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Long non-coding RNAs (lncRNAs) are crucial modulators in various biological processes. However, little is known about the function of lncRNAs in the development of Asian honey bee (*Apis cerana*) larval guts. In this work, on the basis of our previously obtained deep-sequencing data from the 4-, 5-, and 6-day-old larval guts of *A. cerana* workers (Ac4, Ac5, and Ac6 groups), an in-depth transcriptome-wide investigation was conducted to decipher the expression pattern, regulatory manners, and potential roles of lncRNAs during the developmental process of *A. cerana* worker larval guts, followed by the verification of the relative expression of differentially expressed lncRNAs (DElncRNAs) and the targeting relationships within a competing endogenous RNA (ceRNA) axis. In the Ac4 vs. Ac5 and Ac5 vs. Ac6 comparison groups, 527 and 498 DElncRNAs were identified, respectively, which is suggestive of the dynamic expression of lncRNAs during the developmental process of larval guts. Additionally, it was found that 79 and 76 DElncRNAs as potential antisense lncRNAs may, respectively, interact with 72 and 60 sense-strand mRNAs. An investigation of competing endogenous RNA (ceRNA) networks suggested that 75 (155) DElncRNAs in the Ac4 vs. Ac5 (Ac5 vs. Ac6) comparison group could target 7 (5) DEmiRNAs and further bind to 334 (248) DEMRNAs, which can be annotated to 33 (29) functional terms and 186 (210) pathways, including 12 (16) cellular- and humoral-immune pathways (lysosome pathway, necroptosis, MAPK signaling pathway, etc.) and 11 (10) development-associated signaling pathways (Wnt, Hippo, AMPK, etc.). The RT-qPCR detection of five randomly selected DElncRNAs confirmed the reliability of the used sequencing data. Moreover, the results of a dual-luciferase reporter assay were indicative of the binding relationship between MSTRG.11294.1 and miR-6001-y and between miR-6001-y and ncbi_107992440. These results demonstrate that DElncRNAs are likely to modulate the developmental process of larval guts via the regulation of the source genes' transcription, interaction with mRNAs, and ceRNA networks. Our findings not only yield new insights into the developmental mechanism underlying *A. cerana* larval guts, but also provide a candidate ceRNA axis for further functional dissection.