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DEPARTMENT OF HEALTH AND HUMAN SERVICES

PUBLIC HEALTH SERVICE

FOOD AND DRUG ADMINISTRATION

CENTER FOR BIOLOGICS EVALUATION AND RESEARCH

VACCINES AND RELATED BIOLOGICAL PRODUCTS ADVISORY COMMITTEE

MEETING

Friday, January 29, 1999

The meeting took place in Versailles Rooms I II, Holiday Inn, Bethesda, MD, at 8:30 a.m., Patricia L. Ferrieri, M.D., Chair, presiding.

PRESENT:

PATRICIA L. FERRIERI, M.D., Chair NANCY CHERRY, Executive Secretary REBECCA E. COLE, Member (telephonically) ROBERT S. DAUM, M.D., Member KATHRYN M. EDWARDS, M.D., Member MARY K. ESTES, Ph.D., Member HARRY B. GREENBERG, M.D., Member CAROLINE B. HALL, M.D., Member ALICE S. HUANG, Ph.D., Member KWANG SIK KIM, M.D., Member STEVE KOHL, M.D., Member GREGORY A. POLAND, M.D., Member DIXIE E. SNIDER, Jr., M.D., Member ROBERT BREIMAN, M.D., Invited Participant NANCY COX, Ph.D., Invited Participant THEODORE EICKHOFF, M.D., Invited Participant CHARLES HOKE, Jr., M.D., Invited Participant EDWIN KILBOURNE, M.D., Invited Participant DR. ROLAND LEVANDOWSKI, FDA Participant KEIJI FUKUDA, M.D., MPH, Presenter LINDA C. CANAS, Presenter KUNIAKI NEROME, Ph.D., Presenter

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MARIA ZAMBON, MB, BS, MA, Ph.D., Present This transcript has not been edited or corrected, but appears as receiv from the commerical transcribing service. Accordingly the Food and Drug Administration makes no representation as to its accuracy.

PRESENT: (Cont'd)

DAN OFFRINGA, Presenter
GREGORY M. SLUSAW, Ph.D., Presenter
JAQUELINE KATZ, Ph.D., Presenter
JOHN J. TREANOR, M.D., Presenter
JOHN WOOD, Ph.D., Presenter
TAOUFIK MABROUK, Ph.D., DMV, Presenter

ALSO PRESENT:

KATHRYN ZOON, Ph.D.
DR. BETHANIE WILKINSON
CHARLES W. WHITAKER, Ph.D.

PUBLIC COMMENT:

FREDERICK RUBEN, M.D.

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1	P-R-O-C-E-E-D-I-N-G-S
2	8:38 a.m.
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4	
5	Thank you. I am Patricia Ferrieri from the University
6	of Minnesota, and I am Chair of this committee and
7	have been for a long time actually. This is my last
8	time as chair here, so it is a very special meeting
9	for me.
10	I would like to gtone
11	I would like to start the meeting by having members of the committee and other guests
12	
13	sitting at the table to introduce themselves, name and
14	institution. We will start with Dr. Greenberg.
	DR. GREENBERG: Harry Greenberg, Stanford
15	University and the Palo Alto VA Hospital.
16	DR. DAUM: I am Robert Daum from the
17	University of Chicago in Chicago.
18	DR. HUANG: Alice Huang from the
19	California Institute of Technology, Pasadena,
20	California.
21	DR. KOHL: Steve Kohl, University of
22	California, San Francisco.
23	DR. SNIDER: Dixie Snider, Centers for
4	Disease Control and Prevention, Atlanta

DR. ESTES: Mary Estes, Baylor College of

1	Medicine, Houston, Texas.
2	DR. KIM: Kwang Sik Kim, Children's
3	Hospital, Los Angeles, California.
4	DR. EDWARDS: Kathy Edwards, Nashville
5	Tennessee, Vanderbilt University.
6	DR. EICKHOFF: Ted Eickhoff, University of
7	Colorado, Denver.
8	MS. CHERRY: Nancy Cherry, FDA.
9	DR. HALL: Caroline Hall, University of
10	Rochester, New York.
11	DR. HOKE: Charles Hoke, Military
12	Infectious Diseases Research Program, Ft. Detrick.
13	DR. POLAND: Greg Poland, Mayo Clinic, the
14	other Rochester.
15	DR. BREIMAN: Rob Breiman, National
16	Vaccine Program Office.
17	DR. KILBOURNE: Edwin Kilbourne, New York
18	Medical College, Valhalla.
19	DR. LEVANDOWSKI: Roland Levandowski,
20	Center for Biologics Evaluation and Research,
21	Bethesda.
22	DR. COX: Nancy Cox, Influenza Branch,
23	CDC, Atlanta.
24	CHAIRPERSON FERRIERI: Thank you very
25	much. I would like to turn it over to Nancy Cherry

for any announcements and then we will move on.

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MS. CHERRY: The first thing I would like to do is welcome all of you to this annual January meeting, and to let you know that my conflict of interest statement is mercifully short this time. This announcement is made a part of the record at this meeting of the Vaccines and Related Biological Products Advisory Committee on January 29, 1999. Drs. Ada Adimora and Dianne Finkelstein are unable to be with us today. Ms. Rebecca Cole is connected to this room by teleconference. And I might add that on your roster of participants you will see the name of Nancy Ms. Sander had graciously accepted the Sander. invitation to stand in for Ms. Cole, but then we were able to hook up Ms. Cole by teleconference. So Ms. Sander will not be here.

Pursuant to the authority granted under the committee charter, the Director for the Center of Biologics Evaluation and Research has appointed Drs. Rob Breiman, Theodore Eickhoff, Edwin Kilbourne and Charles Hoke as temporary voting members.

Based on the agenda made available, it has been determined that all committee discussions at this meeting for the influenza virus vaccine formulation for the years 1999/2000 and an update on influence A

H5N1 viruses present no potential for a conflict of 1 2 interest. In the event that the discussions involve specific products or firms not on the agenda for which 3 FDA's participants have a financial interest, the 4 5 participants are aware of the need to exclude themselves from such involvement and their exclusions 6 will be noted for the public record. With respect to 7 all other meeting participants, we ask in the interest 8 of fairness that you address any current or previous 9 financial involvement with any firm whose products you 10 11 wish to comment on. And that is the end of the 12 statement. CHAIRPERSON FERRIERI: Thank you, Nancy. 13 14 I am sorry I neglected to announce you, Rebecca Cole. 15 Are you still with us? 16 MS. COLE: I am here. 17 CHAIRPERSON FERRIERI: Thank you. Ms. Cole is our consumer representative. 18 We will start the program with some remarks from Dr. Kathy Zoon from 19 20 FDA, Director of CBER. 21 DR. ZOON: Good morning. This is a job 22 that gives me great pleasure but also some remorse because today we are seeing some members of our 23 24 advisory committee for the last time, at least in 25 their capacity at this time. Hopefully many of them

will continue to work with CBER as consultants in dealing with future issues.

I would like to take a few minutes to thank each of these individuals for their service to our advisory committee, particularly for their sage advice that has been so helpful to CBER on so many issues. As we all know, the regulation of vaccines is filled with many difficult issues. This committee and committees before have risen to the occasion to deal with products as they go through the investigational process, dealing with such complex issues as looking at tumor cell lines as vaccine substrates, looking at some of our more recent discussions that we had at the last advisory committee. They also dealt with many difficult issues regarding adequacy of data; example, with the rotavirus and the lyme vaccine. They dealt with other issues with respect to safety such as looking at the issues regarding reverse transcriptase in a number of vaccines.

I think I would say that the advice of this committee has always been wise, filled with knowledge and science that have helped the agency and will continue to do so, and these four members that I am going to recognize today have played a very special part.

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First I would like to take the time and ask Greg Poland to come up. Dr. Poland is from the Mayo Clinic and Foundation. I would like to thank him for his service and we have a memo and plaque for you. Thank you very much.

I would now like to ask Dr. Caroline Hall from the University of Rochester School of Medicine.

Caroline, please come up.

And to you, Rebecca, on the phone, who is telecommuting today, I would like to thank you for your service over the past four years. For many of you who may not know, Ms. Cole came to this advisory committee following the work she had done to have warnings added to corticosteroid labeling relative to chicken pox and measles virus vaccines. I think she has done a wonderful job in providing her input on the varicella vaccine as we considered it for licensure.

Ms. Cole, thank you. I heard you have your plaque.

We will miss you.

And last but not least, our Chairperson, Dr. Ferrieri, we want to thank you very much for your service. She has been a member of our advisory committee from 1987 to 1990 and then from 1994 to the present. You are an honorary CBER person, for heaven's sake. And she has been our distinguished

chair since 1996. I personally, speaking for myself and CBER, want to thank you. You have led this group very artfully, focused, getting the answers to very difficult questions, and we will miss you. Thank you, Pat.

If I could take a minute or two extra, Madam Chair, I just want to say a few comments that we have this year lost a very dear member of our CBER family, who we are desperately trying to get as an SGA. Dr. Hardegree retired this year. For those of you who know Carolyn, and I think everybody in this room does, she will be sorely missed. Carolyn has given 37 years of dedicated service to the Public Health Service, many of which have focused on the vaccines and both the safety and efficacy of vaccines given to the public and especially our children. And I would like to take this moment that we all recognize Carolyn, because I know how strongly you feel about her. So thank you.

CBER is actually doing a search for a new director of the Office of Vaccines, but we have selected an acting director. Dr. Bill Egan will be the acting director for the Office of Vaccines. Bill, can I ask you to stand up? And just recently we selected the acting deputy director for Vaccines, Dr.

Norman Bayler. Norman, would you please stand? 2 Thank you very much. With that, I will turn it over to the chair. Thank you very much. 3 4 CHAIRPERSON FERRIERI: Thank you very much, Dr. Zoon. I will turn it back to Ms. Cherry 5 now, who may have other announcements and deal with 6 7 the Open Public Hearing. 8 MS. CHERRY: I have no other announcements 9 at this time, except to announce an open public 10 Is there anyone in the audience that would 11 like to make a statement? If not, then we will 12 proceed with the meeting. 13 CHAIRPERSON FERRIERI: Thank you. We will move then into Session 1 on Influenza Virus Vaccine 14 15 formulation and I will turn it over Dr. Levandowski. Roland? 16 17 DR. LEVANDOWSKI: Thank you, Dr Ferrieri. 18 Good morning, everybody. I too would like to thank 19 Dr. Ferrieri for the leadership she has given us on 20 the committee over the past several years. We very 21 much appreciate it and we are going to miss her when she is no longer in the chair. But we hope that we 22 23 will be working with her in some capacity, as was 24 mentioned -- as a consultant or perhaps come back to

our committee one day.

I think everybody knows why we are here this morning. And if somebody could turn on the slides over there perhaps and we might need to dim the lights. I will get started. I will apologize in advance. I know that some of my slides are not going to be very visible for people who are way at the back of the room. And I would encourage you all, if you really want to see some of these things, to move as far forward as you can, understanding that there are some obstructions, like other people sitting in the front row.

As everybody knows, we are here today to begin the process of selecting the influenza virus strands that we will include in the vaccines that will be prepared for the 1999/2000 season. As you are also probably aware, the match between the antigen and the influenza vaccine and the circulating strains is probably the most important feature in the potential efficacy of inactivated influenza vaccines.

The question to be answered by the committee today is shown in this slide. That question is, what strain should be recommended for the antigenic composition of the 1999/2000 inactivated influenza virus vaccine? In order to answer that question, information is needed, and quite a lot of

information is needed. We are prepared to supply some of that information this morning to assist in formulating the answer. The data that are needed include most importantly information on the appearance of new influenza viruses. If new viruses are identified, we also need to know how widespread they have become. This helps greatly in judging the urgency and considering changing a component of the vaccine to know how broad the effect is of those new strains that are being identified.

demonstrate the capability for broad dissemination, it is important to know whether or not the current vaccines are likely to provide some measure of protection. And if it appears likely that current vaccines could be suboptimal, then it is still necessary to know if we have any virus strains that will grow well enough to permit manufacture of vaccine within the current constraints. Actually, I am going to need the overhead projector for just one minute if I could get somebody to put it back up here.

The vaccines that are being prepared now must be available by early fall to insure administration of vaccine before the onset of influenza season in winter months. This overhead

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information about how much influenza some vaccine is being produced. The production and the distribution of vaccine seen from a manufacturer's viewpoint is one of having continuous deadlines, and failure at any point can potentially derail the efforts to deliver vaccine, which currently reached really staggering numbers of doses. presented information last year to indicate that I thought the production capacity was plateauing at about 80 million doses. But as you can see from this slide, what we are projecting for this current season is that approximately 90 million doses of trivalent and inactivated vaccine have been produced. appears from feedback that we have had throughout the year that the demand for influenza vaccine is actually still increasing. So I guess the expectation is at this point that there may be further increases in production capability to keep up with that demand, at least we hope that will be true.

The balancing act that is required to have as much information as possible to insure that we get the correct strains in the vaccine also has to be balanced with the need by the manufacturers to get started in manufacturing. So we are at that point in the year where there is some urgency to get the

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manufacturers going and they need to know at least one of the strains to use in the vaccine today.

During the past year, recommendations have been made for the vaccines that are currently in use, and I would just like to mention a few other things that are happening now in the influenza world. In the past year, the World Health Organization has made formal what was previously an informal recommendation for influenza vaccines to be used in the Southern Hemisphere. That development reflects the growing global demand for influenza vaccine, not only in the United States but everywhere the demand is growing, and also a recognition of the utility of influenza vaccines in reducing morbidity and mortality.

With the now twice yearly formal review of influenza virus vaccines, WHO has committed to updating its recommendation two times a year to help support the orderly and coordinated global efforts that go on to produce and use influenza vaccines. One effect of this activity is to enhance the continuing efforts to improve and insure safe and effective influenza vaccines. And currently recommendations by the WHO for both hemispheres are the same as what our committee's recommendations were for the past year for vaccines. That includes an A/Sydney/5/97 like H3N2

virus, an A/Beijing/262/95 like H1N1 virus, and a B/Beijing/184/93 like virus, which for everybody means a B/Harbin/7/94 like strain.

We will begin this morning, as we always do, with information on surveillance. We know that the schedule is quite tight, so I will just remind the speakers that we do want to try to stay on target in terms of timing or for presentations. We would expect that the committee may have questions as we go along with the presentations, and we would certainly want to answer all of the concerns of the committee as we are able to. So Dr. Keiji Fukuda from the Centers For Disease Control and Prevention is going to give us some information on U.S. Surveillance.

CHAIRPERSON FERRIERI: Before you start, Dr. Fukuda, I would like to mention that the Chair will only recognize people who have hands up, and then when you are called upon, you will announce your name because everything is transcribed. This may sound rigid, but it is the best for CBER and recording.

DR. FUKUDA: Good morning. Thank you, Dr. Ferrieri, and thank you, Dr. Levandowski. Just to remind everybody about the past season. The past season in the United States, the 1997/1998 season, was predominantly an influenza A/Sydney season, and it was

a relatively severe season. I think the other thing that I think people remember, at the same time this year, we had just come out of the H5N1 outbreak in Hong Kong, so I will pick up from there.

So we were hoping for a quiet summer, but really we had a fairly eventful summer in the United States. And the most eventful thing was that there was really a quite large outbreak of Influenza A in Alaska and the Yukon Territory. Just to put this in context, the population of Alaska is about 652,000 people, and it is a quite young population with a median age of 32. It also has a very large tourist season which goes from May to September, during which about 840,000 people come into the state and up to about 70,000 people per week. About one-third of these tourists enter by cruise ship, and last year there were about 28 ships entering the Alaska region with about 1,000 to 2,000 passengers per ship. quite different from the native population, the median age of these tourists is about 62 years.

Now beginning in May, there was a very large outbreak of Influenza A in the state. You can see it began sometime about May. This line here tells you when the cruise ships entered into the area and when they left, and you can see that this outbreak

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went over a period of about five months and it really didn't come to an end. Basically the ships just left the region and then the outbreak came to an end.

Now the cases -- there are about 5,350 cases of acute respiratory illness which were counted by a rapidly set-up surveillance system. Most of these cases, 74 percent, were located in tourists and another 24 percent in tourism workers. Only about 2 percent of the cases were identified in Alaska residents. 420 clinical specimens were collected during the investigation and 99 respiratory viruses were isolated, of which 66 were Influenza A, and of these, 33 were subtyped and all these were A/Sydney viruses. The remainder viruses were predominantly things like rhinoviruses.

Now it is a little bit unclear how often this sort of outbreak occurs, but at least if we look at data from 1997 from ships leaving the Alaska region and then compare it with 1998 data, we can see that there was a much larger number of cases occurring in 1998 and the relative risk was about 2.2.

So in summary, we had a large outbreak of Influenza A/Sydney virus in Alaska and the Yukon Territory. This outbreak lasted well over 5 months and it involved predominantly over-land and sea

travelers. And basically this unusual outbreak was sustained by a continuous influx of people into the region.

Now there are several things that are very interesting about this outbreak, but I will just point to two of them that we are working on at CDC and The first question is whether large elsewhere. tourist groups -- whether this kind of outbreak and others which have been reported recently indicate that large tourist groups are at increased risk for exposure to influenza during the off-season or during the summertime, predominantly because you have a mix of international travelers coming together. second question is also whether these large tourist groups are an important way that influenza is being spread. I will just note here that the cases occurred in people from over 47 countries and all 50 states, and these people went back to their sites of origin.

