami, and (ii) islands impacted by the offshore tsunami. Thus, mega-landslides are expected to promote the ocean deposition and rafting of significantly more organic material than that associated with the landslide itself, although the altitude of secondary deposition will be a function of the tsunami height. In the context of island biogeographic theory, for which colonisation is a fundamental component (MacArthur & Wilson, 1963, 1967), mega-landslides may be an important driver of colonisation, mediated by ocean currents and archipelago geomorphology.

Limitations and further considerations

A general limitation that applies to the present study is a lack of power to estimate the timing of colonisation of mtDNA lineages, which are expected to be synchronous when driven by a mega-landslide event, and consistent with the timing of the mega-landslide event. This is because the estimation of colonisation times of mtDNA lineages that are derived from coalescent mtDNA variation within a source population is subject to multiple sources of error, including unsampled or

extinct haplotypes (see Fig. 5, and Fig. 2 for a conceptual explanation), mean substitution rate uncertainty and high rate variance over a coalescent time-scale. We suggest that some of these challenges may be alleviated in future studies with reduced representation genome sequencing approaches, such as restriction site-associated DNA sequencing (RADseq). With access to geographically referenced patterns of relatedness across potentially thousands of nuclear loci, it may be possible to estimate demographic parameters such as the number of founding events, their timing, and their founding population size(s).

For a given mega-landslide event, ocean currents and archipelago geomorphology will influence the dispersal of organic material deposited into the ocean, potentially providing for model-based hypothesis testing. However, obtaining supporting evidence is expected to be challenging for older mega-landslide events. This is because lineage sorting will erode patterns of shared genetic variation across islands with time, until all individuals coalesce back to a single source lineage. Thus, the older a landslide event is, the less likely it will be to find signatures of colonisation involving multiple individuals. We therefore suggest that it will be advantageous to investigate mega-landslides of recent geological origin. Given the potential for mega-landslides to result in the synchronous colonisation of a large number species to a neighbouring island, we also suggest sampling multiple species with distributions that could be explained by a mega-landslide. Taking a multi-species, multi-locus approach, with a focus on geologically recent mega-landslides should shed light on their general importance in oceanic island biogeography.

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Peer Review

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Supporting information

Additional supporting Information includes one figure and three tables and can be found with this article:

- Appendix S1:** Details of documented landslides in the island of Tenerife
- Appendix S2:** Details of sampling locations and the taxonomic assignment of samples, and the Bayesian phylogenetic tree constructed from 194 unique mtDNA haplotypes.
- Appendix S3:** Altitudinal sampling data for the *L. tessellatus* complex in Tenerife, and photographic evidence of floating vegetation resulting from the 1980 eruption of Mount St. Helens.

Data accessibility

The accession number for the DNA sequence alignment reported in this paper is Dryad: http://to_be_included_upon_acceptance.

Biosketch

The research team have complementary interests in the geology and biodiversity of oceanic islands, and the application of molecular data to understand the origin and maintenance of species and communities of species. This work is a synthesis of these different interests.

578 Author contributions: BCE, VGO and HL conceived and coordinated the study with input from JP,
579 NA, AM, JCC and VS. BCE, VGO and HL undertook the fieldwork, with input from AMC. VGO carried
580 out all laboratory procedures and data analysis, with input from BCE, HL and JP. VGO, HL and BCE
581 wrote the paper with input from other authors.

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583 Editor: Kostas Triantis

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For Peer Review

Table 1. Pairwise F_{ST} (below) and N_{ST} (above) values calculated using mtDNA COII sequence data for the *Laparocerus tessellatus* complex sampled from the Orotava Valley, Tenerife (excluding the Orotava valley) and La Palma. P-values indicate the probability that F_{ST} is significantly different from zero after 10.000 permutations of specimens among the three regions. P-values for N_{ST} indicate the probability that N_{ST} is significantly different from F_{ST} after 10.000 permutations of the matrix of genetic distances among haplotypes.

