

Figure A4.1. Majority-rule consensus tree of 230 taxa within Thymelaeaceae, as inferred through Bayesian analysis of a five-gene (nuclear + plastid) data set using MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.2. Phylogram of 230 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of a five-gene (nuclear + plastid) data set using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.3. Majority-rule consensus tree of 225 taxa within Thymelaeaceae, as inferred through Bayesian analysis of a five-gene (nuclear + plastid) data set using MrBayes. In this analysis, we removed all *Thecanthes* spp. From the data set to determine whether the sister relationship between *Thecanthes* and *Pimelea haematostachya*+*Pimelea venosa* was the product of long-branch attraction. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.4. Phylogram of 225 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of a five-gene (nuclear + plastid) data set using RAxML. In this analysis, we removed all *Thecanthes* spp. From the data set to determine whether the sister relationship between *Thecanthes* and *Pimelea haematostachya*+*Pimelea venosa* was the product of long-branch attraction. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.5. Majority-rule consensus tree of 228 taxa within Thymelaeaceae, as inferred through Bayesian analysis of a five-gene (nuclear + plastid) data set using MrBayes. In this analysis, we removed *Pimelea*

haematostachya+*Pimelea venosa* from the data set to determine whether the sister relationship between these species and *Thecanthes* was the product of long-branch attraction. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.6. Phylogram of 228 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of a five-gene (nuclear + plastid) data set using RAxML. In this analysis, we removed *Pimelea haematostachya*+*Pimelea venosa* from the data set to determine whether the sister relationship between these species and *Thecanthes* was the product of long-branch attraction. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.7. Majority-rule consensus tree of 207 taxa within Thymelaeaceae, as inferred through Bayesian analysis of a five-gene (nuclear + plastid) data set. To obtain this tree, we removed 23 putative rogue taxa from the set of sampled trees from our Bayesian analysis, and then produced a new consensus tree. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.8. Phylogram of 207 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of a five-gene (nuclear + plastid) data set. In this analysis, we removed 23 putative rogue taxa from the best-scoring tree from RAxML and the corresponding bootstrap replicate trees, and then calculated the support for the newly pruned tree. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.9. Majority-rule consensus tree of 230 taxa within Thymelaeaceae, as inferred through Bayesian analysis of a four-gene (plastid) data set using

MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.10. Phylogram of 230 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of a four-gene (plastid) data set using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.11. Majority-rule consensus tree of 223 taxa within Thymelaeaceae, as inferred through Bayesian analysis of a nuclear ribosomal DNA marker (ITS) using MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.12. Phylogram of 223 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of a nuclear ribosomal DNA marker (ITS) using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.13. Majority-rule consensus tree of 127 taxa within Thymelaeaceae, as inferred through Bayesian analysis of the *matK* chloroplast marker using MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.14. Phylogram of 127 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of the *matK* chloroplast marker using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.15. Majority-rule consensus tree of 127 taxa within Thymelaeaceae, as inferred through Bayesian analysis of the *trnL*-F chloroplast marker using MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.16. Phylogram of 127 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of the *trnL*-F chloroplast marker using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.17. Majority-rule consensus tree of 127 taxa within Thymelaeaceae, as inferred through Bayesian analysis of the *rbcL* chloroplast marker using MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.18. Phylogram of 127 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of the *rbcL* chloroplast marker using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.19. Majority-rule consensus tree of 127 taxa within Thymelaeaceae, as inferred through Bayesian analysis of the *rps16* chloroplast marker using MrBayes. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.

Figure A4.20. Phylogram of 127 taxa within Thymelaeaceae, as inferred through maximum-likelihood analysis of the *rps16* chloroplast marker using RAxML. The scale bar represents substitutions per site. Taxon names ending with an asterisk are those that were newly sequenced for the present study.