

4. The caffeine showed synergistic effect in this study when used combination with statin against influenza infection.

**Conclusions:** It indicates that the statin showed anti-influenza virus infectious activity in a murine model. Moreover, it is inexpensive and available, so the statin may meet the challenge of the next influenza pandemic.

**PP-073** Progress in research on the factors of triggering the resistance of influenza viruses to anti-flu drugs such as oseltamivir and the methods of monitoring and prevention of the drug resistance

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Amantadine, rimantadine, zanamivir, oseltamivir are the most common used anti-flu drugs in clinic, the inappropriate use of them could cause resistance and reduce therapy efficacy. The review was focused on the factors of triggering the resistance of influenza viruses to anti-flu drugs such as oseltamivir, the methods of surveillance, monitoring and prevention of the drug resistance. The review would provide theoretical guidance to the reasonable application of anti-flu drugs to reduce the resistance and bring the effect of the drugs to full play.

**PP-074** Influenza-related Host Gene Database (IHGDB): an integrated information resource for influenza-related host's genes

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Influenza A is a serious respiratory illness that can be debilitating and may cause complications leading to hospitalization and death. Like all viruses, influenza viruses rely on the host cellular machinery to support their life cycle. Accordingly, in order to understand the mechanisms of the virus life cycle, identification of the host functions co-opted for viral replication is needed and also we can find new targets for the development of antiviral compounds. In this study, we manually gathered approximately 1500 influenza-related host genes from literatures, which were mainly supported experimentally via RNAi-based genome-wide screening.

**IHGDB Influenza-related Host Gene Database**  
Northwest A&F University, CHINA College of life sciences

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View: Any Title

**Browse & Quick Search**

- Browse all genes
- Browse by chromosome region
- Browse by different viruses
- Browse by different methods
- Search by gene name
- Help

**Major references**  
Influenza A is a serious respiratory illness that can be debilitating and may cause complications leading to hospitalization and death. Like all viruses, influenza viruses rely on the host cellular machinery to support their life cycle. Accordingly, identification of the host functions co-opted for viral replication is of interest to understand the mechanisms of the virus life cycle and to find new targets for the development of antiviral compounds.

**Major references**  
In this study, we manually gathered approximately 1500 influenza-related host genes from literatures, which were mainly supported experimentally via RNAi-based genome-wide screening. We used these data to build an influenza-related Host Gene Database (IHGDB, <http://vir.nwsuaf.edu.cn/IHGDB/>), which contains genes' information like Gene Name, Entrez ID, Ensembl ID through CrossRef ID Converter (<http://biomarker.biocloud.net/crossrefconverter.php>). We divided all information into 3 levels that are Gene, Protein and Function.

**Major references**  
Influenza-related Host Gene Database (IHGDB) is thus developed as an integrated information resource of influenza-related host genes for genetic, genomic, and phylogenetic studies of influenza virus life cycle.

**Influenza related Host Gene Database structure**

- Gene\_information
  - Entrez\_Gene\_ID VARCHAR(20)
  - Ensembl\_Gene\_ID VARCHAR(20)
  - Gene\_name VARCHAR(100)
  - UniGene\_ID VARCHAR(50)
  - Gene\_Description VARCHAR(200)
  - CDS VARCHAR(100)
  - Ensembl\_Chr VARCHAR(2)
  - Start (bp) VARCHAR(20)
  - End (bp) VARCHAR(20)
  - Strand VARCHAR(2)
  - Reference\_ID VARCHAR(20)
- Protein\_information
  - Entrez\_Gene\_ID VARCHAR(20)
  - Swiss-Prot\_Name VARCHAR(20)
  - Gene VARCHAR(100)
  - UniGene\_ID VARCHAR(50)
  - Protein\_ID VARCHAR(20)
  - IP VARCHAR(20)

We used these data to build a Influenza-related Host Gene Database (IHGDB, <http://vir.nwsuaf.edu.cn/IHGDB/>), which contains 3 levels information that are gene, protein and function.

Influenza-related Host Gene Database (IHGDB, <http://vir.nwsuaf.edu.cn/IHGDB/>) is thus developed as an integrated information resource of influenza-related host Genes for genetic, genomic, and phylogenetic studies of influenza virus life circle. It provides a user-friendly interface by which interested genes can easily retrieved by searching engine.

**Poster Session – Gastro-intestinal Infections**

**PP-075** Obstructive jaundice promotes intestinal barrier dysfunction and bacterial translocation: experimental study

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**Background:** Although clinical and experimental studies have demonstrated a correlation between obstructive jaundice and the development of sepsis, the mechanism has not been fully elucidated.

**Aim:** to investigate the influence of biliary obstruction on bacterial translocation as a possible source of infection in cases of obstructive jaundice.

**Material and Methods:** Two groups of 12 Wistar rats were examined: rats subjected to common bile duct (CBD) ligation (group A) and rats subjected to a sham operation (group B). After 7 days blood samples were taken and liver, spleen, and mesenteric lymph nodes (MLN) from the ileocaecal area were removed, divided into small pieces and cultured. Quantitative culture results were determined by the number of colony-forming units (CFU) per ml homogenate. Bacterial translocation was defined as the presence of a positive culture of mesenteric lymph nodes, blood, liver and/or spleen. Samples for histopathological examination were taken from the mucosa of the ileum and the colon and evaluated for inflammatory and destructive changes.

**Results:** There was no evidence of bacterial translocation to MLN, blood, spleen or liver detected in any of the 12 sham-operated control rats. In contrast, bacterial translocation was demonstrated in 8 of the 12 CBD ligated rats ( $P < 0.01$ ). In all 8 cases in which translocation occurred, *Escherichia coli* were cultured from the mesenteric lymph nodes. There were no histological changes in the mucosal samples of the control animals. In the CBD ligated rats hyperemia, vacuolization, reduction of goblet cells, decreased mitotic activity and infiltration by lymphocytes and PMNLs were detected. Cases in which translocation occurred were significantly associated with decreased mitotic activity in the colon ( $r = -0.5$ ,  $p < 0.01$ ) and higher infiltration by PMNLs in the ileum ( $r = -0.62$ ,  $p < 0.05$ ).

**Conclusion:** Obstructive jaundice in a rat model predisposes to bacterial translocation.

**PP-076** Impaired Kupffer cell function: a major predisposing factor of septic complications in obstructive jaundice

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Obstructive jaundice is frequently associated with septic complications.

**Aim:** The aim of this study was to investigate the effect of obstructive jaundice on Kupffer cell functions and its role in septic complications.