Before I go on to this slide, I want to point out that this investigation required a huge effort and it was really spearheaded by the Division of Quarantine and also Health Canada with the assistance of the Influenza Branch in the State of Alaska. So you can see that between May and September, we had this large outbreak going on in

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Alaska. In addition, we were having reports of outbreaks going on in Montana, Florida, Tennessee and California, and these outbreaks were leading us to wonder whether we are going to see unusually heavy and early activity during the fall time. But in fact, activity in the fall time was relatively quiet in terms of outbreak reports to CDC. Although we can now see that in December and January, the number of outbreaks being reported to CDC have picked up.

Now in terms of the viruses which have been collected through the WHO laboratory system, again we can see that it has been somewhat of a mixed The green bars are Influenza A viruses which have not been subtyped. The red bars represent Influenza A H3N2 viruses and the yellow bars represent Influenza B viruses. So, again, it has predominantly an Influenza A season, and of the viruses which have been subtyped, predominantly Influenza A H3N2 Sydney viruses. But about 18 percent of the viruses have been Influenza B viruses.

In parallel to this increasing number of virus isolations for influenza, we can see that the activity being reported by sentinel physicians or the activity being reported by the state epidemiologists have picked up in the country also. So as of the end

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of last week, we had 8 states and New York City reporting widespread influenza activity in their states or influenza-like illness activity, and another 21 states reporting regional activity in their states. And then again in parallel to this sort of reporting, we see that among the sentinel physicians we have had increased activity reported in the last few weeks. So we are now having about 3 percent influenza-like activity being reported by the Sentinel physicians.

Now this map here shows you which states are reporting elevated levels of influenza activity, and down here we can see that in red, these states here, these are the states which are reporting widespread activity. The states in purple are the states which are reporting regional activity. So you can see that activity really is spread out throughout the country. We are seeing activity on the Eastern seaboard and on the Western seaboard, but also in the middle of the country.

In terms of mortality -- pneumonia and influenza-related mortality, these measurements have been bouncing around the baseline, but so far we remain below the threshold, the so-called epidemic threshold. So unlike last year, we have not yet seen a sustained elevation in pneumonia and influenza-

related mortality. So I think that sums up 1 activity in the country so far. 2 Are there any 3 questions? 4 CHAIRPERSON FERRIERI: Yes, Dr. Edwards? 5 DR. EDWARDS: Could you comment whether there appeared to be any efficacy of influenza vaccine 6 for the travelers in the outbreak? Whether there 7 appeared to be any protection afforded from vaccine 8 from the year before or was that looked at in the 9 10 outbreak? 11 DR. FUKUDA: It is being looked at. There are actually a large number of cohorts which were 12 followed or retrospectively followed in that outbreak 13 investigation. Those analyses are still going on. I 14 suspect it will take some number of weeks before those 15 data are analyzed, but it will be looked at. 16 17 CHAIRPERSON FERRIERI: Yes, Dr. Kohl? 18 DR. KOHL: Kohl, UCSF. We are getting reports in California and Seattle and Portland of many 19 individuals having influenza-like illnesses after 20 previously being immunized with the current vaccine. 21 Are you getting any reports similar to that or do we 22 have any current efficacy data going on right now? 23 24 DR. FUKUDA: Yes. Every year we get a number of similar reports, and California and some 25

other states have called us with questions about that. 1 There has been a couple of outbreak investigations in 2 which preliminary vaccine effectiveness estimates have 3 4 been made. There was an outbreak actually in 5 California. and I believe among the staff the effectiveness estimates were somewhere in the range of 6 7 about 45 to 55 percent. But, again, these are pretty preliminary estimates from small outbreaks. But that 8 is about the only data that we have so far. One thing 9 10 to note though is that last year CDC was able to obtain data from three HMO's to look retrospectively 11 12 over the season to see what vaccine effectiveness estimates there were for the entire season, and we 13 will be doing that again for this season. But those 14 data won't be available until the summertime. 15 16 CHAIRPERSON FERRIERI: Dr. Kilbourne? 17 DR. KILBOURNE: Ι think the Alaska

DR. KILBOURNE: I think the Alaska epidemic is fascinating because it is not an Alaska epidemic. In other words, the venue is probably very unimportant, don't you think, from your data? It is a cruise ship phenomenon and a crowding phenomenon. Do you think Alaska has anything to do with it or it could have been any other port with that level of tourism?

DR. FUKUDA: Yes, I think you are right,

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	ed: I chink that one of the things which has
2	characterized the travel industry is that there is a
3	really rapidly increasing number of people who go on
4	these sorts of cruises and there are large
5	conglomerations of people which get together, and I
6	think that this probably could have happened anywhere.
7	I think the really important characteristic is that
8	you just have a lot of people coming together from a
9	lot of parts of the globe at one place. In fact, we
10	are seeing the same kind of activity aboard some ships
11	in other parts of the world right now.
12	CHAIRPERSON FERRIERI: Yes, Dr. Hall?
13	DR. HALL: Dr. Hall, University of
14	Rochester. I am interested in the B isolates that you
15	gotten. In my lab, we have had quite a few B isolates
16	recently, much more than what I expect. And you
17	mentioned that there are 18 percent, I believe, that
18	you know. Are any of those in outbreaks and do you
19	know what strain they are?
20	DR. FUKUDA: Why don't I defer that to
21	Nancy, because I think she will be covering that in
22	detail.
23	DR. HALL: Okay. Thank you.
24	CHAIRPERSON FERRIERI: Any other
25	questions? Dr. Daum?

DR. DAUM: Bob Daum, University I would like to hear your comment and Chicago. perhaps Dr. Levandowski's as well, but I was pretty surprised by the shape of the vaccine uptake curve in that it looked like it was flat for many years and now almost going up exponentially. And I wonder if you or Dr. Levandowski would care to comment on what the factors are that have put the vaccine uptake that high and that big an increase.

Well, Roland may want to DR. FUKUDA: comment on this also. I think that that was a vaccine production curve. But I think that one of the big things which has really happened in terms of vaccine uptake is that the vaccination levels have really increased among people 65 years and above. And probably one of the big things which has driven that is that Medicare has started paying for those vaccinations. But in the latest survey data from the BRFSS survey, vaccination levels in the elderly have risen up to about 65.5 percent. This is really a pretty marked increase over the past decade. That is probably what is largely driving that sort of increased production. Roland?

DR. LEVANDOWSKI: Yes, I will just comment on that also. I agree, I think that is right.

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HCFA demonstration project for making 1 vaccine a Medicare benefit started around 1990, and it 2 is just at that point that the production of vaccine 3 started to go up. I think that has been a very major 4 force behind it. Permitting vaccine manufacturers to 5 increase their production because they know that there 6 will be a demand there to take the vaccine that they 7 are producing. 8 The slide that I showed was for production and not for use of vaccine, so those two 9 10 curves may be different. CHAIRPERSON FERRIERI: Dr. Breiman? 11 Did 12 you have your hand up also, Dr. Poland? DR. POLAND: Keiji, do you think this was 13 14 a reporting and surveillance phenomena? 15 DR. FUKUDA: You mean Alaska? DR. POLAND: That this has been happening 16 on cruise ships all along and for some reason we just 17 picked up on it, or is this something new? 18 19 DR. FUKUDA: Well, I think it is a little bit of both. When you go back to the literature -- in 20 fact, back to some of the earlier pandemics, you can 21 see that in the Alaska region, outbreaks were reported 22 23 aboard ships. They are not reported very often, but 24 it has been reported in the past. But again, keeping with Ed's observation, the travel industry 25

really has been changing a lot in that you are having more and more people assemble for these sorts of voyages. And in a sense someone has coined the phrase that these are virtual populations because they come together for a short period of time and then they disperse again. But I think that with the advent of air travel and so on, you can have people coming from all over the world and getting together for a short period of time and then dispersing. So I think that these outbreaks are not unique, but we probably will be hearing about them more and more often.

DR. POLAND: Your observation brings up my second question, and that is having never been on one, I kind of assume people come together for this cruise and then they are gone. What sustained this over 5 months? Is it the workers?

DR. FUKUDA: Well, I think that --

DR. POLAND: That is kind of an unusual --

DR. FUKUDA: It was probably a little bit of a shifting site of transmission in that the early transmission in the outbreak appeared to be occurring predominantly on land. And then some of the transmission began shifting over to ships as you had outbreaks occurring on ships. And I think that the tourism workers, the people working in staffing hotels

and the crews on these ships are one of the links between this large number of people coming in and out, and we think that they are probably an important part of the link, but I think that is not really so clear.

CHAIRPERSON FERRIERI: Dr. Hall?

DR. HALL: I noticed -- I read somewhere that the age of those on cruise ships has recently -- the average age has gone up, and there was obviously a great dichotomy in the age that you noticed on land and whatever. Do you know the vaccination status then? Since many of these must have been at least eligible for the routine immunization.

DR. FUKUDA: For the Alaska outbreak, again as part of those cohort studies, I think those data were collected, but I don't know what they were. But that dichotomy in age also brings up a potential artifact for this kind of outbreak in that it may be that the people who are older are a little bit more likely to the physicians who were to go the surveillance physicians and the younger people may have stayed away. So that apparent dichotomy between the population and the travelers may be a little bit less than what it appears. But nonetheless, we do think that it was predominantly located among the tourists.

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CHAIRPERSON FERRIERI: Dr. Snider and then Dr. Edwards. DR. SNIDER: Dixie Snider, CDC. another point of information. Not only has the cruise industry been growing quite rapidly, but the size of the ships has also been increasing. So you have much larger numbers of people on cruise ships these days than used to be the case. So that is another factor, I think, that needs to be considered. CHAIRPERSON FERRIERI: Dr. Edwards?

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DR. EDWARDS: With the remarkable increase in the number of people over 65 receiving vaccine, is there any data from the CDC that suggests that the morbidity and mortality with influenza related illnesses is indeed going down, or is it staying the same?

DR. FUKUDA: This is one of the really tough questions. I think that this has been a really difficult question to answer for a couple of different reasons in that the hospitalizations and the mortality that you see from season to season tends to vary so much for factors unrelated to vaccination. recently there has been some -- particularly France, some groups which have looked at how you might calculate how many deaths and hospitalizations are

being averted because of vaccination programs. 1 that is one of the things that we are going to be trying to do this summer to begin calculating those figures for the United States. I mean, this would take me almost a half an hour to go into to just explain why we think that this is a reasonable approach for trying to get at what you are asking. it is a roundabout way of saying that we are going to try to begin to get at that. CHAIRPERSON FERRIERI: If there are no further questions, then we will move on. Dr. Greenberg?

DR. GREENBERG: Just a follow-up on Dixie's point. Is there -have you found correlation between either size of cruise ships or duration of cruising? Is there a time period under which this doesn't happen and are you seeing similar things in airplanes?

DR. FUKUDA: I don't think that we can really tease out duration and size of ships, because most of these cruise ship vacations last about one That is the average time. What you typically see is that the outbreak begins to take off and then people leave the ship. So we couldn't really tell what would happen to a single ship if it were out there for

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three or four weeks.

In terms of airplanes, no, we haven't -- again, there have clearly been reports of outbreaks of influenza occurring on airplanes. Notably, there was an airplane which developed engine trouble and was parked on the ground for some number of hours and there was an outbreak which occurred among the passengers, but we haven't had the same kind of reports that we have had from the cruise industry.

CHAIRPERSON FERRIERI: Any final questions for Dr. Fukuda? Thank you very much. We will move on then. Dr. Levandowski?

DR. LEVANDOWSKI: Okay. We now will hear from Dr. Nancy Cox from CDC on world surveillance strain characterization and molecular analysis of the strains.

DR. COX: Good morning. It is a pleasure to be here once again. I think we will start with the first overhead. I will try to condense what is really a tremendous amount of data that has been developed over the past year in an understandable, palatable way. There really is so much information that we have to leave out of what we present today in order to get it packaged so that it really can be understood. So I hope that all of you will ask questions, even

interrupt me in the course of presenting a particular overhead, so that we can clarify things as we go along.

As Roland has already mentioned, our vaccine strain selection is dependent on our detection of the emergence and spread of variant viruses, and we are looking for variant viruses by testing, using hemagglutination inhibition tests with post-infection sera. For anyone new in the room, these particular methods have been used for many years and have been found to be sensitive for detecting differences in strains which are significant epidemiologically.

In the past 10 to 15 years, we have also begun to rely fairly heavily on sequence data of the hemagglutinin gene. We find that these data are very, very useful as an adjunct to the serologic data. They help define precisely what relationships exist between circulating viruses where the HI data may be a little bit less definitive.

We are looking for significant influenza activity associated with these variant viruses, and we rely heavily on reports to the World Health Organization or domestic reports of high levels of influenza-like illness during the time that these variant viruses are being isolated. And, of course,

we also in recent years have begun to rely more heavily on looking at the post-vaccine immune response to these variant viruses in comparison to the human response to the vaccine strain itself.

I would just like to remind you of the time table for vaccine production and use in the United States which Roland alluded to. Here we are at the end of February, and we need to know one or more strains that will be included in the formula. By March, we need to have precise formulation; that is, we need to know exactly what viruses are going into the vaccine.

I am going to just briefly summarize global activity for each of the virus groups that we will be dealing with. This particular overhead is on page 9 of your package. We will start with Influenza A H1N1 viruses, and as has been typical in the past, we often tend to start with the group of viruses that to us appears to be the easiest to get our arms around. And that can be for a variety of reasons. One of the reasons we are starting with the H1N1 viruses this year is that if you concentrate first on the time period between October 1998 and January 1999, you will see that we really have had relatively little Influenza A H1N1 activity worldwide. We have only had

a couple of sporadic isolates in the United States. There has been sporadic activity reported in Europe. There was a single isolate of Bayern-like strain which was isolated in December in South Africa. There have been reports of sporadic H1N1 isolates in Asia and I think Dr. Nerome will speak a bit more about some of those viruses.

I we step back and look what happened in the Southern Hemisphere, we saw a similar picture. There was a bit more H1 activity, particularly in New Zealand, where Bayern-like strains circulated fairly widely. However, there really was only sporadic activity over all. There was somewhat more activity last winter during the 1997/1998 season for us, and in Asia in February, there were actually outbreaks caused by H1N1 viruses.

So if we move on to the next page in the handout, page 10, we will look at the antigenic properties of these H1N1 viruses that are circulating at fairly low levels. And as you might remember from looking at the data last year, there are really two very distinct groups that one can sort out using post-infection ferret sera. I would like to remind you that we are looking for constant four-fold differences or greater differences in the hemagglutination

inhibition titers. I have tried to simply things a bit. We have the homologous titers between the Bayern virus and its ferret antiserum shown in read here and Johannesburg shown in red here and Moscow shown in red here. And you can see that this group of viruses, these three viruses, are similar to each other in their patterns of reactivity.

In contrast, we have the Beijing 262 and Harbin 4 strains here, which are really quite different. Antisera to the Bayern, Johannesburg and Moscow strains do not inhibit these viruses very well. And conversely, antisera to the Beijing and Harbin strains do not inhibit these viruses very well.

So it is very clear we have two groups of viruses. There are genetic correlates as well, which I will talk about a bit later. And so we will look at some of the viruses that we have tested since we last met. These test antigens 1 through 3 were isolated in the Southern Hemisphere during the summer months, during their influenza season. And they are clearly Bayern and Johannesburg-like. These three strains all isolated from Russia, where some of the European Beijing 262-like strains that we noted last year at this time, and we can see that they are well inhibited -- reasonably well inhibited by antisera to the

Beijing 262 and Harbin strains. We also have additional strains from Europe -- two from Hong Kong and two from Japan which fall into the Beijing 262 group.

Now we are looking at the very latest tests that we have. As I mentioned, we don't have a lot of very recent strains. This is the single strain that we have had in our hands from the United States to analyze. We have one more U.S. strain, which we will be testing next week or the week after. Here is a fairly recent strain from China and one from Russia. Then the rest of these are from Asia. These last two strains were isolated in November of this year, and Dr. Nerome may mention a bit more about them.

But let's look first at the Bayern-like strains here, test antigens 1 and 2. They are well inhibited by the reference antisera and are clearly Bayern-like without much change. What we are seeing when we look at the Beijing 262-like strains is just there are some viruses which are less well inhibited. These are 8-fold down. The Ishikawa Japanese strains are 8-fold down with a reference Beijing 262 and Harbin antisera. And I must remind you that Beijing 262 is the vaccine -- the H1N1 vaccine component.

So we have looked at some of these strains

in some detail. Additional strains were examined during the WHO meeting in September to select strains for the Southern Hemisphere vaccine for next year. And I will have a bit more to say about these strains as we go on and as I talk about options for strain selection after lunch.

So here is a frequency table. There is really not a lot of data, of course, for the most important recent period, October 1998 to January 1999. We have the two low-reacting Beijing 262-like viruses from Japan, which were sent to us because they were low reactors. We don't know what proportion of the strains in Japan fall into this category, and I hope Dr. Nerome will clarify that for us. And then we have the one Bayern-like strain from the U.S.

