**Supplementary Material**

**Table S1**. Forward and reverse primer sequences and annealing temperatures (*Tm*) used for the amplification of the seven microsatellite loci.

|  |  |  |  |
| --- | --- | --- | --- |
| *Locus* | GeneBank Accession Nº | Primer Sequences (5’-3’) | *Tm* (ºC) |
| ***cmrGb4.11B*** | AF3314145 | CCTGAGTGCTTAAAGAGGA  GAGGAGGAGACGATGAAA | 55 |
| ***cmrGb5.9*** | AF3314147 | AGGGTCACTTTCAGTTTTA  TGCAGAACACACTCCAC | 56 |
| ***cmrGb4.2A*** | AF3314148 | ATCGGGCAGTTCCTTGCTAT  GGGAAGCTTTTGTGAGCATC | 56 |
| ***cmrGb5.2B*** | AF3314149 | CGGTCTGAGCAATGATACGA  TACAGAGGGGAGGTAAATCAAGTC | 55 |
| ***cmrGb4.2B*** | AF3314152 | GAGTTGGTGTTTGCCCTGA  GTCTGGAGTGTTTTGGATCATT | 54 |
| ***cmrGb3.8.1*** | AF3314158 | ACGAACACGCAGAAGGAC  GGTCGTTTCAGGACATTACA | 53 |
| ***cmrGb2.6.1*** | AF3314150 | AGAACTAAACCAGCAGAATC  CACAACAAGAGGGAACTC | 53 |

**Table S2.** Genetic diversity estimators by locus of *Genypterus chilensis* from COQ (n = 55).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *Locus* | *N* | *Na* | *Ar* | *Ho* | *He* | *PIC* | *F(null)* | *Fis* |
| *cmrGb5.2B* | 55 | 14 | 10.2 | 0.945 | 0.901 | 0.884 | -0.032 | -0.050 |
| *cmrGb3.8.1* | 55 | 9 | 8.1 | 0.836 | 0.867 | 0.884 | 0.015 | 0.036 |
| *cmrGb5.9* | 55 | 14 | 9.6 | 0.891 | 0.884 | 0.865 | -0.009 | -0.007 |
| *cmrGb4.11B* | 55 | 16 | 10.2 | 0.927 | 0.888 | 0.869 | -0.028 | -0.044 |
| *cmrGb2.6.1* | 55 | 12 | 8.8 | 0.927 | 0.877 | 0.855 | -0.035 | -0.058 |
| Mean | 55 | 13 | 9.3 | 0.905 | 0.884 | 0.863 | -0.018 | -0.025 |

*Na*: number of alleles, *Ar*: allelic richness, *Ho*: observed heterozygosity, *He*: expected heterozygosity, *PIC*: polymorphic information content, *PE*: probability of exclusion, *Null*: null alleles frequency.

**Table S3.** Genetic diversity estimators by locus of *Genypterus chilensis* from ZAP (n = 31).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *Locus* | *N* | *Na* | *Ar* | *Ho* | *He* | *PIC* | *F(null)* | *Fis* |
| *cmrGb5.2B* | 31 | 11 | 9.2 | 0.903 | 0.895 | 0.869 | -0.014 | -0.009 |
| *cmrGb3.8.1* | 31 | 5 | 4.6 | 0.677 | 0.700 | 0.643 | 0.006 | 0.032 |
| *cmrGb5.9* | 31 | 13 | 9.4 | 0.742 | 0.892 | 0.865 | 0.085 | 0.170 |
| *cmrGb4.11B* | 31 | 11 | 8.2 | 0.742 | 0.845 | 0.810 | 0.057 | 0.123 |
| *cmrGb2.6.1* | 31 | 12 | 9.3 | 0.968 | 0.878 | 0.850 | -0.062 | 0.104 |
| Mean | 31 | 10.4 | 8.1 | 0.806 | 0.813 | 0.807 | 0.015 | 0.084 |

*Na*: number of alleles, *Ar*: allelic richness, *Ho*: observed heterozygosity, *He*: expected heterozygosity, *PIC*: polymorphic information content, *PE*: probability of exclusion, *Null*: null alleles frequency.

**Table S4.** Genetic diversity estimators by locus of *Genypterus chilensis* from LAG (n = 12).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *Locus* | *N* | *Na* | *Ar* | *Ho* | *He* | *PIC* | *F(null)* | *Fis* |
| *cmrGb5.2B* | 12 | 11 | 11 | 0.833 | 0.920 | 0.871 | 0.031 | 0.098 |
| *cmrGb3.8.1* | 12 | 8 | 8 | 1.000 | 0.829 | 0.755 | -0.132 | -0.234 |
| *cmrGb5.9* | 12 | 11 | 11 | 0.917 | 0.906 | 0.854 | -0.026 | -0.013 |
| *cmrGb4.11B* | 12 | 7 | 7 | 0.750 | 0.783 | 0.720 | 0.016 | 0.044 |
| *cmrGb2.6.1* | 12 | 7 | 7 | 1.000 | 0.873 | 0.815 | -0.091 | -0.153 |
| Mean | 12 | 8.8 | 9 | 0.900 | 0.860 | 0.803 | -0.040 | -0.051 |

*Na*: number of alleles, *Ar*: allelic richness, *Ho*: observed heterozygosity, *He*: expected heterozygosity, *PIC*: polymorphic information content, *PE*: probability of exclusion, *Null*: null alleles frequency.

