Table. Maximum Likelihood analysis of substitution models

Model	Parameters	BIC	AICc	InL	(+I)	(+G)	R	f(A)	f(T)	f(C)	f(G)	r(AT)	r(AC)	r(AG)	r(TA)	r(TC)	r(TG)
TN93+G+I	86	9582.803	8813.371	-4320.554	0.57	0.58	2.89	0.245	0.255	0.219	0.282	0.032	0.028	0.095	0.031	0.264	0.035
K2+G+I	82	9588.590	8854.934	-4345.347	0.61	0.57	2.93	0.250	0.250	0.250	0.250	0.032	0.032	0.186	0.032	0.186	0.032
T92+G+I	83	9599.789	8857.189	-4345.472	0.61	0.57	2.93	0.250	0.250	0.250	0.250	0.032	0.032	0.187	0.032	0.187	0.032
GTR+G+I	89	9600.516	8804.253	-4312.985	0.58	0.59	2.87	0.245	0.255	0.219	0.282	0.048	0.019	0.096	0.046	0.264	0.048
HKY+G+I	85	9621.091	8860.603	-4345.173	0.61	0.57	3.01	0.245	0.255	0.219	0.282	0.032	0.027	0.211	0.030	0.164	0.035
TN93+I	85	9631.786	8871.298	-4350.520	0.72	n/a	2.50	0.245	0.255	0.219	0.282	0.036	0.031	0.101	0.034	0.246	0.039
K2+I	81	9634.552	8909.840	-4373.803	0.74	n/a	2.59	0.250	0.250	0.250	0.250	0.035	0.035	0.180	0.035	0.180	0.035
T92+I	82	9645.764	8912.108	-4373.934	0.74	n/a	2.59	0.250	0.250	0.250	0.250	0.035	0.035	0.180	0.035	0.180	0.035
GTR+I	88	9647.595	8860.275	-4342.000	0.72	n/a	2.52	0.245	0.255	0.219	0.282	0.052	0.020	0.100	0.050	0.248	0.055
HKY+I	84	9667.059	8915.514	-4373.632	0.74	n/a	2.65	0.245	0.255	0.219	0.282	0.035	0.030	0.204	0.033	0.159	0.039
TN93+G	85	9812.653	9052.165	-4440.954	n/a	0.17	2.79	0.245	0.255	0.219	0.282	0.033	0.028	0.083	0.031	0.272	0.036
JC+G+I	81	9813.675	9088.963	-4463.365	0.69	2.04	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083
GTR+G	88	9828.215	9040.895	-4432.310	n/a	0.17	2.78	0.245	0.255	0.219	0.282	0.050	0.017	0.083	0.048	0.272	0.050
K2+G	81	9837.147	9112.435	-4475.101	n/a	0.15	2.69	0.250	0.250	0.250	0.250	0.034	0.034	0.182	0.034	0.182	0.034
JC+I	80	9837.652	9121.884	-4480.828	0.74	n/a	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083
T92+G	82	9848.139	9114.482	-4475.122	n/a	0.15	2.69	0.250	0.250	0.250	0.250	0.034	0.034	0.182	0.034	0.182	0.034
HKY+G	84	9868.704	9117.160	-4474.454	n/a	0.15	2.76	0.245	0.255	0.219	0.282	0.034	0.029	0.207	0.033	0.161	0.037
JC+G	80	10054.186	9338.418	-4589.095	n/a	0.17	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083
TN93	84	10147.008	9395.463	-4613.606	n/a	n/a	2.00	0.245	0.255	0.219	0.282	0.042	0.036	0.090	0.040	0.233	0.046
GTR	87	10169.682	9391.305	-4608.518	n/a	n/a	2.01	0.245	0.255	0.219	0.282	0.052	0.030	0.090	0.050	0.234	0.057
K2	80	10198.506	9482.739	-4661.255	n/a	n/a	1.99	0.250	0.250	0.250	0.250	0.042	0.042	0.166	0.042	0.166	0.042
T92	81	10209.501	9484.789	-4661.278	n/a	n/a	1.99	0.250	0.250	0.250	0.250	0.042	0.042	0.166	0.042	0.166	0.042
HKY	83	10232.272	9489.672	-4661.713	n/a	n/a	1.99	0.245	0.255	0.219	0.282	0.043	0.037	0.187	0.041	0.146	0.047
JC	79	10391.784	9684.961	-4763.369	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

NOTE.-- This table presents the goodness of fit for multiple substitution models, including their parameter estimates. The Bayesian Information Criterion (BIC) scores are used to select the optimal model. Each model's Maximum Likelihood value (lnL), corrected Akaike Information Criterion (AICc) value, BIC, and the number of parameters are presented (refer to Chapter 8 in [1] for more information). Evolutionary rate variation among sites was modeled using a discrete Gamma distribution (+*G*) with 5 rate categories [2] and a fraction of sites were allowed to be evolutionarily invariant (+*I*). Estimates of gamma shape parameter and fraction of invariant sites are also shown, as appropriate. 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. The sum of *r* estimates is set to 1 for each model making comparisons across models easier. The ML analyses were conducted using an automatically generated tree topology [3]. The analytical procedure encompassed 41 nucleotide sequences with 1.409 positions in the final dataset. Evolutionary analyses were conducted in MEGA12 [4] utilizing up to 10 parallel computing threads.

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

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4. Kumar S., Stecher G., Suleski M., Sanderford M., Sharma S., and Tamura K. (**2024**). Molecular Evolutionary Genetics Analysis Version 12 for adaptive and green computing. *Molecular Biology and Evolution* **41**:1-9.