Figure S4. MrBayes trees of haplotypes for each locus sequenced. Loci are **A.**

PITG_11126, **B.** *PUA*, **C.** *β-tubulin*, and **D.** *TRP1* in *Phytophthora infestans*. Haplotypes

shown for each branch tip, correspond to those in Tables S5, S6, S7 and S8. Bayesian

posterior probabilities are shown above branches and bootstrap support values obtained

by maximum likelihood are shown below branches. Values are not shown for branches

that had less than 80% probability/support by both methods. Pie charts represent the

number of isolates that contain a particular haplotype within each of the three clusters.

Clusters were defined based on the occurrence of *P. infestans* isolates over time in the

United States. Numbers within parentheses indicate the number of individuals that

contain that haplotype.