**From:** Barnes, John R. (CDC/NCIRD/ID) <fzq9@cdc.gov>
**Sent:** Monday, April 8, 2024 2:27 PM
**To:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>; Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>; Stevens, James (CDC/NCIRD/ID) <fwb4@cdc.gov>; Olsen, Sonja (CDC/NCIRD/ID) <sco2@cdc.gov>; Kniss, Krista (CDC/NCIRD/ID) <krk9@cdc.gov>; Kirby, Marie (CDC/NCIRD/ID) <pbi0@cdc.gov>; Kondor, Rebecca J. (CDC/NCIRD/ID) <dqy5@cdc.gov>
**Cc:** Dugan, Vivien (CDC/NCIRD/ID) <lny1@cdc.gov>
**Subject:** FW: Respiratory Virus Roundup 23-24:6 | Influenza A(H5) Guidance and Network Funding Opportunity

We are getting peppered on the following guidance APHL submitted. The highlighted is really confusing labs. I didn't know if this came as cleared language or if APHL wrote it but labs are very confused.
I rewrote the guidance that was in the blast please edit so I can send back to Kelly so we can get this straightened out.

(b)(5)

Thanks,
John

**From:** Warren, Melissa <melissa.warren@aphl.org>
**Sent:** Friday, April 5, 2024 1:07 PM
**To:** Barnes, John R. (CDC/NCIRD/ID) <fzq9@cdc.gov>
**Subject:** Respiratory Virus Roundup 23-24:6 | Influenza A(H5) Guidance and Network Funding Opportunity

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# Respiratory Virus Roundup 23–24:6 | *Influenza A(H5) Guidance and Network Funding Opportunity*

## First Case of HPAI (H5N1) Virus Infection in a Person in the US

On Monday, April 1, 2024 The Texas Department of State Health Services reported the first human case of novel avian influenza A(H5N1) in Texas. The patient became ill following contact with dairy cows presumed to be infected with avian influenza. The Centers for Disease Control and Prevention (CDC) also released a statement and is recommending that clinicians consider the possibility of avian influenza A(H5N1) virus infection in people who have symptoms of influenza and relevant exposure history. This includes people who have had close contact with a person with suspected or confirmed avian influenza A(H5N1) infection, affected animals, or unpasteurized milk from dairy farms with suspected avian influenza A(H5N1). CDC has Interim Recommendations for Prevention, Monitoring, and Public Health Investigations available.

- **Specimen Collection and Testing Guidance**
  Public health laboratories are encouraged to review influenza A(H5N1) testing guidance, ensure they have in date testing kits available and connect with their State Veterinarian and State Agriculture department counterparts. Individuals that meet clinical and epidemiologic criteria for influenza A(H5N1) testing, should have a nasopharyngeal (NP) swab and a nasal swab combined with an oropharyngeal swab (e.g., two swabs combined into one viral transport media vial) collected. The individual that tested positive in Texas had conjunctivitis. Individuals with conjunctivitis should have both a conjunctival swab and NP swab collected. The CDC Human Influenza Virus Real-Time RT-PCR Diagnostic Panel – Influenza A(H5) Assay does not have conjunctival swabs included as a specimen type. CDC is working on additional guidance related to conjunctival swabs. In the interim, it is imperative that paired conjunctival and NP swabs are collected if the individual being tested is experiencing conjunctivitis as a symptom.

  Specimens that test positive using the CDC Human Influenza Virus Real-Time RT-PCR Diagnostic Panel – Influenza A(H5) Assay are considered presumptively positive and must be sent to CDC for confirmation. A specimen is only presumptively positive for influenza A/H5 if all three targets (InfA, H5a and H5b) are positive. A result is inconclusive for A/H5 if the test is positive for InfA and has only one of the two H5 markers testing positive. Remember that any specimens that test positive for Influenza A are unsubtypable using the CDC kit should also be sent to CDC for further testing.

- **Specimen Shipping of Presumptively Positive Specimens**
  USDA has agreed that specimens that test presumptively positive may be shipped as Category B specimens until they are confirmed by CDC. Specimens that are to be shipped to CDC should be stored frozen (-20°C or lower) until shipped.

