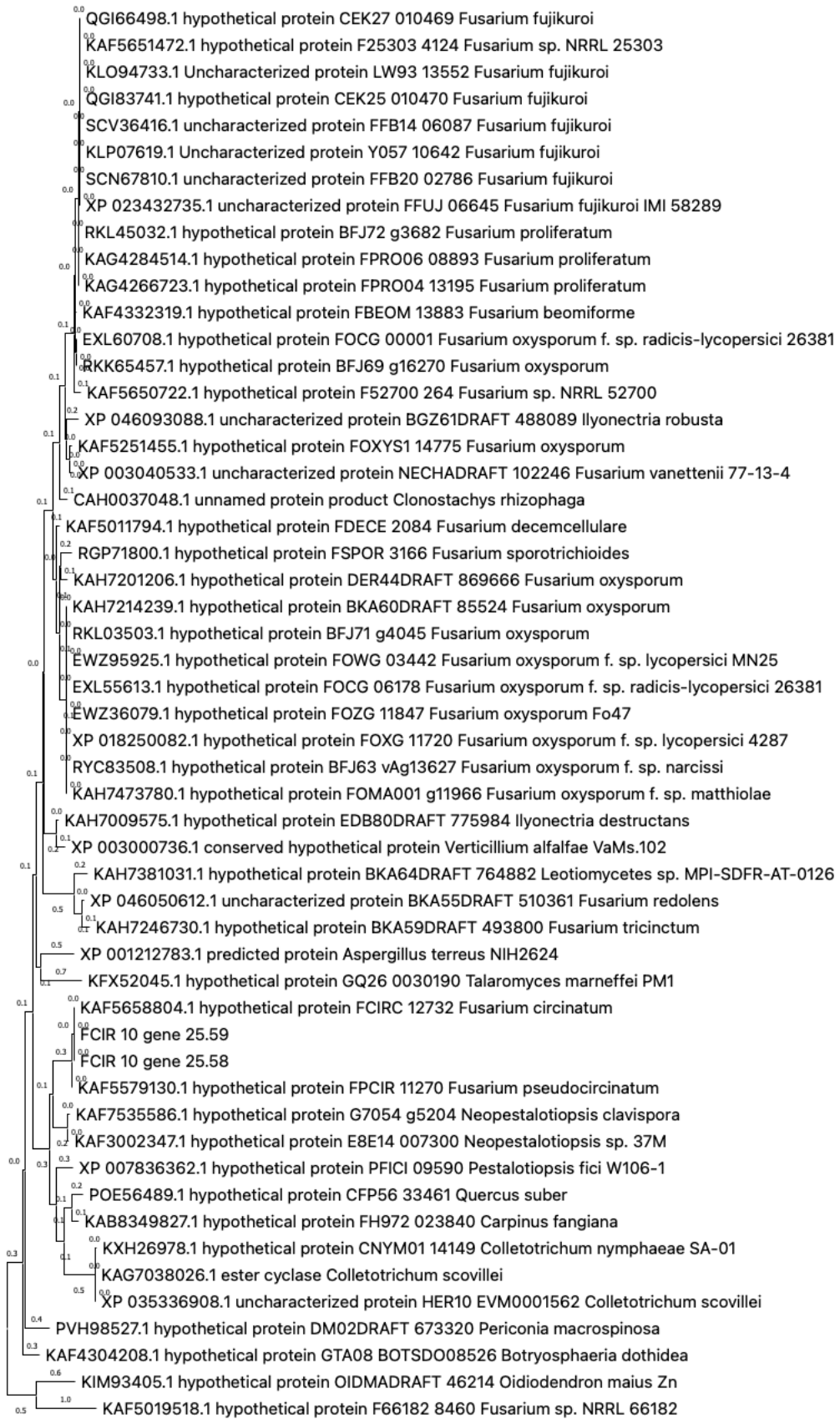


Figure S1. Phylogenetic relationship of paralogs with regards to the respective host-range-associated gene. FCIR = *Fusarium circinatum*; FFRAC = *Fusarium fracticaudum*; FPIN = *Fusarium pininemorale*; FSUB = *Fusarium subglutinans*.