I think we will just go on to the next overhead. So when we moved to Beijing 262 for last year's vaccine, we were dependent on a couple of different pieces of information. One was that these viruses, which had been circulating only in China for a period of time, now had been detected, not just in Asia but also in Europe, Africa, and the U.S. We knew that this was a travel-related case, but we knew it had been introduced into the United States, and we knew that there were a number of isolates in France,

in the Czech Republic and in Russia that detected last winter. And then during a previous period, there had been a number of isolates detected in Senegal and in South Africa. So that was one of the key pieces of information. We can really see that the viruses haven't spread that much more since then.

The evolutionary tree or the dendrogram that is in your package is really much more complex than what I have here on the overhead. I have tried to simplify things a bit for the overhead but give you more information in your package for you to peruse later on. Here we have the two distinct antigenic and genetic groups of viruses. Here is our Beijing 262-like group here shown in green with the Beijing 262 vaccine strain shown in red. This is the Bayern-like group shown in blue. And I have just asterisked viruses with are egg isolates, and therefore are potential vaccine strains.

This strain designated here as Russia 209-98, in other slides it might be mentioned by other individuals with a slightly different designation as Ulan Ude, which is in Russia. So we called it Russia in this particular slide.

Now what we have been able to determine is that there are some of the viruses -- you know, with

our HI test, we have noticed that some of these viruses are not well inhibited by antisera to the Beijing 262. And these viruses are scattered about a bit. The Malaysia virus was one of those. Hong Kong 503, which isn't shown on this slide but which is in your package, was also a low reactor.

Now the problem for us has been that we haven't been able to find signature sequence changes corresponding to this low reactivity that we see in HI tests. And furthermore, when we take these low reactors and infect ferrets, we get antisera which are very poorly cross-reacted. They have low homologous titers and they are very poorly cross-reacted. So any of the low reacting viruses, that is those that are less well inhibited by the Beijing 262-95 ferret antisera, have not proven to be good candidates.

We are always trying to keep up with the ball game here, and since we are always tracking a virus that is moving rapidly, we are looking always at potential vaccine candidates. We won't spend but half a second on this, but we do have some egg isolates that are related to Bayern that represent updated strains, and we are looking at the number of differences from the consensus sequence. We do that

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because we have found in the past that those viruses that are closest in sequence, that have HA's closest in sequence to the consensus sequence, tend to produce very antisera, which are most broadly cross-reactive against the circulating strains. So we are always trying to keep up and make sure that if the picture should change rapidly, we have in our back pockets strains which could be used as vaccine candidates. And so for the Beijing 262 group of viruses, we also have a number of vaccine candidates available.

Now I am not going to talk very much at all about the post-vaccination human serologic testing that we do, because that will be summarized later on But I would like to remind you that the reason that we -- one of the reasons that we moved to the Beijing 262-95 antigen as the H1N1 component of the vaccine is that not only does it induce a good response to the vaccine strain itself, but it also induces a very nice cross-reactive antibody response to viruses which are on the Bayern lineage. was the previous Bayern-like strain in the vaccine, and we see we have an even higher post-vaccination geometric mean titer among human subjects who have received the Beijing 262-like vaccine than they do to the vaccine strain itself. And this has

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confirmed in a number of labs using quite a large number of antigens by this time.

So I think unless there are any questions about H1N1 viruses, I will move on to the ${\rm H3N2}$ strains.

CHAIRPERSON FERRIERI: Let us move on then.

DR. COX: Okay. The H3N2 viruses are always a bit more exciting. Over the past 5 years at least, have had H3N2 viruses predominating we worldwide and causing extensive morbidity and mortality in a number of different countries. start with last season, as Keiji reminded you, we had a great deal of H3N2 activity. Certainly in the United States, we had epidemic level activity in January and February caused by Sydney-like strains. There is a similar picture in Canada. Activity was a bit less intense in Europe, but certainly Sydney virus circulated very widely. And in Asia, in countries like Japan, Sydney viruses had quite a large impact.

In the Southern Hemisphere during our summer season and their winter season, Sydney-like viruses circulated widely causing epidemics in Central and South America in Australia and in Oceania. What has happened since October of 1998 to the present time

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is that there have been sporadic isolates and outbreaks in North America and Europe and activity is really on the increase now. We are hearing about more institutional outbreaks as we move on through the month of January toward February. And I would like to mention, as I imagine most of you have heard, that there has been quite intense Influenza A H3N2 activity in China, particularly in the north of China, and we have been very interested in getting viruses from China, and I will be talking about those very shortly.

When we look at the antigenic profiles of Influenza A H3N2 viruses, we don't see at the present time such clear differentiation as we do for H1N1 and Influenza B viruses. Here we have our old previous vaccine strain that we are just keeping in to show that the viruses really are evolving and moving on. Here is our Sydney homologous titer of 640. And so we are looking for viruses that have titers of 160 or lower. And then we want to see how those viruses -- what sort of a pattern we have for those particular viruses, both in terms of geographic distribution and in terms of their sequence analysis and so on.

We received a shipment of viruses from China. The viruses had been isolated between May and September. This shipment was received sometime in the

fall, I think, in about October or early November. And among those viruses, we found that there were a number of strains, two of them are here -- Sichuan/418 and 346. You will hear more about those as we move through my presentation and the following presentations, which certainly were reduced in titer with the Sydney antisera.

Here I have a block of viruses from the U.S. Most of these were isolated in November and December. And you will see that there are occasional strains which are less well-inhibited by the Sydney antiserum. But by and large, the majority of the isolates from the United States are very well inhibited by antisera to the Sydney strain. So we are looking to see what genetic characteristics these particular strains might have that are low reactors.

I mentioned that we had this package from China that had a lot of strains from Sichuan that had been isolated during the summer and fall, and among those, there were a number of strains which were less well inhibited by the Sydney antiserum as well as by additional antisera that we had developed for our reference battery because we felt they were interesting strains and important in some way as representing outbreaks that had occurred. And we can

see that we have, for the Sichuan/418 a nice homologous titer in this particular test of 1280 and a slightly lower homologous titer of 320 for the Sichuan/346. We also had strains from Japan, which were Sydney-like -- solidly Sydney-like -- in this particular test.

I will go through this slide very quickly. We see that there are -- we like to see absolute consistency from HI test to HI test. But as you all know, for serologic assays there is some inherent variation. And here you can see that the Sichuan/346, which will be noted later in the human serologic results, is really quite poorly inhibited by antiserum to the Sydney strain. And this in additional tests has proven to be the case. This strain reacts less well with our battery in general than the Sichuan/418.

Now let's just look at these strains from the U.S. Again, we see that there are occasional strains which are less well inhibited, but by and large U.S. isolates are well inhibited by the Sydney antisera. We also have a few strains from Hong Kong which are less well inhibited. Here we have some Korean strains isolated in December which are solidly Sydney-like.

And now we move on to the viruses that we

have received most recently. And on this particular 1 overhead, you will see at the bottom starting with 2 3 test antigen number 12 and going on through test antigen 20 a series of viruses which we received on 4 5 January 20. This was a very large package of viruses from China which included over 130 strains isolated 6 7 between September and the end of December. And there 8 are some strains among this group which we have analyzed which are lower in titer with the Sydney 9 10 antiserum. But there are also many strains which are 11 very well inhibited. They are clearly Sydney-like 12 And so perhaps the table has been turned a bit. Northern China was not particularly hard-hit by Sydney-like strains last year, and it would be very unusual to have this sort of picture. But as we know, 15 16 influenza is unpredictable. And even though we can generalize, there are always exceptions to every rule with influenza. And it appears to us that they had their Sydney epidemic a year after we did in northern China. But nevertheless, we are looking very closely at these strains which are less well inhibited and trying to see if there is a pattern in their reactivity and a pattern in the sequence analysis and so on.

These are the most recent strains that we

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have from the United States. They are all Sydneylike. And we have a series of recent strains from Hong Kong which are also Sydney-like.

Now for this frequency table, I am going to concentrate primarily on the two panels at the First of all, I would like to look at the bottom. period between April 1998 and September 1999. would like to note that there were some Sydney-like low reactors. On your page 26, the low reactors are actually designated. That was left off this overhead to try to make it a bit prettier. But where I have those numbers little black X's, here reflecting the number of low reactors to the Sydney antiserum. They are related to Sydney, but they are low reactors.

So we see that we do have a number of viruses that are less well inhibited by the Sydney antiserum. I think it is very important to note that in Australia, approximately 30 percent of the viruses that they have tested are reduced four-fold or greater in titer with Sydney antiserum. And that was a fairly large number of strains. Using a smaller number of strains from Thailand, analyzed by Alan Hampson in Australia, approximately 50 percent of those viruses were less well inhibited by the Sydney antiserum.

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That is, they were four-fold -- they had four-fold or greater reductions in titer.

So as we moved along with the Sydney strains, we have from the very beginning seen the occasional low reactor. And we have been looking for sequence patterns that would give us a clue about what is going on with these low reactors. And what we have been seeing up until very recently is that low reactors were distributed throughout our dendrogram, throughout our HA dendrogram. So there was no real pattern. There wasn't a signature sequence that could be identified with these low reacting viruses.

More recently, we have seen that we have got clustering of some of our low reacting viruses. example, we have our Sichuan low clustering up here at the top of our dendrogram. then this we have cluster here, which is representative of the most recent strains that we received from China. The CNIC stands for the National Influenza Center in Beijing. So what we are trying to figure out, and we do not have enough sequence data yet, because we had to choose the viruses that we were going to sequence. Because we received the package on January 20, we had to go ahead and select viruses for sequence analysis before we could get the antigenic

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analysis. And now that we have got a number of these viruses run in HI tests, we are going to go back to do some additional sequencing and see if we can sort out some of the low reacting strains here and how they might relate to some of these other low reacting strains.

So we feel that it is unfortunate that we received the package from China as late as we did, but we have a wealth of viruses to look at and we need some additional time to sort out exactly what is going on.

But we are trying to keep up with all of our egg isolates, and where there are holes, try to get some additional egg isolates. One of the things happened in China is that has that they have discovered, as the rest of the world had discovered a number of years ago, that many influenza viruses are not well -- are not easily isolated in eggs. And those that are circulating at the current time are great examples of this, particularly the H3N2 strains. So several of the labs in China have moved toward using Madin Darby canine kidney cells and PCK cells as a substrate for isolating viruses. This means we get more viruses from China, but we have fewer strains which are suitable for vaccine production because of

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the passage history.

So we have a number of isolates which have a pure egg passage history. This one was isolated in chick kidney, and of course if viruses have been isolated in chick kidney cells, they are also suitable for vaccine production. And here we see the number of differences from the consensus sequence of the current strains.

Again, I am only going to just touch very, very lightly on the human serologic data that we have developed so far. I would just like to move straight away to this column where we are looking at the post-vaccine GMTs. And we have a post-vaccine GMT for Sydney of 143. For this Sichuan/346, we can see a considerable reduction in post-vaccination GMT.

In contrast, the Alaskan strain that is shown here is a very typical Sydney-like strain that is recently isolated, and we have a nice robust response to that particular strain. I think that is all I will say because that will be summarized later. If there are any questions about H3N2 strains, I would be happy to answer them. Any burning questions? Otherwise, I will move on to Influenza B activity.

Influenza B viruses have continued to circulate world-wide. They have not caused epidemics

during the past couple of years. However, they have caused outbreaks. And at the current time, Influenza strains are predominating in some European As Keiji mentioned, Influenza B viruses constitute about 18 percent of the strains that have been characterized in the United States. certainly was Influenza B activity during the summer months, and we had some of these strains to look at. I think that is about all I will say about this except to remind you that there are two distinct groups of influenza B viruses circulating in Asia. Both the B/Beijing/184-like and the B/Victoria-like viruses are circulating in Asia. I will mention more about that as we go along.

Just to orient you, we will look first at our reference battery at the top. The Beijing 243 and Shangdong 7 strains are Victoria-like. They are recent Victoria-like strains isolated in 1997. And it is very, very easy to distinguish these strains from the Beijing 184 Harbin 7-like strains which are circulating world-wide. These have not been detected outside of Asia, and I will show you a map later on that shows the distribution.

On this particular slide, I have viruses that were isolated in Georgia actually in November and

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December of 1998. These strains were of particular interest because we noted that while the vaccine strain B Harbin 794 has a homologous titer of 640, a number of strains from the United States, and I ticked them here in black, are 8-fold down in their titers as compared to the homogolous titer here. If we look at strains from Europe, we can see that again there are a number of strains that have a four-fold or greater reduction in titer as compared to the Harbin homologous titer.

The viruses are somewhat better inhibited by the Beijing 184 strain, and we have really learned a lot about the differences, both the genetic and antigenic differences between these two strains, which are pretty similar, but they can be distinguished both antigenically and genetically. And we weren't nearly as clear about this when they were first emerging and were considered more or less antigenically equivalent.

Now we have on this slide a number of strains from the U.S. represented here by test antigens 1 through 8. Of course, all of them are in the Beijing 184 Harbin group of viruses. Again, I have ticked those strains that have a four-fold or greater reduction in titer as compared to the homogolous Harbin titer. Again, I would like you to

note that the Beijing 184 antiserum covers strains better.

We have a number of Harbin Beijing 184 strains from Asia that were isolated during the summer and fall up through November. And there are a number of these strains which are also less well inhibited. Here we have two Victoria-like strains from China -- one from China and one from Japan that were isolated relatively recently.

These -- this test was done very recently, just a few days ago. And the reason that I am showing you this test is that we were actually able to go around the corner to the State Health Department in Georgia and get some original clinical material from some of these isolates where the MDCK isolates had a reduced titer and put the original clinical specimens into eggs. And now we have this particular strain here, B/Georgia/498, which is an egg isolate. And you can see that after re-isolation in eggs, it continues to be reduced in titer with the B Harbin antiserum. And again, I have ticked a number of strains. Here we have a couple of strains from the Caribbean. This fairly recent isolate from a sporadic case in Chile, and we have some additional Asian strains.

This Georgia/498 virus has not yet been

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sequenced. It has just recently been put into ferrets, and we expect that we will have reciprocal HI tests with this particular candidate vaccine strain within the next couple of weeks.

So if we look at the frequency table here, we can see that we don't have a tremendous number of Influenza B viruses characterized, but a respectable number -- 76 that were isolated between April and September of 1998, and a total of 50 isolated between October 1998 and January 1999. And we have about 35 percent of the viruses isolated in the U.S. which are reduced in titer to the Harbin vaccine antiserum.

I should also note that when I was reading Dr. Nerome's overhead that he also sees a number of viruses that are reduced in titer to the Harbin antiserum. And in Europe, I understand, they are seeing a similar picture with viruses being very well inhibited by Beijing 184 antiserum but not so well inhibited by the antiserum to the vaccine strain itself.

This map, which shows the geographic distribution of B/Victoria-like viruses really has not changed since September, when we had our WHO consultation on vaccine strain selection for the Southern Hemisphere. We have B/Victoria-like viruses

continuing to circulate only in Asia, and we have been looking at the same picture for a number of years. We do not understand why these viruses have not moved out of Asia as there is a growing susceptible population world-wide, particularly among children who are less than 10 years old. We would expect that there would be a very high proportion of these children who would be susceptible to B/Vic-like viruses. But these viruses simply have not spread outside of Asia. I think Thailand was the country that was added to the map since we met last March.

So if look we at the evolutionary relationships among Influenza B hemagglutinin genes, we see that it is very, very easy to distinguish the Victoria-like strain shown down here in green from what we used to call the Yamagada lineage. you who have been with us for a long time would recognize the Yamagada virus. So this is the Yamagada lineage, which contains both the Beijing 184 virus shown in purple here and our Harbin vaccine strain and the viruses most closely related to it shown in this turquoise color here.

Now what we are trying to sort out and which we still haven't been able to do is to sort out a sequence signature that corresponds to this lower

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reactivity. But what we have determined is viruses which are on this particular sublineage, that is, the viruses shown in purple, tend to produce antisera which are more broadly cross-reactive against all of these strains here than viruses which are in this group here. So we are pursuing that line. And of course the Georgia strain, which we haven't sequenced and which is not on here is in this purple group.

The viruses that were shown previously in purple and in turquoise are sometimes difficult to distinguish antigenically, but they are very easily distinguishable using restriction analysis or RFLP analysis. so we have been trying to keep up with what is going on in different geographic regions with regard to whether the purple team or the turquoise team are winning, and we haven't really seen a great deal of change. What we know is that the Beijing-like or B -- we will just call them B and B* viruses -have continued to circulate exclusively in North America. So all of the viruses that we have analyzed in using RFLP in the U.S. have belonged in this group, the purple group or the Beijing/184 group. In contrast, in Asia we see both the purple and the turquoise viruses circulating -- the Beijing/184-like

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and the Harbin-like viruses circulating and continuing to circulate. So there really hasn't been much change there.

I think we will skip this one. Now we are looking very carefully at our egg isolates and we see that when we look at Harbin-like, that is, turquoise group of viruses, when we look at that group of virus and make a consensus sequence for the HAs from those viruses, we see that the viruses have started to move on a bit and the Harbin strain itself has 7 amino acid differences from the consensus. then we have some egg isolates that have fewer changes from the consensus. Now remember I had mentioned that antisera from the other group, the purple group, have tended to provide better coverage for both groups, and we have a number of candidates here. The Beijing virus itself has 9 amino acid differences from the And we have this virus, Yamanashi/166/98 sent to us by Dr. Nerome, which has only two amino acid differences from the consensus and its antiserum does seem to cover viruses fairly well.

