Maximum Likelihood Model Parameters

The nucleotide substitution model for each data-set was selected using the Bayesian Information Criterion (BIC).

28S rRNA data-set

GTR model with gamma distributed rate heterogeneity (four categories). Rate matrix parameters were Alpha (0.488), Beta (3.648), Gamma (1.951), Delta (0.228) and Epsilon (5.938). Shape of the gamma distribution was 0.339 and there were zero invariant sites.

CO1 data-set

TN93 model with gamma distributed rate heterogeneity (four categories).

Model parameters specific to each partition (codon position):

Parameter	1st	2nd	3rd
Transition between purines	1.718	7.761	3.142
Transition between pyrimidines	6.733	0.613	4.359
Shape of gamma distribution	0.763	0.192	0.871
Proportion of invariant sites (%)	0	0	0

Concatenated 28S rRNA + CO1 data-sets

TN93 model with gamma distributed rate heterogeneity (four categories).

Model parameters specific to each partition:

Parameter	28S rRNA	CO1: 1st	CO1: 2nd	CO1: 3rd
Transition between purines	2.942	2.071	5.678	3.439
Transition between pyrimidines	5.763	8.216	0.706	4.850
Shape of gamma distribution	0.392	0.471	0.177	0.333
Proportion of invariant sites (%)	0	0	0	0