



Figure S1 - Phylogeny of elements of the *Harbinger* superfamily of DNA-transposons.

The conserved DDE-transposase domain (~200 aa) was used for phylogenetic analysis using the maximum likelihood algorithm. The tree was rooted using the outgroup *ISL2EU* and the numbers at nodes are bootstrap values of 100 replicates (only values >50% are shown). *Harbinger* elements from rust are colored in purple, those from *Phytophthora infestans* are in red, and those from plants are in green. All sequences used are available in Repbase. The elements were obtained from the following species: Fungi [*Puccinia striiformis* f. sp. *tritici* (PSt), *Puccinia graminis* (PGr), *Melampsora larici-populina* (MLP, Mlarici), *Allomyces macrogynus* (AllMac), *Ascosphaera apis* (AAp), *Phycomyces blakesleeanus* (PB), *Pleurotus ostreatus* (PleOst), *Talaromyces stipitatus* (TSt), *Tuber melanosporum* (TMe)]; Plants [*Arabidopsis lyrata* (ALy), *Fragaria vesca* (FV), *Malus x domestica* (Mad), *Medicago truncatula* (Mt), *Oryza sativa* (OS), *Populus trichocarpa* (PTr), *Selaginella moellendorffii* (Smoe), *Sorghum bicolor* (SBi), *Triticum aestivum* (TA), *Vitis vinifera* (VV), *Zea mays* (ZM)]; Oomycetes [*Phytophthora infestans* (PI)]; Animals [*Aedes aegypti* (AA, AAe), *Anopheles gambiae* (AG), *Branchiostoma floridae* (BF), *Ciona savignyi* (Cis), *Danio rerio* (DR), *Drosophila willistoni* (DW), *Drosophila yakuba* (DYa), *Gasterosteus aculeatus* (GA), *Hydra magnipapillata* (HM), *Nematostella vectensis* (NV), *Strongylocentrotus purpuratus* (SP), *Xenopus tropicalis* (XT)]; Protists [*Ectocarpus siliculosus* (ES), *Emiliana huxleyi* (EmiHux), *Monosiga brevicollis* (MBr), *Naegleria gruberi* (Ngru), *Thalassiosira pseudonana* (TP), *Trichomonas vaginalis* (TV)].