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Dynamics and regulatory role of circRNAs in Asian honey bee larvae following fungal infection

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Non-coding RNA (ncRNA) plays a vital part in the regulation of immune responses, growth, and development in plants and animals. Here, the identifcation, characteristic analysis, and molecular verifcation of circRNAs in Apis cerana cerana worker larval guts were conducted, followed by in-depth investigation of the expression pattern of larval circRNAs during Ascosphaera apis infection and exploration of the potential regulatory part of diferentially expressed circRNAs (DEcircRNAs) in host immune responses. A total of 3178 circRNAs in the larval guts of A. c. cerana were identifed, with a length distribution ranging from 15 to 96,007 nt. Additionally, 155, 95, and 86 DEcircRNAs were identifed in the in the 4-, 5-, and 6-day-old larval guts following A. apisinfection. These DEcircRNAs were predicted to target 29, 25, and 18 parental genes relevant to 12, 20, and 17 GO terms as well as 144, 114, and 61 KEGG pathways, including 5 cellular and 4 humoral immune pathways. Complex competing endogenous RNA (ceRNA) regulatory networks were detected as being formed among DEcircRNAs, DEmiRNAs, and DEmRNAs. The target DEmRNAs were engaged in 36, 47, and 47 GO terms as well as 331, 332, and 331 pathways, including 6 cellular and 6 humoral immune pathways. Further, 19 DEcircRNAs, 5 DEmiRNAs, and 3 mRNAs were included in the sub-networks relative to 3 antioxidant enzymes. Finally, back-splicing sites within 15 circRNAs and the diference in the 15 DEcircRNAs' expression between uninoculated and A. apis–inoculated larval guts were confrmed based on molecular methods. These fndings not only enrich our understanding of bee host–fungal pathogen interactions but also lay a foundation for illuminating the mechanism underlying the DEcircRNA-mediated immune defense of A. c. cerana larvae against A. apis invasion.