



Figure 4. RecA parsimony tree.

Tree was generated from the multiple sequence alignments using the protpars method of the program Phylip according to the methods described in the text. Regions of ambiguous alignment and indels were excluded from the analysis (see Methods). Consensus clades representing groups found in all phylogenetic methods are highlighted. Branch lengths and scale bars correspond to estimated number of amino-acid substitutions. Bootstrap values when over 70 are indicated by ** and when between 40 and 70 by *. Not published in the Journal of Molecular Evolution article.