

**Table. Maximum Likelihood analysis of 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)
T92+G	48	7980.553	7594.819	-3749.307	n/a	0.82	3.12	0.230	0.230	0.270	0.270	0.028	0.033	0.205	0.028	0.205	0.033	0.028
K2+G	47	7983.835	7606.133	-3755.968	n/a	0.81	3.12	0.250	0.250	0.250	0.250	0.030	0.030	0.189	0.030	0.189	0.030	0.030
T92+I	48	7984.953	7599.218	-3751.506	0.44	n/a	3.11	0.230	0.230	0.270	0.270	0.028	0.033	0.205	0.028	0.205	0.033	0.028
HKY+G	50	7986.551	7584.753	-3742.265	n/a	0.81	3.13	0.183	0.276	0.286	0.255	0.034	0.035	0.192	0.023	0.216	0.031	0.023
K2+I	47	7988.127	7610.425	-3758.114	0.44	n/a	3.11	0.250	0.250	0.250	0.250	0.030	0.030	0.189	0.030	0.189	0.030	0.030
T92+G+I	49	7990.594	7596.827	-3749.307	0.00	0.82	3.12	0.230	0.230	0.270	0.270	0.028	0.033	0.205	0.028	0.205	0.033	0.028
HKY+I	50	7991.410	7589.612	-3744.695	0.44	n/a	3.11	0.183	0.276	0.286	0.255	0.034	0.035	0.192	0.023	0.215	0.031	0.023
TN93+G	51	7991.882	7582.053	-3739.911	n/a	0.79	3.13	0.183	0.276	0.286	0.255	0.033	0.035	0.225	0.022	0.189	0.031	0.022
K2+G+I	48	7993.876	7608.141	-3755.968	0.00	0.81	3.12	0.250	0.250	0.250	0.250	0.030	0.030	0.189	0.030	0.189	0.030	0.030
TN93+I	51	7995.856	7586.027	-3741.897	0.44	n/a	3.11	0.183	0.276	0.286	0.255	0.034	0.035	0.227	0.022	0.187	0.031	0.022
HKY+G+I	51	7996.591	7586.761	-3742.265	0.00	0.81	3.13	0.183	0.276	0.286	0.255	0.034	0.035	0.192	0.023	0.216	0.031	0.023
TN93+G+I	52	8001.923	7584.062	-3739.911	0.00	0.79	3.13	0.183	0.276	0.286	0.255	0.033	0.035	0.225	0.022	0.189	0.031	0.022
GTR+G	54	8019.411	7585.488	-3738.614	n/a	0.79	3.12	0.183	0.276	0.286	0.255	0.024	0.034	0.225	0.016	0.189	0.031	0.022
T92	47	8020.831	7643.129	-3774.466	n/a	n/a	3.05	0.230	0.230	0.270	0.270	0.028	0.033	0.204	0.028	0.204	0.033	0.028
GTR+I	54	8023.412	7589.489	-3740.615	0.44	n/a	3.11	0.183	0.276	0.286	0.255	0.025	0.034	0.227	0.016	0.187	0.031	0.022
K2	46	8024.136	7654.466	-3781.139	n/a	n/a	3.05	0.250	0.250	0.250	0.250	0.031	0.031	0.188	0.031	0.188	0.031	0.031
HKY	49	8027.705	7633.939	-3767.862	n/a	n/a	3.05	0.183	0.276	0.286	0.255	0.035	0.036	0.191	0.023	0.214	0.032	0.023
GTR+G+I	55	8029.451	7587.497	-3738.614	0.00	0.79	3.12	0.183	0.276	0.286	0.255	0.024	0.034	0.225	0.016	0.189	0.031	0.022
TN93	50	8033.366	7631.568	-3765.672	n/a	n/a	3.05	0.183	0.276	0.286	0.255	0.034	0.035	0.217	0.023	0.193	0.032	0.023
GTR	53	8060.956	7635.064	-3764.407	n/a	n/a	3.05	0.183	0.276	0.286	0.255	0.026	0.033	0.218	0.017	0.193	0.032	0.021
JC+G	46	8274.975	7905.304	-3906.558	n/a	0.86	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+I	46	8278.567	7908.897	-3908.354	0.43	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
JC+G+I	47	8285.015	7907.312	-3906.558	0.00	0.86	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC	45	8312.107	7950.469	-3930.144	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

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), Akaike Information Criterion, corrected (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 24 nucleotide sequences. The partial deletion option was applied to eliminate all positions with less than 95% site coverage resulting in a final data set comprising 962 positions. Evolutionary analyses were conducted in MEGA12 [4] utilizing up to 4 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.

1. Nei M. and Kumar S. (2000). *Molecular Evolution and Phylogenetics*. Oxford University Press, New York.
2. Yang Z. (1994) Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: Approximate methods. *Journal of Molecular Evolution*. **39**:306-314.
3. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution* **28**: 2731-2739.
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.

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