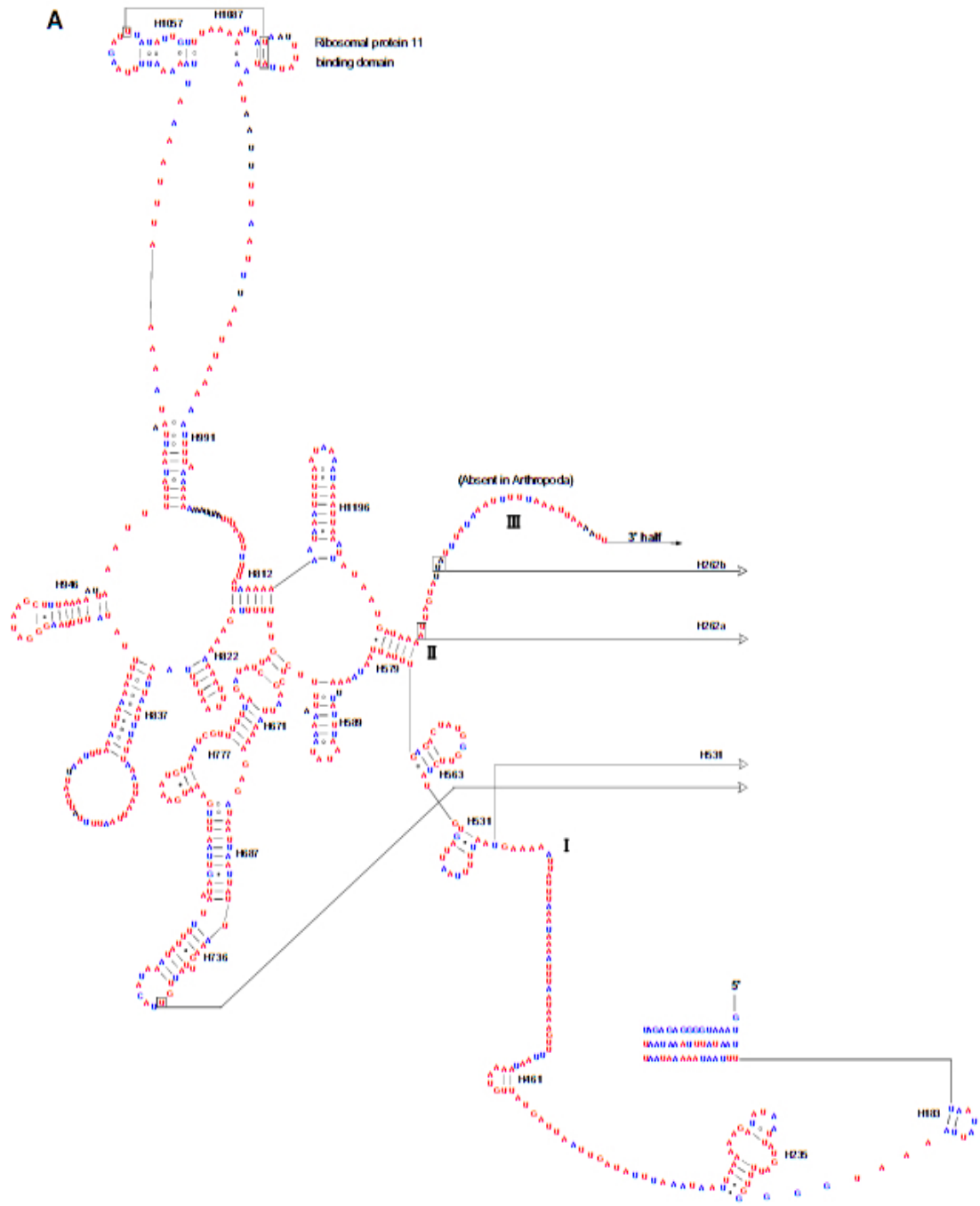


Fig. S1 Inferred secondary structures for 22 typical tRNAs of the *Chilo suppressalis* mitogenome. The tRNAs are labeled with the abbreviations of their corresponding amino acids. Base-pairing is indicated as follows: Watson-Crick pairs by lines, wobble GU pairs by dots and other noncanonical pairs by circles.

