Phylogenetic tree construction by Neighbour-Joining Method

gi|160212994|gb|ABX10940.1| maturase K (chloroplast) Rhynchostylis retusa

gi|758740151|gb|AJO71768.1| maturase K (chloroplast) Smitinandia micrantha

gi|758740021|gb|AJO71703.1| maturase K (chloroplast) Acampe papillosa

gi|76667735|dbj|BAE45639.1| maturase K (chloroplast) Acampe ochracea

gi|584478976|gb|AHJ08651.1| maturase K (chloroplast) Aerides odorata

gi|51831262|gb|AAU09848.1| maturase K (chloroplast) Aerides multiflora

gi|229610185|gb|ACQ83622.1| maturase K (chloroplast) Papilionanthe teres

gi|1835942984|gb|QJF73261.1| maturase K (chloroplast) Geodorum densiflorum

gi|1809269079|gb|QIA92480.1| maturase K (chloroplast) Cymbidium aloifolium

gi|675912510|gb|AIM18028.1| maturase K (chloroplast) Phaius tancarvilleae

gi|523586367|gb|AGQ52178.1| maturase K (chloroplast) Dendrobium moschatum

gi|523586421|gb|AGQ52204.1| maturase K (chloroplast) Dendrobium transparens

gi|1002165311|ref|YP 009235424.1| maturase K (chloroplast) Dendrobium nobile

gi|1215847351|ref|YP 009401734.1| maturase K (chloroplast) Dendrobium jenkinsii

gi|1215847729|ref|YP 009402094.1| maturase K (chloroplast) Dendrobium fimbriatum

gi|1215846444|ref|YP 009400655.1| maturase K (chloroplast) Dendrobium aphyllum

gi|987312724|gb|AMD78048.1| maturase K (chloroplast) Goodyera procera

0.100   0.080   0.060   0.040   0.020   0.000

Evolutionary relationships of taxa:

The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.47505180 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. This analysis involved 17 amino acid sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 526 positions in the final dataset. Evolutionary analyses were conducted in MEGA X.