Just in case, we are always trying to make sure that we have egg isolates for the Victoria lineage, just in case those viruses do begin to spread and would spread quite rapidly. We have a number of

candidates. As you might remember from the past, and as you will be reminded during Roland Levandowski's presentation, there was an experimental vaccine trial done with a virus on the Victoria lineage last year, and there is an additional vaccine trial going on with the Shangdong/7/97 strain in Australia right now. It is just finishing up and we hope to have those sera tested in time for the Geneva meeting. So needless to say, we do have some egg isolates from the Victoria -- recent ones from the Victoria lineage that would be appropriate vaccine candidates. But since the viruses do not appear to be spreading, we are just keeping these in our back pockets.

When we do our serologic studies in humans for the Influenza B viruses, at CDC we typically use ether-treated antigen. And, of course, we always have to keep in mind when we are looking at these results that we are increasing the sensitivity but decreasing the specificity of the antibody reactions. And what we are seeing is pretty consistent solid cross-reactivity between the antibody induced by the B/Harbin vaccine strain and other strains that we have chosen thus far. We have not yet tested the Georgia strain. But when we use viruses on the Victoria lineage, we see a reduction in the post-vaccination

geometric mean titer. A lot more about that will be said later.

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Now finally I would just like to -- I didn't have time to do a proper overhead, but I did want to acknowledge a number of people in Influenza Branch. I don't normally do this, but I wanted to do this today. In particular, I would like to acknowledge Alexander Klimov, who heads the Strain Surveillance Section, and in that group I would like to mention Henrietta Hall, Inger Baker, Cuca Perez, Jim Love and a whole variety of visitors from China and Vietnam and other countries who have contributed to the antigenic analysis of the strains that we are getting in. We are actually receiving twice as many strains at CDC as we did three years ago or four years ago, and so it has been a tremendous challenge to figure out how to get these analyzed, prioritize these and get them analyzed in a way that serves us best for vaccine strain selection. I would like to acknowledge Keiji Fukuda and his epidemiology in particular Lynette Brammer section, Schmeltz, who are very integral parts of the U.S. Domestic Surveillance System. And I would like to acknowledge Jacqueline Katz, not so much for what I presented today, but she and her section have worked

very, very hard in producing some of the results that 1 you will see this afternoon for the experimental H5 2 3 vaccine trial. And the, of course, I would like to acknowledge Dr. Kata Subbarao and her molecular 4 5 genetics section, in particular Huang Jing, Catherine Bender, and Xu Xiyan for getting all the sequencing 6 7 done in such a timely manner. 8 Okay, now I would like to throw it open 9 for questions. CHAIRPERSON FERRIERI: 10 Thank you very 11 much, Dr. Cox. Dr. Snider? 12 DR. SNIDER: Yes. Dixie Snider, CDC. 13 Nancy, as a context for what you have presented, you 14 alluded to the fact that you are getting more strains 15 in. What is your assessment of the representativeness 16 of the strains as a reflection of world-wide influence 17 or activity, and what has been the trend? representativeness improved over the last couple of 18 19 years? 20 DR. COX: Ι would say that the representativeness has improved globally and that if 21 22 you look at the really big picture, which is the whole 23 WHO global influence network and the work that we are 24 doing in parallel with the work that is being done at

Millhill in Melbourne and in Tokyo, that we really

have a much better handle on what is going on. But I think you have to pull it all together. We are getting a lot more viruses from South America and a few more from Central America. We are getting a lot more viruses from Asia. There are still areas of the globe that are not well covered, and obviously we are doing our best to try to enhance surveillance and work with our partners in the military and elsewhere to try to plug some of those gaps. But I would say that we have -- generally speaking, we have a much better handle on what his actually circulating out there at the present time than we did 10 years ago.

CHAIRPERSON FERRIERI: Dr. Kim?

DR. KIM: Dr. Kim, Los Angeles. I have some questions on HI, the titer. It appears that -you indicated that titers of let's say 640 is better
than 160 and 320 is better than 80. Again, I am not
a virologist, but are there data indicating that
better means biologically relevant? That means 640 in
this is biologically better that 160? That is my
first question.

DR. COX: Okay. We have a lot of experience looking at hemagglutination inhibition tests using post-infection ferret sera, and this is the common method used world-wide to distinguish

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antigenic variance. We know that there is sort of an inherent two-fold variation in HI tests. And of course an HI test done on one day may have higher titers generally than an HI test done on another day. We have found through many years of experience that if we consistently see that there are reductions of fourfold or greater in titer of a test antigen compared to what we see for the homologous antigen antiserum interaction, that this is significant and we need to pay attention to it and use our sequence analysis and pull that in and try to see if there are genetic correlates. And the way that we really try to put that all together is to look for patterns, both geographic patterns and sequence patterns.

DR. KIM: All right. The second related question is that it appears that looking at the numbers, your post GMT titer appeared to correlate with the somewhat pre-GMT titer. I wonder whether that is sort of your impression post-GMT titers?

DR. COX: Yes. And I am sure that Roland and others may comment about that. But, yes, that is true to some extent. That if you have higher prevaccination geometric mean titers, which often means — it can mean a couple of different things, but it often means that you have a primed population and you

often have a higher post-vaccination geometric mean titer for that particular strain.

DR. KIM: And then looking to the speculation of why let's say some individuals may have higher pre-GMT titers compared to others, does that perhaps relate to any preexisting -- different kinds of influencing activity? For example, if someone has a vaccine and then has antibodies being induced and then has exposure or has the influence of H3N2, perhaps that individual's antibody may decrease and then resulting in lower pre-GMT titer and therefore that person might not be better antibody inducers in the following season?

DR. COX: I am not quite sure I --

DR. KIM: What I am trying to get into is that perhaps endogenous decay of antibody may depend on the exposure to a homologous or related antigen that perhaps may determine the titers of a pre-GMT. This is entirely speculation. I just want to see --

DR. COX: Yes. I think that the population's exposure both to vaccine and to previously circulating strains certainly will have an impact on the pre-vaccination geometric mean titers.

CHAIRPERSON FERRIERI: Are there other questions? Yes, please.

DR. HOKE: Charles Hoke, Fort Detrick. As you attempt to correlate the sequence changes with the changes perhaps in HAI, you express the information in terms of numbers of mutations and so forth. And I know that you are sequencing through an area that is important, but are all mutations equal?

DR. COX: No, certainly not. And we have a limited amount of time today, so I am trying to present what I think will be the most useful data at this point in time. But we actually look in much greater detail at the changes that occur and oftentimes -- I mean, you have probably seen graphic representations of the three dimensional structure of the HA and where the changes are in the HA, whether they are in antigenic sites or not. And whether or not they are conservative changes -- conservative amino acid changes or whether they are more dramatic changes which we would expect to have a greater impact on antiqenicity.

Very often when we see a significant antigenic variant, there are a number of signature changes as we have come to call them that we see in association with the antigenic change. It is very hard to dissect out which of those signature changes -- often there are three or more signature changes --

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and it is very often hard to dissect out which of those changes are most important for the antigenic changes that we see. But nevertheless, we do look at those in relation to the three-dimensional structure, which antigenic site they are in, and whether or not they are conservative or more dramatic changes. CHAIRPERSON FERRIERI: Dr. Levandowski? DR. LEVANDOWSKI: I have one comment that I would like to make. I think Nancy mentioned it, but

just wanted to comment on the B status, the Influenza B virus vaccine component. The fact that we are using B/Harbin/7/94 in the vaccine relates to the fact that the B/Beijing/184/93, which was actually the strain that was named, does not grow well enough to be useful for manufacturing. But I think I would just like to emphasize that. I think Nancy touched on that, but I think everybody needs to be clear on why that strain was substituted at the time that it was.

> CHAIRPERSON FERRIERI: Thank you.

I didn't mention that and I DR. COX: should have, Roland. Thank you for bringing that up. The B/Beijing/184 grew very, very poorly. I think all the manufacturers had similar experiences with it and it just was not suitable for production.

> CHAIRPERSON FERRIERI: We have time for

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one brief question and brief answer. Dr. Huang?

DR. HUANG: You focused on the low reactants and even pulled them out in your data presentation. I am not sure that I understand why you did that.

DR. COX: We seek -- I focused on those viruses that are reacting lower because we are looking for the next variant. And the only way we are going to do that is by focusing on those low reactors and comparing their sequence -- their genetic sequence to the sequences of the viruses that are typical. I perhaps didn't give enough emphasis to that. So we --

DR. HUANG: But don't you always have a background of those?

DR. COX: That is right, you do. But you've got to be looking at those, or you will never know what the new strain is until it is on you. So you focus on the low reactors. We have learned this from all of our past experience. You've got to look for those low reactors. You have got to know where the sequence changes are, what the signature is, what the antigenic and the genetic signatures are so that you can pick up the next one and the next one and see where they are, so that you can get a pattern. You don't want to just pull a low reactor out of one of

your tests or a couple of them and say, okay, this is 1 probably our next epidemic strain. And you don't want 2 to wait until it is upon you, because then it is far 3 too late. So you are constantly sifting through your 4 data in that way, comparing the low reactors to the 5 6 typical viruses. 7 CHAIRPERSON FERRIERI: Thank you, Nancy, for a very comprehensive presentation. 8 We will move on to Ms. Linda Canas, who will present on additional 9 10 surveillance. 11 DR. LEVANDOWSKI: Dr. Ferrieri, could I 12 just --13 CHAIRPERSON FERRIERI: Yes? 14 DR. LEVANDOWSKI: Could I just comment on this presentation and the ones that are coming up? 15 16 CHAIRPERSON FERRIERI: Yes. 17 DR. LEVANDOWSKI: Many of you know that there is a long history of military involvement with 18 influenza vaccines, and we probably wouldn't 19 20 sitting here today if the military had not wanted to 21 have inactivated influenza vaccines licensed back in the 1940's. For many, many years, we have been very 22 fortunate to have information collected through 23 24 extensive networks within the military in the United 25 States, and a lot of our most important efficacy data

comes from studies that have been done. We were very pleased and happy that we were able to get Linda Canas, who is the chief of diagnostic virology at Brooks Air Force Base to come here today to give us some information on the military's current status in terms of surveillance. And I think you will hear that it is a fairly global activity as well. And that will be followed up by some of our international visitors. So thank you for that.

CHAIRPERSON FERRIERI: Thank you.

MS. CANAS: Good morning. The Department of Defense has long recognized that the trivalent vaccine is currently the most effective measure of preventing influenza illness, and in fact it is a requirement that every active duty individual be vaccinated annually. It is in our institutional interest as well as the global interest that this vaccine be right. And we are very happy to present our data for your consideration.

The program has been in existence since 1976 and was started by the Air Force to determine what influenza was doing in the local communities and the impact that it would have on those bases as well as to establish control measures. We do collect throat swabs today, but in the early days, they

actually did have the patients gargle.

Today, it is a tri-service operation. It is headed by the global emerging infection system located here in Washington and the Army, Navy and Air Force do participate along with some very creative partnerships with other federal and international organizations. This program is evolving as we speak. It is probably one of the strengths that we can be as flexible as we have been, and there is a good deal of excitement about what we are doing.

To give you a very brief overview of how the program works, the people in the global emerging infectious system office, the epidemiologists at the local level, and laboratories for each of the three services decide on the sentinel sites. I will be presenting the Air Force data because we have the international component.

These sites are chosen on the basis of their location as well as the mission. Are they a training site? Is this a port of entry into the country? Do we have troops that are going out to other areas of the world of interest? Or perhaps that base itself is a location we are interested in. In addition, we have been able to collaborate with other areas to establish surveillance in more non-

traditional areas. These have represented clinics that have been established and have a fairly long-running history with other areas of the service, and we have been able to establish surveillance in conjunction with other efforts. We now have a pretty good established program in Nepal, Thailand, Argentina and Peru. The Navy has a lab in Cairo, and they are attempting to establish surveillance sites in Egypt and Syria. We are currently not collaborating with them and sharing resources and information, but we hope that this can be another component of our program in the future.

We also have some very real possibilities for expanding our surveillance, some of them quite creative. One of them that is very real and probably will come about shortly is being able to put liquid nitrogen tanks on board air craft carriers so that samples can be collected from shipboard personnel and at clinics at the various sites where those ships may stop. We also look for increased surveillance in South America and more in Asia.

This is just a quick view of what our map looks like today. We send out collection supplies to each of the sentinel sites along with information on how to store and ship these specimens and ask that

they collect according to a case definition. This case definition is consistent with influenza-like illness. We ask that the specimens be collected from the active duty population. They will serve as a sentinel for vaccine efficacy. The dependent population are less likely to be vaccinated and they will be likely to give us an idea of what is going on in their local community.

The specimens are then shipped to our laboratory in San Antonio, Texas. If there is one component of this whole program that should be at the top of the list of importance, it is probably the shipping issue. Getting timely specimens is important to the submitting facility to know what is going on, but also for the viability of the virus. And I would mention that our laboratory is a reference laboratory -- a full service reference laboratory with customers around the world. And in that regard, we established Federal Express contracts. So we receive 2,000 to 3,000 specimens per day in our lab for any tests. Our project gargle specimens are easily added in to those shipments. And even those non-Air Force sites that are using us are usually in a position to be able to get the samples to our sites. We have been able to hook onto some other arrangements. But this

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basic contract to get the specimens to us quickly has greatly increased the programs capabilities.

In our laboratory, we have our laboratory procedure for how we are going to isolate those viruses. When we do get a flu virus, we have just this year begun doing our own subtyping. We do share what we get with the CDC to make sure that you all have the information that we have and so it available for your vaccine decisions. It is a full service lab and we are going to report any virus that we happen to isolate. Just as a point of interest, we do expect to get a specimen in an average of about four days. Influenza grows rather quickly and we have been able to get most of those results out within the first test, which will come off at 48 hours. We don't work on the weekends, so it comes out a little bit I would say that by the time a negative is reported out, we have done at least two screening tests and have held the culture for at least 10 days.

In addition to our laboratory, the result is put into our computer where the submitting facility receives it as a patient report for those records. We also e-mail the results to the Public Health Office, so they have real-time data on what is going on in their area. This can be used then for public health

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decisions or command decisions that may need to be made. This has also been an important addition to the program. The submitting facility is now getting something back. When we were just giving patient reports, it was very difficult for the public health people to get that information. So with the minimal effort of putting it into e-mail, they have some information to make their program worthwhile, and their physicians are much more likely to collect also.

We are attempting to establish the epidemiology. This is a real strength. We have this information. We know vaccination status and travel histories. It is just a matter of getting it all together. That is an ongoing process, but one that we expect to be able to work on and one that we collaborate closely again with the CDC. And here is an idea of where our isolates have come from in the last year.

We collect and report anything we get throughout the year, but it has officially run October through May. As we add more of South America, I expect that will change. I notice the numbers got cut off on this graph. Just as a point of reference -- if I find it -- the January peak, we received 540 specimens and we isolated 160 Flu A's. That was last

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year, but it is just to give you an idea. As you are well aware, every year has its own personality of influenza. And last year was pretty much exclusively Flu A for us. We had five B's in the entire year from all of our sites. We are seeing a few more this year, but it still is exclusively influenza A.

Now looking at our recent data, divide up our sites into areas, when we look at Asia, last year we had 53 specimens that were typed in this area, and all of them came back as A/Sydney H3N2. would say that this year has been fairly light until last week. This data is current until last Friday. From Monday until Wednesday before I left, we had received 85 specimens and had reported out additional 34 influenzas. So I will add those as we And 31 of those specimens came from Asia, and 8 of those influenza isolates came from this area. In December, we saw an outbreak in Korea. of our isolates from this area came from Korea. of those were in active duty individuals. We don't have confirmed vaccination status on those, but we do know that our vaccination status overall in this population is 90 percent. So we have sequenced -- or excuse me, not sequenced, but we have typed 15 of and they have all been the A/Sydney.

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The ones that we have received this week were from Japan. We haven't had quite as many lately from Korea, but we are now starting to see them in Japan.

We have three sites in Europe. England has Lakenheath Air Force Base, Ramstein, Germany, and Incirlik, Turkey. I would also comment that the Army has a lab at Lonstull, Germany, where they run a similar program although on a smaller scale. Bosnia is supposed to be conducting surveillance and sending through them. The data I have seen has been small, but their isolates have also been the H3 Sydney. We are continuing to receive more from them. We have this week reported 5 more A's and one B, the one B being in Germany.

Most of our specimens do come from the United States. We have 8 sentinel sites, but these public health officers move around and know about the program. Flu, of course, is becoming a much more important topic, even in the lay press. So we get specimens from a lot more sites than just our sentinel sites who are required to send to us. We are really seeing an increase in activity. We are picking up -- in California, we are starting to pick up more, and we have had two B's in Texas so far. That is the only

B's we have seen in our United States population.

And to comment on our work with the Nepalese and South America. This has been a very exciting part of our program, mainly because it works. It takes a tremendous amount of cooperation to collect the samples in these remote communities and get them to a place -- in Nepal, they go to Bangkok -- where they are repacked in dry ice and then shipped to us. We have had wonderful success from Nepal. We have had a total over two years of four shipments, and we have had good isolation. This year out of two shipments, we had 91 samples. We had a 44 percent isolation of viruses in those shipments. 34 percent of those were influenzas. Of the 28 influenza A's that we received, 21 have thus far been identified as being the ${\tt H3N2}$ A/Sydney. We have had 3 B's altogether.

