**Fig. 3.6. Bayesian 50% majority rule concatenated *Apn2* + *BenA* + *TEF1α* consensus tree containing representative *Diaporthe* isolates.** Culture collection, GenBank, or JB Tanney personal collection accession numbers are followed by the species name. Ex-type or type strains are indicated in bold. All branches have Bayesian posterior probability values of 1.0; values lower than 1.0 are presented at nodes. The tree was rooted to *Diaporthe citri* AR3405 and scale bars indicate expected changes per site per branch.