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<?xml version="1.0" standalone="yes"?>

<!-- Generated by BEAUTi v1.7.3 -->
<!-- by Alexei J. Drummond, Andrew Rambaut and Marc A. Suchard -->
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<!-- Institute of Evolutionary Biology, University of Edinburgh -->
<!-- David Geffen School of Medicine, University of California, Los Angeles-->
<!-- http://beast.bio.ed.ac.uk/ -->
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  <!-- The list of taxa to be analysed (can also include dates/ages). -->
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[illegible]

This image shows a blank sheet of handwriting practice paper. It features ten sets of horizontal dashed lines, each set consisting of three parallel lines (top, middle, and bottom) to guide letter formation. The lines are evenly spaced across the page, providing a structured environment for practicing cursive or other handwriting styles.

[illegible]

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ATTTCTCTTATTGGATCATTGTGCGAAAGCTCA-ATTTGTACTATATCGGGTCATCCTATTAGTAAACCAA-TCTGGACCG-
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<taxon idref="Goodyera_procera"/>

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GTTGT-----

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GGTTTTGTATCGTATAAAGTATATAC-----
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        </sequence>
    </alignment>

    <!-- The unique patterns from 1 to end -->
    <!-- npatterns=1157 -->
    <patterns id="Matrix in file 'cymb ITS1_2.nexus'.patterns" from="1" strip="false">
        <alignment idref="alignment1"/>
    </patterns>

    <!-- The unique patterns from 1 to end -->
    <!-- npatterns=581 -->
    <patterns id="Matrix in file 'cymbidium_matk.nexus'.patterns" from="1"
strip="false">
        <alignment idref="alignment2"/>
    </patterns>

    <!-- Calibrated Yule: Heled J, Drummond AJ (2011), Syst Biol, doi: 10.1093/sysbio/
syr087-->
    <yuleModel id="yule" units="substitutions">
        <birthRate>
            <parameter id="yule.birthRate" value="0.4" lower="0.0"/>
        </birthRate>
    </yuleModel>

    <!-- This is a simple constant population size coalescent model -->
    <!-- that is used to generate an initial tree for the chain. -->
    <constantSize id="initialDemo" units="substitutions">
        <populationSize>
            <parameter id="initialDemo.popSize" value="100.0"/>
        </populationSize>
    </constantSize>

    <!-- Generate a random starting tree under the coalescent process -->
    <coalescentTree id="startingTree">
        <constrainedTaxa>
            <taxa idref="taxa"/>
            <tmrca monophyletic="true">
                <taxa idref="Cymbidium"/>
            </tmrca>
            <tmrca monophyletic="true">
                <taxa idref="Dendrobium_Earina"/>
                <uniformDistributionModel id="Dendrobium_Earina-
uniformDist">
                    <lower>
                        20.0

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        </lower>
        <upper>
            120.0
        </upper>
    </uniformDistributionModel>
</tmrca>
<tmrca monophyletic="true">
    <taxa idref="Goodyera"/>
</tmrca>
</constrainedTaxa>
<constantSize idref="initialDemo"/>
</coalescentTree>

<!-- Generate a tree model -->
<treeModel id="treeModel">
    <coalescentTree idref="startingTree"/>
    <rootHeight>
        <parameter id="treeModel.rootHeight"/>
    </rootHeight>
    <nodeHeights internalNodes="true">
        <parameter id="treeModel.internalNodeHeights"/>
    </nodeHeights>
    <nodeHeights internalNodes="true" rootNode="true">
        <parameter id="treeModel.allInternalNodeHeights"/>
    </nodeHeights>
</treeModel>

