



Figure S1. Alignment of putative amino acid sequence of protein coded by effector gene PITG_06099. Dots represent sequence positions without amino acid substitutions when compared to the reference sequence of genome T-30.



Figure S2. Alignment of putative amino acid sequence of protein coded by effector gene PITG_08944. Dots represent sequence positions without amino acid substitutions when compared to the reference sequence of genome T-30.



Figure S3. Alignment of putative amino acid sequence of protein coded by effector gene PITG_12737. Dots represent sequence positions without amino acid substitutions when compared to the reference sequence of genome T-30.



Figure S4. Alignment of putative amino acid sequence of protein coded by effector gene PITG_15980. Dots represent sequence positions without amino acid substitutions when compared to the reference sequence of genome T-30.

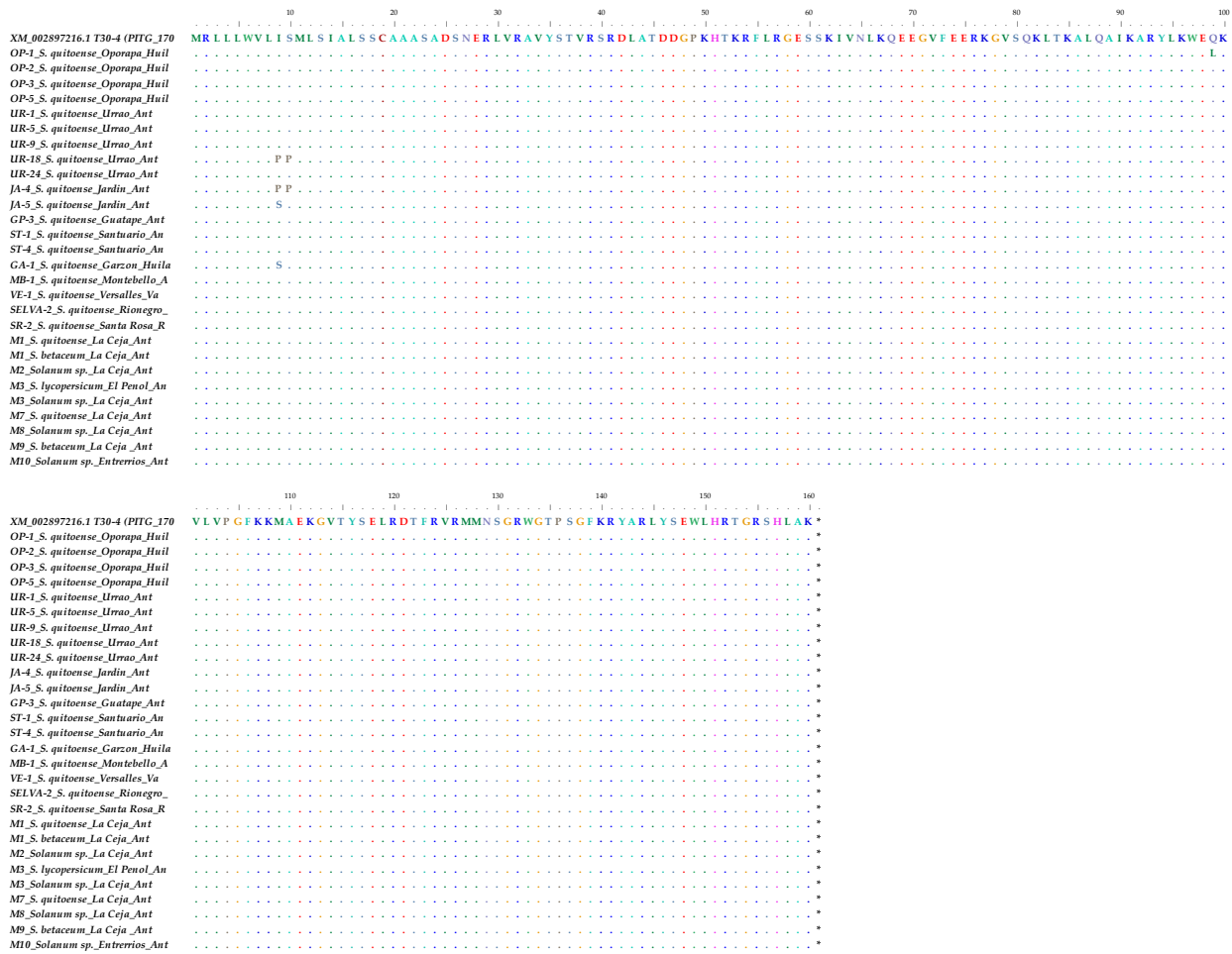


Figure S5. Alignment of putative amino acid sequence of protein coded by effector gene PITG_17063. Dots represent sequence positions without amino acid substitutions when compared to the reference sequence of genome T-30.

