CDC Institutional Biosafety Committee (IBC) Meeting Minutes

Date: February 27, 2026
Time: 10:30 AM – 12:00 PM
Location: MS Teams meeting

Member	Attendance	Member	Attendance
1. NCEZID/DVBD1	☒	13. NCEZID/DCLSR2	☐
2. NCIRD/DVD	☒	14. IOD/OLSS3	☒
3. NCEZID/DHCPP1	☒	16. NCEZID/DCLSR3	☒
4. IOD/OLSS1	☐	17. NCEZID/OD	☐
5. OCOO/OSSAM/OHC	☐	18. IOD/OLSS4	☒
6. NCEZID/DVBD2	☐	19. NCHHSTP/DHP2	☒
7. IOD/OLSS2	☒	20. Outside Member/Atlanta1	☒
8. NCHHSTP/DHP1	☒	21. Outside Member/Atlanta2	☒
9. NCHHSTP/DTE	☒	22. Outside Member/Fort Collins	☒
10. NCIRD/ID	☒	23. Outside Member/Puerto Rico	☐
11. NCIRD/CORVD	☐	24. CDC/GHC/OD	☐
12. NCEZID/DCLSR1	☒	**Visitor(s)**	**4**

Agenda

1. **10:32 am EST-** Welcome.
2. Review and approval of **January 30, 2026** Meeting Minutes.
3. Review of IBC registrations:
    1) IBC-2025-212 Renewal
    2) IBC-2025-214 Renewal
    3) IBC-2025-216 Renewal
    4) IBC-2025-217 Renewal
    5) IBC-2025-299 Renewal
4. Other Business

Principal Discussion

- Quorum confirmed.
- Meeting called to order at 10:32 am
- Review and approval of **January 30, 2026** Meeting Minutes.
- Review of IBC Registrations
- Other Business

Review of IBC Registrations

1. **IBC-2025-212 Renewal**
   General Project Description: Hepatitis A virus (HAV) is unusual in that after infection it doesn't try to take over the replication machinery of the infected host cell but uses cellular resources that are underutilized

by the host cell. Because of this it can take at least 10 days for HAV to form plaques in cell culture there is a need to develop a more rapid method to detect levels of HAV replication in cell culture. This study will use an HAV clone with a luciferase gene inserted into its genome to develop a more rapid assay through the detection of this luciferase activity with a luminometer.
Approximate percentage of the viral genome used: >2/3
Applicable Sec of NIH Guidelines: III-D-1-a, III-D-2-a
Required biological containment level for the work to be implemented: BSL-2
General Points Discussed:

- **Section 2.12:** check Yes for III-D-3
- **Section 3:**
  - Add host viruses, and remove the Huh7 cell line, which is not a host for the recombinant molecules.
  - Add *E coli* strain
- **Section 4.2:** Please include the external lab (Stanley Lemon lab) described in Section 1.3

Committee Action: Approved with changes

2. **IBC-2025-214 Renewal**
General Project Description: PCR amplification and cloning of whole HBV genomes from different genotypes. Cloned HBV genomes will be transfected into hepatocytes. Expression of surface antigen, e antigen, and core antigen will be measured in cells and cell culture supernatant. HBV RNA and DNA will be detected by Northern and southern blotting, and PCR.
Approximate percentage of the viral genome used: >2/3
Applicable Sec of NIH Guidelines: III-D-1-a, III-D-2-a
Required biological containment level for the work to be implemented: BSL-2
General Points Discussed:
   - **Section 2.7: check Yes**
   - **Section 4: Please include campus, Bldg. number, but not specific room number.**

