Supplementary Table 10. Number of probable first-generation immigrants verified in each population of *S. furcifera* in 2014 and of its putative source population at threshold of *a* = 0.05 and *a* = 0.01 (in parentheses).

|  |  |  |  |
| --- | --- | --- | --- |
| Country | Population | Test statistic1 | Putative source population |
| JC | TA | BA | SA3 | WD | CW | KP | NYJ | GS | MY | CH1 | CH3 | CH3 | CH4 |
| Korea | JC | *L*home/*L*max | - |  |  |  |  |  |  |  | 7(4) |  |  |  | 1(1) |  |
|  | TA | *L*home/ *L*max |  | - | 2(0) |  |  |  | 1(1) |  | 3(0) | 2(1) |  |  |  |  |
|  | BA | *L*home/ *L*max | 1(1) | 1(0) | - |  |  | 1(1) |  | 1(1) |  |  |  | 3(3) |  |  |
|  | SA3 | *L*home/ *L*max | 1(1) | 2(2) |  |  |  | 2(0) | - |  |  |  |  |  | 1(1) | 1(1) |
|  | WD | *L*home/ *L*max |  |  |  | 2(1) |  | 4(2) | 1(1) | - |  | 1(1) |  |  |  |  |
|  | CW | *L*home/ *L*max | 4(1) | 2(1) |  |  |  |  | 1(0) |  | - |  |  |  |  |  |
|  | KP | *L*home/ *L*max |  | 4(2) | 4(1) |  | 4(2) |  |  |  | 1(0) | - |  |  |  |  |
|  | NYJ | *L*home/ *L*max | 1(1) | 1(1) |  |  |  |  |  |  | 1(1) |  | - |  | 2(1) |  |
|  | GS | *L*home/ *L*max |  |  |  |  |  | 1(1) |  |  |  |  |  |  |  | - |
|  | MY | *L*home/ *L*max |  |  |  |  |  | 1(0) |  |  |  | 1(0) | 1(0) |  | 2(1) | 1(0) |
| China | CH1 | *L*home/ *L*max |  |  |  |  |  |  | 1(0) |  |  |  |  |  |  |  |
|  | CH2 | *L*home/ *L*max |  | 2(0) | 2(0) |  |  |  |  |  |  | 3(1) |  |  |  |  |
|  | CH3 | *L*home/ *L*max | 1(1) |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | CH4 | *L*home/ *L*max | 1(0) |  |  | 1(0) |  |  |  |  | 2(1) |  |  |  |  |  |

The analysis applied the assignment criterion explained by Rannal & Mountain (1997) and the Monte Carlo resampling method reported by Paetkau *et al*. (2004).

1 L= likelihood of immigrant detection (Paetkau *et al*., 2004)