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**Fig. S1.** *wsp* gene detection of *Wolbachia* in samples from 8 different geographical populations. A: Yuhang; B: Liyang; C, Langxi; D: Xinchang; E: Guiyang; F: Nanchang; G: Yingde; H: Enshi; P: Positive control used the genomic DNA of *E. grisescens* as template; N: Negative control used ddH2O as template, Samples from A, B, C wereidentified as *E. obliqua*, and those from D, E, F, G, H wereidentified as *E. grisescens*.



**Fig. S2.** *wsp* gene detection of *Wolbachia* in samples from 2 different geographical populations of Yuhang and Xinchang. P: Positive control; N: Negative control, Samples from Yuhang wereidentified as*E. obliqua*, and those from Xinchang wereidentified as*E. grisescens*.



**Fig. S3.** *wsp* gene detection of *Wolbachia* in samples from 2 different geographical populations of Liyang and Guiyang. P: Positive control; N: Negative control, Samples from Liyang wereidentified as *E. obliqua*, and those from Guiyang wereidentified as *E. grisescens*.



**Fig. S4.** *wsp* gene detection of *Wolbachia* in samples from 2 different geographical populations of Langxi and Nanchang. P: Positive control; N: Negative control, Samples from Liyang wereidentified as *E. obliqua*, and those from Guiyang wereidentified as *E. grisescens*.



**Fig. S5.** *wsp* gene detection of *Wolbachia* in samples from 2 different geographical populations of Yingde and Enshi. P: Positive control; N: Negative control, Samples from Yingde and Enshi were identified as *E. grisescens*.

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**Fig. S6.** *wsp* gene detection of *Wolbachia* in samples used for bacterial community analysis. P: Positive control; N: Negative control, Samples O1-10 were identified as *E. obliqua*, and Samples G1-10 wereidentified as *E. grisescens*.