**Table A.** Showing the locations, source, number of sample amplified for mitochondrial Dloop ($n^{mt}$), with microsatellites ($n^{n}$), and grid reference (Latitude, Longitude) of all new samples used in this study.

| Map ID | Location | Source | $n^{mt}$ | $n^{n}$ | Grid Ref. | |
|---|---|---|---|---|---|---|
| IRL | Belfast, Northern Ireland | Wing punch | 11 | 8 | 54.579089 | 5.916139 |
| | Tollymore, Northern Ireland | Wing punch | 5 | 17 | 54.221081 | 5.924617 |
| | Dungannon, Northern Ireland | Wing punch | 5 | 4 | 54.498611 | 6.755636 |
| | Coalisland, Northern Ireland | Wing punch | 1 | 1 | 54.536694 | 6.703625 |
| | Jordanstown, Northern Ireland | Wing punch | 5 | 13 | 54.688333 | 5.898439 |
| | Downpatrick, Northern Ireland | Wing punch | 5 | 8 | 54.367744 | 5.580544 |
| | Kesh, Northern Ireland | Wing punch | 5 | 9 | 54.521247 | 7.724792 |
| | Crom Estate, Northern Ireland | Wing punch | 5 | 16 | 54.186394 | 7.562217 |
| | Askeaton, Ireland | Wing punch | 3 | | 52.601031 | 8.977186 |
| | Oughtergard, Ireland | Wing punch | 5 | 18 | 53.431653 | 9.319042 |
| | Baldwinstown, Ireland | Wing punch | 5 | 17 | 52.238356 | 6.579333 |
| | Timoleague, Ireland | Wing punch | 7 | 15 | 51.643436 | 8.567794 |
| | Crosshaven, Ireland | Wing punch | 5 | 14 | 51.803319 | 8.298853 |
| | Ardpatrick, Ireland | Wing punch | 8 | | 52.340297 | 8.522353 |
| IOM | Union Mills, Isle of Man | Faecal sample | 7 | | 54.168656 | 4.522597 |
| GBR | Bristol, England | Wing punch | 10 | | 51.455314 | 2.591903 |
| | Essex, England | Faecal sample | 3 | | 51.685033 | 0.433931 |
| | London, England | Faecal sample | 4 | | 51.581664 | 0.145525 |
| | Notts, England | Faecal sample | 1 | | 53.224717 | 1.076947 |
| | Newton Stewart, Scotland | Faecal sample | 1 | | 55.064372 | 4.580525 |
| | Nairn, Scotland | Faecal sample | 2 | | 57.583522 | 3.875178 |
| FRA | Precy-sous-Thil, France | Wing punch | 9 | 126 | 47.386567 | 4.309678 |
| | Saint-Brisson, France | Wing punch | 4 | 19 | 47.272544 | 4.088256 |
| | Saint-Romans, France | Wing punch | 2 | | 45.118117 | 5.325744 |
| | Sidiailles, France | Wing punch | 4 | | 46.507869 | 2.318269 |
| | Bourges, France | Wing punch | 1 | | 47.080992 | 2.398778 |
| | Troncias, France | Wing punch | 1 | | 46.640508 | 2.719722 |
| | Orleans, France | Wing punch | 1 | | 47.174108 | 2.379514 |
| | Champniers, France | Wing punch | 2 | | 45.714889 | 0.205214 |
| | Guénin, France | Wing punch | 1 | | 47.514692 | 2.399394 |
| | Saint Genis les Ollières, France | Wing punch | 1 | | 45.757283 | 4.726022 |
| | Fontenay, France | Wing punch | 1 | | 48.845594 | 2.480367 |
| PRT | Tondela, Portugal | Wing punch | 8 | | 40.516544 | 8.080647 |
| CHE | Burgistein, Switzerland | Wing punch | 1 | | 46.78635 | 7.499681 |
| | Interlaken, Switzerland | Wing punch | 1 | | 46.685989 | 7.867303 |
| DEU | Wiebelsdorf, Germany | Wing punch | 2 | | 50.715267 | 11.950478 |
| HUN | Felsötorkany, Hungary | DNA | 2 | | 47.962008 | 20.432575 |
| GRC | Kaepension, Greece | DNA | 2 | | 38.917244 | 21.794369 |
| | Prusos, Greece | DNA | 1 | | 38.742497 | 21.653433 |
| | Agia Anastasia, Greece | DNA | 1 | | 39.561781 | 20.736408 |