	Orotava Valley	Tenerife	La Palma
Orotava Valley	-	0.130***	0.377***
Tenerife	0.022***	-	0.452***
La Palma	0.042***	0.041***	-

***P < 0.001.

Figure 1. Mega-landslides on the island of Tenerife. Seven of the 11 documented landslides are sufficiently unaffected by subsequent volcanic activity to be able to identify their geographic limits. Landslides are colour-coded according to the inset that provides approximate ages for each mega-landslide. See Table S1.1 in Appendix S1 for more details.

Figure 2. Biotic consequences of a volcanic flank collapse. (A) Flank collapse is initiated near sea-level, causing the downslope movement of a block of terrain. The surface of the affected terrain suffers limited transformation, with maximum transformation occurring along the sliding plane. (B) A consequence of the dynamic described in A is that much of the organic surface layer may enter in the ocean practically intact, with a high proportion remaining on the surface due to its high floatability. (C) The ocean surface will contain a vast amount of organic debris derived from the surface of the landslide, including living animals and plant material. This flotsam, together with favourable winds and marine currents, would favour the dispersal of animals and plant species between islands.

Figure 3. Inferring sets of potential colonist (geographically shared) haplotypes, and the minimum number of colonising haplotypes. Haplotypes from an ancestral island (X) are represented as black filled circles. Haplotypes from a colonised island (Y) are represented as white filled circles. Haplotypes found on both X and Y are shown in hatching. Large circles represent sampled haplotypes. Small circles represent missing (extinct or unsampled) haplotypes, whose *potential* geographic states are inferred based on the known geographic states of immediately ancestral and descendent sampled haplotypes. For each of the scenarios A-G, asterisks indicate the set of haplotypes from which a minimum of one haplotype is inferred to have colonised from X to Y. (A) represents no haplotype extinction and sampling of all haplotypes, while C-E represent the same scenario but with some extinct or unsampled haplotypes, while F-G represent alternative scenarios with coalescence. (A) 5 is identified as the colonising haplotype as it is shared across both islands. (B) Either 4 or 5 is the colonising haplotype: 4 colonised Y and is unsampled or extinct on Y, or 5 colonised Y and is unsampled or extinct on X. (C) Either 5 or 6 is the colonising haplotype: 5 colonised Y and is unsampled or extinct on Y, or 6 colonised Y and is unsampled or extinct on X. (D) Either 4, 5 or 6 is the colonising haplotype: 4 colonised Y and is unsampled or extinct on Y, or 5 colonised Y and is unsampled or extinct on both islands, or 6 colonised Y and is

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627 unsampled or extinct on X. (E) Any of haplotypes 2-9 may have colonised from X to Y: 2 colonised Y
628 and is unsampled or extinct on B, or one of haplotypes 3-8 colonised Y and is unsampled or extinct
629 on both islands, or 9 colonised Y and is unsampled or extinct on X. (F) At least two colonising
630 haplotypes are inferred, due to the sampling of haplotypes 2 and 10 on X, with a minimum of one
631 shared haplotype between haplotypes 2-9, and the other between 10-17. (G) Similar to F, but
632 unsampled or extinct haplotypes 2 and 10 result in a minimum inference of 1 colonising haplotype.

633
634 **Figure 4. Map of sampling sites for the *Laparocerus tessellatus* complex.** The eleven
635 taxonomically defined species within the complex are all single island endemics. Gran Canaria (5
636 species): *L. microphthalmus* Lindberg, 1950, *L. obsitus* Wollaston, 1864, *L. osorio* Machado, 2012, *L.*
637 *tirajana* Machado, 2012, and *L. sp. aff. tirajana*. Tenerife (4 species) *L. tessellatus* (Brulle, 1839), *L.*
638 *freyi* Uyttenboogaart, 1940, *L. punctiger* Machado, 2016, and *L. canescens* Machado, 2016. La
639 Palma (1 species): *L. auarita* Machado, 2016. El Hierro (1 species): *L. bimbache* Machado, 2011.
640 Sampling sites are colour coded to be consistent with island colour coding in Figure 5 and Figure
641 S1. Geographic coordinates of sampling sites, and the taxonomic species assignment of samples
642 from each location are provided in Table S2.2 in Appendix 2. Also shown is a polygon describing
643 the minimum geographic range of mtDNA haplotypes and their descendants from Tenerife that
644 are ancestral to La Palma haplotypes (see text). Sampling sites from Faria *et al.* (2016) are
645 indicated with a white dot inside the coloured circle.