A



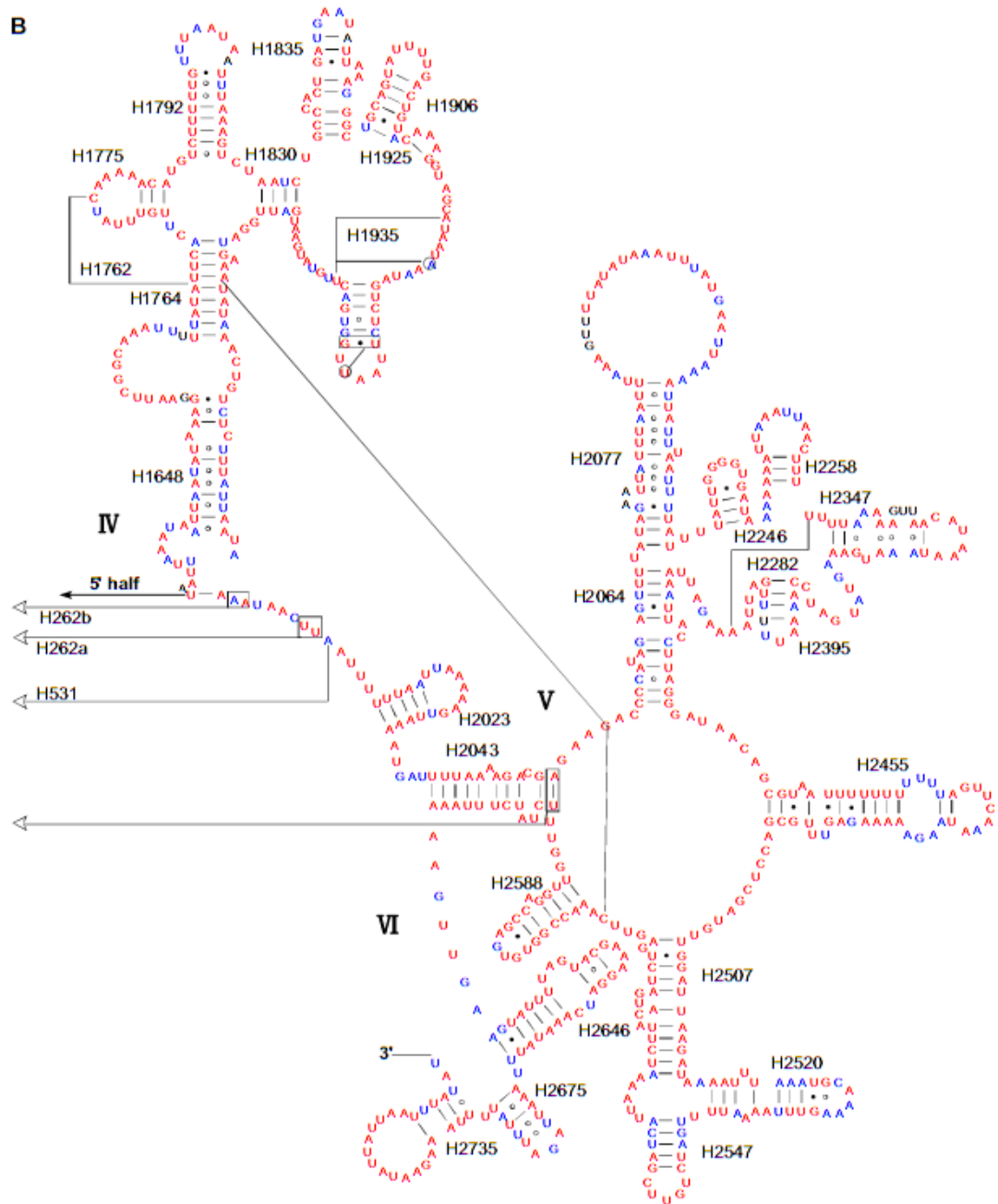


Fig. S2 Predicted secondary structure of the *rrnL* gene in the *Chilo suppressalis* mitogenome.