And this gives some idea -- we just finished -- Wednesday, as I was leaving, we just finished the latest shipment. So not all of those are represented here, but we have had a very broad range of the time scale. The latest we had was in November. Another important point is how flexible it is. Dr. Cox mentioned all the discussion about activity in China. So our contact in Thailand put out the word to the providers to be alert and got a call that they had

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an Embassy official who had just returned from Thailand and was very ill and they were able to actually get that specimen in the shipment. We isolated parainfluenza 3, but they had the result back in 7 days.

In our results in South America, we had a little more problematic beginning in the shipment. It was a learning experience. It got held up in Customs There wasn't enough dry ice once. So we had a couple of shipments where we got nothing. But this last shipment that we received in October, we had quite a nice selection of viruses and age groups. again what we have seen have identifications on these yet, but it seems that they are still being the Sydney that we are seeing.

As any program moves on, it continues to develop, and we are growing too. Our latest component is that we are going to add the molecular and be able to do our own sequencing. Dr. Lohman has just joined our lab in October. I am not the only one standing outside his door with priorities, but he is here today and I think that shows our corporate commitment and his personal enthusiasm for what we have to do. He is coordinating closely with CDC so that we are doing the same thing. We can share our resources and not

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duplicate our efforts but maximize the information that we have to present to you. We are very pleased with our program. It is actually a lot of fun. My techs get overworked, but they are very committed to it. It is important to them to know that you are interested in their work and it helps them to work a little harder. And we thank you. Would there be any questions?

CHAIRPERSON FERRIERI: Yes, Dr. Breiman, a brief question.

DR. BREIMAN: Rob Breiman. This sounds like a wonderful adjunct to the global surveillance information. I wonder -- you mentioned that shipping has been or can be a problem or it could be the weak link. Do you have an idea -- have you been able to look at viability to see what proportion of specimens have had some effect to them during transport so that you had loss of viability and inability to grow the organisms?

MS. CANAS: We actually have very good results. The ones from Nepal that we just received were actually collected in April and May. So the average was five months that they had stored it. So the trick is to be stored properly. It doesn't matter how long, as long as it is -- and those were held in

liquid nitrogen and then shipped to us on dry ice. 1 South America stores at -70, and they shipped on dry 2 3 ice, and the average that they held them was over two 4 months. So that has not been the problem. It is 5 maintaining that cold link in transit. 6 CHAIRPERSON FERRIERI: One brief last 7 question. Dr. Hall? 8 DR. HALL: I just wondered, is viral isolation the only means of diagnosis you are using or 9 are you using the antigen detection tests in addition? 10 11 Currently we are only using MS. CANAS: the culture because we want to have the strain. 12 DR. HALL: 13 Right. 14 MS. CANAS: This is certainly an area that would help tremendously in these remote areas if we 15 could use the antigen test. They would get something 16 17 out of it more quickly. Expense comes in there. We also then hope to work on that as far as our molecular 18 19 The other problem with those direct goes also. 20 antigen tests, at least stateside, is they do them and they know what is going on and they forget to give us 21 22 the culture. 23 CHAIRPERSON FERRIERI: Thank you, very 24 I wonder, Dr. Levandowski, if you would please

introduce our next two presenters, our international

reports.

DR. LEVANDOWSKI: Okay. Thank you. We are fortunate to have some guests to fill in some of the information that Nancy Cox was alluding to earlier in her presentation. First on our list is Dr. Kuniaki Nerome from the NIH in Japan. He, as you know, works at one of the WHO influenza centers, the most recently established one in Japan, and he too will give us some information on the status of surveillance.

DR. NEROME: Good morning, ladies and gentlemen. It gives me great pleasure to give a presentation about the situation of flu activity in Japan. I am also grateful to the staff of the CDC and the FDA for providing this chance to attend this meeting.

I left all color slides in the airplane between Atlanta and Washington. I think this is another type of risk due to jet lag. But I overcome this risk by the aid of the staff of the FDA. Thank you very much.

Our flu activity in Japan starts with first isolation of the H3N2 antibodies in the southern part of Japan. Antigenic analysis indicates that this --

CHAIRPERSON FERRIERI: Can you turn it up?

DR. NEROME: Antigenic analysis of these past isolates indicated a close identity to A/Sydney vaccine. Second are reports of isolation of H3N2 viruses from the southern part of Japan, Okinawa. And now H3N2 virus has spread all over the country. First of all, I'd like to show the differences of the epidemic strain by two colors. The darkened bar indicates the isolation of the A viruses, H3N2 viruses. This dark bar indicates the number of isolations of H3N2 viruses. This white bar indicates the number of isolations of Influenza B viruses. So H3N2 and B viruses cocirculate in Japan.

So we have used five indices to understand epidemic occurrence in and the magnitude of the outbreak. This information was collected in grammar school and junior high and high school. This affords a good indicator for understanding the immunizations in Japan. This is the virus isolation in primary school.

CHAIRPERSON FERRIERI: Excuse me, Dr. Nerome, would you please speak louder? I am afraid the acoustics are not good enough for people to pick up in the back of the room. So louder, please. And maybe you can help over here our assistant.

DR. NEROME: You can see here whole

indices to understand epidemic occurrence and the magnitude of the outbreak. This information was collected in schools such as primary school, junior high and high school through absentees, class closures and school closures. These big peaks through the indices portray in dark last season. But this season, only a very small peak can be seen here. This slide shows activity in Japan, very small.

The Japanese government decided to start a nationwide serological surveillance of all age groups before the start of the flu season. You can see here antibody distribution of A/Beijing/262 H1N1 viruses. This is borderline to prevent epidemic at this time. All age groups, the antibody titer of this age group rested on this borderline. This is very important information to predict the next epidemic strain.

This table shows the antigenic analysis of H1N1 viruses. Could you look at this slide here? So the Okinawa isolates show directly to a higher titer to Beijing 262, the antigen similar to the vaccine strain. The remaining three viruses are isolated in the western part of Japan, Ishikawa 42, Ishikawa 43, correlate directly to a low titer to the vaccine strain like this.

These slides show the evolutionary pathway of H1N1 influenza viruses. You can see most of the isolates are isolated from this scene are located in new branch across here and the second branch located here. These two -- this one is related to vaccine strain to Beijing.

This slide shows the antibody distribution to two Influenza B viruses. Above here is the antibody distribution to all age groups. You can see here that most of the age groups contain antibodies to higher than 40 --? So this data suggests to us that this Harbin-like strain cannot cause intense strain in the coming season. Please remember this antibody distribution. And the other figure indicates antibody distribution to B/Beijing/243/97. This is a Victorialike variant. This is a Harbin-like variant. These two viruses were quite different originally.

The Japanese isolates reacted to the low titer to reactive strain Beijing/243 as you can see here. And one European strain isolated in France, B/Pasteur/266, reacted to low titer to reactive strain. The antigenic analysis of the B influenza viruses, one French strain reacted to low titer to the vaccine Harbin/07/94 strain.

This here is very interesting for us. So

last season, Japan recommended Harbin-like variant of the vaccine B viruses, but I was beginning to wonder if this Beijing-like strain may appear or not. But as a result, two types of B variant cocirculated in Japan, one variant, a Harbin-like vaccine strain, and the second variant a Beijing-like strain. These viruses cannot -- a vaccine cannot contain this variant. By a lower antibody distribution. So B/Beijing-like variant, Victoria-like variant, could circulate a major strain like this here.

This pie chart indicates the proportion of the isolates of B viruses. So 62.8 percent isolates to Victoria-like variant, B/Beijing/243, and the remaining 37.2 percent is Harbin strain. So the B/Beijing-like variant or the Victoria-like variant is predominant in Japan as the major strain. This is very important to understand the choice of the vaccine strain for next season.

This is the geographical distribution of the two B variants. The red indicates the number of isolates of Harbin-like viruses. And blue indicates the area where B/Beijing-like viruses are isolated. And light blue is mixed. You can see here that in most of the areas, the two variants are cocirculating. This is very interesting data for us.

This is an evolutionary tree of B influenza viruses. Most of the recent influenza B viruses have evolved into two evolutionary lineages. This is the first lineage, the Yamagata-like variant and this is the Victoria-like variant. So most of the recent isolates are located in this top branch cluster here. And second, the Victoria-like viruses in Japan, Shizouka, Shiga, Chiba, Osaka and Chinese Shangdong viruses belong to the top branch cluster of Victoria-like genus.

In the last slide, the figures indicate the antibody distribution to the H3N2 viruses. This top figure indicates antibody distribution to all age groups to A/Sydney/5/97 strain. All age groups, particularly the lower age groups, contain a higher HI antibody titer than had been considered. So this Sydney-like strain may not cause a major strain in this season. This bottom figure indicates the antibody distribution to the Yokohama-like variant. Roughly, these two antibody distribution of the two viruses are similar to each other.

So all isolates from Japan antigenically are very similar to A/Sydney/5/97 strain. This is the substrain Samara and Scichan, and the Scichan isolate reacted to a low titer to A/Sydney vaccination, around

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Two Sichuan strains were sent from CDC and we captured them again. Dr. Nancy Cox already pointed out that, these two strains are directly related to the vaccine strain in Chile in 1997. This is a proportion of the isolate in the 1996/1997 season, the Wuhan strain was the prevalent strain. In the last season, this Sydney-like strain increased in proportion like this. And this season, all isolates were actually 5/97 strain.

This is an evolutionary tree, a Sydney-like variant, an Okinawa or Japanese strain to top branch. This is related to vaccine Sydney-like virus here.

In conclusion, first in 1998/99 influenza activity in Japan was characterized by epidemic influenza A/Sydney/5/97-like activity.

Second, cocirculating influenza B viruses were antigenically and phylogenetically separated into two lineages. The first lineage, B/Yamagata-like viruses (B/Harbin/07/974-like viruses). Second, the Victoria-like viruses (B/Beijing/243/97-like viruses). Third, a few A H1N1 viruses from sporadic cases drifted from A/Beijing/262/95 viruses similar to A/Harbin/04/97 viruses.

Serological studies conducted several months before the start of the 1998/99 season indicate the following. Antibody levels to A/Sydney/5/97-like viruses were highest in the lower age group, primary school, junior high school and high school students. Mean antibody titers to A(H1N1) viruses in groups ranging from young adults to the elderly were low and below protective levels.

So even though antibody titers were low to A/Beijing/262/95 H1N1 viruses, a few drifted variants were isolated in this season. Antibody titers to B/Harbin/07/96 were elevated in persons over 49 years of age. Antibody titers to B/Victoria/2/87-like viruses were very low in all age groups except in persons 20 to 29 years of age.

With regard to the vaccine strain recommendations, a few points should be considered. A/Sydney/5/97-like virus variants may cause little activity in the coming season. New antigenic variants should be considered to replace the A/Sydney/5/97 virus component. In Japan, B/Beijing/243/97 viruses, variants of the B/Victoria/2/87-like viruses, appeared to cause major activity.

For the B component, should we consider B/Harbin/07/96-like strains? Second,

B/Beijing/243/97-like strains? Or third, strains which efficiently cover the above two strains? And how should the few A/H1N1 variants, drifted from A/Beijing/262/95, be evaluated?

Regarding new potential pandemic influenza viruses, Avian influenza A/H5N1 viruses disappeared at the end of 1997. In Southern China, avian A/H9N2 viruses have been isolated from poultry and pigs.

It was Sunday night or Monday night -anyway, it was midnight. I received some information from the southern part of China. A large number of H9N2 viruses were isolated in humans from some lady who travelled in China. I was beginning to wonder if this new H9N2 virus may cause the next pandemic strain and tried to confirm it with the Chinese Government, and then with the party who has authority over the southern part of China. Finally I confirmed that this information is very wrong. So the large number of H9N2 viruses were isolated from Southern China, but all of them were avian viruses, not human. So that is wrong information. So we have to carefully handle this kind of information. So it turns out that we are still waiting at the starter gate and looking for a tail of the pandemic strain. Thank you for your attention.

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CHAIRPERSON FERRIERI: Thank you, Dr. Nerome. I am afraid we have to move on or we won't be on time for the open public session later in the day and some of you want to apparently leave early. So we have a maximum of 15 minutes to present by Dr. Zambon of the Public Health Laboratory Service in the United Kingdom.

DR. ZAMBON: Good morning, ladies and gentlemen. It is a pleasure to be here. In England, just as in the United States and in Japan and in many countries of the world, we use many different ways of monitoring clinical influenza activity. The one which we place the most reliance on through experience really in terms of its usefulness is a consultation index derived from continuous morbidity registration by sentinel physicians scattered throughout country. This allows us to derive a population-based rate for influenza-like illness in the community, and we term this the RCGP index.

We know over the last 10 years or so that we can recognize activity above a baseline of about 50 consultations per 100,000 in association with circulating influenza viruses. And we describe activity above baseline usually for somewhere between 6 and 12 weeks every year. An activity between 50 and

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200, we describe as normal seasonal activity and we would expect to see this in most years. In unusual years, such as in 1989, when there was a circulation of a novel influenza H3N2 variant, we saw consultation rates of well over 400 per 100,000. And in maybe 3 years out of 10, we see consultation rates of between 200 and 400, which we describe as higher than normal seasonal activity.

So if we come to look at this season, the 1998/99 season, we have had a consultation rate of somewhere of approximately 270 per 100,000. So very similar in terms of impact to the season of 1996/97, when we had circulation of a new influenza H3N2 variant, the Wuhan variant. Shown in color here along the index are the actual virus isolates which we have had, and this season so far in England has been predominantly influenza A H3N2.

This is confirmed from the total laboratory isolates, where we have seen laboratory reports from all hospital laboratories, predominantly Influenza A activity with very little Influenza B activity. This line here should actually be labeled 1996/97. The reason for the comparison is that the death registrations that we have had are very similar in terms of total impact to the season of 1996/97.

And as I should also point out, our peak consultation was in week 1 of the year, and we have seen a downturn in the consultation index, which indicates that we are tailing off in terms of flu activity.

We have looked -- one of the problems of making slides for this meeting is that they are very rapidly outdated. Here we had, when I prepared this slide towards the end of last week, we had actually looked at some 300 viruses, and we have now looked at well over 400, the vast majority of which have been H3N2 viruses with only a handful of Influenza B isolates. The viruses themselves have actually been obtained from all regions of the country, almost in equal measure between northern/central and southern parts of England with some Scottish, Northern Ireland and Welsh isolates.

As I have mentioned, one of the things that have in England is a community-based surveillance system. And we have linked that community-based surveillance system with continuous morbidity registration to sampling for influenza in particular. So that individuals presenting with flulike illness to certain sentinel physicians automatically swabbed, and those swabs sent centrally. So that allows us a very rapid, timely handle on

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influenza isolates coming directly from the community as opposed to from the hospitalized population. And what we see there is the onset of influenza activity towards the end of the year and peaking from the community point of view around the turn of the year. And the hospital isolates are just now starting to come in from other laboratories, although we have the same picture in the community as compared with the hospital in that we have predominantly H3 activity in both sides with very little Influenza B.

In terms of the age distribution of the isolates which we have looked at, in the community isolates and in the hospital isolates, we do see some differences in the age distribution, not surprisingly in that the hospital isolates reflect the populations with which become hospitalized influenza, in particular the very young. I haven't disaggregated this data in the under 5's, but the vast majority of these are actually from the under 1's as opposed to the 1 to 5's and in the elderly. Whereas in the community, the majority of isolates that we get are from the working age population. Unusually for us, we have seen rather more isolates from the elderly than we would normally expect, and although we don't have the complete disaggregated consultation data, this

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also reflects the preliminary evidence that for some reason -- we don't have a good explanation for it -- Influenza A or Influenza this year has been particularly hard on the elderly population in the United Kingdom.

I have mentioned that we have seen Influenza H3 and Influenza B virus. We have not seen any influenza H1N1. But for the sake of completeness, I have included the HI data on the very last H1N1 virus that we had in the last season which was isolated in February/March of 1998. And the main point to notice there is that it was very similar in properties to the Bayern-like viruses, and indeed very similar to other influenza viruses circulating throughout the United Kingdom during the last season.

If we turn now to the influenza H3N2 isolates. As Ι have mentioned, we approximately 400 or so isolates which we have looked The vast majority of these isolates have shown reactivity with Sydney 5 antiserum. Very recently, though, in January, we have had isolates from a variety of different sources in the United Kingdom which we can see have a four-fold or more reduced reactivity to Sydney 5. We do not yet have molecular information about these viruses.

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you can see, the dates of the specimen are actually very recent indeed. So it will be sometime next week before we have molecular data pertaining to those. So the molecular data, if you will, that I am about to present on the H3N2 really pertains to the first strains that we have isolated.

I should draw your attention to this one, A/656, which still continues to show good reactivity to Sydney 5 in this HI test, but which was actually obtained from a person who had been vaccinated. And of some interest is the fact that it had rather lower reactivity to older, earlier strains.

In terms of the molecular analysis of viruses, we don't really have anything much which we can comment on in terms of important differences or features that we could identify as being perhaps evolution of new lines of influenza. But of some importance, perhaps, in the virus recovered from the vaccinated individual, we do see an isolated leucine to asparagine change here which potentially creates a novel glycosylation site and then some changes here in position 192, which is antigenic site B, which may possibly account for that escape from vaccination, although that may well be a rather speculative conclusion at this time.

