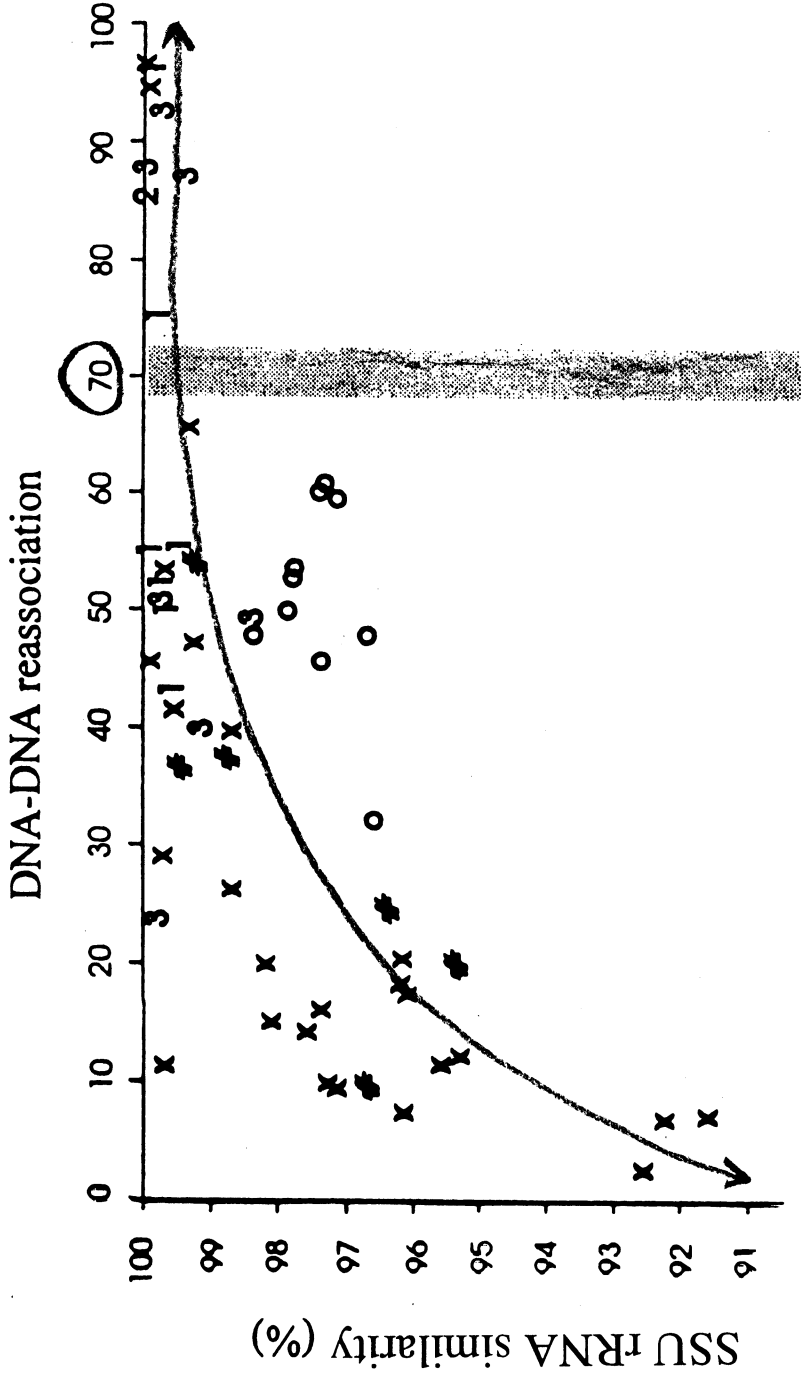


Hybridization Data yield whole-genome similarities – do NOT confuse with molecular sequence comparisons.



Summary:

- Classical physiological descriptors of microbes constitute a taxonomy, but do NOT provide relationships (except as might be inferred subjectively).
- Methods such as DNA-DNA reassociations establish relationships ONLY if closely related.
- Molecular sequence comparisons (e.g., SSU rRNA similarity) contain evolutionary relationship information.

