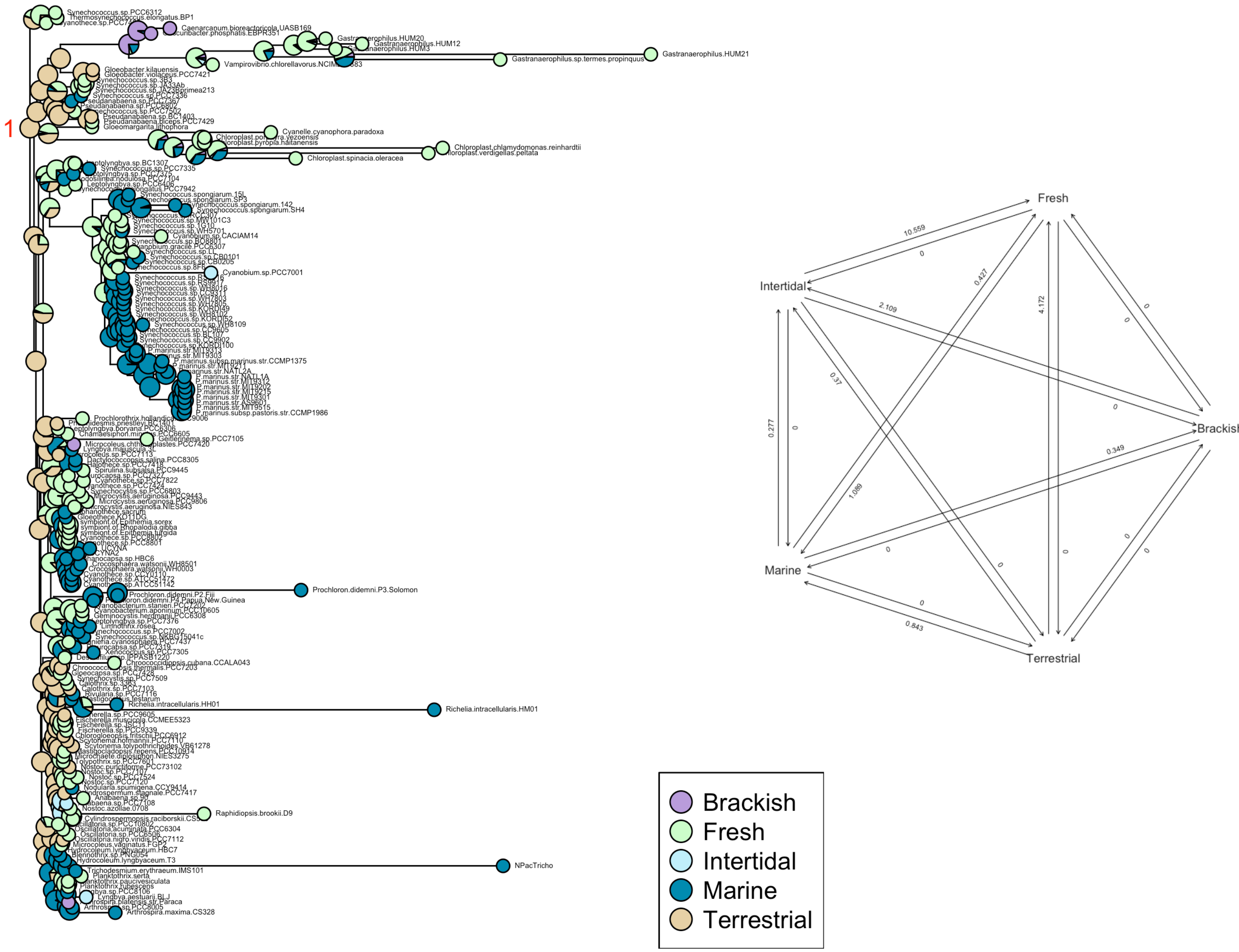
```
          df      AIC
fitP.ER    1 377.5706
fitP.ARD  20 331.1087
fitP.SYM  10 347.1306
```

- **ER** is an `equal-rates` model of where a single parameter governs all transition rates
- **SYM** is a `symmetric` model where forward and reverse transitions share the same parameter
- **ARD** is an `all-rates-different` model where each rate is a unique parameter