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This slide should actually read H3N2 here. So of the data that we have so far, the phylogenetic analysis of the sequence data indicates that the England strains looked and mapped very closely to Sydney 5, and I would point out that these are viruses which continue to show good antigenic reactivity to the Sydney 5 antiserum. They are not the viruses

which have the rather lower reactivity which we have

seen and cannot attribute just yet.

We have had a sporadic number of Influenza B's, a total of about 23 or 24 from a variety of sources, both hospitals and communities. And as has already been remarked upon by Dr. Nancy Cox, some of the characteristics of the viruses are overt. react rather better with the Beijing/184 antiserum than they do with the Harbin. In our England strains, we do see a four-fold reduction in reactivity to vaccine strains or antiserum rates to vaccine strain. However, it is also fair to say that when we have analyzed these strains, at least the ones that we have sequenced, we have seen a number οf sequence differences, as you would expect from the vaccine strain itself. But we are not necessarily able to attribute, if you will, importance to the particular amino assay changes that we have seen, and I would

guess that in order to do that, this type of data needs to be pooled with data that is available that is available world-wide to give a picture of what is actually happening with Influenza B, and in particular the importance of the reduced reactivity that we seen in hemagglutination inhibition.

To conclude then, our Influenza B's look very similar in terms of phylogeny to the more recent Influenza B's that we have had from the last season and are showing a little bit of movement from the Beijing 184, perhaps slightly closer to the Harbin in terms of phylogeny.

So in conclusion then in England we have had moderately severe influenza season in association primarily with influenza H3N2 A/Sydneylike virus. We have seen one or two variants from Sydney/05 virus, which have low reactivity, although we don't yet have molecular correlates of that. also have Influenza B viruses associated with sporadic cases which have a slightly reduced reactivity to antiserum raised in the vaccine strains, and I would suggest that more data needs to be accumulated on the importance of that observation. Thank you.

CHAIRPERSON FERRIERI: Thank you, Dr. Zambol. We have time for -- we don't have time, but

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we will take it anyway. Does anyone have a question for Dr. Zambol? Dr. Breiman?

DR. BREIMAN: Rob Breiman. When you look at the homologous responses to your A/Sydney, your scale is quite a bit different than the one that CDC showed in the sense that it is 2,500, and I think their homologous was 640. Is there that much lab to lab variation that is expected? And I guess the corollary is then when you look and try to extrapolate to these new viruses, particularly the new Scottish and England isolates, would you then -- instead of looking at them as 320, if one wanted to compare with the results that Nancy gave, would they be more likely to be like 80 in that vaccine?

DR. ZAMBON: Okay. Well perhaps if I could answer the question broadly. There is often variation in HI tests, laboratory to laboratory. But if you look at the numerical values, that is perhaps, if you like, more emphasized if you concentrate solely on the numerical side of things. If, on the other hand, you look at, if you will, the overall meaning of those results, what we found historically, I think, is that our data correlate usually pretty well with the CDC data in terms of meanings of tests.

The second point to make is that we are a

	97
1	national influenza center and that our representative
2	portion of our isolates always goes to one of the
3	world influenza centers. So that our data can be
4	confirmed in HI testing. And I think in some ways
5	that answers the second part of your question, which
6	is relating to the numerical values that you see. I
7	think they are less important than the scale of
8	differences that you find.
9	CHAIRPERSON FERRIERI: Thank you. I think
0	we will take a break now and then resume at
1	approximately 11:30. Thank you.
2	(Whereupon, at 11:18 a.m., off the record

until 11:37 a.m.)

CHAIRPERSON FERRIERI: We will need to get to our seats right away. Will all committee members please come to the table? We will start with vaccine responses, and Dr. Levandowski is going to lead off. This is a very critical part of our meeting this morning before we adjourn for lunch, so that we try to remember information presented, options for strains, Roland, please start. and so on.

DR. LEVANDOWSKI: If I could get Okay. somebody to turn on the slides for me, please? And I again need the lights down. I will apologize if you are not able to see some of these things in the back

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row. Some of these actually are better seen by Gestalt anyway, so it may be all right.

I am going to be talking about the 1998 vaccine studies that were done to get information about serologic responses of people who have been immunized with the current vaccines. For the convenience of the committee, the handout includes the slides and the overheads that are being used to present this information, so you can follow along on those. What I am going to try to do is summarize what is really very voluminous information from many collaborating centers to provide information for this purpose, for the function of making strain selections.

Now this slide -- and maybe that is not in focus. I can't really tell from here whether it is or not. So maybe someone can help me with that. This slide shows the serum panels that were used for the serologic studies, and they include four separate serum panels from adults and elderly in Australia, Europe, and the United States. The vaccines used for the immunizations are shown here. And I will call your attention to the vaccine used in Australia, which includes as the H1N1 component 8 Johannesburg 82/96. Data for the H1N1 viruses for the Australian sera are not going to be presented because of that because it

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is not representative of the vaccines that are being used here.

The laboratories participating in performing the serologic testing to be discussed include the WHO Influenza Center in Melbourne, Australia, the National Institute of Biological Standardization and Control in London, the Centers for Disease Control and Prevention in Atlanta, the Centers for Biologics Evaluation and Research in Bethesda, and the University of Rochester in New York.

The first four labs, I should point out, share the first three sets of sera that are shown in the table here. And that includes about approximately 172 serum pairs. And then the University of Rochester supplies an additional 200 serum pairs for these kinds of studies.

Now this slide shows the H1N1 antigens, and I am sure you won't be able to see these in the back, but these are the antigens that were used for the serologic testing. And I don't think it is really critical to see all the names up here, because I will discuss some of them more specifically. But you can see that there are quite a few different antigens that have been used for testing. Not every antigen was used by all the laboratories in order that some of

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these strains could be explored more discretely, but there is a core of the different strains that are used for testing in each of the laboratories, and that is used as a gauge for confirming when there is a signal, since there are, as has been pointed out in some of the previous discussions, some technical differences between laboratories doing hemagglutination inhibition tests.

The serologic studies that I am going to describe have been performed in two separate campaigns that coincide with the WHO recommendations for the Southern Hemisphere in September of 1998, and the current evaluation of influenza viruses that is going on now. The antigens shown include representative strains for both of the H1N1 lineages that are circulating, including the A/Beijing/262, which is our current vaccine strain, and the A/Bayern/7/95-like strains, which was our previous vaccine component.

Now I would like to turn the slides off for a minute and use some overheads here. And, Dan, if you can put up the overhead from page 3. That is the same page number that is in the hand-out, so it may be more convenient for you to look at them that way. This overhead shows the results that were obtained in September of 1998 from two of the

laboratories using a panel of sera from adults in Europe. And by the way, I am going to just pick and choose here to try to make some points from the serologic testing that was done. The table includes data on geometric mean titers, percent greater than or equal to 32 of 40, and percent four-fold rises. data that are shown here are from NIBSC at the top and from the WHO Influenza Center in Melbourne at the bottom. The vaccine strain for these tests was the A-Beijing/262/95 strain. The vaccine used was clearly immunogenic and it produced brisk homologous antibody responses. And in this particular instance. A/Shanghai is a Beijing/262-like strain, Johannesburg, A-Prague and A-Aukland are Bayern/7/95like strains. In both cases, the A-Beijing 262 vaccine produced antibodies that cross-reacted very well with the Beijing/262-like strain and also with the Bayern 7-like strains.

If I can get the next overhead for page four. This overhead shows the results obtained in January of 1999 from two of the laboratories using a panel of sera from elderly in Europe. These data are from CDC at the top and CBER at the bottom. The vaccine strain, again, was A/Beijing/262/95. A/Hong Kong/4847 is a Beijing/262-like strain, and

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A/Johannesburg and A/Michigan/24 are both Bayern/7/95-like strains. Although the absolute antibody titers are somewhat lower than in the previous overhead, and this is again because of technical differences and also partly because these sera are from elderly patients, the vaccine did elicit response to the homologous and the heterologous antigens. And although the response to the Hong Kong strain was reduced, the difference here was less than a two-fold difference in geometric mean titer.

The next overhead for page 5. This overhead shows the results obtained in January of 1999 using a panel of sera from adults in the United These data are from the CDC at the top and from NIBSC at the bottom. The data from the CDC indicate a greater than two-fold difference between the vaccine strain and the Hong Kong strain, but quite good titers for A/Michigan. Conversely, the data from NIBSC indicate a greater than two-fold reduction in the geometric mean titer for A/Michigan, which again is a Bayern-like strain, and A/Ulan Ude, which Nancy being mentioned as from Russia, which is Beijing/262-like strain. There was no difference seen here for the other Bayern-like strain, A/Madrid, as shown in the NIBSC information.

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Then I am going to skip the next overhead there and go back to the slides. If you can turn the overhead off. This slide shows the H3N2 antigens that were used for serologic testing, and all of the antigens chosen represent strains that are related to the A/Sydney/5/97 current vaccine strain. So I don't really want to dwell on those, but just again to reiterate that there are a number of strains that are tested.

Go back to the overheads, the overhead for page 8. This overhead will show results that were obtained in September of 1998 using a panel of sera from adults in the United States. The data shown here are from the CDC at the top and from NIBSC at the bottom. The data are similar in both instances and show again that the vaccines used are immunogenic. They also demonstrate that the current vaccine strain produces antibodies that cross-react reasonably well with the other new H3N2 viruses such as A/Chile/37/92, A/Shanghai/72 and Johannesburg/29.

The overhead for page 9 shows the results obtained in September of 1998 using a panel of sera from elderly in Europe. The data are from the CDC at the top and from CBER at the bottom. And although the absolute titers are lower in the elderly than seen

with the adult serum panel just before, the vaccine responses to the new H3N2 strains appears similar to the vaccine except for the Johannesburg/3/98 virus, which shows a result that is more than a two-fold reduction in the CBER test.

The overhead for page 10 shows results obtained in January of 1999 for sera that were from elderly in Australia. These data are from NIBSC at the top and CBER at the bottom. And they demonstrate that the current vaccine strain produces antibodies that cross-react reasonably well with other new H3N2 viruses such as the A/Genoa/5/98, the A/Genoa/8/98, the Sichuan/346 and the Sichuan/418.

The overhead for page 11. This overhead shows results obtained in January of 1999 for adults in Europe. The data are from NIBSC at the top and from the WHO Center in Melbourne at the bottom. The data here demonstrate that the current vaccine produces antibodies that cross-react well with the other strains such as Genoa/5 and Genoa/8 and also Sichuan/418. However, the results here suggest a two-fold reduction for the Sichuan/346 strain.

You can take the overheads off again, please. This slide shows the antigens used for the B component of the serologic testing. These antigens

include representative strains for both of the B lineages that are circulating and include strains that are related to the B/Harbin/7/94 current vaccine strain and also similar to the B/Victoria/287-like strains.

Back to the overheads, page 13. overhead shows results that were obtained in September 1998 using a panel of sera from adults Australia. The data are from the WHO Flu Center in Melbourne at the top and CBER at the bottom, and the data again demonstrate that the current vaccine strain produces antibodies that cross-react reasonably well with the newer B/Harbin-like strain, which here is the B/Romania/318/98, which I think I remember was in the cluster that Nancy indicated was more like the Beijing/184/93. But the antibody titers are extremely low against the newer B/Victoria-like strains such as B/Beijing/243/97 and B/Shanqdong/7/97. And actually, this is very consistent with the experience that we have been noting over the past several years for the B/Victoria-like strains.

We can skip page 14 and go to page 15.

This overhead will show the results that were obtained in January of 1999 using a panel of sera from the United States with data from CDC at the top and CBER

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at the bottom. They demonstrate that the current vaccine strain again produces antibodies that cross reasonably well with other new Harbin-like strains such as B/Foshan/396 and B/Delaware/2/98. And again, the antibody titers are very low for the B/Victoria-like strain, the B/Shangdong/7/97.

Although the reduction is not as great as two-fold, the results for the B/Singapore/35 strain are on the low side for a B/Harbin-like virus. I don't know if I have got both slides and overheads for this. Would you turn the overhead off and I will see if the slide projects here. Actually, I think, let's put the overhead up. I think that will probably show up better. This should be H1N1 viruses.

So to try to summarize all of the information, of which I have given you some flavor from the bits that have been presented so far, we have taken the information and converted it so that we can show you the frequency with which we found new test antigens giving a 50 percent or greater reduction in geometric mean titer compared to the current vaccine strain. We use 50 percent because that is a fairly dramatic difference for a geometric mean titer. A two-fold reduction in geometric mean titers is actually fairly marked. The data included in this

table are only for those antigens where more than one lab is tested. So I am not showing you -- there is more information in the specific handouts from each of the places, but I have tried to summarize where we have some level of confirmation from other laboratories.

For the first four labs that are indicated here, the serum panels were shared. And again, for the H1N1, the Australian serum panels were excluded because the vaccine antigen was not A/Beijing/262/95. The top two antigens on this panel are the Beijing/262-like strains and the lower three are the Bayern/7-like strains.

Paying attention for the moment just to the total results here -- the column that says total the data for Shanghai/2, A/Johannesburg and A/Moscow uniformly indicate that there is no reduction in the geometric mean titer. However, the results for the Hong Kong/4847 and the Michigan/24 are somewhat mixed, with some laboratories showing some reduction and some and even differences within not, the laboratory for the particular virus. However, on the average, the reductions for all of these strains are less than 50 percent, which is shown in that last trying to take the average of all

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serologic panels that were examined and showing you a range of the differences that were found.

The next overhead. This should be a summary for the H3N2 viruses. There is a typo at the bottom that says something about Beijing/262, please ignore that. All of these strains are Sydneygenerally the A/Chile/37/92 and Sichuan/418 viruses appear to be well inhibited by sera from person who were immunized with the current vaccines. However, the Johannesburg/3 virus and the Sichuan/346, which represent Sydney-like variants, did not appear to be well inhibited, and there is more uniformity in finding reduced antibody titers compared to the vaccine strain for the different laboratories that are testing. On average, the responses to both of these viruses are reduced by more than 50 percent in the labs testing, and I think that gives some indication of the degree of divergence.

The next one, please? This slide shows summary data for the Influenza B viruses. And most of these panels are done with ether-treated antigen. Where that information was available, if we didn't have that information, I have included information for non-ether-treated antigen. And in some instances, there is not really a difference in the relative

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proportion of the antibodies, but sometimes there is as Nancy was pointing out. There are differences in specificity and sensitivity for those different ways of looking at the Influenza B serologies. data shows -- this slide shows the summary data for the B viruses, and the top two strains are B/Victorialike, and the bottom three strains are like the vaccine strain, which is B/Harbin. And generally the B/Harbin-like viruses appear to be well inhibited by the sera from persons who are immunized with the current vaccines, although there is a suggestion that some antigenic drift is occurring. And I would point out that the data for B/Delaware here, where there seemed to be more than a 50 percent reduction, actually is somewhat remarkable with non-ether-treated antigen to see differences. So I think that is something that we need to take into account.

As would be expected, the B/Victoria viruses do not appear to be well inhibited and there is more uniformity in finding the reduced antibody titers for these strains as compared to the vaccine. And on average, the responses to both of B/Victoria-like strains is a bigger difference than 50 percent in all of the laboratories.

We can turn that off and turn the lights

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So in summary, the vaccines used for the 1 clinical studies appeared to be immunogenic in the 2 populations that were tested. For all three of the 3 vaccine component strains, there is some evidence of 4 antigenic drift, which is possibly most notable for 5 the H3N2 virus strains representing drift variance of 6 the current vaccine strain. And as we have known for 7 8 several years now, the B/Victoria lineage persisting and the current vaccines may be 9 limited in their protection against those strains. 10 So I will stop there. I hope we 11 getting back on time. And if there are questions or 12 13 comments, I will take them. 14 CHAIRPERSON FERRIERI: Thanks, Roland. 15 Yes, Dr. Estes? 16 DR. ESTES: Mary Estes. Would you clarify for me the importance of the ether treatment? I don't 17 remember hearing about this before. Apparently it is 18 only used for the B viruses, and is this something 19 20 is new this year or just put that 21 perspective? 22 DR. LEVANDOWSKI: No, it is not new. Ιt is something that has been done for many, many years. 23 There are a number of studies that suggest serologic responses for Influenza B viruses are more

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comparable to what would be found for
hemagglutination inhibition assays for B viruses with
ether-treated antigen are more comparable to
neutralizing antibody. The correlation is much
better. And I don't think that has been entirely
explained on a chemical basis, but it is something
that has been noted in many different studies. My
personal feeling is that I would find the ether-
treated antigen hemagglutination inhibition titers to
be a better representation of what protective effect
there might be from the vaccine. But I don't think
that we should ignore the titers that we get
otherwise. What usually happens is that it is a
flatter looking curve. It is more difficult to show
a difference at all if there is one there with the
non-ether-treated antigen. And of course what we are
trying to do here with both the ferret sera and the
human sera is to see can we detect differences between
immunologic differences between the current vaccine
strain and the newer strains. So our comparison is
not really to show that these vaccines are being
protective, but really to have that comparative
difference between the strains. And we think maybe we

CHAIRPERSON FERRIERI: Dr. Daum and then

equalize things with ether treatment for B.

Dr. Greenberg.

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DR. DAUM: Just a quick question, I think.

