

IQ-TREE 1.5.0a built Oct 28 2016

Input file name: cp_batatas_mafft.fasta
Type of analysis: tree reconstruction
Random seed number: 785392

SEQUENCE ALIGNMENT

Input data: 192 sequences with 266726 nucleotide sites
Number of constant sites: 256633 (= 96.216% of all sites)
Number of invariant (constant or ambiguous constant) sites: 256633 (= 96.216% of all sites)
Number of distinct site patterns: 11570

SUBSTITUTION PROCESS

Model of substitution: GTR+F

Rate parameter R:

A-C: 0.9989
A-G: 1.3292
A-T: 0.4514
C-G: 1.0446
C-T: 1.3488
G-T: 1.0000

State frequencies: (empirical counts from alignment)

$\pi(A) = 0.3104$
 $\pi(C) = 0.1904$
 $\pi(G) = 0.1854$
 $\pi(T) = 0.3138$

Rate matrix Q:

A	-0.8142	0.2678	0.347	0.1994
C	0.4365	-1.305	0.2727	0.5958
G	0.5808	0.28	-1.303	0.4418
T	0.1972	0.3616	0.261	-0.8199

Model of rate heterogeneity: Uniform

STATISTICAL TESTS

Tree 1 = Sweet potato monophyletic

Tree 2 = Sweet potato non-monophyletic

Tree	logL	deltaL	bp-RELL	p-KH	p-SH	p-WKH	p-WSH	c-ELW	p-AU
1	-514713.615	209.489	0.0664 +	0.0686 +	0.0686 +	0.0686 +	0.0686 +	0.0664 +	0.0652 +
2	-514504.126	0.000	0.9335 +	0.9314 +	1.0000 +	0.9314 +	0.9314 +	0.9336 +	0.9348 +

deltaL : logL difference from the maximal logl in the set.

bp-RELL : bootstrap proportion using REll method (Kishino et al. 1990).

p-KH : p-value of one sided Kishino-Hasegawa test (1989).

p-SH : p-value of Shimodaira-Hasegawa test (2000).

p-WKH : p-value of weighted KH test.

p-WSH : p-value of weighted SH test.

c-ELW : Expected Likelihood Weight (Strimmer & Rambaut 2002).

p-AU : p-value of approximately unbiased (AU) test (Shimodaira, 2002).

Plus signs denote the 95% confidence sets.

Minus signs denote significant exclusion.

All tests performed 100000 resamplings using the REll method.