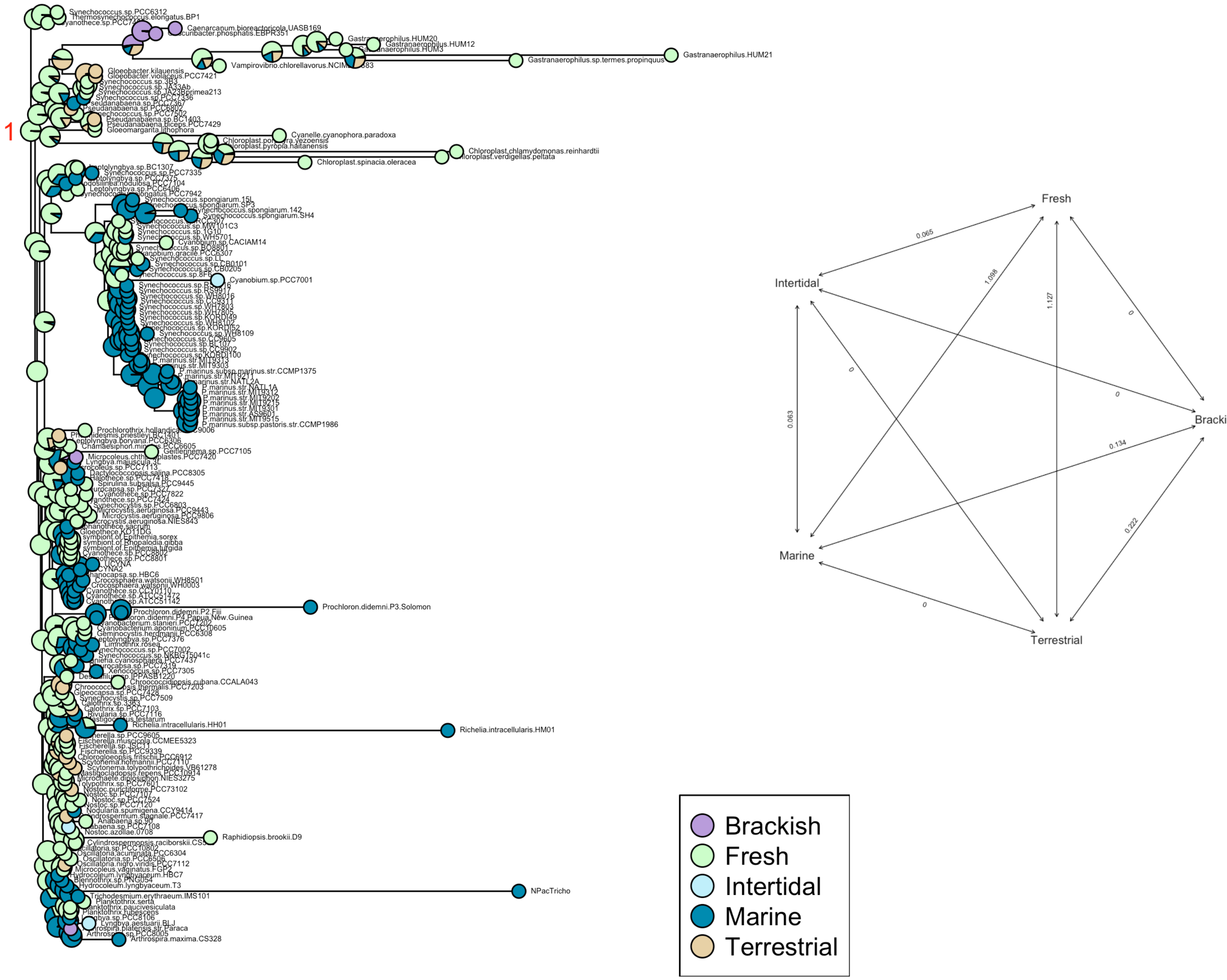
ARD is the best model among the three because of the low AIC score.

Below are trees with pie charts at nodes representing the posterior probabilities for each location. The roots are labeled with a red ‘1’. The pentagons next to them show the transition rates between different locations.