<!-- Taxon Sets -->
<tmrcaStatistic id="tmrca(Cymbidium)" includeStem="false">
    <mrca>
        <taxa idref="Cymbidium"/>
    </mrca>
    <treeModel idref="treeModel"/>
</tmrcaStatistic>
<monophylyStatistic id="monophyly(Cymbidium)">
    <mrca>
        <taxa idref="Cymbidium"/>
    </mrca>
    <treeModel idref="treeModel"/>
</monophylyStatistic>
<tmrcaStatistic id="tmrca(Dendrobium_Earina)" includeStem="false">
    <mrca>
        <taxa idref="Dendrobium_Earina"/>
    </mrca>
    <treeModel idref="treeModel"/>
</tmrcaStatistic>
<monophylyStatistic id="monophyly(Dendrobium_Earina)">
    <mrca>
        <taxa idref="Dendrobium_Earina"/>
    </mrca>
    <treeModel idref="treeModel"/>
</monophylyStatistic>
<tmrcaStatistic id="tmrca(Goodyera)" includeStem="false">
    <mrca>
        <taxa idref="Goodyera"/>
    </mrca>
    <treeModel idref="treeModel"/>
</tmrcaStatistic>
<monophylyStatistic id="monophyly(Goodyera)">
    <mrca>

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        <taxa idref="Goodyera"/>
    </mrca>
    <treeModel idref="treeModel"/>
</monophylyStatistic>

<!-- Generate a speciation likelihood for Yule or Birth Death -->
<speciationLikelihood id="speciation">
    <model>
        <yuleModel idref="yule"/>
    </model>
    <speciesTree>
        <treeModel idref="treeModel"/>
    </speciesTree>
    <calibration correction="exact">
        <point>
            <taxa idref="taxa"/>
            <normalDistributionModel>
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                    39.0
                </mean>
                <stdev>
                    5.5
                </stdev>
            </normalDistributionModel>
        </point>
    </calibration>
</speciationLikelihood>

<!-- The uncorrelated relaxed clock (Drummond, Ho, Phillips & Rambaut (2006) PLoS
Biology 4, e88 )-->
<discretizedBranchRates id="branchRates">
    <treeModel idref="treeModel"/>
    <distribution>
        <logNormalDistributionModel meanInRealSpace="true">
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                <parameter id="ucl.d.mean" value="1.0" lower="0.0"/>
            </mean>
            <stdev>
                <parameter id="ucl.d.stdev" value="1.0"
lower="0.0"/>
            </stdev>
        </logNormalDistributionModel>
    </distribution>
    <rateCategories>
        <parameter id="branchRates.categories"/>
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</discretizedBranchRates>
    <rateStatistic id="meanRate" name="meanRate" mode="mean" internal="true"
external="true">
        <treeModel idref="treeModel"/>
        <discretizedBranchRates idref="branchRates"/>
    </rateStatistic>
    <rateStatistic id="coefficientOfVariation" name="coefficientOfVariation"
mode="coefficientOfVariation" internal="true" external="true">
        <treeModel idref="treeModel"/>
        <discretizedBranchRates idref="branchRates"/>
    </rateStatistic>
    <rateCovarianceStatistic id="covariance" name="covariance">
        <treeModel idref="treeModel"/>

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        <discretizedBranchRates idref="branchRates"/>
    </rateCovarianceStatistic>

    <!-- The general time reversible (GTR) substitution model -->
    <gtrModel id="Matrix in file 'cymb_ITS1_2.nexus'.gtr">
        <frequencies>
            <frequencyModel dataType="nucleotide">
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            </frequencyModel>
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        <rateAG>
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        </rateAG>
        <rateAT>
            <parameter id="Matrix in file 'cymb_ITS1_2.nexus'.at" value="1.0"
lower="0.0"/>
        </rateAT>
        <rateCG>
            <parameter id="Matrix in file 'cymb_ITS1_2.nexus'.cg" value="1.0"
lower="0.0"/>
        </rateCG>
        <rateGT>
            <parameter id="Matrix in file 'cymb_ITS1_2.nexus'.gt" value="1.0"
lower="0.0"/>
        </rateGT>
    </gtrModel>

