

Phylogenetic tree showing the relationships between various bacterial strains based on 16S rDNA sequences. The tree is rooted on the left. Strains are labeled with names and numbers, color-coded by group: blue for H9, H8, H10, M3, M11, K1, H4, B5*, B3*, M2, B4*, K10, H1, M7, M9, GP2, B7*, M5, H6, H2, M8, H5, M12, M13, M1, B6*, M10, H3, M6, B2*, and M14. Green labels include GP1, B1-B*, B1-A*, GP3, *M. intestinale*, GP4, *H. arabinoxylanisolvans*, H7, M2, K1, M9, GP2, B7*, M5, H6, H2, M8, H5, M12, M13, M1, B6*, M10, H3, M6, B2*, and M14. A scale bar at the bottom right indicates 0.2 substitutions per site.