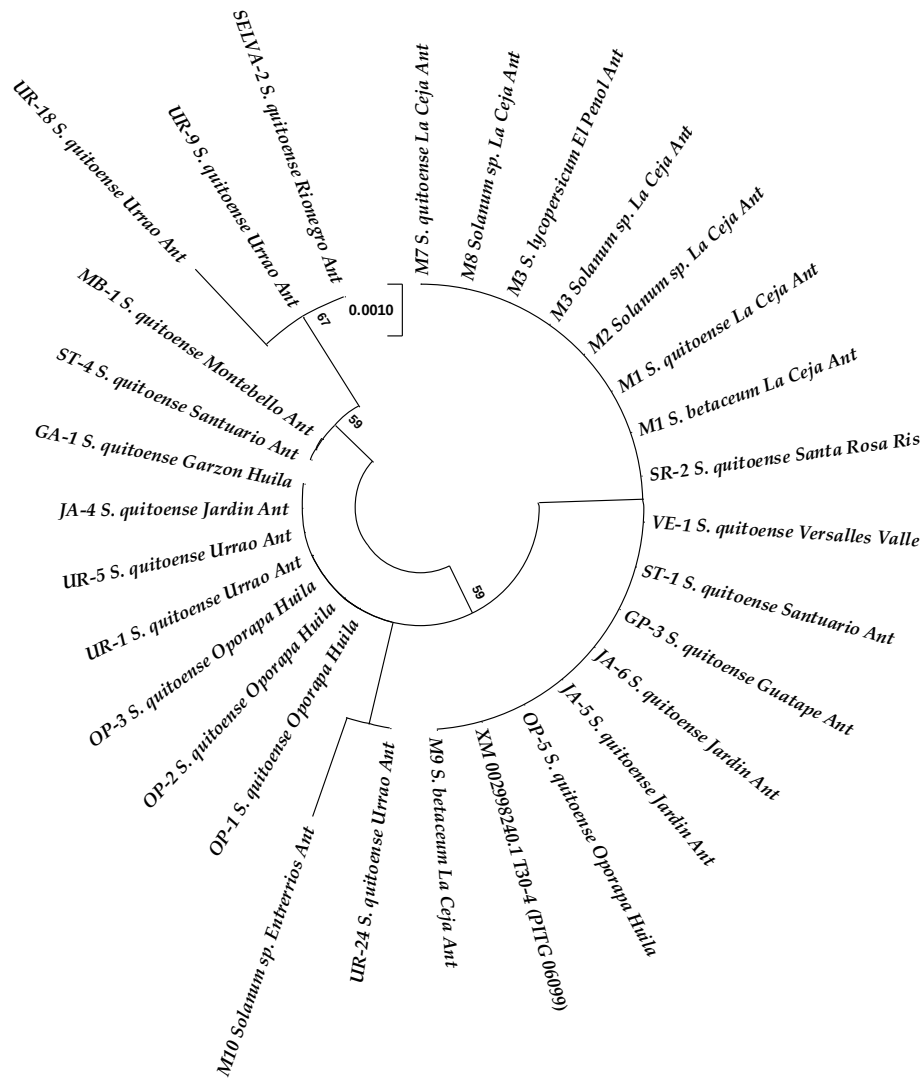


Figure S6. Molecular Phylogenetic analysis by Maximum Likelihood method of gene 06099.

The evolutionary history was inferred by using the Maximum Likelihood method and Jukes-Cantor model. The tree with the highest log likelihood (-727.66) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. 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 Jukes-Cantor model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 30 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 489 positions in the final dataset. The bootstrap consensus tree was inferred from 1000 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. Labels are organized as follows: first, isolate code in Table 1; second, host scientific name (e.g., *Solanum quitoense*, *S. betaceum*, *S. lycopersicum*, *Solanum* sp.); third, Municipality and Department of Colombia from where corresponding isolate was collected (e.g., La Ceja Ant). Ant: Department of Antioquia, Colombia. Valle: Department of Valle del Cauca, Colombia. Ris: Department of Risaralda, Colombia. Evolutionary analyses were conducted in MEGA X [58].