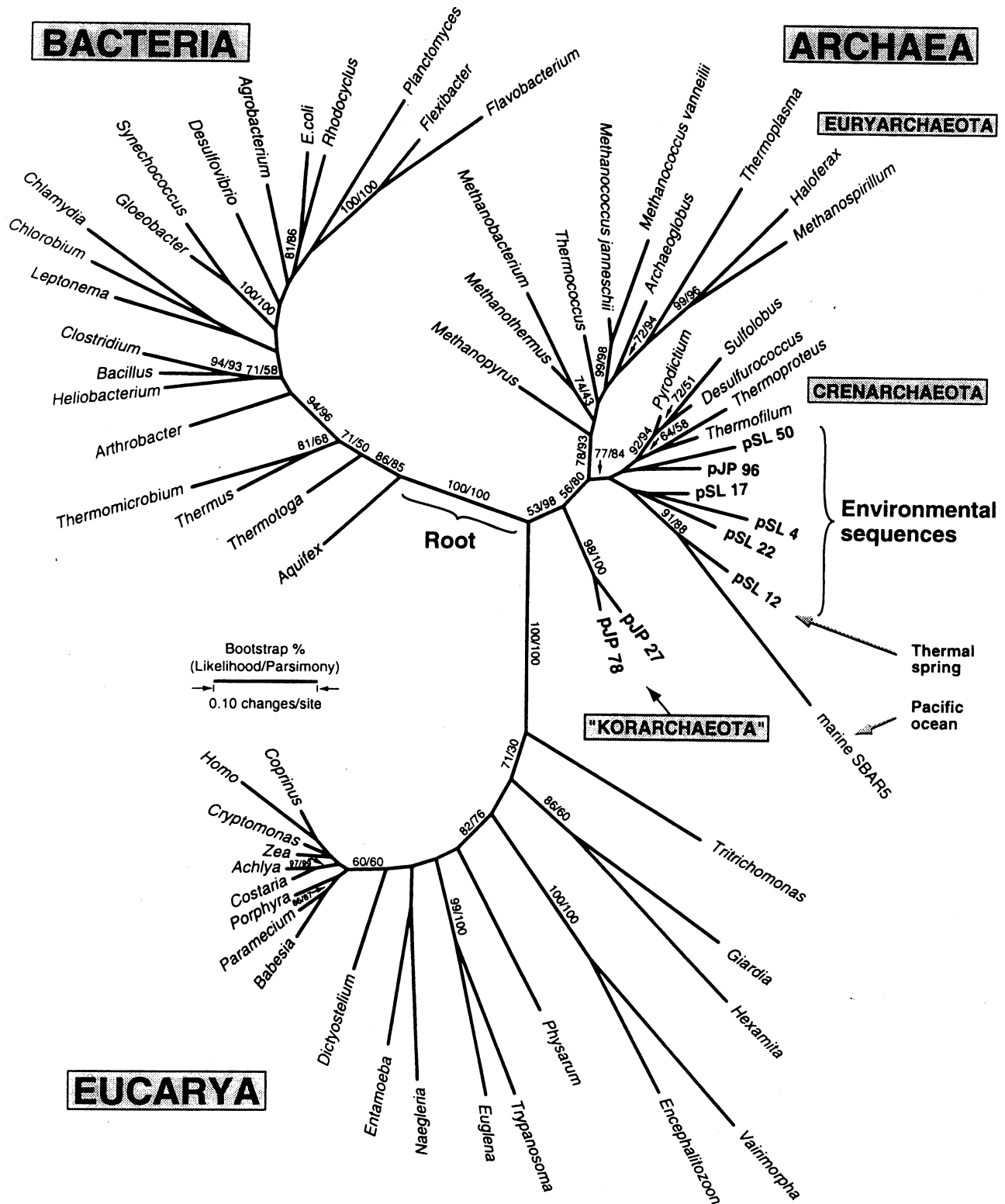


FIG. 2. "Universal" unrooted phylogenetic tree showing positions of major groups of sequences recovered from the Obsidian Pool community. Tree was inferred by ML analysis of 1620 homologous nucleotide positions of sequence from each organism or clone. Numbers indicate percentage of bootstrap resamplings that support indicated branches in ML (before slash) and MP (after slash) analyses for those groups only that attained >60% support with at least one of the two methods. Analyses of duplicated protein genes have placed the root of the tree on the branch at the base of the Bacteria (20, 21).