   Committee Action: Approved with changes

3. **IBC-2025-216 Renewal**
General Project Description: Recently there has been renewed interest in hepatitis Delta (HDV) as a virus of concern. HDV needs a helper virus, hepatitis B virus (HBV), to provide the HBV surface protein to encapsulate the HDV genome for the creation of progeny HDV. HDV only occurs as a co-infection or superinfection with HBV, causing severe complications in individuals infected with HBV. This research intends to create HDV transfection clones from genotypes 1 to 8 for assay development and drug discovery.
Approximate percentage of the viral genome used: >2/3
Applicable Sec of NIH Guidelines: III-D-2-a, III-D-3-a
Required biological containment level for the work to be implemented: BSL-2
General Points Discussed:
   - **Section 2.6:** Please list the plasmids containing the HBV genome underneath the description "PCR-XL-TOPO with HBV whole genome inserts GenBank accession numbers MT426088 to MT426118".
   - **Section 2.8:** should be Yes
   - **Section 3:**
     - List the host HBC and HDV instead of the cell lines
     - Specify E.coli strain
   - **Section 4:** Please include campus, Bldg. number, but not specific room number

   Committee Action: Approved with changes
4. **IBC-2025-217 Renewal**

General Project Description: Cloning of genomic or sub-genomic fragments of hepatitis viruses in E.coli to meet our needs for consistent availability of positive PCR control materials from the HAV and HCV genotypes 1a, 1b, 2 and 3a, most prevalent in the USA.; HBV genotypes A, B, C, D, E, F, G and H and HEV genotypes 1, 2, 3 and 4. These small sub-genomic targets are derived and correspond to our existing genotyping assays.
Approximate percentage of the viral genome used: >2/3
Applicable Sec of NIH Guidelines: III-D-1-a, III-D-2
Required biological containment level for the work to be implemented: BSL-2
General Points Discussed:

- **Section 2.6c:** Section 1.3 description does not support that >2/3 virus genomes were used. Please clarify in Section 1.3 and make the necessary edit in Section 2.6c.
- **Section 2.8:** should be Yes
- **Section 2.12:**
  - III-D-1 should be No
  - III-D-2-a should be Yes
- **Section 3:** Specify E coli strain
- **Section 4:** Check BSL-1, although CDC does not have a BSL-1 lab

Committee Action: Approved As Written

5. **IBC-2025-299 Renewal**

General Project Description: The purpose of the study is to delineate both cellular and molecular basis of human immune response to influenza. In order to evaluate and improve future vaccines, we will assess the B cells that are the basis for the serum antibodies which can protect individuals from influenza infection, morbidity and mortality. This will also allow us to understand the molecular nature of antibody-mediated protection from influenza.
Approximate percentage of the viral genome used: N/A
Applicable Sec of NIH Guidelines: III-D-3, III-D-4-a, III-D-7, III-F-8
Required biological containment level for the work to be implemented: BSL-2
General Points Discussed:

- **Section 1.3:** Please clarify whether the wild-type or recombinant/RG influenza virus is used in the study.
- **Section 2.12**: III-D-3 should be No, if only WT influenza virus was used in the study and the virus does not serve as a host for recombinant or synthetic molecules.
- **Section 2.9c:** Provide expiration date for the IACUC protocols (3179 & 3180) in Section 2.9c
- **Section 3:** Remove the influenza virus if only WT virus was used in the study, and the virus does not serve as a host for recombinant or synthetic molecules.
- **Section 4:** Please include campus, Bldg. number, but not specific room number

Committee Action: Approved with changes

Other Business

- **IBC Charter**
- **Committee Rapporteur (CR)**
  - The CR role shall be rotated among the voting members
  - The CR shall lead discussion of IBC registrations during the full committee meeting
  - Initially, each CR will be assigned fewer than 3 registrations
- **Meeting Agenda**
  - Any committee member can propose agenda items for discussion
  - The IBC Administrator finalizes the meeting agenda through check-in meetings with the Chairs
- **Meeting adjourned at 11:53am**

REYNOLDS M. SALERNO - S

Digitally signed by REYNOLDS M. SALERNO -S
Date: 2026.04.17 09:39:36 -04'00'

Reynolds M Salerno, PhD
Director, Office of Laboratory Systems and Response