  **Links to Additional Information**

- 2023–24 Influenza Surveillance Testing Guidance
- Highly Pathogenic Avian Influenza A(H5N1) Virus in Animals: Interim Recommendations for Prevention, Monitoring, and Public Health Investigations | Avian Influenza (Flu) (cdc.gov)
- 2022–2024 Detections of Highly Pathogenic Avian Influenza (usda.gov)
- Highly Pathogenic Avian Influenza Emergency Response (usda.gov)
- CDC Press Release

## APHL RFP: Strengthening Respiratory Virus Surveillance Networks

APHL, in conjunction with the CDC's National Center for Immunization and Respiratory Diseases (NCIRD), is soliciting applications to award one-time funding for up to 25 state or local public health laboratories (PHLs) for the purpose of rebuilding and enhancing their respiratory virus surveillance networks. Full details on the project are available in the RFP at www.aphl.org/rfp. Learn more by reviewing the RFP and contact Courtney Demontigny at courtney.demontigny@aphl.org or 240.638.2000 with questions. A letter of intent is due by April 22, 2024 and final proposals (outlined in the RFP) are due by May 10, 2024 at 5:00 pm ET.

This publication was supported by Cooperative Agreement number # NU60OE000104, funded by the Centers for Disease Control and Prevention. Its contents are solely the responsibility of the authors and do not necessarily represent the official views of the Centers for Disease Control and Prevention or the Department of Health and Human Services.

**Association of Public Health Laboratories**
7700 Wisconsin Avenue, Suite 1000 • Bethesda, MD 20814
**P** 240.485.2745 • **F** 240.485.2700

APHL Blog APHL.org Unsubscribe

**From:** Jordan, Douglas E. (CDC/NCIRD/ID)
**Sent:** Fri, 26 Apr 2024 13:32:13 +0000
**To:** Burns, Erin (CDC/NCIRD/ID); Budd, Alicia (CDC/NCIRD/ID); Kniss, Krista (CDC/NCIRD/ID)
**Cc:** McCreavy, Claire (CDC/NCIRD/ID); Spratling, Robin (CDC/NCIRD/ID); Garg, Shikha (CDC/NCIRD/ID); Swyers, Victoria (CDC/NCIRD/ID); Uyeki, Timothy M. (CDC/NCIRD/ID)
**Subject:** RE: TA Request 37867: Clarification on the type of specimens collected to test for HPAI A(H5N1)

Looping in Shikha and Victoria, because I think we are in the process of updating some of these older guidance documents to be consistent with the Interim Guidance. Similar things will need to be done with the new Worker protection guidance.

---

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Friday, April 26, 2024 9:13 AM
**To:** Budd, Alicia (CDC/NCIRD/ID) <acp4@cdc.gov>; Kniss, Krista (CDC/NCIRD/ID) <krk9@cdc.gov>
**Cc:** McCreavy, Claire (CDC/NCIRD/ID) <rua5@cdc.gov>; Spratling, Robin (CDC/NCIRD/ID) <qbm9@cdc.gov>; Jordan, Douglas E. (CDC/NCIRD/ID) <fud7@cdc.gov>
**Subject:** RE: TA Request 37867: Clarification on the type of specimens collected to test for HPAI A(H5N1)

Yea, just tell me exactly what you need us to do.
Thanks,
Erin

---

**From:** Budd, Alicia (CDC/NCIRD/ID) <acp4@cdc.gov>
**Sent:** Friday, April 26, 2024 8:22 AM
**To:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>; Kniss, Krista (CDC/NCIRD/ID) <krk9@cdc.gov>
**Subject:** RE: TA Request 37867: Clarification on the type of specimens collected to test for HPAI A(H5N1)

If we are saying different things at different places on our website we should rectify that or clarify that the intent of the pages is different (if that's the case). It looks like the first link has last updated in June 2023 so if it is outdated, can it be removed?

