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Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASW_J (Monsoon season of ASSBY). The trees were constructed based on partial sequences (1200 bp) of 16S rRNA genes retrieved 16S rRNA gene clone libraries and neighbouring RDP sequences. The trees were constructed using the neighbour-joining algorithm with Kimura 2 parameter distances in MEGA 4.0 software. Numbers at nodes indicate percent bootstrap values above 50 supported by 1000 replicates. Bar indicates Jukes-Cantor evolutionary distance. Numbers in parentheses indicate RDP-ID numbers of neighbouring sequences downloaded from the Ribosomal Database Project (RDP-II)

Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSW_J (Monsoon season of ASSBY). The trees were constructed based on partial sequences (1200 bp) of 16S rRNA genes retrieved 16S rRNA gene clone libraries and neighbouring RDP sequences. The trees were constructed using the neighbour-joining algorithm with Kimura 2 parameter distances in MEGA 4.0 software. Numbers at nodes indicate percent bootstrap values above 50 supported by 1000 replicates. Bar indicates Jukes-Cantor evolutionary distance. Numbers in parentheses indicate RDP-ID numbers of neighbouring sequences downloaded from the Ribosomal Database Project (RDP-II)

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