Tertiary interactions and base triples are shown connected by continuous lines. Fig. S2-A represents the 5' half of *rrnL*, with the remaining 3' half in Fig. S2-B. Base-pairing is indicated as follows: Watson-Crick pairs by lines, wobble GU pairs by dots and other noncanonical pairs by circles.

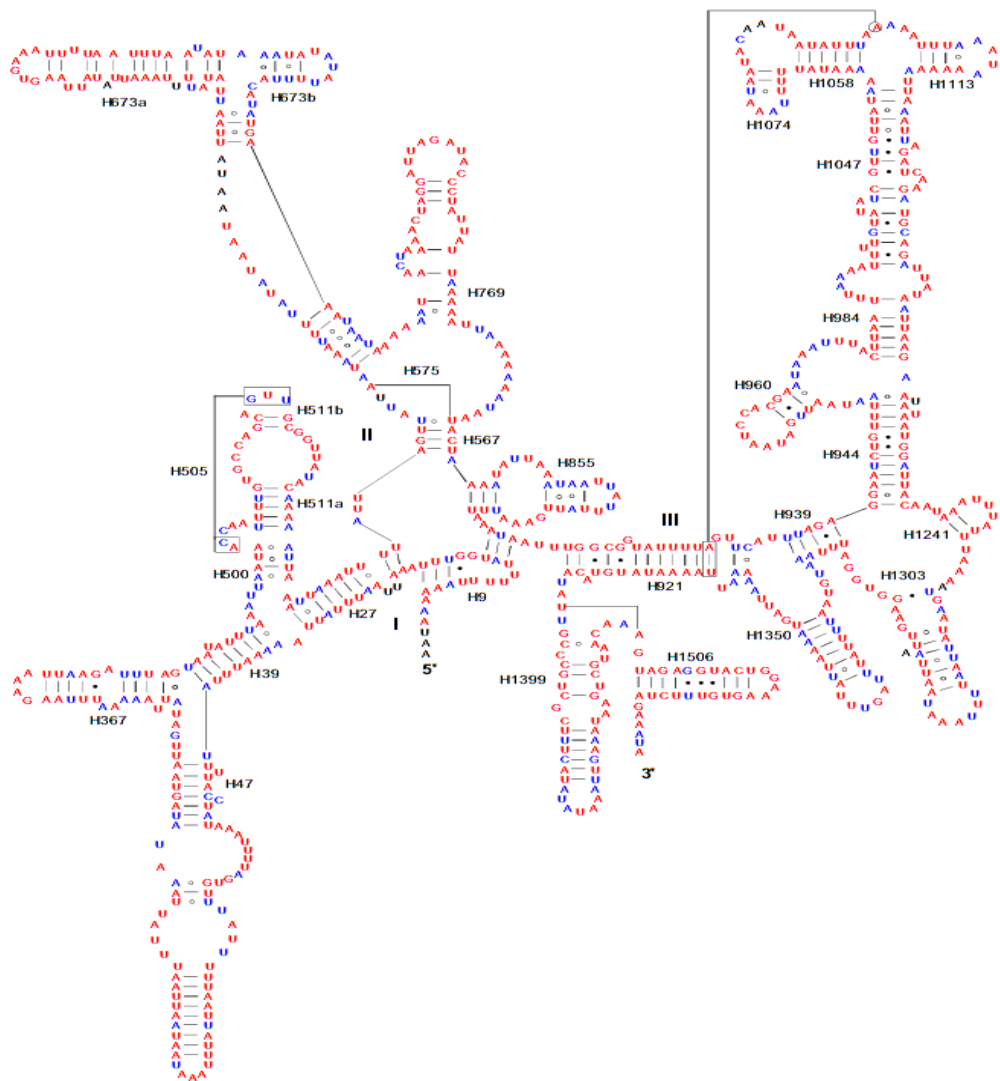


Fig. S3 Predicted secondary structure of the *rrnS* gene in the *Chilo suppressalis* mitogenome.

Tertiary interactions and base triples are shown connected by continuous lines. Base-pairing is indicated as follows: Watson-Crick pairs by lines, wobble GU pairs by dots and other noncanonical pairs by circles.