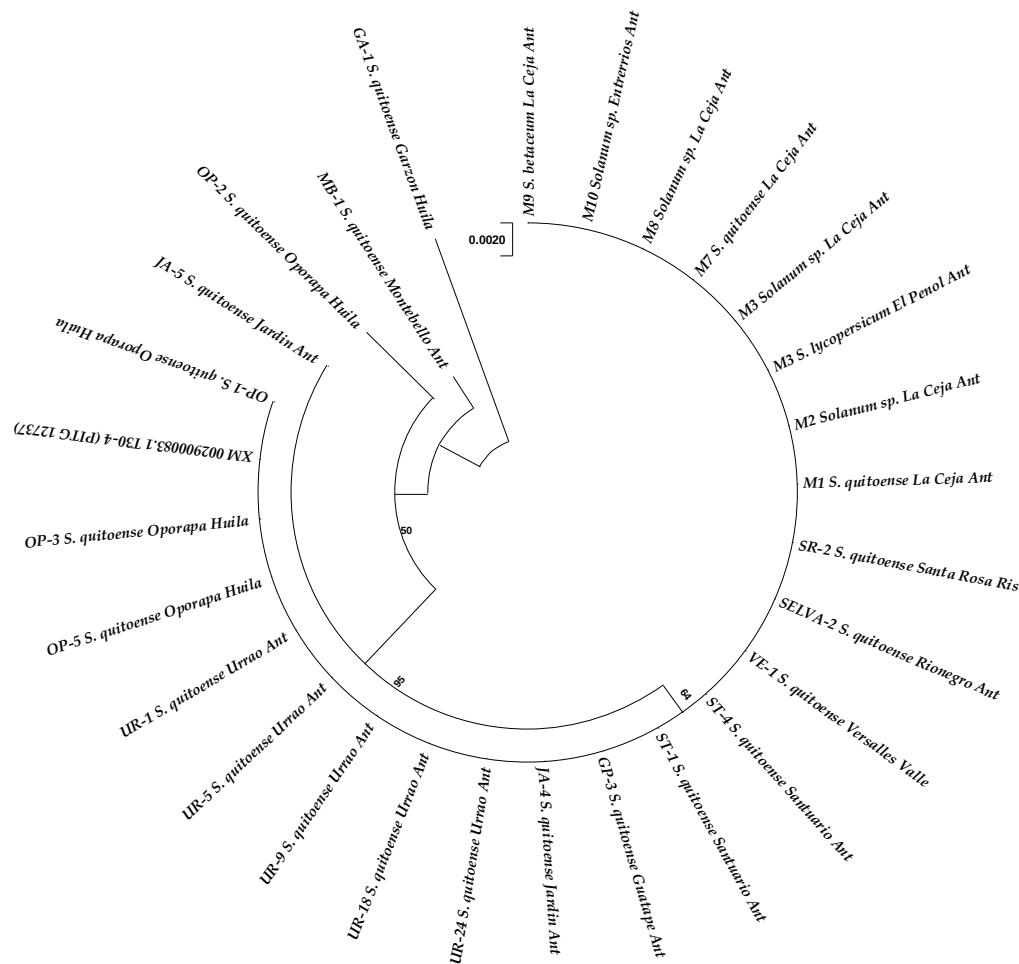


Figure S7. Molecular Phylogenetic analysis by Maximum Likelihood method of gene 12737.