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647 **Figure 5. Haplotype network.** A resolved haplotype network representing the relationships among
648 195 mtDNA haplotypes obtained from 633 bp of mtDNA sequence data for the COII gene for 396
649 individuals of the *Laparocerus tessellatus* complex. Haplotypes are colour coded with respect to
650 island: yellow - Gran Canaria, blue - Tenerife, green - La Palma, pink - El Hierro. Haplotypes from
651 Tenerife that are ancestral to La Palma, or closely related to haplotypes that are ancestral to La
652 Palma (referred to as TF-LP haplotypes in the text), are shown in light blue. Extinct or unsampled
653 haplotypes are shown as small black filled circles. The grey arrow indicates the most recent
654 common ancestral haplotype of the complex, determined by rooting with the closely related
655 species *L. vicinus* Lindberg, 1953. Coloured pointed rectangles represent sets of potential ancestral
656 haplotypes, from which at least one haplotype colonised a new island, with colonisation direction
657 indicated by a colour gradient and pointed end to the rectangle (see Figure 3).

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SUPPORTING INFORMATION

Evidence for mega-landslides as drivers of island colonisation

Victor García-Olivares, Heriberto López, Jairo Patiño, Nadir Alvarez, Antonio Machado, Juan Carlos Carrecedo, Vicente Soler and Brent C. Emerson

Appendix S1. Details of documented landslides on the island of Tenerife

Table S1.1 Summary of documented landslides on the island of Tenerife, with marine deposit data when known. The area of each major plant community affected was calculated for those landslides where the limits of the surface area affected are clearly described by geomorphological evidence, such as landslide scars on island flanks. GIS shapes for the limits of the affected landslide areas were created based on previous published approximations, and on scars visualized on maps within the Canary Island cartography website (<http://visor.grafcan.es/visorweb/>). GIS shapes were then imported into maps of potential vegetation, and areas of each plant community were estimated using proprietary tools within the grafcan website.

Landslide	Age (Ma)	Marine deposits			Area of the landslide in inland (km ²)						Total
		Length (km)	Area (km ²)	Volume (km ³)	High mountain scrub	Pine forest	Laurel forest	Thermophilous woodland	Xeric shrub	Other	
Masca	5.89-6.65 ^{a,b}	-	-	-	-	-	-	-	-	-	-
Carrizales	5.89-6.27 ^{a,b}	-	-	-	-	-	-	-	-	-	-
Teno	6 ^{c,d,e}	35 ^e	400 ^e	-	-	-	-	-	-	-	-
Anaga	4.1-4.7 ^f	33 ^e	>400 ^d , 500 ^{e,g}	36 ^g	0	0	5.6	6.26	3.53	0	15.39
Tigaiga	2.3-2.6 ^{c,e}	30 ^e	200 ^e	-	1.38	14.34	18.8	7.12	0.31	0	41.95
Bandas del Sur	<2 ^h	30 ^h	500 ^h	25 ^h	-	-	-	-	-	-	-
Roques de García	0.6-1.3 ^{c,i}	95 ^e ; 130 ^d	2200-4500 ^{e,d}	500 ^{c,d}	-	-	-	-	-	-	-
Micheque	0.83 ^j	25 ^k	400 ^k	100 ^k	-	-	-	-	-	-	-
Güímar	0.83-0.85 ^{l,m} ; 0.78-0.84 ^d	85 ^e ; >50 ^d	1600 ^{d, h} ; 2600 ^e	120 ^{d, h}	5.14	38.68	5.01	15.07	37.71	28.39	130
La Orotava	0.54-0.69 ^e ; 0.5-0.8 ^h	75 ^e ; 90 ^d	2100 ^d ; 2200 ^e	500 ^d	23.64	23.71	65.43	14.92	8.35	0	136.05
Icod	0.15-0.17 ^d ; 0.165 ⁿ	105 ^d	1700 ^{d,i}	320 ⁿ	-	-	-	-	-	-	-