    <!-- site model -->
    <siteModel id="Matrix in file 'cymb_ITS1_2.nexus'.siteModel">
        <substitutionModel>
            <gtrModel idref="Matrix in file 'cymb_ITS1_2.nexus'.gtr"/>
        </substitutionModel>
        <gammaShape gammaCategories="4">
            <parameter id="Matrix in file 'cymb_ITS1_2.nexus'.alpha"
value="0.5" lower="0.0"/>
        </gammaShape>
        <proportionInvariant>
            <parameter id="Matrix in file 'cymb_ITS1_2.nexus'.pInv"
value="0.5" lower="0.0" upper="1.0"/>
        </proportionInvariant>
    </siteModel>

    <!-- The general time reversible (GTR) substitution model -->
    <gtrModel id="Matrix in file 'cymbidium_matk.nexus'.gtr">
        <frequencies>
            <frequencyModel dataType="nucleotide">
                <frequencies>
                    <parameter id="Matrix in file
'cymbidium_matk.nexus'.frequencies" value="0.25 0.25 0.25 0.25"/>
                </frequencies>
            </frequencyModel>
        </frequencies>
    </gtrModel>

```

```

        <rateAC>
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.ac"
value="1.0" lower="0.0"/>
        </rateAC>
        <rateAG>
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.ag"
value="1.0" lower="0.0"/>
        </rateAG>
        <rateAT>
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.at"
value="1.0" lower="0.0"/>
        </rateAT>
        <rateCG>
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.cg"
value="1.0" lower="0.0"/>
        </rateCG>
        <rateGT>
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.gt"
value="1.0" lower="0.0"/>
        </rateGT>
    </gtrModel>

    <!-- site model -->
    <siteModel id="Matrix in file 'cymbidium_matk.nexus'.siteModel">
        <substitutionModel>
            <gtrModel idref="Matrix in file 'cymbidium_matk.nexus'.gtr"/>
        </substitutionModel>
        <gammaShape gammaCategories="4">
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.alpha"
value="0.5" lower="0.0"/>
        </gammaShape>
        <proportionInvariant>
            <parameter id="Matrix in file 'cymbidium_matk.nexus'.pInv"
value="0.5" lower="0.0" upper="1.0"/>
        </proportionInvariant>
    </siteModel>

    <!-- Likelihood for tree given sequence data -->
    <treeLikelihood id="Matrix in file 'cymb ITS1_2.nexus'.treeLikelihood"
useAmbiguities="false" stateTagName="Matrix in file 'cymb ITS1_2.nexus'.states">
        <patterns idref="Matrix in file 'cymb ITS1_2.nexus'.patterns"/>
        <treeModel idref="treeModel"/>
        <siteModel idref="Matrix in file 'cymb ITS1_2.nexus'.siteModel"/>
        <discretizedBranchRates idref="branchRates"/>
    </treeLikelihood>

    <!-- Likelihood for tree given sequence data -->
    <treeLikelihood id="Matrix in file 'cymbidium_matk.nexus'.treeLikelihood"
useAmbiguities="false" stateTagName="Matrix in file 'cymbidium_matk.nexus'.states">
        <patterns idref="Matrix in file 'cymbidium_matk.nexus'.patterns"/>
        <treeModel idref="treeModel"/>
        <siteModel idref="Matrix in file 'cymbidium_matk.nexus'.siteModel"/>
        <discretizedBranchRates idref="branchRates"/>
    </treeLikelihood>

    <!-- Define operators -->
    <operators id="operators">
        <scaleOperator scaleFactor="0.75" weight="0.1">
            <parameter idref="Matrix in file 'cymb ITS1_2.nexus'.ac"/>
        </scaleOperator>