The evolutionary history was inferred by using the Maximum Likelihood method and Jukes-Cantor model. The tree with the highest log likelihood (-820.95) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. 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 Jukes-Cantor model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 28 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 507 positions in the final dataset. The bootstrap consensus tree was inferred from 1000 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. Labels are organized as follows: first, isolate code in Table 1; second, host scientific name (e.g., *Solanum quitoense*, *S. betaceum*, *S. lycopersicum*, *Solanum* sp.); third, Municipality and Department of Colombia from where corresponding isolate was collected (e.g., La Ceja Ant). Ant: Department of Antioquia, Colombia. Valle: Department of Valle del Cauca, Colombia. Ris: Department of Risaralda, Colombia. Evolutionary analyses were conducted in MEGA X [58]

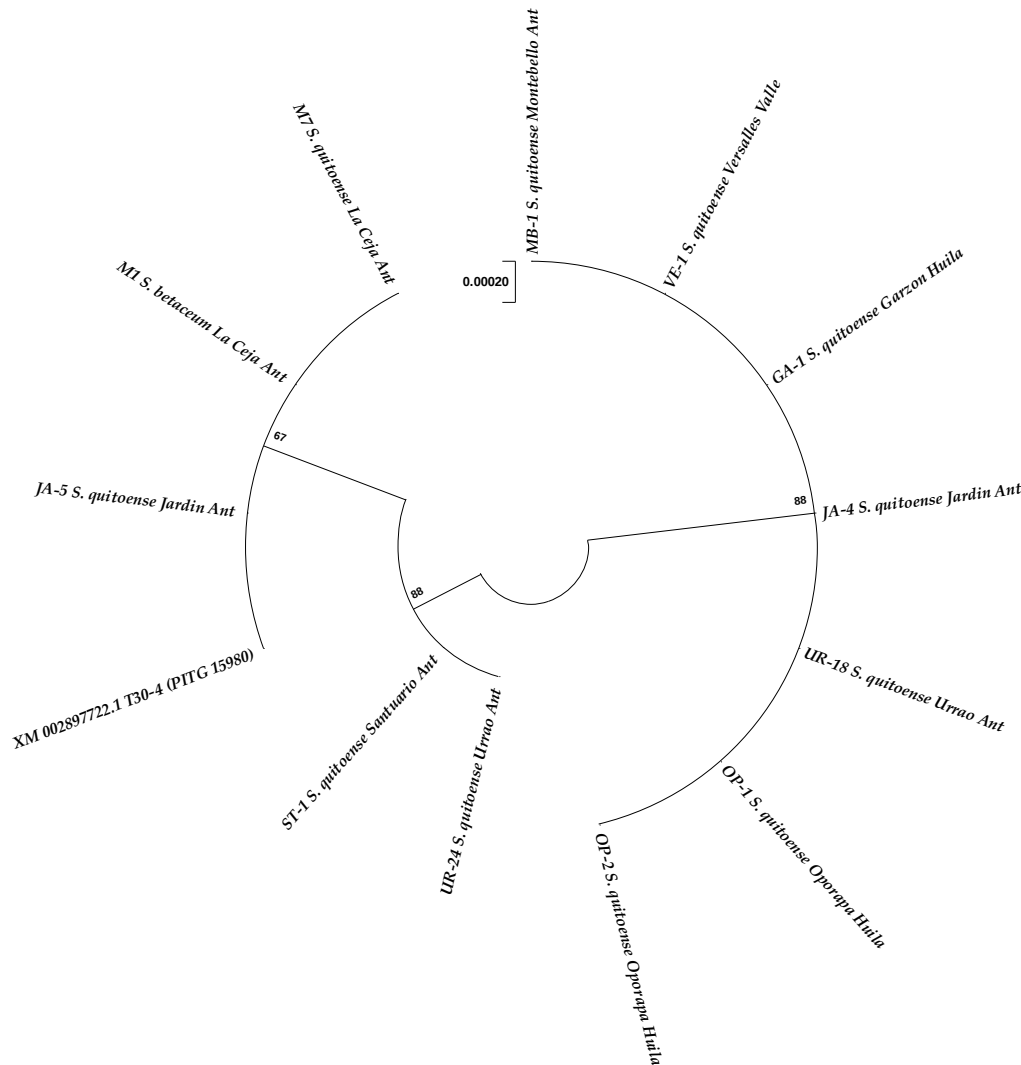


Figure S8. Molecular Phylogenetic analysis by Maximum Likelihood method of gene 15980.

