**ONLINE RESOURCES 2-5**

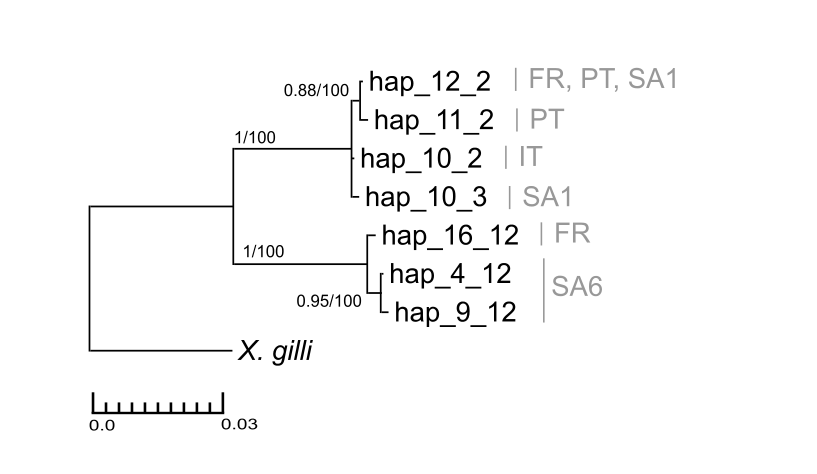
**Unequal contribution of native South African phylogeographic lineages to the invasion of the African clawed frog, *Xenopus laevis*, in Europe**

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**Online Resource 2.**



**Fig.** MP and BI tree of unique concatenated Cytb-16S haplotypes. First number in the label refers to the Cytb allele and the second number refers to the 16S allele. Numbers at the branches are Bayesian posterior probabilities and Parsimony bootstrap values (if > 0.70). Geographical regions are indicated in grey.

**Online Resource 3.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Table.** PCR cycle conditions | | | | | | | |
| **Cytb** | Temp (°C) | Time (s) | Cycles | **mastl** | Temp (°C) | Time (s) | Cycles |
| Initial denaturation | 96 | 120 |  | Initial denaturation | 94 | 240 |  |
| denaturation | 96 | 10 |  | denaturation | 94 | 30 |  |
| Annealing | 50 | 5 | 25x | Annealing | 51.4 | 45 | 35x |
| Extension | 60 | 240 |  | Extension | 72 | 45 |  |
| Final extension | 60 | 300 |  | Final extension | 72 | 480 |  |
|  | 15 | hold |  |  | 15 | hold |  |
|  |  |  |  |  |  |  |  |
| **16S** | Temp (°C) | Time (s) | Cycles | **AR** | Temp (°C) | Time (s) | Cycles |
| Initial denaturation | 94 | 120 |  | Initial denaturation | 94 | 120 |  |
| denaturation | 94 | 30 |  | denaturation | 94 | 60 |  |
| Annealing | 46 | 30 | 35x | Annealing | 55 | 60 | 36x |
| Extension | 72 | 60 |  | Extension | 72 | 60 |  |
| Final extension | 72 | 300 |  | Final extension | 72 | 600 |  |
|  | 15 | hold |  |  | 16 | hold |  |
|  |  |  |  |  |  |  |  |
| **prmt6** | Temp (°C) | Time (s) | Cycles |  |  |  |  |
| Initial denaturation | 94 | 240 |  |  |  |  |  |
| denaturation | 94 | 30 |  |  |  |  |  |
| Annealing | 53 | 45 | 35x |  |  |  |  |
| Extension | 72 | 45 |  |  |  |  |  |
| Final extension | 72 | 480 |  |  |  |  |  |
|  | 15 | hold |  |  |  |  |  |
|  |  |  |  |  |  |  |  |

**Online Resource 4.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table.** Pairwise Population *Fst* values (below diagonal) based on pairwise nucleotide differences for 16S and probability (above diagonal) based on 999 permutations. All *Fst* values were significant, except those in bold. | | | | | | | | | |
| FR | PT | SA1 | SA2 | SA3 | SA4 | SA5 | SA6 | SA7 |  |
|  | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.027 | **0.145** | 0.000 | FR |
| 0.78768 |  | **0.139** | **0.439** | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 | PT |
| 0.79837 | **0.10422** |  | **0.072** | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | SA1 |
| 0.78083 | **0.00986** | **0.08146** |  | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | SA2 |
| 0.70636 | 0.80591 | 0.81981 | 0.78144 |  | 0.037 | 0.000 | 0.000 | 0.000 | SA3 |
| 0.78227 | 0.97634 | 0.96253 | 0.96715 | 0.1537 |  | 0.000 | 0.000 | 0.000 | SA4 |
| 0.05685 | 0.98533 | 0.97399 | 0.97868 | 0.84435 | 0.95997 |  | **0.198** | 0.000 | SA5 |
| **0.04906** | 0.98476 | 0.9737 | 0.97826 | 0.84792 | 0.96 | **0.02886** |  | 0.000 | SA6 |
| 0.79863 | 0.97907 | 0.96794 | 0.97269 | 0.58859 | 0.82648 | 0.96726 | 0.96696 |  | SA7 |

**Online Resource 5.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table.** Pairwise Population *Fst* values (below diagonal) based on nuclear allele frequencies and probability (above diagonal) based on 999 permutations. All *Fst* values were significant except those in bold. | | | | | | | | | |
| FR | PT | SA1 | SA2 | SA3 | SA4 | SA5 | SA6 | SA7 |  |
|  | 0.001 | 0.001 | 0.001 | 0.025 | 0.001 | 0.001 | 0.001 | 0.001 | FR |
| 0.244 |  | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | PT |
| 0.092 | 0.141 |  | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | SA1 |
| 0.077 | 0.249 | 0.073 |  | 0.011 | 0.001 | 0.001 | 0.001 | 0.001 | SA2 |
| 0.036 | 0.329 | 0.105 | 0.054 |  | 0.001 | 0.001 | 0.001 | 0.001 | SA3 |
| 0.185 | 0.476 | 0.269 | 0.197 | 0.124 |  | 0.001 | 0.001 | 0.001 | SA4 |
| 0.181 | 0.521 | 0.317 | 0.225 | 0.162 | 0.128 |  | **0.079** | 0.001 | SA5 |
| 0.178 | 0.543 | 0.315 | 0.211 | 0.144 | 0.098 | **0.017** |  | 0.001 | SA6 |
| 0.338 | 0.644 | 0.463 | 0.446 | 0.414 | 0.386 | 0.370 | 0.375 |  | SA7 |