a: Longpré et al. (2009); b: Walter and Schmincke (2002); c: Cantagrel et al. (1999); d: Masson et al. (2002); e: Acosta et al. (2003); f: Walter et al. (2005); g: Llanes et al. (2003); h: Krastel et al. (2001); i: Watts and Masson (1998); j: Carracedo et al (2011); k: Ablay and Hürlimann (2000); l: Hunt et al. (2013); m: Giachetti et al. (2011); n: Wynn et al. (2002).

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SUPPORTING INFORMATION
Evidence for mega-landslides as drivers of island colonisation
V́ctor Garća-Olivares, Heriberto Ĺpez, Jairo Patiño, Nadir Alvarez, Antonio Machado, Juan Carlos Carrecedo, Vicente Soler and Brent C. Emerson

Appendix S2. Details of sampling locations and the taxonomic assignment of samples, and the Bayesian phylogenetic tree constructed from the 194 unique mtDNA haplotypes obtained from the sequences of 394 individuals.

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Figure S2.1. Bayesian phylogenetic tree constructed from 195 haplotypes for the mtDNA COII gene sampled from the *Laparocerus tessellatus* complex. Haplotype colour represents island of origin (see Fig. 3). See Supplemental Experimental Procedures for more details.

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Table S2.2. Details of sampling locations, the number of individuals sampled at each location, and their taxonomic assignment.

