

The B2 consensus sequence was from RepeatModeler based on the published TE library and was not identified by machine learning; thus, the classification was reliable. It indicated that the SINE/B2 either was an independently evolved subfamily in *T. ni* or probably was horizontally transferred from other Lepidopteran species. The insertion was estimated from 60 Mya with a peak propagation around 20–30 Mya. However, where the B2 subfamily came from and how it integrated into the *T. ni* genome requires further study.

4.2. TE Expansion Activity Correlated with Phylogeny of Noctuidae Species

In addition to being the main contribution factor to the genome size of Noctuidae species, we also investigated which class/subfamily of TE was correlated with the phylogeny of Noctuidae. Among the four classes of TE, only LINE showed a phylogenetic signal with high confidence, indicating the essentially vertical inheritance characteristics of LINE elements in Noctuidae. In particular, four LINE subfamilies, CR1, L2, RTE, and R1, showed a high correlation with Noctuidae phylogeny, all abundant in copy number. In contrast, despite the high copy number