Method for MrBayes run:

To validate the accuracy of certain splits in our maximum likelihood tree, we used Bayesian inference as a second method to reconstruct the expansin gene tree. The same alignment as used for maximum likelihood reconstruction was used, except that *Vitrella brassicaformis* and *Emiliania huxleyi* were removed as they represented extremely divergent and long branches which may have interfered with convergence of the Bayesian model. We used MrBayes (v 3.2.6) on the XSEDE cluster to reconstruct a Bayesian tree. Two separate runs were performed each with six chains for 10 million generations. We used metropolis coupling with a heating parameter of 0.005 and swap frequency of 1. The substitution model was the Whelan and Goldman (WAG) matrix with four gamma distributed rate categories. The chain was sampled every 500 generations and the first 25% of samples were discarded as burn-in. The log likelihood of both runs plateaued after ~2.5 million generations and both runs converged on a similar tree (standard deviation of split frequencies between runs = 0.020738. All parameters of the MCMC algorithm are listed below. A majority rule consensus tree was constructed from the sampled trees of run 1.

**MrBayes on XSEDE - Parameters**

|  |  |
| --- | --- |
| **Covarionopts\_** | false |
| **Nbetacatopts\_** | 5 |
| **Ngammacatopts\_** | 4 |
| **Parsmodelopts\_** | false |
| **aamodelpropts\_** | fixed(wag) |
| **allchainsval\_** | allchains=Yes |
| **brlensprexp1\_** | 10.0 |
| **brlenspropts\_** | unconstrained:exponential |
| **burninfracval\_** | 0.25 |
| **codingopts\_** | all |
| **covswitchpropts\_** | uniform |
| **covswitchuni1\_** | 0.0 |
| **covswitchuni2\_** | 100.0 |
| **flagdatatype\_** | protein |
| **mcmcdiagnval\_** | mcmcdiagn=Yes |
| **minpartfreqval\_** | 0.1 |
| **mrbayesblockquery\_** | false |
| **nchainsval\_** | 6 |
| **ngenval\_** | 10000000 |
| **nocharsets\_** | 0 |
| **nrunsval\_** | 2 |
| **nstopts\_** | 1 |
| **nswapsval\_** | 1 |
| **nucmodelopts\_** | 4by4 |
| **ordertaxaval\_** | Ordertaxa=Yes |
| **pinvarpropts\_** | uniform |
| **pinvarpruni1\_** | 0.0 |
| **pinvarpruni2\_** | 1.0 |
| **precision\_** | 15 |
| **rateopts\_** | gamma |
| **ratepropts\_** | fixed |
| **relburninval\_** | relburnin=Yes |
| **reportsiterateopts\_** | false |
| **revmatopts\_** | dirichlet |
| **run\_version\_** | 6 |
| **runtime\_** | 168 |
| **samplefreqval\_** | 500 |
| **sbrlensval\_** | Savebrlens=Yes |
| **scientific\_** | false |
| **set\_beagle\_params\_** | false |
| **shapeprdir2\_** | 50.0 |
| **shapepropts\_** | uniform |
| **shapepruni1\_** | 0.0 |
| **statewfreqprdir1\_** | 1.0 |
| **statewfreqpropts\_** | dirichlet |
| **stopruleval\_** | stoprule=Yes |
| **stopval\_** | 0.01 |
| **sump\_burninfrac\_** | 0.25 |
| **sump\_relburnin\_** | Yes |
| **sumpburnin\_** | 10 |
| **sumpnruns\_** | 2 |
| **sumt\_burninfrac\_** | 0.25 |
| **sumt\_conformat\_** | Figtree |
| **sumt\_relburnin\_** | Yes |
| **sumtburnin\_** | 10 |
| **sumtcontype\_** | contype=Halfcompat |
| **sumtdisplaygeq\_** | 0.05 |
| **sumtnruns\_** | 2 |
| **sumtntrees\_** | 1 |
| **sumtshowtreeprobs\_** | showtreeprobs=No |
| **swapfreqval\_** | 1 |
| **symdirihyperpropts\_** | fixed(infinity) |
| **tempval\_** | 0.005 |