Island	Locality	Locality Code	Lat.	Long.	Taxonomic assignment	No. Individuals	Source
Gran Canaria	Las Huertecillas	C01	28.08554312	-15.55989249	<i>L. obsitus</i>	2	This study
Gran Canaria	Las Huertecillas	C01	28.08554312	-15.55989249	<i>L. osorio</i>	1	Faria et al. 2015
Gran Canaria	Degollada de Osorio	C02	28.07254322	-15.55794230	<i>L. sp. aff. tirajana</i>	5	Faria et al. 2015
Gran Canaria	Laguna de Valleseco	C03	28.06506291	-15.56382636	<i>L. obsitus</i>	2	This study
Gran Canaria	Barranco Oscuro	C04	28.06775026	-15.58813215	<i>L. obsitus</i>	4	Faria et al. 2015; this study
Gran Canaria	Barranco Oscuro	C04	28.06775026	-15.58813215	<i>L. osorio</i>	6	Faria et al. 2015; this study
Gran Canaria	Barranco los Cazadores	C05	28.04327617	-15.59488702	<i>L. obsitus</i>	2	This study
Gran Canaria	Barranco los Cazadores	C05	28.04327617	-15.59488702	<i>L. osorio</i>	3	Faria et al. 2015
Gran Canaria	Casa Forestal de Tamadaba	C06	28.05323863	-15.69192219	<i>L. microphthalmus</i>	9	Faria et al. 2015; this study
Gran Canaria	Pico del Majadal	C07	28.03067996	-15.67753554	<i>L. microphthalmus</i>	2	This study
Gran Canaria	Cruz de Tejeda	C08	28.00513303	-15.59791167	<i>L. microphthalmus</i>	3	This study
Gran Canaria	Infra Cruz de Tejeda	C09	27.99958826	-15.60048465	<i>L. obsitus</i>	2	This study
Gran Canaria	Barranco de la Mina	C10	27.99852595	-15.58727789	<i>L. obsitus</i>	2	Faria et al. 2015
Gran Canaria	Barranco de la Mina	C10	27.99852595	-15.58727789	<i>L. osorio</i>	3	This study
Gran Canaria	Las Casillas	C11	27.99277738	-15.52195750	<i>L. obsitus</i>	2	This study
Gran Canaria	Degollada de Becerra	C12	27.98854334	-15.59328465	<i>L. obsitus</i>	2	This study
Gran Canaria	Barranco de los Cernicalos	C13	27.96126336	-15.53148454	<i>L. sp. aff. tirajana</i>	5	Faria et al. 2015; this study
Gran Canaria	Cumbre. Pico Redondo	C14	27.96466481	-15.55926738	<i>L. sp. aff. tirajana</i>	5	Faria et al. 2015; this study
Gran Canaria	Llanos de la Pez	C15	27.96539529	-15.58548187	<i>L. obsitus</i>	2	This study
Gran Canaria	Supra Ayacata	C16	27.96511834	-15.60155445	<i>L. tirajana</i>	2	This study
Gran Canaria	Lomo Aserrador	C17	27.95949872	-15.62689883	<i>L. tirajana</i>	4	This study
Gran Canaria	Casa forestal Pilacones	C18	27.92719590	-15.59940314	<i>L. tirajana</i>	1	This study
Gran Canaria	Barranco Tirajana	C19	27.92605460	-15.57921238	<i>L. tirajana</i>	3	Faria et al. 2015; this study
Gran Canaria	San Bartolome de Tirajana	C20	27.91562810	-15.57493941	<i>L. tirajana</i>	2	This study
Gran Canaria	San Bartolomé, Km 1	C21	27.91213562	-15.57252269	<i>L. tirajana</i>	12	Faria et al. 2015
El Hierro	Monte Ajares, 600 m	H02	27.80306251	-17.91735339	<i>L. bimbache</i>	2	Faria et al. 2015
El Hierro	Piedras Blancas, San Andrés	H06	27.75615779	-17.96588963	<i>L. bimbache</i>	2	Faria et al. 2015
