V. CONCLUSION AND SUGGESTION

A. Conclusions

From the results and discussion of this research, the following conclusions can be drawn:

1. The Reverse Transcription Polymerase Chain Reaction (RT-PCR) technique was successfully utilized to detect Influenza virus in clinical nasopharyngeal (NP) swab samples.
2. In Batur District, Banjarnegara, a moderate 30% of children with Acute Respiratory Infection (ARI) had influenza infection.
3. Among the assessed factors, community ARI history (76.19%) and household cigarette smoke exposure (66.67%) were identified as the leading contributors to ARI incidence in children with Influenza in Batur District. Meanwhile, incomplete immunization (38.10%) appeared less influential and did not emerge as a dominant risk factor in this study.

B. Suggestion

This study was limited to detecting Influenza viruses only at the genus level. For future research, it is advisable to optimize molecular procedures by quantifying cDNA and ensuring proper storage conditions to avoid repeated freeze–thaw cycles that may reduce nucleic acid integrity. The application of more advanced approaches such as Sanger sequencing, whole-genome sequencing (WGS), and phylogenetic analysis is recommended to achieve subtype or strain-level identification and to broaden our understanding of the genetic diversity of circulating Influenza viruses. Beyond molecular analysis, preventive strategies at the community level remain crucial. Priority should be given to reducing children's exposure to household tobacco smoke, promoting complete immunization, and strengthening public health education among parents and communities about maintaining a healthy environment and adhering to timely vaccination schedules.