SUPPLEMENTAL MATERIAL

Phylogenetic analysis of the *P. avellanae mut* genes

The sequences of the *P. avellanae mutS* and *mutL* putative genes were translated into amino acid sequences and compared with the Mut proteins of medically and environmentally relevant bacterial species of interest. We also compared the amino acid sequences with those from all plant pathogenic bacteria sequenced thus far. For the analyses, we used the neighbour-joining, minimum evolution and UPGMA algorithms. Dendrograms constructed from the neighbour-joining algorithm show the relationship between the putative MutS and MutL proteins of *P. avellanae* with those of other species (Figs. **1** and **2**). Both the MutS and MutL dendrograms revealed that the *P. avellanae* mismatch repair proteins are very similar to the homologues of other plant pathogenic pseudomonads (i.e., *P. syringae* pathovars *phaseolicola*, *syringae* and *tomato*) even though they are not identical. All of the other pseudomonads assessed (*P. aeruginosa, P. enthomophila, P. fluorescens*, *P. putida*, *P. stutzeri*) form different subclusters generated out of the same cluster. *Xanthomonas* species and *Xylella fastidiosa* were placed into a separated cluster. Members of the *Enterobacteriaceae* clustered separately and displayed distinct subclusters. Bootstrap analysis revealed that most of the branches shown in the dendrograms are highly robust (values > 80%). Dendrograms constructed using the UPGMA and minimum evolution algorithms provided highly similar strain clustering (data not shown).

Fig. (1). Dendrogram based on the amino acid sequence of the *Pseudomonas avellanae* MutS protein, compared to other bacterial species.

The results were obtained using the neighbour-joining algorithm. The percentages of bootstrap replicates, based on 1,000 bootstrap samples, are placed at the tree nodes. The bar scale indicates the rate of substitution per amino acid.

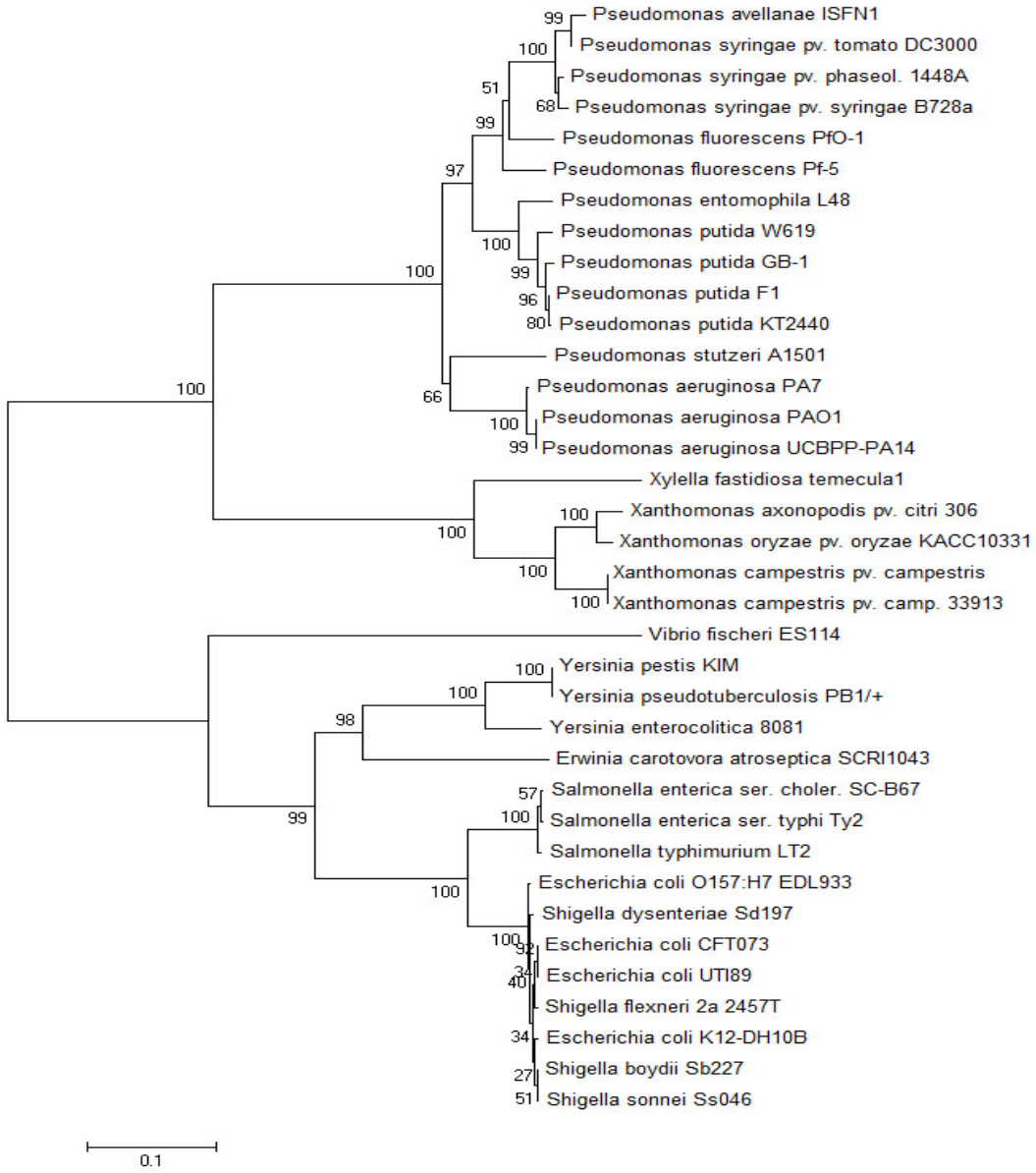

Fig. (2). Dendrogram based on the amino acid sequence of the *Pseudomonas avellanae* MutL protein, compared to other bacterial species.

The results were obtained using the neighbour-joining algorithm. The percentages of bootstrap replicates, based on 1,000 bootstrap samples, are placed at the tree nodes. The bar scale indicates the rate of substitution per amino acid.