Figure S1. The phylogenetic tree of *Phytophthora infestans RAD23* sequences was reconstructed using a Neighbor-joining (NJ) approach embedded in the MEGA 7.0.21 program and displayed and annotated using the online tool Interactive Tree of Life (https://itol.embl.de/). The bootstrap values were calculated from 1,000 replications and are represented by red circles at the middle of the tree graph.