---

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Thursday, April 25, 2024 4:28 PM
**To:** Kniss, Krista (CDC/NCIRD/ID) <krk9@cdc.gov>; Budd, Alicia (CDC/NCIRD/ID) <acp4@cdc.gov>
**Subject:** FW: TA Request 37867: Clarification on the type of specimens collected to test for HPAI A(H5N1)

Don't know if this person needs additional help.
Erin

**From:** Lawal, Modinat (CDC/IOD/ORR/DSLR) (CTR) <tkz5@cdc.gov>
**Sent:** Thursday, April 25, 2024 3:56 PM
**To:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Cc:** CDC IMS STLT Program Liaisons <eocevent441@cdc.gov>; CDC IMS 2024 Influenza A/H5N1 Response CoS <eocevent289@cdc.gov>; Pierce, Carrie (CDC/IOD/ORR/DSLR) <cby3@cdc.gov>; Green, Jamilla (CDC/IOD/ORR/DSLR) <qwq7@cdc.gov>
**Subject:** TA Request 37867: Clarification on the type of specimens collected to test for HPAI A(H5N1)

Good afternoon,

My name is Modinat Lawal, and I am the Program Liaison Officer for the Jurisdictional Readiness and Response Support Branch (JRR) within DSLR. Through close contact with jurisdictions, JRR receives inquiries from health departments which are triaged and routed through our team who reach out to the appropriate point of contact in CDC. We are reaching out to you today to share an inquiry that we received from the California Department of Public Health that might be causing some public confusion. Please see the full inquiry below.

"I had a question about the recommendations for testing for HPAI.

On Interim Guidance on Testing and Specimen Collection for Patients with Suspected Infection with Novel Influenza A Viruses with the Potential to Cause Severe Disease in Humans | Avian Influenza (Flu) (cdc.gov) it recommends either an NP swab or nasal aspirate swab or nasal + OP swab for testing.

On Highly Pathogenic Avian Influenza A(H5N1) Virus in Animals: Interim Recommendations for Prevention, Monitoring, and Public Health Investigations | Avian Influenza (Flu) (cdc.gov), it is recommended to obtain both an NP and nasal and oropharyngeal swab. It also adds that if a person has conjunctivitis a conjunctival swab should be obtained.

Should we be obtaining both an NP and nasal + OP swab with suspect HPAI cases?"

In response, I shared recommendations within Highly Pathogenic Avian Influenza A(H5N1) Virus in Animals: Interim Recommendations for Prevention, Monitoring, and Public Health Investigations | Avian Influenza (Flu) (cdc.gov) is specific for HPAI as well as the Interim Considerations for Advanced Readiness and Preparedness for Highly Pathogenic Avian Influenza A(H5N1) Virus document.

Please include the HD LNO, Carrie Pierce, on any responses.

Thank you,

Modinat

**Modinat Lawal, MPH, CHES (She/Her/Hers)**
Program Liaison Officer
Jurisdictional Readiness and Response Support Branch (JRR)
Division of State and Local Readiness
Office of Readiness and Response

**Centers for Disease Control and Prevention (CDC)**
Contractor | Goldbelt Professional Services
678.836.4410 Cell
Tkz5@cdc.gov | eocevent441@cdc.gov

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID)
**Sent:** Wed, 24 Apr 2024 15:42:16 +0000
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID)
**Subject:** RE: Timothy sent a message

Ok thanks, will hold off

---

**From:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Sent:** Wednesday, April 24, 2024 11:40 AM
**To:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Subject:** RE: Timothy sent a message

Hi Tim.

I'd suggest not changing. I'm worrying about a situation where a lab skips H1 and H3 testing and go straight to fluA and H5.

(b)(5) APHL has clear guidance on this for PHLs.
Todd

---

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Sent:** Wednesday, April 24, 2024 9:00 AM
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Subject:** RE: Timothy sent a message

I'm making some very minor tweaks to the Technical Report before posting. Are you okay with these edits for clarity (highlighted):

(b)(5)

---

**From:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Sent:** Wednesday, April 24, 2024 8:52 AM

**To:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Subject:** RE: Timothy sent a message

OK – we've been preparing for chance to update NEJM so keep me posted.

