

**Table. Maximum Likelihood fits of 24 different nucleotide substitution models**

Model	Parameters	BIC	AICc	lnL	(+I)	(+G)	R	f(A)	f(T)	f(C)	f(G)	r(AT)	r(AC)	r(AG)	r(TA)	r(TC)	r(TG)	r(CA)	r(CT)	r(CG)	r(GA)	r(GT)	r(GC)
HKY+G+I	745	21714.080	13827.218	-6166.714	0.56	1.36	5.40	0.272	0.286	0.255	0.187	0.022	0.020	0.158	0.021	0.215	0.015	0.021	0.241	0.015	0.230	0.022	0.020
TN93+G+I	746	21726.666	13829.224	-6166.712	0.56	1.36	5.40	0.272	0.286	0.255	0.187	0.022	0.020	0.159	0.021	0.214	0.015	0.021	0.240	0.015	0.231	0.022	0.020
T92+G+I	743	21742.326	13876.628	-6193.429	0.56	1.39	5.16	0.279	0.279	0.221	0.221	0.022	0.018	0.186	0.022	0.186	0.018	0.022	0.234	0.018	0.234	0.022	0.018
GTR+G+I	749	21745.931	13816.745	-6157.457	0.56	1.44	5.38	0.272	0.286	0.255	0.187	0.033	0.025	0.156	0.032	0.220	0.009	0.027	0.247	0.004	0.227	0.014	0.005
GTR+G	748	21800.181	13881.576	-6190.878	n/a	0.20	4.84	0.272	0.286	0.255	0.187	0.027	0.026	0.159	0.026	0.208	0.021	0.028	0.234	0.003	0.231	0.032	0.004
K2+G+I	742	21825.842	13970.725	-6241.483	0.56	1.55	4.66	0.250	0.250	0.250	0.250	0.022	0.022	0.206	0.022	0.206	0.022	0.022	0.206	0.022	0.206	0.022	0.022
GTR+I	748	21830.645	13912.040	-6206.110	0.59	n/a	4.21	0.272	0.286	0.255	0.187	0.043	0.028	0.165	0.041	0.194	0.012	0.030	0.218	0.004	0.240	0.018	0.006
HKY+I	744	21831.996	13955.716	-6231.968	0.59	n/a	2.89	0.272	0.286	0.255	0.187	0.037	0.033	0.139	0.035	0.189	0.024	0.035	0.212	0.024	0.203	0.037	0.033
TN93+I	745	21853.488	13966.627	-6236.418	0.59	n/a	2.86	0.272	0.286	0.255	0.187	0.037	0.033	0.129	0.035	0.200	0.024	0.035	0.225	0.024	0.187	0.037	0.033
T92+I	742	21855.473	14000.356	-6256.298	0.59	n/a	2.90	0.279	0.279	0.221	0.221	0.035	0.028	0.165	0.035	0.165	0.028	0.035	0.208	0.028	0.208	0.035	0.028
K2+G	741	21868.624	14024.088	-6269.169	n/a	0.20	4.82	0.250	0.250	0.250	0.250	0.021	0.021	0.207	0.021	0.207	0.021	0.021	0.207	0.021	0.207	0.021	0.021
K2+I	741	21907.897	14063.361	-6288.806	0.59	n/a	3.73	0.250	0.250	0.250	0.250	0.026	0.026	0.197	0.026	0.197	0.026	0.026	0.197	0.026	0.197	0.026	0.026
HKY+G	744	21920.340	14044.060	-6276.140	n/a	0.52	3.98	0.272	0.286	0.255	0.187	0.029	0.025	0.150	0.027	0.204	0.019	0.027	0.229	0.019	0.218	0.029	0.025
TN93+G	745	21931.583	14044.721	-6275.466	n/a	0.52	4.00	0.272	0.286	0.255	0.187	0.029	0.026	0.140	0.027	0.215	0.019	0.027	0.241	0.019	0.203	0.029	0.026
T92+G	742	21941.815	14086.698	-6299.469	n/a	0.52	3.90	0.279	0.279	0.221	0.221	0.028	0.022	0.176	0.028	0.176	0.022	0.028	0.223	0.022	0.223	0.028	0.022
JC+G+I	741	22696.688	14852.152	-6683.201	0.57	3.16	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+I	740	22729.363	14895.408	-6705.835	0.59	n/a	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+G	740	22742.683	14908.728	-6712.495	n/a	0.23	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
GTR	747	23143.033	15235.009	-6868.599	n/a	n/a	2.50	0.272	0.286	0.255	0.187	0.057	0.046	0.130	0.055	0.191	0.024	0.049	0.214	0.005	0.188	0.036	0.006
T92	741	23159.767	15315.231	-6914.741	n/a	n/a	2.90	0.279	0.279	0.221	0.221	0.035	0.028	0.165	0.035	0.165	0.028	0.035	0.208	0.028	0.208	0.035	0.028
HKY	743	23163.633	15297.935	-6904.083	n/a	n/a	2.89	0.272	0.286	0.255	0.187	0.037	0.033	0.139	0.035	0.189	0.024	0.035	0.212	0.024	0.203	0.037	0.033
TN93	744	23171.771	15295.491	-6901.856	n/a	n/a	2.89	0.272	0.286	0.255	0.187	0.037	0.033	0.128	0.035	0.202	0.024	0.035	0.227	0.024	0.185	0.037	0.033
K2	740	23189.456	15355.501	-6935.881	n/a	n/a	2.88	0.250	0.250	0.250	0.250	0.032	0.032	0.186	0.032	0.186	0.032	0.032	0.186	0.032	0.186	0.032	0.032
JC	739	23918.491	16095.118	-7306.695	n/a	n/a	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083

NOTE.-- Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best. For each model, AICc value (Akaike Information Criterion, corrected), Maximum Likelihood value (*lnL*), and the number of parameters (including branch lengths) are also presented [1]. Non-uniformity of evolutionary rates among sites may be modeled by using a discrete Gamma distribution (+G) with 5 rate categories and by assuming that a certain fraction of sites are evolutionarily invariable (+I). Whenever applicable, estimates of gamma shape parameter and/or the estimated fraction of invariant sites are shown. Assumed or estimated values of transition/transversion bias (*R*) are shown for each model, as well. They are followed by nucleotide frequencies (*f*) and rates of base substitutions (*r*) for each nucleotide pair. Relative values of instantaneous *r* should be considered when evaluating them. For simplicity, sum of *r* values is made equal to 1 for each model. For estimating ML values, a tree topology was automatically computed. The analysis involved 371 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 797 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2].

Abbreviations: GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; TN93: Tamura-Nei; T92: Tamura 3-parameter; K2: Kimura 2-parameter; JC: Jukes-Cantor.

1. Nei M. and Kumar S. (2000). *Molecular Evolution and Phylogenetics*. Oxford University Press, New York.
2. Tamura K., Stecher G., Peterson D., Filipi A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

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