Bob Daum, Chicago. What does the ether do?

DR. LEVANDOWSKI: Ether disrupts the virus by dissolving the lipid envelope. Influenza viruses are lipid envelope viruses and it is one way to do it. It is actually used in manufacturing the vaccines to make the subunit vaccine. One manufacturer uses ether as their solvent, whereas others may use detergents, but it is the same concept.

DR. DAUM: Why only B?

DR. LEVANDOWSKI: There are some studies with Influenza A as well, but I don't believe -- and somebody could correct me if I am wrong -- but they don't seem to show as much difference as Influenza B. We talk about these two viruses. They both are obviously orthomyxo viruses, but they are structurally somewhat different and physiologically or pathophysiologically, they may be somewhat different. I don't think I really want to get too deeply into that, but there are differences between Influenza A and Influenza B, and we call them that because of the disease that they produce, which is the febrile respiratory illness, but they probably are somewhat different.

1 CHAIRPERSON FERRIERI: Harry? 2 DR. GREENBERG: Harry Greenberg, Stanford. The lack of cross-reactivity between Harbin 3 Victoria on the B side, that has been the same for 4 5 several years, correct? 6 DR. LEVANDOWSKI: Yes. 7 GREENBERG: DR. Is there anything different now, this year, for B than there was last 8 I mean last year the same thing, that 9 year for B? Victoria was different but limited basically to China. 10 11 DR. LEVANDOWSKI: Right. Well, in terms of the serologic results, I would say I guess that 12 there is some evidence of antigenic drift going on in 13 the B/Harbin-like strains that I 14 think detecting in these serologic studies as well. 15 years, when we have done comparisons between the 16 vaccine strain and the non-vaccine strains, often the 17 antibody titers have been even higher against the non-18 19 vaccine strains. So I think we are seeing some reductions here, and I think that corresponds with 20 what was being described earlier for characterization 21 of the strains. There are antigenic differences that 22 can be distinguished with the ferret antisera. 23 24 DR. GREENBERG: But that is related to

other Harbin-like strains, not to the Victoria-like

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1	strains, right?
2	DR. LEVANDOWSKI: Right. Well, those are
3	two different issues. There are two lineages of
4	Influenza B that are cocirculating. But amongst the
5	B/Harbin strains, which are predominant everywhere, it
6	appears that there are some antigenic changes.
7	DR. GREENBERG: I was asking on the other
8	side, vis-a-vis the Victoria things are pretty much
9	status quo?
10	DR. LEVANDOWSKI: I don't think we can
11	gauge that from the serologic studies because we are
12	not immunizing at least and I am not going to
13	discuss any of the studies that Nancy was eluding to.
14	But I don't know if John Wood or Nancy Cox might have
15	something to add about the experimental vaccine
16	studies that have been done to try to if that in
17	some way indicates anything about what is happening
18	with the B/Victoria-like strains. I mean obviously
19	they have antigenic changes going on also that are
20	clearly detected by the ferret antisera, but I don't
21	think I can answer the question you are asking about
22	serologic responses in people.
23	CHAIRPERSON FERRIERI: Yes, Dr. Edwards.

And then this will be the last question.

DR. EDWARDS:

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In the past you have had

some pediatric serology. Is it felt that the pediatric responses so clearly mimic the adult responses that they don't provide additional information, or do you have that information and it is not here?

DR. LEVANDOWSKI: We would dearly love to have that information, but it is not very easy to find someone who can immunize children and provide the sera in a timely manner so that we can use that. We would very much like to have access to those kind of sera. As you know, we had a contract at FDA to support that for a number of years, and we are no longer able to do And we have been searching to find others who could help out in that regard. We do get some support from Vanderbilt and from the University of Rochester in providing some of these sera, but we just have not been extremely successful in finding a good, stable place to make it possible. Particularly for the very young children. It is a little easier for older children. But for the very young children who give a response that is not influenced by any previous exposure, we have a very hard time finding those.

CHAIRPERSON FERRIERI: Thanks, Roland.

Our next speaker is Dr. Offringa from FDA, who will speak on the availability of strains and reagents. My

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voice is altered due to a respiratory infection this week that was flu-like, but having been vaccinated and being adamantly attached to the protectiveness of flu vaccine, I do not believe that I have an influenza illness. I prefer to think it was adenovirus -- maybe.

RSV or paraflu, we have lots of affinities here.

DR. OFFRINGA: Good morning. I am going to give a brief overview of the status of candidate vaccine strains and potency reagents. I will begin with the Influenza B vaccine strains.

The current В vaccine strain is B/Harbin/794. As you have heard earlier, the name strain is B/Beijing/184/93. Currently, reassortants are not made for B strains, and Harbin is used for vaccine production because it is antiquenically similar the Beijing strain but has better characteristics. As you can see, it is a moderate to high yield growth strain. There are two candidate strains listed, B/Shangdong/7/97, which is in the B/Victoria lineage, and B/Foshan/396/98, which is a The B/Shangdong/7/97 strain has B/Harbin variant. been sent to manufacturers and has a moderate growth character. We are preparing to send the B/Foshan strain early next week, and as Dr. Cox mentioned earlier, there are also some other B variants which

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may be better candidates, such as B/Romania/318/98 and B/Bucharest/311/98. These strains will be included in the shipments as well.

If I could move on to the H1N1's. The current vaccine strain is A/Beijing/262/95. The reassortant being used for vaccine production is X127, which has a high yield growth character. At this time, we have no candidate strains identified for H1N1. As Dr. Cox mentioned earlier, there have been a few Beijing low reactors isolated, but there is no general trend in any particular antigenic direction.

Influenza H3N2, the current vaccine strain is A/Sydney/5/97. There are two reassortants being used for this, IVR-108 and RESVIR-13. Both of these reassortants have a median to high yield growth character. I have two candidate strains listed, A/Sichuan/346/98 and A/Sichuan/418/98. Both of these are Sydney-like variants and have been sent out to the manufacturers. Dr. Kilbourne's laboratory and our lab are both currently working on reassortants for these viruses, but at this time none have yet been isolated. The wild type strains have a moderate growth character.

For the potency reagents -- for the current vaccine strains, reference antigens and

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antisera used for the potency testing are available 1 for all strains, B/Harbin/794, A/Beijing/262/95, and 2 A/Sydney/5/97. Based on previous years experience, if 3 a new strain is chosen or new strains are chosen, 4 reagents would be available in May at the earliest. 5 6 Are there any questions? 7 CHAIRPERSON FERRIERI: Committee members? 8 Now is your chance. 9

DR. OFFRINGA: Thank you.

CHAIRPERSON FERRIERI: Thanks very much. will move on then to Dr. Slusaw from Pharmaceutical Research and Manufacturing Association, and he will present on behalf of the manufacturers. Apparently the current pharmaceutical firms that will making vaccine are Wyeth, Pasteur Connaught, Evans in the UK, and Parke Dale, related to Parke Davis. Pardon me? The other Rochester. Okay.

DR. SLUSAW: Thank you. Dr. Levandowski had asked me to give a brief discussion of some of the logistics and other timing issues that are of concern to the manufacturers. Kind of an explanation of why the manufacturers tend to look perplexed at various times during the strain selection process. thought I would recap some of that information for you.

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pieces of the puzzle that have to fall into place in order to successfully manufacture the number of vaccine doses that we have seen have been distributed

Although there are a lot of critical

three most important pieces are first of all insuring

and released over the last few years, probably the

that a supply of embryonated eggs is available to

produce the vaccine. And this is a process that

really begins far in advance, actually a year in

advance of the current vaccine manufacturing cycle.

And the critical part of the egg supply is not only

making sure they are there, but once the supply is

started and that flow of eggs is turned on, it is

impossible to turn off. And right now, the

manufacturers in the U.S. probably have about half a

million eggs per day available that need to be made

into some sort of monovalent concentrates.

Strain selection is also very critical, the activity that we are doing here today. And there are two components to that, both the timing of the strain selection as well as having suitable viruses with high growth characteristics, particularly the availability of high growth reassortants of the A strains, and having vaccine strains that we can purify and inactivate in our manufacturing processes.

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And then the third important piece of the

puzzle is the availability of the potency test

reagents for the SRID test. For new strains that are

selected each year, until these reagents are produced

and standardized, we really don't have a good handle

on how much monovalent we are manufacturing, as well

as we can't formulate trivalent vaccine until these

reagents are made.

I would just like to run over a little overview of the time table that Drs. Levandowski and Cox eluded to in their presentations. As I mentioned, the birds to ensure the egg supply have to be ordered about a year in advance. Each year in October or November, those birds are actually moved into the houses and soon begin producing eggs. Also in this time frame, we begin receiving candidate seed viruses from the FDA and from CDC, potential viruses that may be considered for inclusion in the next year's vaccine formulate. And happening kind of in parallel with this is the work on high growth reassortants of some

Manufacturing the first monovalents generally begins -- I think all the manufacturers currently are starting in January and may actually be

of these viruses that look like they may be serious

candidates for the formula.

starting before the official strain selection, taking best our quess based on the scientific and surveillance data that is available at the time and beginning production with one of the strains from the previous vaccine year. Of course with some of the high growth viruses we have these last few years, we can't continue to produce a single strain for a very long time without risking overproducing the number of doses of that strain. So we need to switch to the second and third strains in fairly short order. And typically we would like to have, if possible, second virus strain in February and then the third virus strain for the vaccine formula sometime in March. After some discussion actually in years where it is suitable to make the decision, we would like to see perhaps a provisional recommendation for a second strain pending the decisions that come out of the WHO strain selection meeting in February.

Monovalent concentrate production continues for about a 7 or 8-month period from January through August or so, and for new vaccine strains that have been included, potency test reagent production and standardization of those reagents occurs in parallel and is usually completed by about May or June. We generally target to manufacture the first

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bulk vaccine about the first week of June, and that material is filled and released and the license is typically issued about the first week of July, and the manufacturers begin distribution of the final product at that time. And the final product is distributed in the July through about October time frame, typically anything available later than that, the uptake by our customers and distributors will be very low and much of that material is returned. So we have a fairly narrow time window where all the material that we manufacture has to be sent to our customers.

just to recap from the previous overhead some of the more critical timing issues that concern the logistics and issues that the manufacturers have to consider. There is about a year lead time for the egg supply. We have good systems in place for that and it is generally not a concern. know we need to make vaccine each year. The problem is turning them off if we have to wait for strain selection. About 8 to 10 weeks are generally required to make and analyze a high growth reassortant virus. And I think as Drs. Kilbourne and Levandowski will attest, that is with a good strain. Certainly it can take much longer than that depending on any technical problems that may be encountered.

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1	Once we have a suitable seed virus in the
2	manufacturer's hands, it takes at least about a month
3	and sometimes longer depending on the passage level
4	and so on to produce a working seed that is suitable
5	for use in production. About 10 to 12 weeks are
6	required from beginning to end to manufacture and
7	standardize potency test reagents. And from start to
8	finish, it is about three to four months,
9	approximately 15 weeks, from the inoculation of a
10	monovalent concentrate through the production of a
11	final container of a trivalent vaccine. So one of the
12	issues I would like to emphasize is that although from
13	a scientific standpoint it is often useful to be able
14	to wait for additional data on strain selection, any
15	candidate strains that may be identified say a month
16	from now also have these lead times for reassortant
17	production and working seed production that must be
18	added onto them. So if a candidate strain selection is
19	made very late, there may be several months of
20	activity that is needed to be done by the
21	manufacturers before those strains can actually be
22	brought into production.
23	CHAIRPERSON FERRIERI: Thank you very

CHAIRPERSON FERRIERI: Thank you very much. Questions for Dr. Slusaw? Well, we will be finishing up the morning session then with options for

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strain selection, Dr. Nancy Cox from CDC.

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DR. COX: Okay. So I will try very hard to summarize what we have been hearing today and lay out the options in some kind of a logical framework. I just wanted to remind you that global data were reviewed extensively in September, and the WHO recommendations at. that time for the Southern Hemisphere's 1999 season, which will be coming very soon, are for an A/Sydney-like H3N2 component, a Beijing/262 H1N1-like component, and A/Beijing/184/93-like virus, which of course is the B/Harbin/7/94 in all the countries using vaccine.

I think we need to review the need for a trivalent vaccine. We do have Influenza A H1N1 viruses continuing to circulate worldwide. There are two distinct antigenic and genetic groups, as you have seen. Although they have been isolated rarely during the past four months, if we look back over the past couple of years, we see that there have been outbreaks caused by H1N1 viruses in different areas of the world.

Influenza H3N2 viruses have continued to circulate worldwide in large numbers and to cause significant morbidity and mortality. They have predominated during the past year if you look

globally, and of course the Sydney variant is the 1 2 culprit we are talking about. 3 Influenza B viruses also continue to circulate worldwide. There are two distinct antigenic 4 5 and genetic groups, as you have heard, and they have been isolated fairly frequently in North America and 6 7 Europe. 8 For H1N1 viruses, sporadic isolates have 9 been reported in Asia, Japan, Thailand and China; in Europe, Finland, Italy and Spain; in the United 10 States; and a single strain in South Africa. Overall, 11 activity has been low, as I just said. 12 13 There has been antigenic variation noted among the Asian A/Beijing/262/95-like strains, yet we 14 15 have no clear genetic correlates for these antigenic 16 changes. And when we have taken these strains that 17 have the lower reactivity to the Beijing/262 antiserum 18 and put those strains into ferrets, we found that the 19 antiserum produced really did not either clearly 20 identify these viruses as a group or cross react well. 21 The current H1N1 component induces broadly 22 cross-reactive antibodies versus the Bayern-like strains, and this particular vaccine component was 23 24 updated last year.

So our options -- I will put all the

options up. Of course, I have sort of put them in the order of -- well, in some sort of order. You can judge for yourselves. But we could retain a Beijing/262/95 strain in the vaccine. We know that it induces broadly cross-reactive antibodies. It has known properties.

We could update to a more recent low reacting virus on the Beijing/262 lineage, but we really don't have a good candidate. And there have been so few isolates, we would be stabbing in the dark to some extent.

There is another alternative, which I think is not a very good one, but of course I should list it. We could update the H1N1 component and go back to the other lineage, that is the Bayern lineage. But we already know that viruses from that lineage have not induced broadly cross-reacting antibody to the Beijing/262 lineage strains.

Okay. So now I will summarize what we have seen today regarding Influenza A H3N2 viruses. The Sydney strains have circulated worldwide, both during the 1997/98 influenza seasons, the 1998 season in the Southern Hemisphere, and this season that we are just moving through. There have been widespread outbreaks and epidemics during the 1998/99 season in

Asia, particularly in China. Hong Kong has also had activity. Japan and Korea have also reported H3N2 activity. A number of countries -- a large number of countries in Europe have isolated H3N2 viruses in association with influenza-like activity and Canada and the U.S. have had predominantly H3N2.

So there has been extensive H3N2 activity overall. There is some antigenic heterogeneity observed, although the majority of the strains clearly are still Sydney-like. We have the A/Sichuan/436/98 strain, which is the best characterized of the low reactors, and we have seen that in human serologic tests that the post-vaccination GMTs to this strain are reduced by about 50 percent in some tests in some laboratories.

Now we have a number -- actually a fair number or quite a large number of additional strains to analyze from China, and we have noted variation among those. I just mentioned the reduced post-vaccine response to the Sichuan strains, and we did a rough count before we received 7 more packages of virus yesterday, and we had 200 H3N2 strains that are moving through the system. We did update the vaccine component last year from Nanching to Sydney.

So we could retain the A/Sydney vaccine

component. Most current strains are Sydney-like, although we are seeing evidence that they are changing a bit. The Sydney high growth reassortant has known characteristics, and that is always an advantage. Or we can update the Sydney component. And the reasons that we might think that this would be necessary to do is that this variant has circulated widely for two years. It seems unlikely based on past patterns that we have observed with H3N2 viruses that we would have a third year of circulation of the same strain, particularly given the intensity of circulation.

with more severe disease, including hospitalization and death. And we have detected this particular variant. We have, as I mentioned before, many more viruses to test from Asia, the U.S. and Europe, and I think it would be worth our while to do some additional serologic analyses with the human serum using some of these recent strains from China.

We will move on to Influenza B viruses. Of course, we have two lineages, the B/Victoria and the B/Yamagata groups that are co-circulating -- B/Vic in Asia only. Outbreaks and sporadic activity have been reported this season in Asia. In Europe and the countries that I have asterisked are those in which B

has really been the predominant strain. In the United States, approximately 18 percent of our isolates are type B, and there was a B virus from Chile.

Influenza B activity overall has been fairly moderate worldwide. We have noted that over half of the U.S. viruses that we have characterized that were isolated during this season are four-fold or greater reduced in titer with the B-Harbin serum. And similar results have been seen in Europe.

Now the current B component introduces antibody that cross reacts with many non B/Vic-like viruses in human serology when we are using ethertreated antigen. This vaccine component was last updated in 1995. So we haven't changed our B component for a number of years. And the last time we changed the B component, we were seeing a similar pattern with our ferret antiserum to the vaccine strain, B Panama, not covering the recently isolated strains in Europe and North America. So there is sort of a parallel from the last time that we updated the B component that I can clearly see.

So what are our options? We can retain the B/Harbin component. It does appear to cover most strains tested in our human serologies. This strain has known characteristics. It grows well for the

manufacturers and so on.