---

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Sent:** Wednesday, April 24, 2024 8:51 AM
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Subject:** RE: Timothy sent a message

(b)(5)

For NEJM – it is still in peer-review, I had hoped they would request 48-hour turnaround since they were so eager and requested the submission. I am checking every day.
I'm sure there will be an opportunity to add some revisions even if reviewers have no comments (I have published many times in NEJM and always make changes to the galley proof after acceptance). My preference is to update the text and the Supplementary Appendix as much as possible until right before publication – so yes.
Once I hear back formally from the journal, I'll let you know, fingers crossed.

Thanks,
Tim

---

**From:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Sent:** Wednesday, April 24, 2024 8:44 AM
**To:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Subject:** RE: Timothy sent a message

Hi Tim.

I think the more detailed analysis of USDA sequences (and in the context of human sequence) should go in the other report (link below). I'm afraid its too much detail for the overall Technical Report.

Technical Update: Summary Analysis of Genetic Sequences of Highly Pathogenic Avian Influenza A(H5N1) Viruses in Texas (cdc.gov)

No – no need to add anything about the diagnostic test in the technical report. It's related to only one part of the test so the assay will still work to identify FluA pos unsubtypables but may be 'inconclusive' for H5 at the state lab. Either way, this triggers state to send samples immediately to CDC.

Regarding NEJM… there are some tweaks I'd like to make with USDA sequence public if there is an opportunity for revisions (updated trees). Any news yet about peer review feedback?

Thanks,

Todd

---

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Sent:** Wednesday, April 24, 2024 8:00 AM
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Subject:** RE: Timothy sent a message

Hi Todd- thanks for sharing. Three questions, the first two are priority:
1) Anything you suggest we should add to the Technical Report regarding the USDA sequences – defer to you to add to the attached report.
2) Erin told me last night there are issues with the H5 assay (reagents, target) – anything we should revise in the Technical Report with respect to the CDC H5 assay and H5 diagnostic testing?

3) Lower priority – our case report manuscript is in peer review – any revisions we should make to the manuscript and to the Supplementary Appendix in terms of the USDA sequences and the sequences from the human case?
Thanks,
Tim

---

**From:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Sent:** Wednesday, April 24, 2024 7:27 AM
**To:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Subject:** RE: Timothy sent a message

Hi Tim.

We've had some related questions since the USDA data came out and wrote up the following to describe in more detail. This the text that Sonja mentioned yesterday to add (some of it) to the technical report on the genetic analysis of the Texas human virus.
Todd

The virus that emerged in dairy cattle has been classified as belonging to a genotype of H5N1 viruses that is believed to have emerged in wild birds in the Americas through a series of reassortment events between the original fully Eurasian HPAI H5N1 genotype and pre-existing LPAI American wild bird lineages. This genotype is referred to as genotype B3.13 based on phylogenetic analysis of each of the 8 influenza A gene segments per USDA's genotype classification scheme GitHub - USDA-VS/GenoFLU: Influenza data pipeline to automate genotyping assignment.

- PA, HA, NA and M gene segments have evolved from Eurasian wild bird lineages
- PB2, PB1, NP and NS gene segments have evolved from American wild bird lineages

Viruses with this genome constellation were first identified in wild birds in November 2023 in the U.S. and have been sporadically detected in wild birds, peri-domestic birds and wild mammals (skunk) prior to the first detections in cattle in March 2024. Thus, wild bird gene segments found in B3.13 viruses (that make up the parental branches of phylogenetic trees that gave rise to the cattle outbreak) represent viruses that have diversified since at least November 2023. And, although there is active surveillance for HPAI H5N1 in wild birds in the U.S., sampling of wild birds represents convenience sampling due to the challenges of capture/release or collection of dead or injured birds. Thus, gaps in nucleotide diversity from the November 2023 parental B3.13 virus tree branches to the first detections in cattle are expected because the *actual* diversity among wild birds (that are believed to have initiated the cattle outbreak) is greater than what can be analyzed from available virus sequences.

