Table 2. Values of genetic diversity of 16S, COI and combined gene (COI+16S) of *Conraua goliath* from six localities

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Populations** | **N** | **H** | **S** | **Hd** | **π** | **D** | **Fu’s Fs** |
| **16S** | | | | | | | |
| **Nkebe** | 7 | 2 | 1 | 0.533 | 0.00104 | 0.850 | 0.533 |
| **Bantoum** | 16 | 2 | 1 | 0.125 | 0.00024 | -1.16 | -0.700 |
| **Bipelhe** | 12 | 3 | 2 | 0.345 | 0.00071 | -1.429 | -0.246 |
| **Gounja** | 4 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Mbete** | 8 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Mpoula** | 7 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Overall** | 54 | 4 | 3 | 0.512 | 0.00106 | -0.368ns | -0.605 ns |
| **COI** | | | | | | | |
| **Nkebe** | 6 | 2 | 1 | 0.04 | 0.0006 | -1.816 | 0.090 |
| **Bantoum** | 13 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Bipelhe** | 12 | 1 | 1 | 0.000 | 0.000 | / | / |
| **Goundja** | 4 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Mbete** | 8 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Mpoula** | 7 | 1 | 0 | 0.000 | 0.000 | / | / |
| **Overall** | 50 | 2 | 1 | 0.042 | 0.00007 | -1.10ns | -1.602ns |
| **Combined gene (16S+COI)** | | | | | | | |
| **Nkebe** | 4 | 2 | 1 | 0.667 | 0.00059 | 1.63 | 0.54 |
| **Bantoum** | 15 | 2 | 1 | 0.133 | 0.00012 | -1.15 | -0.649 |
| **Bipelhe** | 8 | 3 | 2 | 0.464 | 0.00045 | -1.31 | -0.99 |
| **Goundja** | 4 | 1 | 0 | 0.0000 | 0.0000 | / | / |
| **Mbete** | 6 | 1 | 0 | 0.0000 | 0.0000 | / | / |
| **Mpoula** | 8 | 1 | 0 | 0.0000 | 0.0000 | / | / |
| **Overall** | 48 | 4 | 3 | 0.508 | 0.00048 | -0.428ns | -0.693 ns |

N indicates the sample size for each species and population, H the number of haplotypes, S number of substitution, Hd haplotype diversity, π the nucleotide diversity, D Tajuma's index**,** Fu's Fs Fs test.