Response to Reviewers

The authors express their sincere gratitude to the reviewers for their insightful and constructive comments, which have significantly enhanced the manuscript. Authors respond to each comment (in the red font, pls see below) and have made tracked changes to the script.

Reviewer Comments:

Reviewer 1

Lines 89–100: The study investigates not only Arsenophonus but also other endosymbionts. Revise the study aim to ensure consistency with the title and results.

Ans. Author thanks the reviewer for pointing out this important oversight. The comment has been addressed by adding the names of other endosymbionts in the sentence. Please see L126-128 of the revised script.

Table 1: The table includes a primer set for Fritschea, which is not mentioned in the Introduction. Include relevant information about this bacterium in the Introduction.

Ans. A sentence related to "*Candidatus Fritschea bemisiae*" has bee added in the revised script. Please see L102-105 of the revised script.

Lines 177–182: Add information to the Introduction about Bemisia tabaci species, particularly their distribution in the study region.

Ans. Authors addressed this comment by adding data related to whitefly distribution in the region. Please see Line 72-78 of the revised script.

Subsection 3.2: Restructure this subsection for clarity. First, report negative PCR results for Asia II-5 and Asia II-7. Then, present all other findings. Clarify the discrepancy: why do 274 whiteflies represent only four species here, when lines 121 and 132 refer to six species? Verify the numbers and rewrite accordingly.

Ans. Reviewer made a highly useful query that helped in substantially improving the section. As two species, Asia II-5 and Asia II-7, didn't yield PCR amplicon, so this study included four species in the subsequent analyses. Please see lines 218-220 of the revised script.

Subsection 3.4: The prevalence percentages for each symbiont do not align with those in Figure 2 (e.g., "Arsenophonus was more common, 80% (100/124) in the Punjab region," but Figure 2 shows 100 (43.1%)). Explain this discrepancy. Standardize the presentation of frequencies throughout (e.g., by frequency then region, or region then frequency).

Ans. Thank you for your important observation. Authors revised section 3.4 to alleviate any discrepancy and standardized to clearly distinguish overall versus regional prevalence.

Lines 218–220: Provide data on cryptic species distribution in the study regions (as described in Subsection 3.1) to support this statement.

Ans. As section 3.4 has been revised and this statement has been omitted.

Subsection 3.5: The term "infection probability" is inappropriate in this context. Replace it with a more suitable term throughout the manuscript and figures, or justify its use.

Ans. Thank you for the comment. Authors substituted "infection probability" to "infection frequency" to better reflect the term, both in the text and figure 3. This change ensures terminological accuracy and better reflects the nature of the data.

Figure 4:

- Explain why Cardinium and Hamiltonella have many more sequences than Arsenophonus, despite the latter's prevalence.

Ans. Authors thank the reviewer for this important observation. *Arsenophonus* was analyzed using both 16S and 23S rRNA. In the original submission, only 16S-based trees were shown, underrepresenting *Arsenophonus*. This has now been corrected by constructing a combined 16S+23S phylogeny, improving its representation.

- On the Arsenophonus tree, three sequences lack GenBank accessions. Correct or explain this.

Ans. This has been corrected in the revised figure.

- Indicate the loci used for tree reconstruction.

Ans. Added in the figure legends.

- Some labels on the Cardinium tree are bolded. Clarify if this has significance.

Ans. Bold text was editing errors that have been rectified in the revised figure.

Lines 286–294: Justify emphasizing Arsenophonus as dominant when Cardinium frequency is nearly as high.

Ans. Although *Cardinium* shows comparable frequency, the emphasis on *Arsenophonus* is based on functional relevance rather than prevalence alone. *Arsenophonus* was the most consistently prevalent across cryptic species and regions, particularly dominating in Asia II-1 populations and virus-endemic areas. In contrast, *Cardinium*, although frequent, showed greater variability and frequent co-infection with *Arsenophonus*, especially in Punjab. This pattern suggests that *Cardinium* may play a complementary or modulatory role, whereas *Arsenophonus* likely represents the primary driver, particularly given its established mechanistic role in virus

transmission. Both these points have already been mentioned in the discussion. Nonetheless, authors briefly mention these points in the revised discussion. Please see Line 352-359.

Line 295: Clarify why reference is made to only two samples when Figure 4 and supplementary materials (SM) show five.

Ans. Thanks for pointing out this oversight. There are five samples and have been updated in the revised script. Please see Line 365 of the revised script.

Lines 376–378: in Supplementary Table: List all GenBank accession numbers for symbionts directly in the cells (replacing letters A, C, H, etc.). Remove the last column, as it is unnecessary. Define abbreviations in the "Prov." column. Explain the yellow highlighting. Improve table formatting overall. Address the absence of Hamiltonella data for sample 213.

Ans. The Table S1 has been updated as per suggestion. Yellow highlighting was just for self reminder.

Minor Comments

Lines 109–110: Report any correlation between host plant and B. tabaci endosymbiont community if possible.

Ans. Authors appreciate this insightful suggestion. However, analyzing correlations between host plant and *B. tabaci* endosymbiont communities is beyond the scope of the current study, as sampling was not designed to systematically compare symbiont profiles across host plants under controlled conditions. Nevertheless, this represents an important direction for future research.

Table 1: Align the primer name "23GISR" at the same level as the primer sequences (currently, it aligns with part of U23GISR).

Ans. Done

Line 173: Clarify "Asia II-1ll the figures were generated…" and define "Asia II-1ll," which is not mentioned earlier.

Ans. This was a typo and has been corrected in the revised script. Pls see L207 in the revised script.

Line 179: prevailed.

Ans. Corrected

Line 180: common biotype

Ans . Done

Line 186: Standardize “Asia 1” or “Asia I” throughout the manuscript, figures, and main text.

Ans. Standardized wherever in the script was applicable.

Subsection 3.3: Consider adding a visualization (e.g., like Figure 2 or a bar chart) for these results.

Ans. Authors appreciate this suggestion but want to continue with the present way of presentation.

Line 200: Define “biotype” (is it synonymous with “cryptic species”)?

Ans. Yes and added in the revised script at Line 238.

Line 216: Add missing bracket.

Ans. Added

Line 351: Clarify “ticks’ spider.”

Ans. Corrected.