We recognize that there are a small number of nucleotide differences in some gene segments between the virus sequenced from the human case compared to the currently available cattle sequences. This suggests genetic variation exists among dairy cattle in Texas and other states with confirmed HPAI A(H5N1) virus infection of dairy cattle. Unfortunately, sequence data from presumably infected cattle on the farm where the infected dairy farm worker was exposed are not available for analysis because no samples were collected. These data would likely help fill gaps between the human case and the currently available sequences from samples collected on different farms.

The observation that *the human sample, according to the HA sequences, is found on the parental branch of the current outbreak, but according to PB2, it clusters together with the current outbreak (and appears to be arising from the base of the branch)* most likely reflects the inherently different mutation rates between the influenza A HA gene and internal polymerase genes, such as PB2. The HA gene typically experiences higher mutation rates than polymerase genes due to greater selective pressure on the HA surface protein in comparison to internal genes, which are more evolutionarily constrained to maintain optimal replication fidelity.

We do expect that some of these gaps in nucleotide diversity will be filled as additional sampling from wild birds and cattle is performed and as sequence data are generated.

---

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID) in Teams <noreply@gcc-email.teams.microsoft.com>
**Sent:** Wednesday, April 24, 2024 1:34 AM
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Subject:** Timothy sent a message

**Hi,**

Your teammates are trying to reach you in **Microsoft Teams**.

TU **Timothy sent a message in chat**

Todd - do you agree with Worobey's assessment that the human case is an outlier and not related to the cow viruses?...

Reply in Teams

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**From:** Uyeki, Timothy M. (CDC/NCIRD/ID)
**Sent:** Wed, 24 Apr 2024 11:59:47 +0000
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID)
**Subject:** RE: Timothy sent a message
**Attachments:** #1033 H5N1 Technical Report updated April 23 2024 revised CLEAN.docx

Hi Todd- thanks for sharing. Three questions, the first two are priority:
1) Anything you suggest we should add to the Technical Report regarding the USDA sequences – defer to you to add to the attached report.
2) Erin told me last night there are issues with the H5 assay (reagents, target) – anything we should revise in the Technical Report with respect to the CDC H5 assay and H5 diagnostic testing?

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Thanks,
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**From:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Sent:** Wednesday, April 24, 2024 7:27 AM
**To:** Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Subject:** RE: Timothy sent a message

Hi Tim.

We've had some related questions since the USDA data came out and wrote up the following to describe in more detail. This the text that Sonja mentioned yesterday to add (some of it) to the technical report on the genetic analysis of the Texas human virus.
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The observation that *the human sample, according to the HA sequences, is found on the parental branch of the current outbreak, but according to PB2, it clusters together with the current outbreak (and appears to be arising from the base of the branch)* most likely reflects the inherently different mutation rates between the influenza A HA gene and internal polymerase genes, such as PB2. The HA gene typically experiences higher mutation rates than polymerase genes due to greater selective pressure on the HA surface protein in comparison to internal genes, which are more evolutionarily constrained to maintain optimal replication fidelity.

We do expect that some of these gaps in nucleotide diversity will be filled as additional sampling from wild birds and cattle is performed and as sequence data are generated.

---

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID) in Teams <noreply@gcc-email.teams.microsoft.com>
**Sent:** Wednesday, April 24, 2024 1:34 AM
**To:** Davis, Charles (Todd) (CDC/NCIRD/ID) <eou8@cdc.gov>
**Subject:** Timothy sent a message

**Hi,**

Your teammates are trying to reach you in **Microsoft Teams**.

TU

**Timothy sent a message in chat**

Todd - do you agree with Worobey's assessment that the human case is an outlier and not related to the cow viruses?...