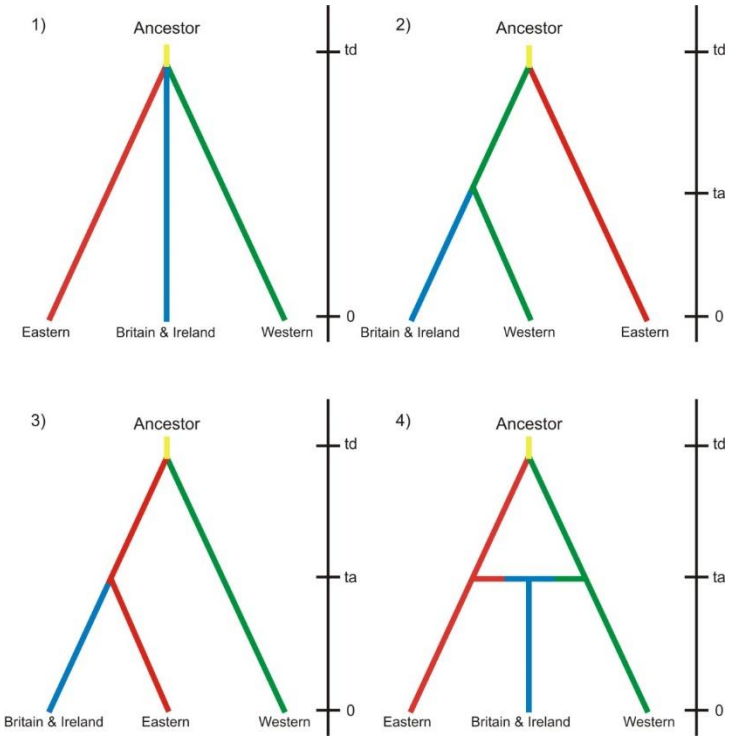
**Table B.** Distribution and numbers (including totals) for Leisler's bat's haplotypes present in each location. See Table 1 and Figure 1 for location code (Ir - Ireland; En – Great Britain; Fr - France; Po - Portugal; Sw - Switzerland; Hu - Hungary; Gr - Greece; Sp - Spain; Tu - Turkey; Cz - Czech Republic; Mo - Morocco; Ma - Madeira; Az - Azores).

| Haplotypes / samples | IRL | IOM | GBR | FRA | PRT | ESP | CHE | DEU | HUN | GRC | TUR | CZE | MNE | MAR | Mad Is. | Can Is. | Az Is. | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Ir1 | 31 | 1 | 3 | | | | | | | | | | | | | | | 35 |
| Ir3 | 9 | 2 | | | | | | | | | | | | | | | | 11 |
| Ir4 | 1 | | | | | | | | | | | | | | | | | 1 |
| Ir5 | 1 | | | | | | | | | | | | | | | | | 1 |
| Ir6 | 1 | | | | | | | | | | | | | | | | | 1 |
| Ir7 | 1 | | | | | | | | | | | | | | | | | 1 |
| Ir8 | 7 | | | | | | | | | | | | | | | | | 7 |
| Ir9 | 1 | | | | | | | | | | | | | | | | | 1 |
| Ir10 | 1 | | | | | | | | | | | | | | | | | 1 |
| Ir11 | 1 | | | | | | | | | | | | | | | | | 1 |
| En1 | | | 1 | 1 | | | | | | | | | | | | | | 2 |
| En2 | | | 2 | | | | | | | | | | | | | | | 2 |
| Fr1 | | | 1 | 2 | | | | | | | | | | | | | | 3 |
| Fr2 | | | | 8 | | | | | | | | | | | | | | 8 |
| Fr3 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr4 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr5 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr6 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr7 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr8 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr9 | | | | 1 | | | | | | | | | | | | | | 1 |
| Fr10 | | | | 1 | | | | | | | | | | | | | | 1 |
| Po1 | 14 | 1 | 8 | 3 | 10 | 1 | 1 | | | 2 | 1 | 1 | | 1 | | | | 43 |
| Po2 | | | | | 20 | | | | 1 | 1 | | | | | | | | 22 |
| Po3 | | | | | 3 | | | | | | | | | | | | | 3 |
| Po4 | | | | | 1 | | | | | | | | | | | | | 1 |
| Po5 | | | | | 1 | | | | | | | | | | | | | 1 |
| Sw1 | | | | | | | 1 | | | | | | | | | | | 1 |
| Sw2 | | | | | | | 1 | | | | | | | | | | | 1 |
| Sw3 | | | | | | | 1 | | | | | | | | | | | 1 |
| Sw4 | | | | | | | 2 | | | | | | | | | | | 2 |
| Sw5 | | | | 5 | | | 1 | | | | | | | | | | | 6 |

