# Response to Reviewer 1

Although the comment that “combining 16S and 23S sequences in a single phylogenetic tree is inappropriate,” the authors have retained this unchanged. Moreover, they consider these distinct loci as separate clades within the tree, which constitutes a substantial error.

Additionally, it remains unclear why the authors employed two loci (16S and 23S) to detect Arsenophonus, whereas other bacteria were assessed using only a single locus. No justification is provided in either the Materials and Methods or Results sections.

Ans. In the revised manuscript, separate phylogenetic trees for 16S and 23S have been added for *Arsenophonus* in Figure 4. The reason for adding both trees is the query by another reviewer. Please see the revised Figure 4.

We also clarified the rationale for using two different loci for *Arsenophonus* in MM section at lines 163-166.

Line 456: Figure S1 requires a legend.

Ans. Figure 4 was substantially revised to address this comment as well as concerns raised by another reviewer. Following these modifications, the information previously presented in Figure S1 became redundant. Therefore, Figure S1 has been removed from the Supplementary Data, and its corresponding legend is no longer required.