Identification of Hierarchical Orthologous Groups (HOGs) in Pseudomonas, Acinetobacter, and Burkholderia:

Genomes and associated proteomes GFF annotation files of strains from the Pseudomonas (228), Acinetobacter (5), and Burkholderia (1) genera were downloaded from the NCBI datasets database. To determine orthologous relationships between protein-coding genes, we used OrthoFinder version 2.5.4. The analysis was performed on an AWS EC2 instance type (c6a.48xlarge) with default settings. OrthoFinder computed hierarchical orthologous groups (HOGs) for each internal node in the species tree. To improve HOG prediction accuracy, an outgroup proteome (Burkholderia) was used to root the resulting species tree. HOGs are sets of proteins descended from a single gene in the ancestral species corresponding to the respective internal node. In this study, we focused on analyzing HOGs associated with the species tree node representing the last common ancestor of all A. Pseudomonas, Acinetobacter, and Burkholderia. Specifically, we examined HOGs containing cbrA, crc, and members of the pel, cupB, and cupC operons.

For visualizing and annotating phylogenetic trees, custom Python scripts were employed to generate the datasets for annotation in the Interactive Tree of Life (iTol) tool (<https://itol.embl.de/>). Jupyter notebooks for downloading genomes from NCBI, processing OrthoFinder results, and creating figures are available on GitHub at https://github.com/JonWinkelman/dash\_app\_pseudomonas.