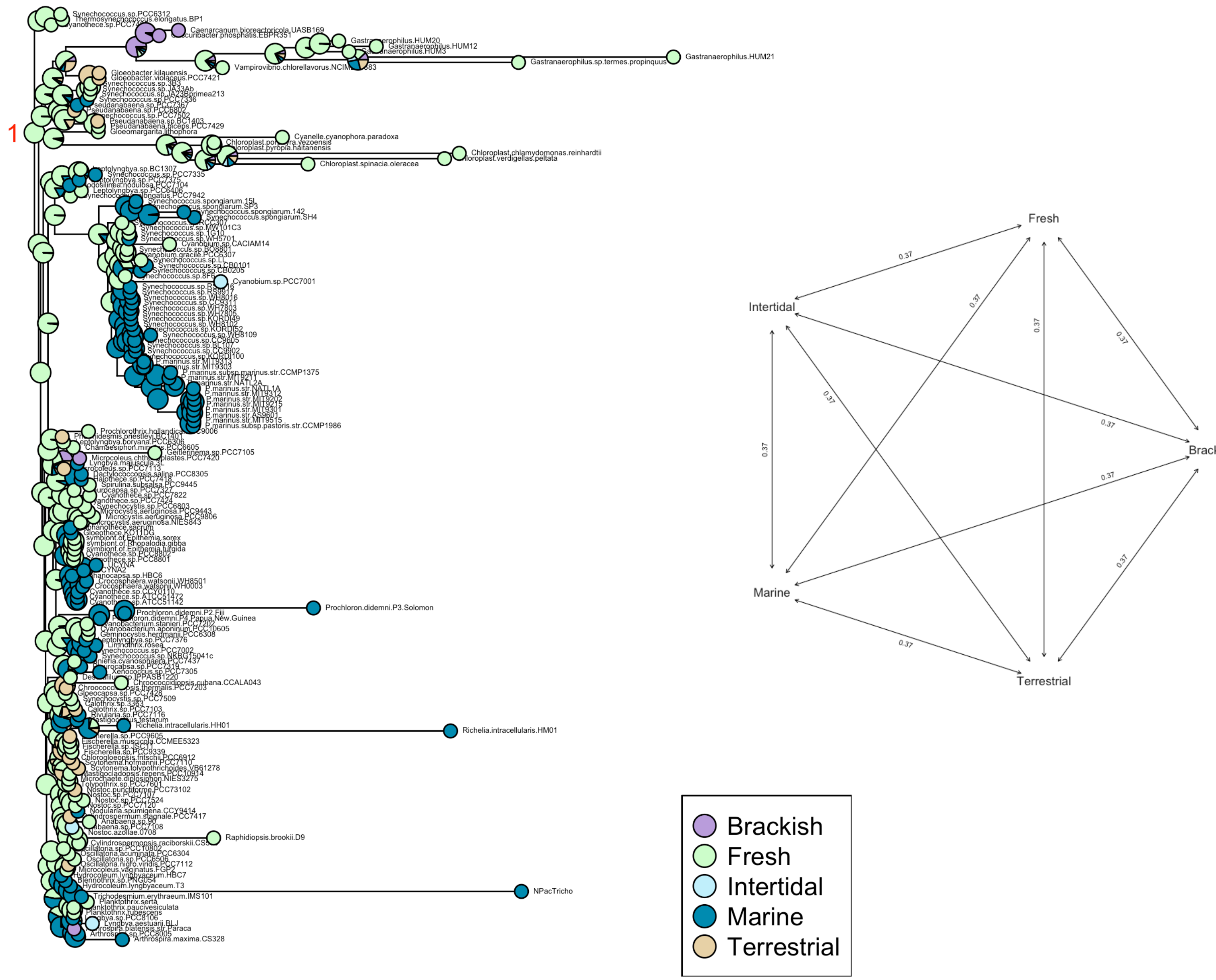
fitP.ARD


1
Synechococcus.sp.PCC6312
Thermosynechococcus.elongatus.BP1
Caenarcanum.bioreactoricola.UASB169
Gastranaerophilus.HUM20
Gastranaerophilus.HUM12
Gastranaerophilus.sp.termes.propinquus
Gastranaerophilus.HUM21
Gloeobacter.kilauensis
Gloeobacter.violaceus.PCC7421
Synechococcus.sp.JA33Ab
Synechococcus.sp.JA23Bprimea213
Synechococcus.sp.PCC7336
Pseudanabaena.sp.PCC6802
Pseudanabaena.sp.BC1403
Pseudanabaena.biceps.PCC7429
Gloeomargarita.lithophora
Cyanelle.cyanophora.paradoxa
Chloroplast.pyropia.haitanensis
Chloroplast.chlamydomonas.reinhardtii
Chloroplast.spinacia.oleracea
Leptolyngbya.sp.BC1307
Synechococcus.sp.PCC7335
Leptolyngbya.sp.PCC6406
Synechococcus.spongiarum.15L
Synechococcus.spongiarum.142
Synechococcus.spongiarum.SH4
Synechococcus.sp.MW101C3
Synechococcus.sp.1G10
Cyanobium.sp.CACIAM14
Synechococcus.sp.LL
Synechococcus.sp.CB0101
Synechococcus.sp.CB0205
Cyanobium.sp.PCC7001
Synechococcus.sp.WH8016
Synechococcus.sp.WH7803
Synechococcus.sp.WH7805
Synechococcus.sp.KORDI49
Synechococcus.sp.WH8102
Synechococcus.sp.WH8109
Synechococcus.sp.BL107
Synechococcus.sp.CC9902
P.marinus.str.MIT9313
P.marinus.subsp.marinus.str.CCMP1375
P.marinus.str.NATL1A
P.marinus.str.MIT9312
P.marinus.str.MIT9202
P.marinus.str.MIT9215
P.marinus.str.MIT9301
P.marinus.str.AS9601
P.marinus.str.MIT9515
P.marinus.subsp.pastoris.str.CCMP1986
Leptolyngbya.boryana.PCC6306
Geitlerinema.sp.PCC7105
Lyngbya.majuscula.3L
Dactylococcopsis.salina.PCC8305
Spirulina.subsalsa.PCC9445
Cyanothece.sp.PCC7822
Cyanothece.sp.PCC7424
Synechocystis.sp.PCC6803
Microcystis.aeruginosa.PCC9443
Microcystis.aeruginosa.PCC9806
Microcystis.aeruginosa.NIES843
Gloeothece.KO11DG
symbiont.of.Epithemia.sorex