**Table S5.** Genetic diversity estimators by locus of *Genypterus chilensis* from LEB (n = 21).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *Locus* | *N* | *Na* | *Ar* | *Ho* | *He* | *PIC* | *F(null)* | *Fis* |
| *cmrGb5.2B* | 21 | 4 | 4 | 1.000 | 0.753 | 0.692 | -0.152 | -0.329 |
| *cmrGb3.8.1* | 21 | 6 | 5.8 | 1.000 | 0.825 | 0.780 | -0.108 | -0.214 |
| *cmrGb5.9* | 21 | 4 | 4 | 1.000 | 0.731 | 0.677 | -0.165 | -0.355 |
| *cmrGb4.11B* | 21 | 9 | 8.5 | 1.000 | 0.879 | 0.853 | -0.073 | -0.129 |
| *cmrGb2.6.1* | 21 | 8 | 7.4 | 0.667 | 0.829 | 0.808 | -0.093 | 0.203 |
| Mean | 21 | 6.2 | 5.9 | 0.933 | 0.861 | 0.762 | -0.118 | -0.165 |

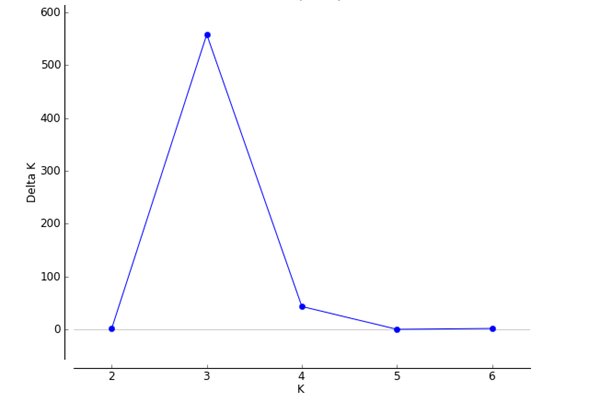
*Na*: number of alleles, *Ar*: allelic richness, *Ho*: observed heterozygosity, *He*: expected heterozygosity, *PIC*: polymorphic information content, *PE*: probability of exclusion, *Null*: null alleles frequency.

**Table S6.** Number of individuals of each population in each identified cluster by DAPC (K=2).

|  |  |  |
| --- | --- | --- |
|  | Cluster I | Cluster II |
| COQ | 55 | 0 |
| LAG | 12 | 0 |
| ZAP | 31 | 0 |
| LEB | 0 | 21 |

**Table S7.** Number of individuals of each population in each identified cluster by DAPC (K=4).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Cluster I | Cluster II | Cluster III | Cluster IV |
| COQ | 26 | 19 | 10 | 0 |
| LAG | 2 | 9 | 1 | 0 |
| ZAP | 2 | 21 | 8 | 0 |
| LEB | 0 | 0 | 0 | 21 |



**Figure S1**. Plot of the Delta K indicating the number of clusters identified by STRUCTURE.

**Table S8**. Allele frequencies for locus *cmrGB5.2B* for each studied population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| cmrGb5.2B | | | | |
| **Alleles** | **COQ** | **ZAP** | **LAG** | **LEB** |
| 120 | 0.0727 | - | 0.0417 | - |
| 124 | 0.0727 | 0.0806 | 0.0417 | - |
| 128 | 0.0545 | 0.0806 | - | - |
| 132 | 0.0909 | 0.0645 | 0.1250 | - |
| 136 | 0.0636 | 0.1129 | 0.0417 | - |
| 140 | 0.1909 | 0.1774 | 0.0833 | - |
| 144 | 0.1273 | 0.0161 | 0.0833 | - |
| 148 | 0.1091 | 0.1452 | 0.1250 | - |
| 152 | 0.1182 | 0.1129 | 0.0833 | - |
| 156 | 0.0273 | - | 0.1250 | 0.2143 |
| 160 | 0.0364 | 0.1452 | 0.2083 | 0.3095 |
| 164 | 0.0091 | 0.0484 | 0.0417 | 0.1905 |
| 168 | 0.0182 | - | - | 0.2857 |
| 176 | - | 0.0161 | - | - |
| 180 | 0.0091 | - | - | - |