El Hierro	Infra Montaña Masilva	H08	27.74329951	-17.97906625	<i>L. bimbache</i>	2	Faria et al. 2015
La Palma	Ermite Santa Cecilia	P01	28.55312588	-17.86759048	<i>L. auarita</i>	2	This study
La Palma	Don Mendo Inferior	P02	28.55635515	-17.86673813	<i>L. auarita</i>	1	This study
La Palma	Don Mendo Superior	P03	28.55918404	-17.85878435	<i>L. auarita</i>	5	Faria et al. 2015; this study
La Palma	Caldereta de Mazo	P04	28.55171613	-17.78852885	<i>L. auarita</i>	4	This study
La Palma	Montaña de Venjobre	P05	28.60832065	-17.78591420	<i>L. auarita</i>	12	Faria et al. 2015; this study
La Palma	Refugio del Pilar	P06	28.61465974	-17.83430130	<i>L. auarita</i>	2	This study
La Palma	Pared Vieja	P07	28.61991369	-17.82330969	<i>L. auarita</i>	5	Faria et al. 2015; this study
La Palma	Fuente Guairín 1400 m	P08	28.64466749	-17.82496467	<i>L. auarita</i>	5	This study
La Palma	Supra El Paso, 870 m.	P09	28.65230896	-17.84558086	<i>L. auarita</i>	7	Faria et al. 2015
La Palma	Supra El Paso, 837 m	P10	28.65633803	-17.85215283	<i>L. auarita</i>	2	This study
La Palma	Cumbre Nueva, 1400 m	P11	28.66020837	-17.82546337	<i>L. auarita</i>	5	This study
La Palma	Pista de la Cumbre Nueva km 6	P12	28.66844581	-17.82710614	<i>L. auarita</i>	5	This study
La Palma	Pista de Ferrer Inferior	P13	28.67692853	-17.84972415	<i>L. auarita</i>	2	This study
La Palma	Barranco de la Madera	P14	28.69902060	-17.78647300	<i>L. auarita</i>	2	This study
La Palma	Montaña Tagoja B	P15	28.71770148	-17.77949856	<i>L. auarita</i>	3	Faria et al. 2015
La Palma	Montaña Tagoja A	P16	28.72455336	-17.78274993	<i>L. auarita</i>	5	This study
La Palma	Fuente de Olén	P17	28.73150875	-17.81321665	<i>L. auarita</i>	5	This study
La Palma	Picos de las Nieves	P18	28.73144181	-17.83024401	<i>L. auarita</i>	2	This study
La Palma	Las Moradas 2000	P19	28.76854840	-17.90470811	<i>L. auarita</i>	3	This study
La Palma	Pinar de la Garafía 1900 m	P20	28.77295172	-17.90463565	<i>L. auarita</i>	2	This study
La Palma	Pinar de la Garafía 1450 m	P21	28.78029274	-17.91932624	<i>L. auarita</i>	2	This study
La Palma	Cueva de la Zarza	P22	28.80500749	-17.90804415	<i>L. auarita</i>	6	This study
La Palma	Montaña de las Varas	P23	28.81950108	-17.90894892	<i>L. auarita</i>	5	This study
La Palma	Juan Adalid, 600 m	P24	28.83406532	-17.90866785	<i>L. auarita</i>	1	This study
La Palma	Barranco de las Traviesas, 924 m	P25	28.80646150	-17.86624023	<i>L. auarita</i>	5	This study
La Palma	Llanada de Barlovento	P26	28.81725810	-17.80925143	<i>L. auarita</i>	5	Faria et al. 2015
La Palma	Laguna de Barlovento	P27	28.81173517	-17.80936941	<i>L. auarita</i>	5	This study
La Palma	Los Tilos	P28	28.79697693	-17.78941412	<i>L. auarita</i>	5	This study
La Palma	Las Lomadas	P29	28.79118302	-17.78605468	<i>L. auarita</i>	5	This study
La Palma	Marcos y Cordero	P30	28.77274777	-17.81202970	<i>L. auarita</i>	5	This study

