**Maximum Likelihood Estimate of Substitution Matrix**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **A** | **T/U** | **C** | **G** |
| **A** | - | *10.72* | *6.09* | **6.46** |
| **T/U** | *9.84* | - | **6.31** | *6.52* |
| **C** | *9.84* | **11.11** | - | *6.52* |
| **G** | **9.77** | *10.72* | *6.09* | - |

NOTE.-- Each entry is the probability of substitution (*r*) from one base (row) to another base (column). Substitution pattern and rates were estimated under the Tamura-Nei (1993) model [1]. Rates of different transitional substitutions are shown in **bold** and those of transversionsal substitutions are shown in *italics*. Relative values of instantaneous *r* should be considered when evaluating them. For simplicity, sum of *r* values is made equal to 100, The nucleotide frequencies are A = 29.67%, T/U = 32.33%, C = 18.36%, and G = 19.64%. For estimating ML values, a tree topology was automatically computed. The maximum Log likelihood for this computation was -105173.804. This analysis involved 37 nucleotide sequences. Codon positions included were 1st+2nd+3rd. All positions containing gaps and missing data were eliminated (complete deletion option). There were a total of 13622 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2]

1. Tamura K. and Nei M. (**1993**). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* **10**:512-526.

2. Kumar S., Stecher G., Li M., Knyaz C., and Tamura K. (**2018**). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* **35**:1547-1549.