symbiont.of.Rhopalodia.gibba
symbiont.of.Epithemia.turgida
Cyanothece.sp.PCC8802
Crocosphaera.watsonii.WH8501
Crocosphaera.watsonii.WH0003
Cyanothece.sp.CCY0110
Cyanothece.sp.ATCC51472
Prochloron.didemni.P3.Solomon
Prochloron.didemni.P2.Fiji
Cyanobacterium.stanieri.PCC7202
Cyanobacterium.aponinum.PCC10605
Geminocystis.herdmanii.PCC6308
Limnothrix.rosea
Synechococcus.sp.NKBG15041c
Xenococcus.sp.PCC7305
Chroococcidiopsis.cubana.CCALA043
Chroococcidiopsis.thermalis.PCC7203
Gloeocapsa.sp.PCC7428
Synechocystis.sp.PCC7509
Calothrix.sp.PCC7103
Rivularia.sp.PCC7116
Richelia.intracellularis.HH01
Richelia.intracellularis.HM01
Fischerella.muscicola.CCMEE5323
Fischerella.sp.PCC9339
Chlorogloeopsis.fritschii.PCC6912
Scytonema.hofmannii.PCC7110
Scytonema.tolypothrichoides.VB61278
Mastigocladopsis.repens.PCC10914
Microchaete.diplosiphon.NIES3275
Tolypothrix.sp.PCC7601
Nostoc.punctiforme.PCC73102
Nostoc.sp.PCC7524
Nostoc.sp.PCC7120
Nodularia.spumigena.CCY9414
Anabaena.sp.90
Nostoc.azollae.0708
Raphidiopsis.brookii.D9
Oscillatoria.acuminata.PCC6304
Oscillatoria.sp.PCC6506
Oscillatoria.nigro.viridis.PCC7112
Microcoleus.vaginatus.FGP2
Hydrocoleum.lyngbyaceum.HBC7
Blennothrix.sp.PNG054
Hydrocoleum.lyngbyaceum.T3
NPacTricho
Trichodesmium.erythraeum.IMS101
Planktothrix.serta
Planktothrix.rubescens
Lyngbya.aestuarii.BLJ
Arthrospira.maxima.CS328
Fresh
Intertidal
Brackish
Marine
Terrestrial
10.559
0
0.427
4.172
2.109
0.37
0.277
1.089
0.349
0.843
Brackish
Fresh
Intertidal
Marine
Terrestrial

fitP.SYM


1
Fresh
Intertidal
Brackish
Marine
Terrestrial
0.065
1.058
1.127
0
0
0
0.063
0.134
0.222
0
Brackish
Fresh
Intertidal
Marine
Terrestrial

fitP.ER


1
Fresh
Intertidal
Brackish
Marine
Terrestrial
0.37
Brackish
Fresh
Intertidal
Marine
Terrestrial