



## Detection of Dabieshan tick virus in Hebei Province of China by Small RNA Sequencing

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Ticks are important haematophagous ectoparasites. Tick-borne viruses are increasingly recognized as important threats to the health of human and livestock. In the present study, the viruses were detected in tick samples of *Haemaphysalis longicornis* collected from Chengde and Pingshan of Hebei province using sRNA-seq method, respectively. A total of 7 pools constructed for virus screen, and all of the samples (4 pools) originated from Chengde were positive for Dabieshan Tick Virus (DBTV), which has not been reported before in Hebei province. The full-length genome sequence of Dabieshan tick virus was obtained through sRNA-seq and Sanger sequencing. The nucleotide sequence of L and N segments of DBTV detected in this study showed 95.8% and 94.3% identity with Hubei strain of DBTV, respectively. The most interesting thing is that all the tick specimens collected from the two regions were engorged nymphs, and molted to adults in the lab. DBTV was detected from newly molted adults of *H. longicornis* indicated that this virus can be transmitted from nymphs to adults, and it might even be transstadial transmission. **Acknowledgements:** This work was supported by the Natural Science Foundation of Hebei Province (C2022205026), the Foundation of Hebei Educational Committee (ZD2020168) and the National Natural Science Foundation of China (31472050), the State Key Laboratory of Veterinary Etiological Biology, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences (SKLVEB2021KFKT006).

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