The evolutionary history was inferred by using the Maximum Likelihood method and Jukes-Cantor model. The tree with the highest log likelihood (-1873.04) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. 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 Jukes-Cantor model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 13 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 1332 positions in the final dataset. The bootstrap consensus tree was inferred from 1000 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. Labels are organized as follows: first, isolate code in Table 1; second, host scientific name (e.g., *Solanum quitoense*, *S. betaceum*, *S. lycopersicum*, *Solanum* sp.); third, Municipality and Department of Colombia from where corresponding isolate was collected (e.g., La Ceja Ant). Ant: Department of Antioquia, Colombia. Valle: Department of Valle del Cauca, Colombia. Ris: Department of Risaralda, Colombia. Evolutionary analyses were conducted in MEGA X [58]

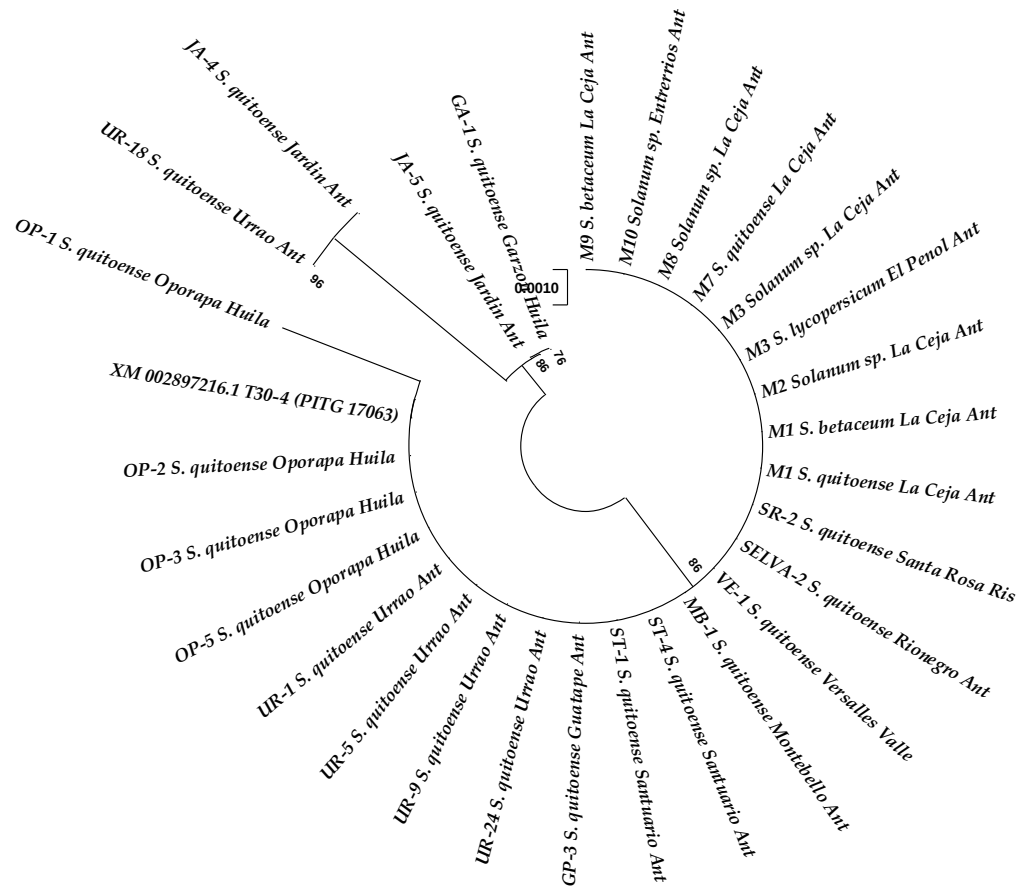


Figure S9. Molecular Phylogenetic analysis by Maximum Likelihood method of gene 17063.

The evolutionary history was inferred by using the Maximum Likelihood method and Jukes-Cantor model. The tree with the highest log likelihood (-721.46) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. 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 Jukes-Cantor model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 29 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 483 positions in the final dataset. The bootstrap consensus tree was inferred from 1000 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. Labels are organized as follows: first, isolate code in Table 1; second, host scientific name (e.g., *Solanum quitoense*, *S. betaceum*, *S. lycopersicum*, *Solanum* sp.); third, Municipality and Department of Colombia from where corresponding isolate was collected (e.g., La Ceja Ant). Ant: Department of Antioquia, Colombia. Valle: Department of Valle del Cauca, Colombia. Ris: Department of Risaralda, Colombia. Evolutionary analyses were conducted in MEGA X [58]