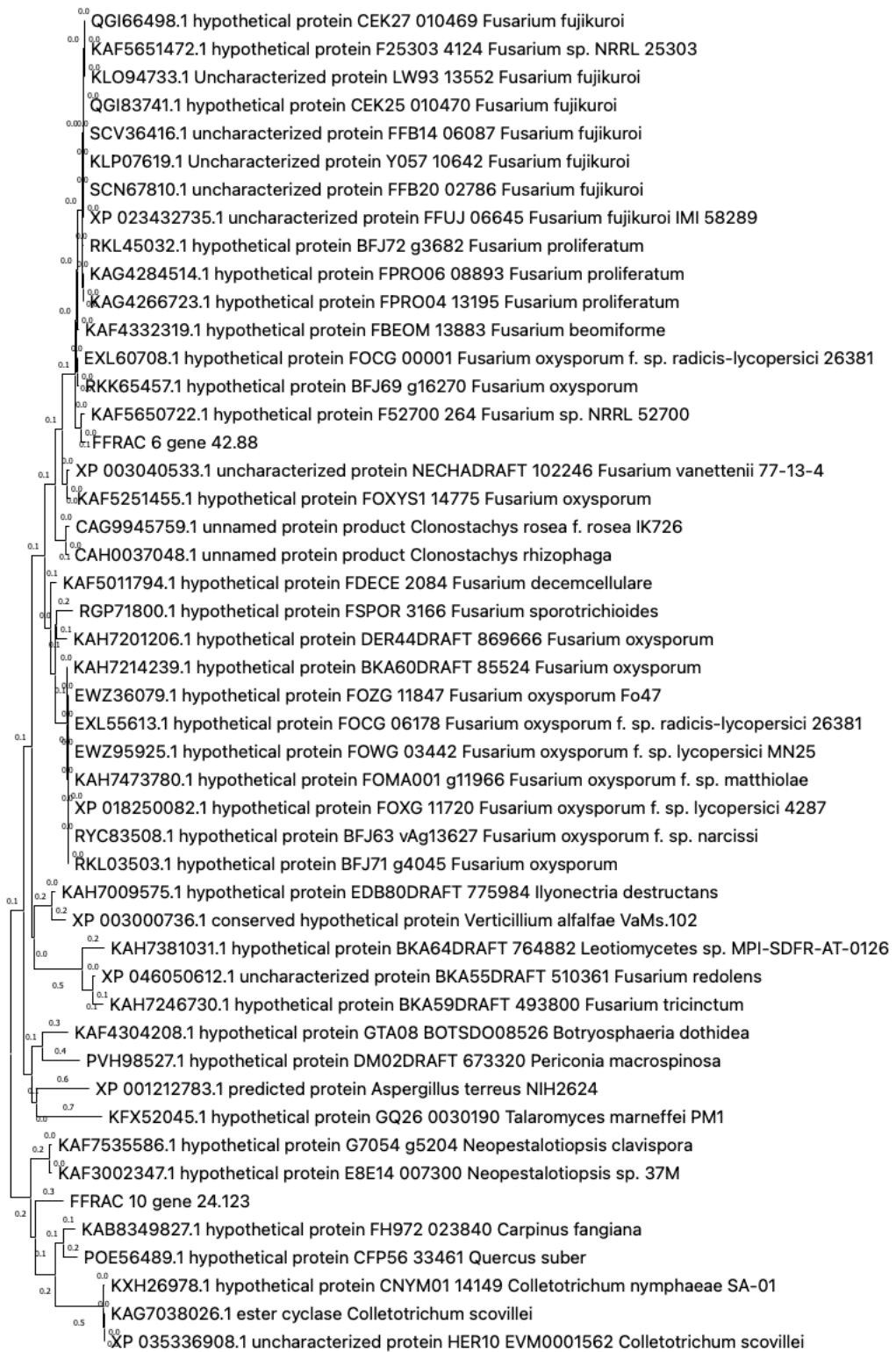


The evolutionary history of FCIR_10_gene_25.58 and its paralog FCIR_10_gene_25.59 was inferred by using the Maximum Likelihood method and JTT matrix-based model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.



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The evolutionary history of FFRAC_10_gene_17.127 and its paralog FFRAC_10_gene_17.128 was inferred by using the Maximum Likelihood method and JTT matrix-based model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.

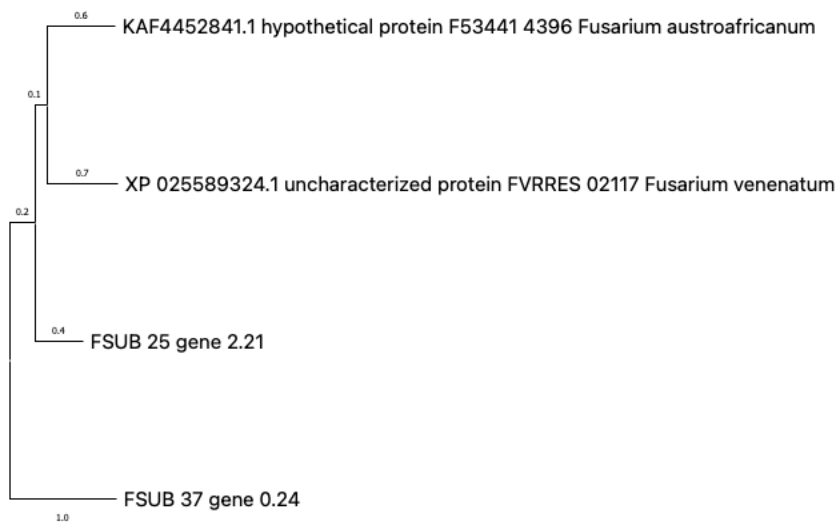


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The evolutionary history of FFRAC_10_gene_24.123 and its paralog FFRAC_6_gene_42.88 was inferred by using the Maximum Likelihood method and JTT matrix-based model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.



The evolutionary history of FPIN_12_gene_2.12 and its paralog FPIN_12_gene_2.24 was inferred by using the Maximum Likelihood method and the Le Gascuel model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.



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The evolutionary history of FSUB_25_gene_2.21 and its paralog FSUB_37_gene_0.24 was inferred by using the Maximum Likelihood method and the Le Gascuel model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.