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(b)(5)

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(b)(5)

(b)(5)

(b)(5)

(b)(5)

**From:** Uyeki, Timothy M. (CDC/NCIRD/ID)
**Sent:** Fri, 19 Apr 2024 21:12:45 +0000
**To:** Burns, Erin (CDC/NCIRD/ID)
**Subject:** RE: TIM/SONJA final sign off please RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

Reviewing now

---

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Friday, April 19, 2024 5:05 PM
**To:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>; Olsen, Sonja (CDC/NCIRD/ID) <sco2@cdc.gov>; Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Cc:** Jhung, Michael (CDC/NCIRD/ID) <dvk3@cdc.gov>; CDC IMS 2024 Influenza A/H5N1 Response Clearance <eocevent519@cdc.gov>; Denty, Robert (RED) (CDC/NCIRD/ID) <otl1@cdc.gov>
**Subject:** TIM/SONJA final sign off please RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you
**Importance:** High

---

**From:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Sent:** Friday, April 19, 2024 5:04 PM
**To:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>; Olsen, Sonja (CDC/NCIRD/ID) <sco2@cdc.gov>; Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Cc:** Jhung, Michael (CDC/NCIRD/ID) <dvk3@cdc.gov>; CDC IMS 2024 Influenza A/H5N1 Response Clearance <eocevent519@cdc.gov>; Denty, Robert (RED) (CDC/NCIRD/ID) <otl1@cdc.gov>
**Subject:** Re: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

Thanks, Erin. We are hoping to get back to the reporter today. Please let me know once this is complete so I can send to OC.

Thank you,

Jasmine Reed
Public Affairs Specialist
National Center for Immunization and Respiratory Diseases
Centers for Disease Control and Prevention
(404) 754-7385

---

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Friday, April 19, 2024 3:51:39 PM
**To:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>; Olsen, Sonja (CDC/NCIRD/ID) <sco2@cdc.gov>; Uyeki, Timothy M. (CDC/NCIRD/ID) <tmu0@cdc.gov>
**Cc:** Jhung, Michael (CDC/NCIRD/ID) <dvk3@cdc.gov>; CDC IMS 2024 Influenza A/H5N1 Response Clearance <eocevent519@cdc.gov>; Denty, Robert (RED) (CDC/NCIRD/ID) <otl1@cdc.gov>
**Subject:** RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

Jasmine, I had some suggestions, but I'm looping in Sonja Olsen and Tim Uyeki for final review. (Also Mike for response ADS if he has time.)
Thanks,
Erin

---

**From:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Sent:** Friday, April 19, 2024 3:31 PM
**To:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Subject:** RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

Can I run this by you:

**Why is CDC limiting testing recommendations to exposed people with certain symptoms? We know that birds and mammals can be infected asymptomatically. Scientists say they need this information to understand the potential scope of human infection.**

(b)(5)

(b)(5)

Thanks,

Jasmine

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Friday, April 19, 2024 12:18 PM
**To:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Subject:** RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

No, I it's really because most H5 patients globally have been symptomatic. The below is tangential. We think we are getting the people who are actually infected.

**From:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Sent:** Friday, April 19, 2024 12:13 PM
**To:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Subject:** RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

Thanks. One last question, what is the bottom line as to why we do not recommend testing asymptomatic people?

Would it be this sentence:

(b)(5)

Thanks,
Jasmine

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Friday, April 19, 2024 12:10 PM
**To:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Subject:** RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

You can, but they are asking about the denominator, which we don't know.

**From:** Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Sent:** Friday, April 19, 2024 11:52 AM
**To:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Subject:** RE: Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

Erin,

For this question, can we use the below:

(b)(5)

**CDC is aware of 23 exposed people in affected states that have been tested.**

Thanks,

Jasmine Reed
Public Affairs Specialist
National Center for Immunization and Respiratory Diseases
**Centers for Disease Control and Prevention**
(404)754-7385

**From:** Burns, Erin (CDC/NCIRD/ID) <eub5@cdc.gov>
**Sent:** Friday, April 19, 2024 10:47 AM
**To:** Denty, Robert (RED) (CDC/NCIRD/ID) <otl1@cdc.gov>; Reed, Jasmine (CDC/IOD/OC) <pvz1@cdc.gov>
**Subject:** Burns, Erin (CDC/NCIRD/ID) shared "H5N1 Flu" with you

## Burns, Erin (CDC/NCIRD/ID) invited you to access a file

Jasmine, This is response cleared, please move it forward in clearance.
Thanks,
Erin

H5N1 Flu

This invite will only work for you and people with existing access.

Open

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CDC Centers for Disease Control and Prevention

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