**Table S9.** Allele frequencies for locus *cmrGB3.8.1* for each studied population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| cmrGb3.8.1 | | | | |
| **Alleles** | **COQ** | **ZAP** | **LAG** | **LEB** |
| 108 | 0.0727 | - | 0.0417 | 0.2381 |
| 111 | 0.1364 | 0.1290 | 0.0833 | 0.1429 |
| 114 | 0.2273 | 0.4677 | 0.3333 | 0.1429 |
| 117 | 0.1727 | 0.0323 | 0.1667 | 0.2143 |
| 120 | 0.0455 | - | 0.0417 | 0.2143 |
| 123 | 0.0545 | - | 0.0417 | - |
| 126 | 0.1000 | 0.1290 | 0.0417 | - |
| 129 | 0.1273 | 0.2419 | 0.2500 | 0.0476 |
| 132 | 0.0636 | - | - | - |

**Table S10**. Allele frequencies for locus *cmrGB5.9* for each studied population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| cmrGb5.9 | | | | |
| **Alleles** | **COQ** | **ZAP** | **LAG** | **LEB** |
| 122 | 0.0818 | 0.0161 | - | 0.3571 |
| 124 | 0.0273 | 0.0161 | 0.0417 | - |
| 126 | 0.1000 | 0.1452 | 0.1667 | - |
| 128 | 0.0182 | - | 0.0417 | 0.1429 |
| 130 | 0.0636 | 0.0645 | 0.0417 | 0.2619 |
| 134 | 0.0364 | 0.0645 | 0.0417 | - |
| 136 | 0.1455 | 0.1452 | 0.1250 | - |
| 138 | 0.0273 | 0.0161 | - | - |
| 140 | 0.1273 | 0.1290 | 0.2083 | - |
| 142 | 0.2273 | 0.1613 | 0.1667 | 0.2381 |
| 144 | 0.1000 | 0.1613 | 0.0833 | - |
| 146 | 0.0182 | 0.0161 | - | - |
| 148 | 0.0091 | 0.0484 | - | - |
| 150 | 0.0182 | - | 0.0417 | - |
| 154 | - | - | 0.0417 | - |
| 156 | - | 0.0161 | - | - |

**Table S11**. Allele frequencies for locus *cmrGB4.11B* for each studied population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| CmrGb4.11B | | | | |
| **Alleles** | **COQ** | **ZAP** | **LAG** | **LEB** |
| 211 | 0.0273 | - | - | - |
| 215 | 0.0455 | - | - | - |
| 217 | 0.0091 | 0.0484 | - | 0.0476 |
| 223 | 0.0091 | 0.0323 | - | - |
| 225 | - | - | - | 0.0952 |
| 229 | - | - | - | 0.0476 |
| 227 | - | 0.0323 | - | - |
| 233 | 0.1545 | 0.2581 | 0.4167 | 0.1190 |
| 235 | 0.1909 | 0.1935 | 0.1250 | 0.1905 |
| 237 | 0.0273 | 0.0323 | - | 0.1190 |
| 241 | 0.1909 | 0.2097 | 0.2083 | 0.1905 |
| 243 | 0.0727 | 0.1129 | - | - |
| 245 | 0.0545 | 0.0161 | 0.0417 | - |
| 247 | 0.0727 | 0.0484 | 0.0833 | 0.0952 |
| 251 | 0.0364 | - | - | - |
| 253 | - | - | - | 0.0952 |
| 259 | 0.0364 | - | 0.0833 | - |
| 263 | 0.0545 | 0.0161 | 0.0417 | - |
| 271 | 0.0091 | - | - | - |
| 287 | 0.0091 | - | - | - |

**Table S12**. Allele frequencies for locus *cmrGB2.6.1* for each studied population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| cmrGb2.6.1 | | | | |
| **Alleles** | **COQ** | **ZAP** | **LAG** | **LEB** |
| 109 | - | - | - | 0.0625 |
| 112 | 0.0182 | 0.0484 | - | - |
| 115 | - | - | - | 0.2500 |
| 121 | 0.0273 | 0.0161 | - | - |
| 124 | 0.0545 | 0.0161 | 0.0417 | - |
| 127 | 0.1818 | 0.2097 | 0.1667 | - |
| 133 | 0.0909 | 0.0645 | 0.1250 | - |
| 136 | 0.1273 | 0.1935 | 0.2083 | - |
| 139 | 0.1909 | 0.1613 | 0.1250 | 0.1250 |
| 142 | 0.1000 | 0.0645 | 0.1250 | - |
| 145 | 0.0273 | 0.0323 | - | 0.1875 |
| 148 | 0.0273 | 0.0484 | 0.2083 | 0.0313 |
| 151 | 0.1455 | 0.1129 | - | - |
| 154 | 0.0091 | 0.0323 | - | 0.1250 |
| 160 | - | - | - | 0.1875 |
| 163 | - | - | - | 0.0313 |