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```

<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.ag"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.at"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.cg"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.gt"/>
</scaleOperator>
<deltaExchange delta="0.01" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.frequencies"/>
>
</deltaExchange>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.alpha"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.pInv"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.ac"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.ag"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.at"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.cg"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.gt"/>
</scaleOperator>
<deltaExchange delta="0.01" weight="0.1">
  <parameter idref="Matrix in file
'cymbidium_matk.nexus'.frequencies"/>
</deltaExchange>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.alpha"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="0.1">
  <parameter idref="Matrix in file 'cymbidium_matk.nexus'.pInv"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="3">
  <parameter idref="ucl.d.mean"/>
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="3">
  <parameter idref="ucl.d.stdev"/>
</scaleOperator>
<subtreeSlide size="4.4" gaussian="true" weight="15">
  <treeModel idref="treeModel"/>
</subtreeSlide>
<narrowExchange weight="15">
  <treeModel idref="treeModel"/>
</narrowExchange>
<wideExchange weight="3">

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```

        <treeModel idref="treeModel"/>
    </wideExchange>
    <wilsonBalding weight="3">
        <treeModel idref="treeModel"/>
    </wilsonBalding>
    <scaleOperator scaleFactor="0.75" weight="3">
        <parameter idref="treeModel.rootHeight"/>
    </scaleOperator>
    <uniformOperator weight="30">
        <parameter idref="treeModel.internalNodeHeights"/>
    </uniformOperator>
    <scaleOperator scaleFactor="0.75" weight="3">
        <parameter idref="yule.birthRate"/>
    </scaleOperator>
    <upDownOperator scaleFactor="0.75" weight="3">
        <up>
            <parameter idref="uclD.mean"/>
        </up>
        <down>
            <parameter idref="treeModel.allInternalNodeHeights"/>
        </down>
    </upDownOperator>
    <swapOperator size="1" weight="10" autoOptimize="false">
        <parameter idref="branchRates.categories"/>
    </swapOperator>
    <uniformIntegerOperator weight="10">
        <parameter idref="branchRates.categories"/>
    </uniformIntegerOperator>
</operators>

<!-- Define MCMC -->
<mcmc id="mcmc" chainLength="10000000" autoOptimize="true"
operatorAnalysis="cym.ops">
    <posterior id="posterior">
        <prior id="prior">
            <booleanLikelihood>
                <monophylyStatistic
idref="monophyly(Dendrobium_Earina)"/>
                <monophylyStatistic idref="monophyly(Goodyera)"/>
                <monophylyStatistic idref="monophyly(Cymbidium)"/>
            </booleanLikelihood>
            <gammaPrior shape="0.05" scale="10.0" offset="0.0">
                <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.ac"/>
            </gammaPrior>
            <gammaPrior shape="0.05" scale="20.0" offset="0.0">
                <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.ag"/>
            </gammaPrior>
            <gammaPrior shape="0.05" scale="10.0" offset="0.0">
                <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.at"/>
            </gammaPrior>
            <gammaPrior shape="0.05" scale="10.0" offset="0.0">
                <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.cg"/>
            </gammaPrior>
            <gammaPrior shape="0.05" scale="10.0" offset="0.0">
                <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.gt"/>