**Table B.** continuation

| Haplotypes / samples | IRL | IOM | GBR | FRA | PRT | ESP | CHE | DEU | HUN | GRC | TUR | CZE | MNE | MAR | Mad Is. | Can Is. | Az Is. | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Ge1 | | | | | | | | 1 | | | | | | | | | | 1 |
| Ge2 | | | | | | | | 1 | | | | | | | | | | 1 |
| Gr1 | | | | | | | | | | 1 | | | | | | | | 1 |
| Gr2 | | | | | | | | | | 1 | | | | | | | | 1 |
| Gr3 | | | | | | | | | | 1 | | | | | | | | 1 |
| Gr4 | | | | | | | | | | 1 | | | | | | | | 1 |
| Hu1 | | | | | | | | | 1 | | | | | | | | | 1 |
| Mad | | | | | | | | | | | | | | | 2 | | | 2 |
| Mar1 | | | | | | | | | | | | | | 2 | | | | 2 |
| Mar2 | | | | | | | | | | | | | | 1 | | | | 1 |
| Mn | | | | | | | | | | | | | 1 | | | | | 1 |
| Can | | | | | | | | | | | | | | | | 1 | | 1 |
| A1 | | | | | | | | | | | | | | | | | 9 | 9 |
| A2 | | | | | | | | | | | | | | | | | 4 | 4 |
| A3 | | | | | | | | | | | | | | | | | 3 | 3 |
| A4 | | | | | | | | | | | | | | | | | 25 | 25 |
| A5 | | | | | | | | | | | | | | | | | 14 | 14 |
| A6 | | | | | | | | | | | | | | | | | 4 | 4 |
| A7 | 7 | 3 | 6 | | | | | | | | | | | | | | 54 | 70 |
| A8 | | | | | | | | | | | | | | | | | 12 | 12 |
| A9 | | | | | | | | | | | | | | | | | 6 | 6 |
| A10 | | | | | | | | | | | | | | | | | 22 | 22 |
| A11 | | | | | | | | | | | | | | | | | 2 | 2 |
| A12 | | | | | | | | | | | | | | | | | 1 | 1 |
| A13 | | | | | | | | | | | | | | | | | 1 | 1 |
| A14 | | | | | | | | | | | | | | | | | 1 | 1 |
| A15 | | | | | | | | | | | | | | | | | 1 | 1 |
| A16 | | | | | | | | | | | | | | | | | 6 | 6 |
| **Grand Total** | **75** | **7** | **21** | **27** | **35** | **1** | **7** | **2** | **2** | **7** | **1** | **1** | **1** | **4** | **2** | **1** | **165** | **359** |

**Fig. A**. Postglacial colonisation scenarios for the *N. leisleri* tested using the ABC phylogeographical approach as implemented in DIYABC. Times of lineage origins are indicated back in time by *td* and *ta*, while 0 represent contemporary samples. Four colonization scenarios were considered. For scenario 1, the samples representing the western, the eastern groups and those in Britain & Ireland were considered to have diverged from a common ancestor at time *td*. For scenario 2, the western and the eastern lineages were considered to have initially diverged from the common ancestor at time *td*, while the group in Britain & Ireland diverged more recently (time *ta*) from the western lineage. Scenario 3 is similar to scenario 2, with the difference that the group in Britain & Ireland would have diverged more recently from the eastern lineage. For scenario 4, the western and the eastern lineages were considered to have initially diverged from the common ancestor at time *td*. At time *ta*, there has been an admixture event between these two lineages giving origin to the group in Britain & Ireland. For microsatellites, given that no equivalent data was available for the Azores, simulations were run with the caveat that terminal sampling was carried out only for the eastern group and Britain & Ireland. Prior distributions of demographic parameters were as follows: Uniform [10; 10000] for effective population sizes (similar for all lineages), Uniform [1; 10000] for *td*, Uniform [1; 10000] for *ta* (with *ta* < *td*), and Uniform [0.001; 0.999] for *ra* (admixture rate). The time parameter was considered as the number of generations (2 years for *N. leisleri*). The mtDNA sequences were considered to follow the two parameter model of Kimura (1980) with a fraction of constant sites fixed to 10% and the shape parameter of the Gamma distribution of mutations among sites equal to 2. The priors for mutation rate (per site per generation) followed a uniform distribution ranging from 6.7% to 25.2% with an average of 20% Myr-$^{1}$. For each one of the four tested competing scenarios, 500 data sets were simulated. For model comparison, the posterior probabilities for each scenario were estimated using logistic regression (Cornuet *et al*. 2008). The posterior probabilities were used to estimate type I and II errors in the choice of each scenario (Excoffier *et al*. 2005).



Additional References:

Excoffier L., Estoup A., Cornuet JM. 2005. Bayesian analysis of an admixture model with mutations and arbitrarily linked markers. *Genetics* **169**, 1727–1738.