La Palma	Infra Marcos y Cordero	P31	28.76956776	-17.78921668	<i>L. auarita</i>	5	This study
La Palma	Cubo de la Galga	P32	28.76701695	-17.76984079	<i>L. auarita</i>	5	This study
Tenerife	Chinobre A	T04	28.55855948	-16.17519235	<i>L. tessellatus</i>	1	Faria et al. 2015
Tenerife	El Pijaral A	T05	28.55558324	-16.18118025	<i>L. tessellatus</i>	12	Faria et al. 2015
Tenerife	Cruz del Carmen	T08	28.53192475	-16.28007026	<i>L. tessellatus</i>	2	Faria et al. 2015
Tenerife	Pista Las Yedras	T10	28.53869269	-16.30013310	<i>L. tessellatus</i>	1	Faria et al. 2015
Tenerife	Los Morros (Altos Vilaflor)	T100	28.17835785	-16.63134339	<i>L. canescens</i>	1	This study
Tenerife	Granadilla (Las Vegas)	T105	28.14503420	-16.54520667	<i>L. canescens</i>	6	Faria et al. 2015
Tenerife	El Contador	T112	28.19143403	-16.52742558	<i>L. canescens</i>	2	Faria et al. 2015
Tenerife	Cumbres de Arico	T113	28.19770104	-16.53115154	<i>L. canescens</i>	3	Faria et al. 2015
Tenerife	Lomo del Retamar	T122	28.29691862	-16.48256482	<i>L. canescens</i>	4	This study
Tenerife	Montaña Las Raíces	T123	28.29323746	-16.44797825	<i>L. punctiger</i>	2	This study
Tenerife	Montaña de Anocheza A	T124	28.29324808	-16.43328514	<i>L. punctiger</i>	5	This study
Tenerife	Las Raíces	T20	28.42382434	-16.37923736	<i>L. punctiger</i>	11	Faria et al. 2015
Tenerife	Montaña Pico las Flores	T21	28.42380586	-16.39610270	<i>L. punctiger</i>	1	This study
Tenerife	Fuente Fria. Tacoronte	T22	28.42011452	-16.40749833	<i>L. tessellatus</i>	1	Faria et al. 2015
Tenerife	Barranco de Bensa	T41	28.39007943	-16.45466060	<i>L. tessellatus</i>	3	Faria et al. 2015
Tenerife	Gorgo	T43	28.35900553	-16.43337186	<i>L. tessellatus</i>	1	This study
Tenerife	Mirador de Chipeque	T46	28.37382697	-16.46375524	<i>L. tessellatus</i>	5	This study
Tenerife	Choza Almadi	T50	28.38142911	-16.47936090	<i>L. tessellatus</i>	4	This study
Tenerife	Las Lajitas	T51	28.39031952	-16.48924102	<i>L. tessellatus</i>	7	This study
Tenerife	Supra La Corujera	T53	28.40303863	-16.49228702	<i>L. tessellatus</i>	5	Faria et al. 2015; this study
Tenerife	El Nogalito	T54	28.40120553	-16.49567039	<i>L. tessellatus</i>	5	This study
Tenerife	Montaña de Ayosa	T55	28.35769475	-16.46666606	<i>L. tessellatus</i>	5	This study
Tenerife	Peña Rajada	T56	28.36350078	-16.49300887	<i>L. tessellatus</i>	5	This study
Tenerife	Corral de los Lucas	T57	28.34126307	-16.47890596	<i>L. punctiger</i>	5	This study
Tenerife	Barranco del Agua. Güimar	T59	28.30806238	-16.44235595	<i>L. punctiger</i>	9	Faria et al. 2015
Tenerife	Lomo los Pajales	T60	28.31639226	-16.48613925	<i>L. punctiger</i>	5	This study
Tenerife	Lomo Chillero	T61	28.35539266	-16.51460597	<i>L. tessellatus</i>	5	This study
Tenerife	Morro Quemado	T62	28.34795435	-16.53172067	<i>L. tessellatus</i>	5	This study
Tenerife	Las Jaritas	T63	28.34422815	-16.54282729	<i>L. tessellatus</i>	2	This study
Tenerife	Montaña Bermeja	T64	28.32716206	-16.53319714	<i>L. freyi</i>	2	Faria et al. 2015
Tenerife	Roque Caramujo	T65	28.30758082	-16.53692392	<i>L. freyi</i>	5	This study
Tenerife	Los Amontaderos	T66	28.34006167	-16.56709584	<i>cf. L. freyi</i>	5	This study
Tenerife	El Portillo	T67	28.30291210	-16.56654085	<i>L. freyi</i>	3	Faria et al. 2015
Tenerife	Infra El Portillo	T68	28.30911349	-16.56722319	<i>L. freyi</i>	2	This study
Tenerife	Vista la Chapa	T69	28.32568840	-16.58786491	<i>L. freyi</i>	3	This study
Tenerife	Cruz de Joaquín	T70	28.34281845	-16.59322010	<i>L. freyi</i>	5	This study
Tenerife	Icod el Alto	T71	28.36095843	-16.59862289	<i>L. freyi</i>	4	Faria et al. 2015
Tenerife	La Corona	T72	28.37783472	-16.60094739	<i>cf. L. tessellatus</i>	2	This study
Tenerife	Lomo Blanco	T73	28.33658388	-16.62065758	<i>L. freyi</i>	2	This study
Tenerife	Hoya Benjamins	T74	28.33271255	-16.65817491	<i>L. tessellatus</i>	2	This study
Tenerife	Llano de los Cuervos	T75	28.31620449	-16.71956612	<i>L. tessellatus</i>	2	This study
Tenerife	Tanque Bajo	T76	28.36146458	-16.77505070	<i>L. tessellatus</i>	1	Faria et al. 2015
Tenerife	Arenas Negras	T77	28.31853497	-16.75554195	<i>L. tessellatus</i>	1	This study
Tenerife	El Lomito	T79	28.32895645	-16.80887055	<i>L. tessellatus</i>	2	This study
Tenerife	Cumbre de Bolico	T80	28.31338338	-16.82018098	<i>L. tessellatus</i>	2	Faria et al. 2015
Tenerife	Ifonche	T94	28.13267228	-16.68803953	<i>L. punctiger</i>	2	Faria et al. 2015
Tenerife	Fuente Fria. Altos Vilaflor	T96	28.18892538	-16.65694869	<i>L. canescens</i>	1	This study