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        </gammaPrior>
        <uniformPrior lower="0.0" upper="1.0">
            <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.frequencies"/>
        </uniformPrior>
        <exponentialPrior mean="0.5" offset="0.0">
            <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.alpha"/>
        </exponentialPrior>
        <uniformPrior lower="0.0" upper="1.0">
            <parameter idref="Matrix in file
'cymb_ITS1_2.nexus'.pInv"/>
        </uniformPrior>
        <gammaPrior shape="0.05" scale="10.0" offset="0.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.ac"/>
        </gammaPrior>
        <gammaPrior shape="0.05" scale="20.0" offset="0.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.ag"/>
        </gammaPrior>
        <gammaPrior shape="0.05" scale="10.0" offset="0.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.at"/>
        </gammaPrior>
        <gammaPrior shape="0.05" scale="10.0" offset="0.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.cg"/>
        </gammaPrior>
        <gammaPrior shape="0.05" scale="10.0" offset="0.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.gt"/>
        </gammaPrior>
        <uniformPrior lower="0.0" upper="1.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.frequencies"/>
        </uniformPrior>
        <exponentialPrior mean="0.5" offset="0.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.alpha"/>
        </exponentialPrior>
        <uniformPrior lower="0.0" upper="1.0">
            <parameter idref="Matrix in file
'cymbidium_matk.nexus'.pInv"/>
        </uniformPrior>
        <exponentialPrior mean="10.0" offset="0.0">
            <parameter idref="ucld.stdev"/>
        </exponentialPrior>
        <uniformPrior lower="1.0E-6" upper="10.0">
            <parameter idref="ucld.mean"/>
        </uniformPrior>
        <uniformPrior lower="0.0" upper="1.0E100">
            <parameter idref="yule.birthRate"/>
        </uniformPrior>
        <speciationLikelihood idref="speciation"/>
    </prior>
    <likelihood id="likelihood">
        <treeLikelihood idref="Matrix in file
'cymb_ITS1_2.nexus'.treeLikelihood"/>
        <treeLikelihood idref="Matrix in file

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'cymbidium_matk.nexus'.treeLikelihood"/>
    </likelihood>
</posterior>
<operators idref="operators"/>

<!-- write log to screen
-->
<log id="screenLog" logEvery="1000">
    <column label="Posterior" dp="4" width="12">
        <posterior idref="posterior"/>
    </column>
    <column label="Prior" dp="4" width="12">
        <prior idref="prior"/>
    </column>
    <column label="Likelihood" dp="4" width="12">
        <likelihood idref="likelihood"/>
    </column>
    <column label="rootHeight" sf="6" width="12">
        <parameter idref="treeModel.rootHeight"/>
    </column>
    <column label="ucl.d.mean" sf="6" width="12">
        <parameter idref="ucl.d.mean"/>
    </column>
</log>

<!-- write log to file
-->
<log id="fileLog" logEvery="1000" fileName="cym.log" overwrite="false">
    <posterior idref="posterior"/>
    <prior idref="prior"/>
    <likelihood idref="likelihood"/>
    <parameter idref="treeModel.rootHeight"/>
    <tmrcaStatistic idref="tmrca(Cymbidium)"/>
    <tmrcaStatistic idref="tmrca(Dendrobium_Earina)"/>
    <tmrcaStatistic idref="tmrca(Goodyera)"/>
    <parameter idref="yule.birthRate"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.ac"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.ag"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.at"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.cg"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.gt"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.frequencies"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.alpha"/>
    <parameter idref="Matrix in file 'cymb_ITS1_2.nexus'.pInv"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.ac"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.ag"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.at"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.cg"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.gt"/>
    <parameter idref="Matrix in file
'cymbidium_matk.nexus'.frequencies"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.alpha"/>
    <parameter idref="Matrix in file 'cymbidium_matk.nexus'.pInv"/>
    <parameter idref="ucl.d.mean"/>
    <parameter idref="ucl.d.stdev"/>
    <rateStatistic idref="meanRate"/>
    <rateStatistic idref="coefficientOfVariation"/>
    <rateCovarianceStatistic idref="covariance"/>
    <treeLikelihood idref="Matrix in file

```

```

'cymb_ITS1_2.nexus'.treeLikelihood"/>
    <treeLikelihood idref="Matrix in file
'cymbidium_matk.nexus'.treeLikelihood"/>
    <speciationLikelihood idref="speciation"/>
</log>

    <!-- write tree log to file
-->
    <logTree id="treeFileLog" logEvery="1000" nexusFormat="true"
fileName="cym.trees" sortTranslationTable="true">
    <treeModel idref="treeModel"/>
    <trait name="rate" tag="rate">
        <discretizedBranchRates idref="branchRates"/>
    </trait>
    <posterior idref="posterior"/>
    </logTree>
</mcmc>
<report>
    <property name="timer">
        <mcmc idref="mcmc"/>
    </property>
</report>
</beast>

```