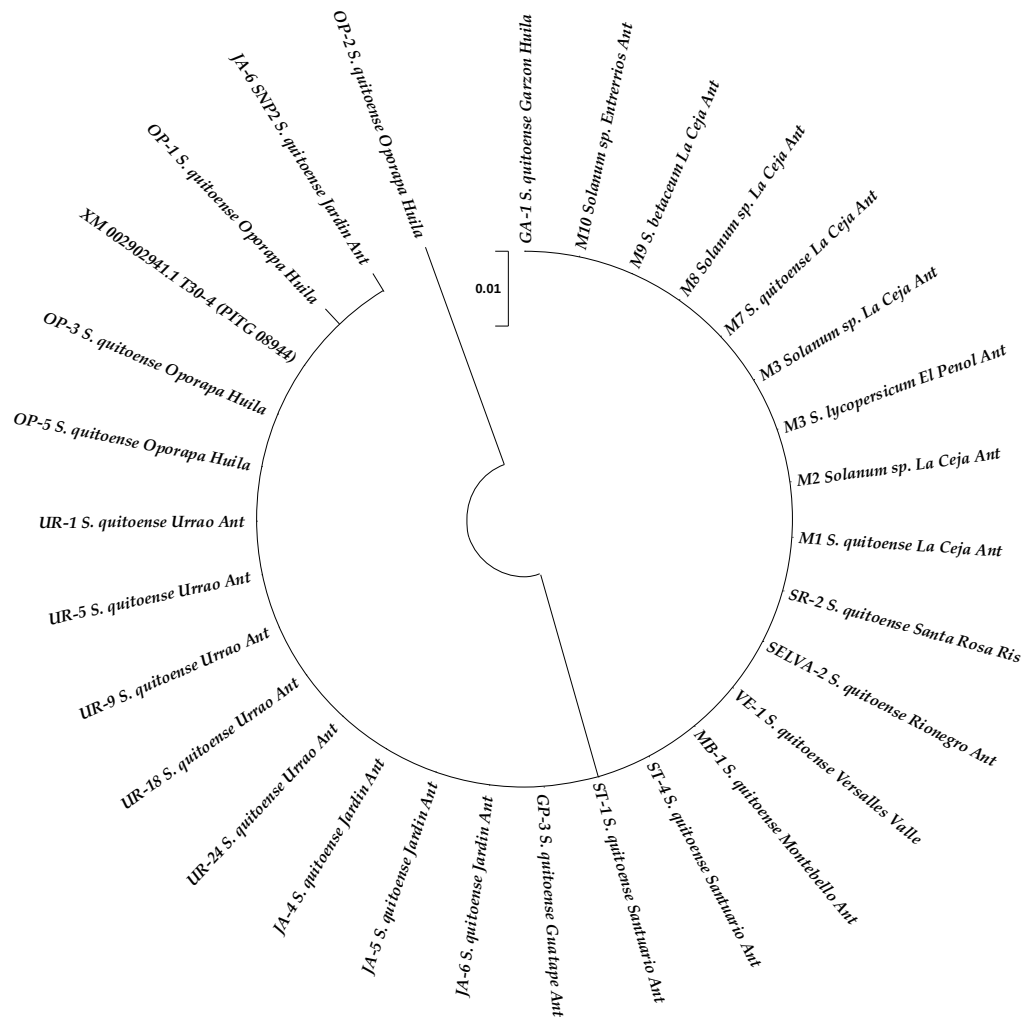


Figure S10. Molecular Phylogenetic analysis by Maximum Likelihood method of gene 08944.

The evolutionary history was inferred by using the Maximum Likelihood method and Jukes-Cantor model. The tree with the highest log likelihood (-1238.15) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. 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 Jukes-Cantor model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 30 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 724 positions in the final dataset. The bootstrap consensus tree was inferred from 1000 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. Labels are organized as follows: first, isolate code in Table 1; second, host scientific name (e.g., *Solanum quitoense*, *S. betaceum*, *S. lycopersicum*, *Solanum* sp.); third, Municipality and Department of Colombia from where corresponding isolate was collected (e.g., La Ceja Ant). Ant: Department of Antioquia, Colombia. Valle: Department of Valle del Cauca, Colombia. Ris: Department of Risaralda, Colombia. Evolutionary analyses were conducted in MEGA X [58]

Table S1. The full list of accession numbers registered at Genbank

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