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Appendix S3. Altitudinal sampling data for the *Laparocerus tessellatus* complex in Tenerife, and photographic evidence of floating vegetation resulting from the 1980 eruption of Mount St. Helens.

Table S3.3. Summary of the number of localities known in Tenerife for the *tessellatus* complex and the other species of *Laparocerus*, in altitudinal intervals of 100 macsl. Locality data from a collection of *Laparocerus* maintained by one of us (AMC) was used to estimate the altitudinal range of the *Laparocerus tessellatus* complex in Tenerife. Six hundred and forty-two sampling localities, encompassing all ecosystems in an altitudinal gradient from sea level to the highest altitudes of the island, were sampled for *Laparocerus*. Data are summarised within altitudinal intervals of 100 macsl in Table S3.3. Two hundred and forty-four localities included samples from the *L. tessellatus* complex, while the remaining 398 were sampled only for other species from the genus. Of the 83 localities sampled for *Laparocerus* at altitudes ≤ 300 macsl, the *L. tessellatus* complex was sampled at only 4, meaning that more than 98% of occurrence records for *L. tessellatus* are > 300 macsl. The *L. tessellatus* complex is typical of altitudes above 764 macsl and below 1424 macsl (first and third quartiles of species distribution records), with a median and mean altitude of 1102 m and 1000 m respectively.

Latitudinal intervals	Frequency <i>L. tessellatus</i>	Frequency other species	Total
0-99	0	35	35
100-199	3	21	24
200-299	1	23	24
300-399	3	21	24
400-499	5	18	23
500-599	10	26	36
600-699	18	30	48
700-799	27	37	64
800-899	30	47	77
900-999	22	20	42
1000-1099	22	30	52
1100-1199	15	10	25
1200-1299	18	11	29
1300-1399	5	4	9
1400-1499	11	8	19
1500-1599	4	5	9
1600-1699	16	12	28
1700-1799	9	4	13
1800-1899	3	3	6
1900-1999	7	1	8
2000-2099	8	8	16
2100-2199	2	9	11
2200-2299	4	7	11
2300-2399	1	2	3

2400-2499	0	0	0
2500-2599	0	2	2
2600-2699	0	2	2
2700-2799	0	0	0
2800-2899	0	0	0
2900-2999	0	0	0
3000-3099	0	2	2
> 3100	0	0	0
Total	244	398	642

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During the eruption of Mt. St. Helens in 1980, a mega-landslide resulted in the deposition of tens of thousands of trees into Spirit Lake, producing a giant log raft that persisted for many years. The following photos, taken between two and three decades after the eruption, demonstrate the high floatability and temporal persistence of plant material deposited into a water body from a mega-landslide.

Photo 1: Agglomeration of logs on Spirit Lake, 22 years after the eruption and landslide (Author: Xpda). Logs are indicated with a black arrow added by the authors.

Photo 2. Trees drifting on Spirit Lake, with the open crater of Mount St. Helens open in the background, 32 years after the landslide and eruption (Author: Stephan Schulz)

Photo 3. Hikers gazing at the logs covering Spirit Lake, near Mount St. Helens, 29 years after the eruption and landslide (Author: Etliebe).