Supplementary Material

Genome, Host Genome Integration, and Gene Expression in Diadegma fenestrale Ichnovirus from the Perspective of Coevolutionary Hosts

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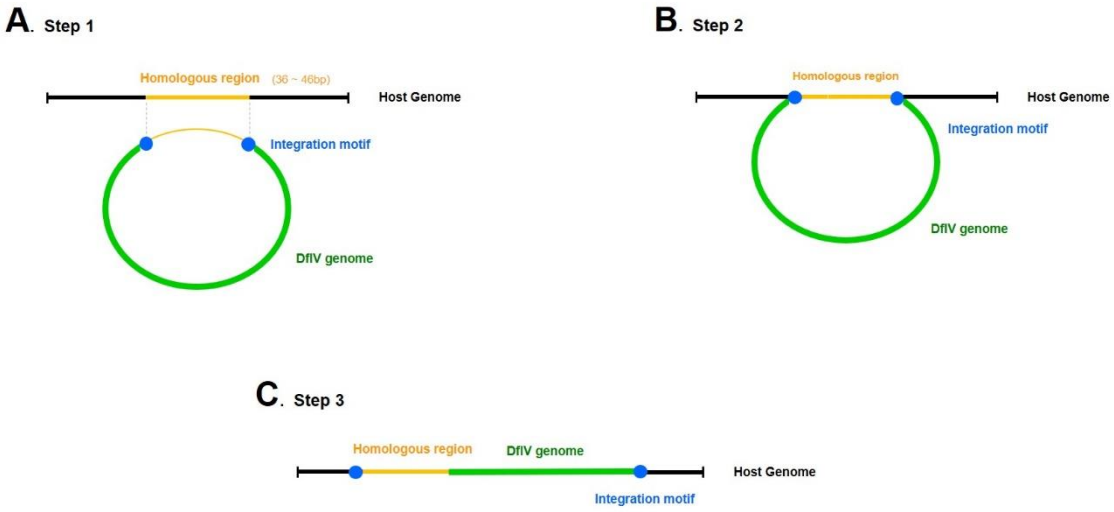
1 Supplementary Figures and Tables



Supplementary Figure 5. A proposed schematic diagram of the integration mechanism between *Diadegma fenestrale* ichnovirus (DfIV) and the diamondback moth (*Plutella xylostella*) genome. **A).** The homologous sequences ranged in length from 36–46 bp between circular viral genomic (DfIV) segments and host genome segments, and integration motifs flanked homologous regions. **B).** Host and viral homologous regions were integrated and surrounded by the flanking sites of the integration motif. **C).** The homologous region and integrated motifs were combined into a partial linearized host genome during the homologous recombination process (Legeai et al., 2020). Detailed information (re-sequencing results, integration motif sequences and their positions in the host genome, homologous sequences and their positions) is provided in supplementary Table S4 and Figure 2.