

OG0000652 249 after

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OG0000652_249_after

The phylogenetic tree illustrates the evolutionary relationships among numerous bacterial strains, primarily from the genera *Glycyphaga* (GLY), *Pharomacrus* (PHA), *Mediterraneanus* (MED), *Arharahy*, *Ardaradu*, *Cecropia* (CEC), *Locustella* (LOC), *Prunella* (PRU), *Popillia* (POP), *Vitellina* (VIT), *Actinotriton* (ACT), *Solenopsis* (SOL), *Helicoverpa* (HEL), *Colletes* (COF), *Cucullia* (CUC), *Mimodes* (MIM), *Liriomyza* (LIR), *Aspilota* (ASP), *Cinetus* (CIN), *Ceratomyza* (CER), *Marissa* (MAR), *Gnathoceros* (GIN), *Nymphaea* (NYM), *Ambrosia* (AMB), *Bracon* (BRA), *Oryctes* (ORY), and *Chiastophora* (CHI). The tree is rooted at the bottom left and branches upwards. Strains are labeled with their respective genus abbreviations followed by a unique identifier. Some labels include additional information such as "gnm1.Arahy.09g01987" or "A08g01354". The color coding is consistent across the tree, allowing for easy identification of related species.

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CTE