Genetic analysis of two spawning stocks of the short-finned squid (*Illex argentinus*) using nuclear and mitochondrial data.

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**Appendix 1.**

**Table S1.** Variable nucleotide positions defining 7 haplotypes in the 556 bp of COI region with respective GenBank accession numbers. Identical nucleotide is indicated with a dot (**·**).

|  |  |  |
| --- | --- | --- |
| COI haplotype | Variable nucleotide position | Accession number |
|  | 136 | 195 | 225 | 330 | 348 | 402 |  |
| Iah1 | C | A | T | A | C | G | KC594174 |
| Iah2 | T | **·** | **·** | **·** | **·** | **·** | KC594175 |
| Iah3 | **·** | **·** | **·** | G | T | **·** | KC594176 |
| Iah4 | **·** | **·** | **·** | G | **·** | **·** | KC594177 |
| Iah5 | **·** | **·** | C | **·** | **·** | A | KC594178 |
| Iah6 | **·** | **·** | **·** | **·** | **·** | A | KC594179 |
| Iah7 | **·** | G | **·** | **·** | **·** | **·** | KC594180 |

**Table S2.** Variable nucleotide positions defining 7 haplotypes in the 439 bp of 16S rDNA region with respective GenBank accession numbers. Identical nucleotide is indicated with a dot (**·**) and absence of nucleotide is indicated with a dash (**−**).

|  |  |  |
| --- | --- | --- |
| 16S rDNA haplotype | Variable nucleotide position | Accession number |
|  | 7 | 68 | 108 | 202 | 203 | 204 | 268 | 303 | 304 |  |
| Iah1 | **−** | **−** | C | **−** | **−** | **−** | T | **−** | **−** | KC594167 |
| Iah2 | T | **−** | **·** | **−** | **−** | **−** | **·** | **−** | **−** | KC594168 |
| Iah3 | **−** | **−** | **·** | **−** | **−** | **−** | **·** | T | A | KC594169 |
| Iah4 | T | G | **·** | **−** | **−** | **−** | **·** | **−** | **−** | KC594170 |
| Iah5 | **−** | **−** | T | **−** | **−** | **−** | **·** | **−** | **−** | KC594171 |
| Iah6 | **−** | **−** | **·** | T | T | A | **·** | **−** | **−** | KC594172 |
| Iah7 | **−** | **−** | **·** | **−** | **−** | **−** | C | **−** | **−** | KC594173 |

**Figure S1.** Median-joining network of COI haplotypes (556 bp) detected for *Illex argentinus*. The area of each circle is proportional to the number of individuals exhibiting that haplotype. Each line in the network represents one mutational step. Summer Spawning Stock (SSS), South Patagonic Stock (SPS).

**Figure S2.** Median-joining network of 16S rDNA haplotypes (439 bp) detected for *Illex argentinus*. The area of each circle is proportional to the number of individuals exhibiting that haplotype. Each line in the network represents one mutational step. Summer Spawning Stock (SSS), South Patagonic Stock (SPS).

