

Bacterial Microbiota of Field-Collected *Helicoverpa zea* (Lepidoptera: Noctuidae) from Transgenic Bt and Non-Bt Cotton

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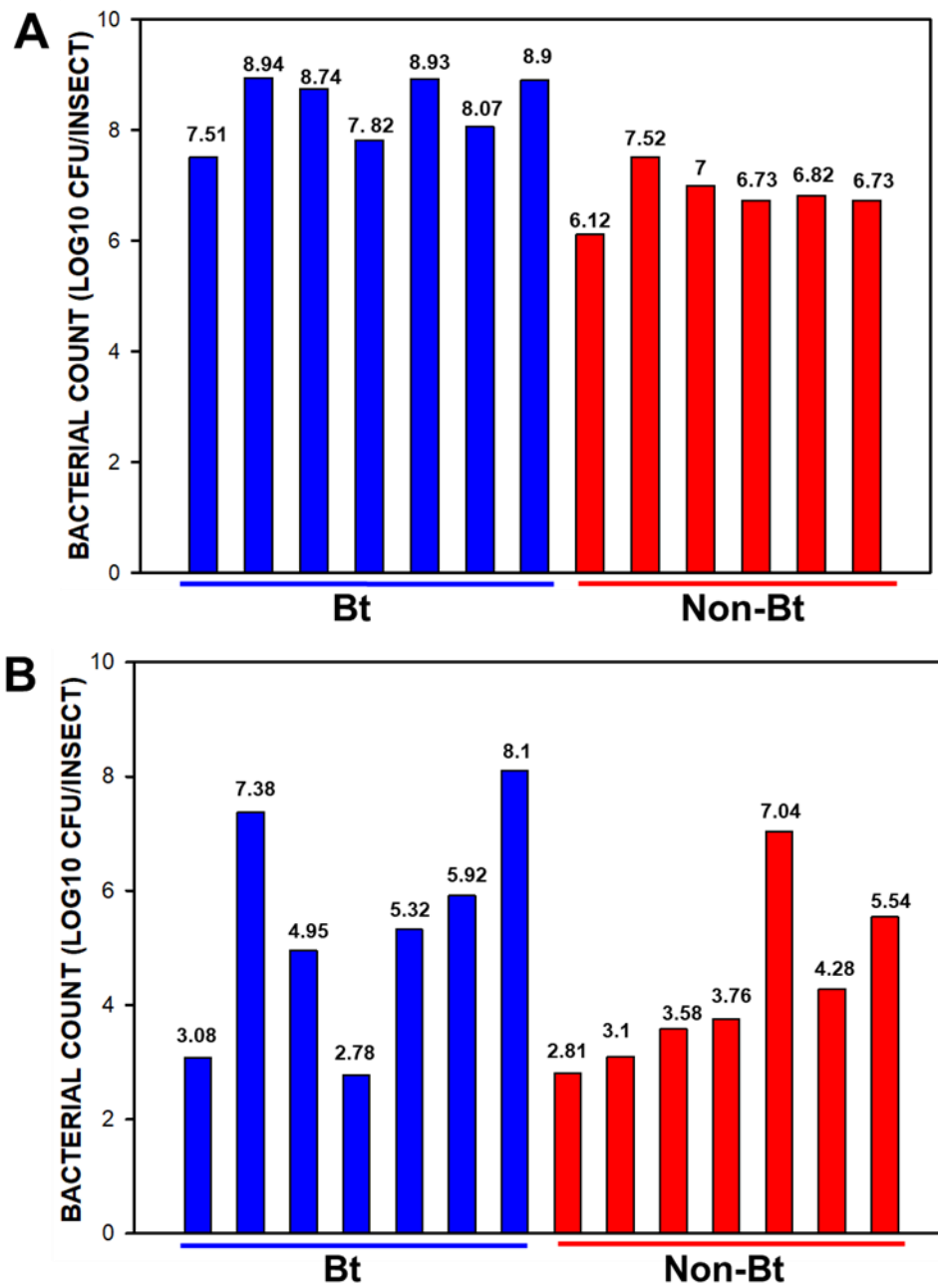


Figure S1. Detailed prevalence (per sample) of cultivable bacterial loads in bollworms from non-Bt cotton versus Bt (Wid-eStrike) cotton from the field. (A) 2nd to 3rd stadium *Helicoverpa zea* larvae collected in August 2016; (B) 3rd stadium bollworms collected in August 2018. Each bar represents the median number (log-converted) of Colony Forming Units.

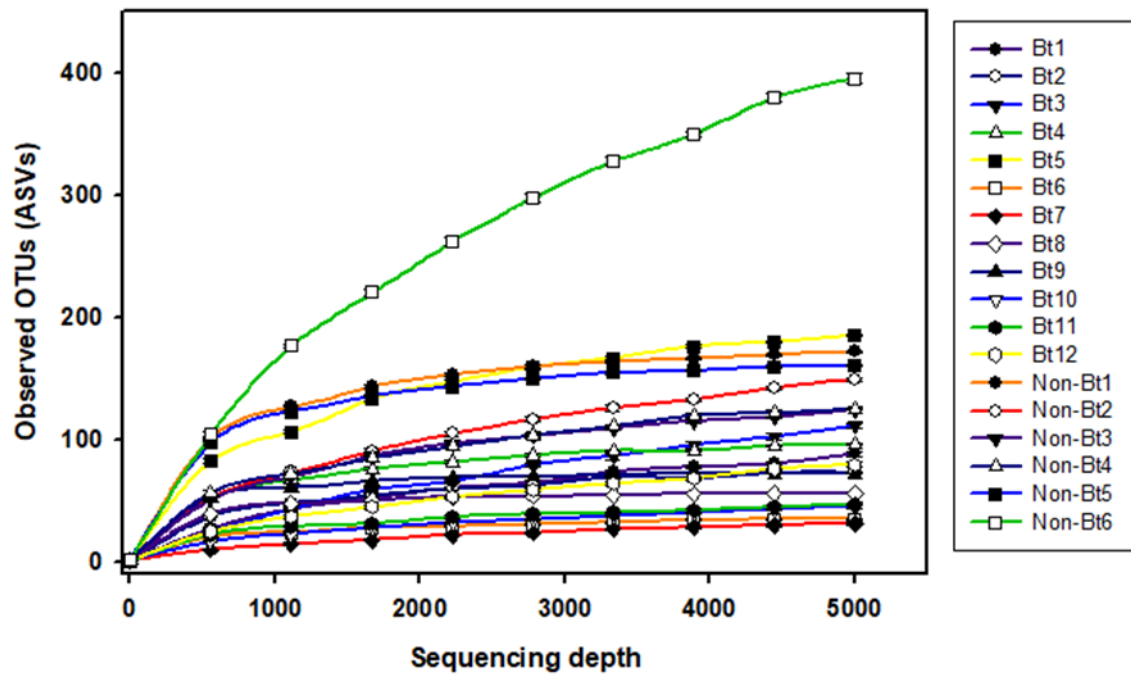


Figure S2. Rarefaction curves of the number of observed OTUs (sequence variants) from internal DNA samples of the cotton bollworm, *Helicoverpa zea*. Bt: sample originating from third stadium larvae from Bt (WideStrike, Cry1Ac + Cry1F) cotton. Non-Bt: sample originating from third stadium larvae from non-Bt cotton. Number after sample origin represents sample number. Sequences were obtained from amplified DNA fragments overlapping the V3–V4 hypervariable regions of the 16S rRNA gene.