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Or we could update the B/Harbin component to another virus, a more recent strain on the same lineage, and we would do this because of the reduced ability of the Harbin ferret serum to inhibit the current strains. We have a number of additional strains to test, and in particular I think it would be useful to assess this B/Georgia virus and the other strains that Dan mentioned.

The other possibility that I must put on the table is that we could update the B/Harbin component to a virus on the B/Vic lineage. discussed this several times in the past, but as you have seen, the B/Victoria viruses remain more or less confined to circulation in Asia and you've seen what WHO recommendations were for t.he Southern But we always need to keep in mind that Hemisphere. there is a growing susceptible population to viruses on this particular lineage. Thank you.

CHAIRPERSON FERRIERI: Thank you, Nancy.

Are there questions for Dr. Cox? Yes, Dr. Breiman?

DR. BREIMAN: Nancy, could I ask a few questions that might clarify things for me? The data for me at least are a little dense and getting through it is, for me, a little challenging. I just want to

make sure I understand a couple of things. One, when 1 you -- is it fair to say that if you look at the 2 Sichuan/418 antisera that it reacted as well with 3 Sydney/05/97 as the homologous antisera? That is the 4 5 way your table reads. So it actually does as well as 6 Sydney? 7 DR. COX: So you are looking at the 8 reciprocal? 9 DR. BREIMAN: Yes. 10 DR. COX: Yes. 11 DR. BREIMAN: Okay. And then you do get with the Sichuan/418 added reactivity against these 12 13 new SI strains that you have mentioned like the 417, 14 the 420 and the 320. 15 DR. COX: Yes. 16 DR. BREIMAN: That wasn't there before with the Sydney. And then there is only one dilution 17 difference from all of the other antigens when you 18 19 compare the two antisera except that 20 A/Okinawa/289, which I don't know if you felt that 21 that was clinically important. The A/Okinawa/289 22 looked like it substantially reacted differently with the Sydney antisera versus the Sichuan/418 antisera. 23 24 DR. COX: I am sorry, which one? 25 DR. BREIMAN: It is the A/Okinawa/289/98.

It had a 2560 titer against Sydney and 640 against 7 2 Is that -- am I --SI/418. 3 DR. COX: Yes. I mean, that is just a strain that is well inhibited by all the antisera. 4 5 DR. BREIMAN: Yes. So I mean -- I guess what I am asking is is that a meaningful difference, 6 7 the fact that there was 2560 for one and 640 for the 8 other? 9 DR. COX: No. No. 10 DR. BREIMAN: So it looks based on that 11 table that you provided that the -- you are only 12 gaining by looking at the Sichuan/418 13 example, you are only gaining additional reactivity 14 against these new strains that you identified this 15 year, the SI/417 and 420. 16 DR. COX: That is right, Rob. And when we 17 look at these patterns year after year, what we are 18 looking for is where the virus is going. You know, we 19 are trying to see where is it going to be next year at 20 And it is a really difficult -- it is 21 tremendously challenging, first of all, to get through 22 all the data. And then to try to understand what you 23 are seeing this year within the context of what you 24 have seen in other years. So if you are just looking

at the data that you are seeing this year, you would

say, well, it is a no-brainer. Stay with the Sydney. 1 2 The majority of the strains are Sydney. You are not going to gain very much. But if we look over the past 3 10 years, you see that it is unlikely -- it is not 4 5 impossible because influenza viruses behave as they will, not as we wish they would. But it is unlikely 6 that there are going to be Sydney-like viruses 7 8 circulating next year. So we need to try to see what -- so we are looking for a virus that is going to give 9 us an advantage next year. So we are looking for the 10 11 patterns and so on. So --12 DR. BREIMAN: I guess I was just wanting to confirm that that was my impression from looking at 13 your table. That it looked like you would actually 14 15 only gain by switching to say the Sichuan/418 type of antisera. I mean a vaccine that would give you that 16 17 kind of coverage. 18 DR. COX: That is right. 19 CHAIRPERSON FERRIERI: Dr. Greenberg? We 20 don't have -- I think everyone knows where we are from 21 So we don't have to announce our institutions. 22 DR. GREENBERG: Harry Greenberg. decision is made to move to a new H3N2, a Sichuan-23 like, what is the time table to pick the ideal?

have a whole bunch of new viruses that have just come

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in and you alluded to the fact that you wanted to test some more of these viruses from China. How much -- I mean, I don't have a real feeling for what that drill is. I just heard from the manufacturers how important it is to identify the specific strain, and I just wondered where one would be in picking a new H3N2 strain, if that was the decision made.

DR. COX: We face this dilemma every single year. And one of the disadvantages -- we are really operating at a bit of a disadvantage. sort of answering in an indirect way. We are operating at a disadvantage this year because influenza activity in the United States and Europe was a bit late getting going. And so the strains weren't coming in as quickly. We are getting a tremendous number in now, and likewise there was a delay in getting the strains from China. So that really puts a lot of pressure on us to get these strains out quickly -- to get them analyzed as quickly as possible and to get them out quickly. Now there are a variety of shortcuts that are taken when we find ourselves in this kind of a situation. Sometimes we have often funneled viruses through FDA and they are sent out through FDA to the manufacturers at exactly the same time so that they get exactly the same passage level

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If we are really pushed, we can send the 1 and so on. strains directly to the manufacturers. In some years, 2 3 been impossible to get a high reassortant, so the manufacturers were forced and 4 actually able quite successfully to use Influenza A 5 strains that weren't high growth reassortants. I thin 6 the last time that occurred was in 1986 with the 7 Taiwan strain. 8 So it is a bit removed from our current experience. But there are a whole variety of 9 things that can be done if they need to be done, and 10 we just try to expedite things the best way we can. 11 I know that both Ed Kilbourne and Roland Levandowski's 12 are working very hard on some high growth 13 reassortants now and we will just do everything we can 14 to expedite things. 15 16 CHAIRPERSON FERRIERI: Dr. Daum and then 17 Dr. Hall and then we are going to quit for lunch.

DR. DAUM: Bob Daum. I am intrigued by this observation that the B/Victoria-like viruses remain in a small part of the world and despite several people admonishing us to listen to the fact that there is a growing number of susceptibles elsewhere. And I would like some clarification from influenza experts as to whether this kind of behavior is typical of influenza viruses and whether we should

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really consider that issue in advising about formulating the B vaccine.

We have been watching the DR. COX: B/Victoria viruses circulate in China and a few other countries in Asia exclusively for -- since about 1991. I think in the 1990/91 season, there were some B/Victoria-like strains isolated in Europe. And then they just died out. But since then, those viruses have continued to circulate and evolve in China. we would wait, I think, to see their spread to other continents as we did for the H1N1 A/Beijing/262/95like strains before we got terribly excited about putting them in. But nevertheless, we have to keep in mind that these viruses are evolving and population is changing.

CHAIRPERSON FERRIERI: Dr. Hall?

DR. HALL: Caroline Hall. Nancy, from -obviously from the H3N2, it would be ideal to have a
candidate that gave very good reactivity to both the
Sichuan and the Sydney components. And a couple of
your isolates, at least from the serology that you
have given us, do look like they can provide that.
The recent ones from Japan, et cetera. Even the
Alaska. Do we know anything about those in terms of
growth or potential candidate vaccines?

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1	DR. COX: The Fukuoka is a cell isolate.
2	And you are talking about the Alaska yes, those are
3	all cell isolates.
4	DR. HALL: Is the Okinawa also a cell
5	isolate?
6	DR. COX: Yes. They are all isolated in
7	NBCK cells.
8	DR. HALL: Have they been tried?
9	DR. COX: No, no. We haven't pursued
10	those getting egg isolates. And perhaps Dr. Nerome
11	would have some egg isolates available in Japan. I am
12	not sure just what he has available.
13	DR. HALL: But they do look like they give
14	broader reactivity.
15	DR. COX: They may. The real test is the
16	cross once you have your ferret antiserum to that
17	particular virus. But, yes, it is possible that one
18	of those would.
19	CHAIRPERSON FERRIERI: Related to that,
20	though, Nancy, am I misinterpreting data that would
21	suggest that the current antibody to A/Sydney does
22	cross react with Sichuan/418/98 in some of the
23	vaccinees at least from Europe some of the data
24	from Europe and Australia?
25	DR. COX: Yes. There is a much greater

difference in reactivity in the human serologic 1 2 studies with the Sichuan/436 strain the 3 Sichuan/418 strain. CHAIRPERSON FERRIERI: Well, let's break 4 Thank you very much, Nancy. We have an hour and 5 15 minutes this afternoon approximately for further 6 discussion and recommendation to CBER on the strain. 7 So we will reconvene at 1:40. 8 9 (Whereupon, at 12:38 p.m., the meeting was adjourned for lunch to reconvene this same day at 1:42 10 11 p.m.) 12 13 14 15 16 17 18 19 20 21 22 23 24

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NEAL R. GROSS

1	A-F-T-E-R-N-O-O-N S-E-S-S-I-O-N
2	1:42 p.m.
3	CHAIRPERSON FERRIERI: Well, I am sure
4	that others will soon join us, but this is an
5	opportunity to have a very thorough discussion of the
6	issues that were presented today and coming up with
7	recommendations for next year's vaccine. Ms. Cole,
8	are you with us? Ms. Cole? Rebecca? I want her to
9	be tuned in with us before we get going.
10	MS. CHERRY: Rebecca, are you there?
11	MS. COLE: Yes, Nancy, I am here.
12	CHAIRPERSON FERRIERI: Can you hear me
13	too?
14	MS. COLE: Yes.
15	CHAIRPERSON FERRIERI: I thought I would
16	start by seeing if there were any members of the
17	committee who think we should take the path of least
18	resistance and just keep all the current components.
19	Do I have a show of hands? Any hands? None.
20	Rebecca, how do you feel about it?
21	MS. COLE: No.
22	CHAIRPERSON FERRIERI: Very good. We are
23	all in consensus then. I am sorry, Dr. Slusaw. I am
24	sure you are not too surprised, though. Well, let's
25	start discussing then perhaps. I want to do it one by

one. But before we start, is there anyone who feels there hasn't been enough information or you feel there is one last important question you must ask that would influence your decision making? Yes, Dr. Hall?

DR. HALL: I almost hesitate to mention this, but I just wondered has there ever been a consideration of adding a fourth component so that if you could not get the ideal virus to cross react between two, if the fourth component -- if there were two, say, candidates that grew well. So this would mean -- I can't imagine what it means in terms of the manufacturing, but at least in terms immunogenicity. If this has ever been a consideration or should be potentially one.

CHAIRPERSON FERRIERI: The closest thing to that, perhaps -- and then I will let someone answer it -- is when someone last year who came to the meeting and spoke from the audience proposed a separate vaccine for children, and that wasn't a real popular suggestion for a number of scientific reasons as well. Roland, would you like to address this briefly and then maybe someone from the audience?

DR. LEVANDOWSKI: Okay. I will take a stab at it, but I think it is something for the manufacturers to talk about. I think it is a very

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The manufacturers, I guess, practical thing. through campaigns for each of the strains, and they have so many days that they can be manufacturing with all of the strains. So if there is another component that is added to that, it takes away from that total number of days that can be used to manufacture the vaccine. So if we just thought about it in terms of simple numbers, if three strains take 12 months, more strains still take 12 months and so you get that much less of each one of the components as a result and less vaccine. I guess my understanding is that not every day in manufacturing is a day that leads to a product that results in distribution, so there some of that that goes on also. I think it would be possibly feasible for manufacturers to do that, but not under the current understanding of how they are distributing vaccines and how much vaccine is being demanded. There would have to be some give somewhere in the system, either more strains or more I guess it is a choice that has to be made. Apart from anything to do with whether it really would add anything to the immunologic responses.

CHAIRPERSON FERRIERI: Dr. Sluslaw, do you want to add anything here? While you are deciding, I would like to announce that we are going to have an

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open public hearing starting immediately now. So if you wish to speak, you can be part of the open public hearing as well as addressing the question. And anyone else who would like to come forward on the subject that we are discussing. Could you please announce your name for the recorders, please?

MR. WHITAKER: Charles Whitaker, Pasteur Merieux Connaught. In relation to the discussion of a fourth strain, as we saw earlier, the increased doses of vaccine which have been manufactured over the last few years have been made possible because of anticipation of manufacturers to meet the demands that have been increasing. The problem with introducing the matter of a fourth strain, such as to cover I quess the B situation where we have two circulating families of B viruses -- introducing that complication into the formula produces a ripple down effect for manufacturing which, of course, now in order to meet the current demand, we are producing early in the year, starting in January as described. The problems of an additional strain now of course compounds the addition of the growth time and development, first of all for a suitable candidate seed, and then the production of that fourth strain to be included, including the reagents and other things.

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time, with the demands that we have on our production facilities to meet current demands with the trivalent, it is really not possible for us to produce the same amount of doses required with the fourth additional strain, and we would certainly want to defer that to a time when the strain might be more widespread than we see it right now. So far the B has been isolated and has not spread further, the B/Victoria-like strains. So we would really take a serious step back, I think, in our production capabilities if we were forced to do that.

CHAIRPERSON FERRIERI: Thank you. The issue is much broader than that. FDA may have an on official line this, but this introduces а completely new product with no data to support it immunologically. You would have to launch massive large-scale trials to do this. So it brings forward more complications than the burden that would be imposed on industry. Brief comments now before I hit my agenda. Dr. Eickhoff and Dr. Greenberg?

DR. EICKHOFF: Dr. Hall, I think, has raised an interesting point. And if I may reflect for just a little bit. There was a time in history, and Dr. Kilbourne knows this problem much better than I actually, when in the late 1950's and early 1960's the

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vaccine used -- and it was made primarily for military use rather than civilian, it had five or six components in it. But it does raise the issue of do we need a trivalent vaccine. We have had a trivalent vaccine now since about 1977 or 1978 or thereabouts. So we have the tradition of 21 years behind a trivalent vaccine, simply because all three major virus types were cocirculating.

Listening to Dr. Cox present her data this morning, I wondered transiently, why don't we just dump in H1N1. And there are a couple of good reasons why we should not just do that. Even though it is not a big, big cause of morbidity and mortality in adults and there is generally little or no excess mortality with H1N1 strains, but it does disenfranchise children, and that was the genesis of the comment last year. And particularly it disenfranchises high risk children who would probably suffer from such a move on But there is no federal regulation that our part. says we have to have a trivalent vaccine. Indeed we don't. We are operating from the background of tradition.

One option -- and I don't think we should spend a whole lot of time discussing this issue today -- but one option to consider at some point when it

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might be appropriate is should we take out a component, like an H1N1 or a B, and instead substitute two cocirculating H3N2 antigens, for example. I don't think this is the year to do that, but at least we are not limited to an H1N1, H3N2 and B. That is purely tradition.

CHAIRPERSON FERRIERI: Harry?

DR. GREENBERG: I was simply going to ask historically is there data when two sort of types of either an H1 or H3N2 are given together, does that work as well? Traditionally the trivalent vaccine has been three different viruses basically. But if you made it two different with two sort of subtypes, do you get appropriate immune responses? For example, if you had two B's in this current vaccine, would you get a good response to both of them? Is that known?

DR. KILBOURNE: No, it is not known. And I thought Ted was going the other way with his comments of the early multiple virus vaccine. Because one concern at that time came up when we were challenged with pandemic viruses and we still wanted to be stuck with a multi-component vaccine at that time. It was a matter of antigenic competition, which is a real business. So as our chairman was reminding us a minute ago, the new immunologic problems that are

going to arise with this are not just regulatory and involved with the vaccine manufacturers. I think you will have to reexamine the whole vaccine in terms of responses to all antigens.

CHAIRPERSON FERRIERI: Well, let's move Anything else? I would like to start with What I think would be best for us to do today is do one at a time and come up with recommendations and we will vote on them. anyone wanted to speak in the open public hearing and no one stood up. Would you like to?

MR. RUBEN: Yes.

CHAIRPERSON FERRIERI: Please. Announce your name and association.

MR. RUBEN: My name is Fred Ruben. I am with Pasteur Merieux Connaught. I just wanted to make a comment about what happened this past year. There were some delays in getting vaccine out to the public due to manufacturing difficulties. And what I am thinking -- I am one of these people that like to think of the worst case scenario, and I am thinking that we do need some time this year to pick an H3N2 that is going to be appropriate for our vaccine. We have got a lot of unknowns given the strains that are coming over from China. So I am thinking that it may

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take well into the spring to come up with the right decision about that.

I am also thinking how horrible it is to be running a public health clinic and not have vaccine when you've got your clinic scheduled and patients are clamoring for it. The media picks up on it and says there is going to be a vaccine shortage. creates a nightmare. And I think as an influenza thinking body and all of us are on the same page, we want to continue to have the public to have confidence in what we are doing. I think we ought to allow for time to make the correct decision about the H3N2. But if we are going to do that, there is always a counter -- there is always an opposite effect. I think we have to make a decision about the other antigens a little bit sooner in order to have time to produce those so you have the luxury of having the time to make the H3N2.

So in the best of worlds, what I would recommend for consideration today would be to make some decisions about the H1N1, the B strains that have been going around for five years in spots here and there, and to go ahead and play a little guesswork with those, but not guess on the H3N2 and allow manufacturing to know what to make with those first

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two antigens, the H1N1 and the B. Then I think we are all going to come out ahead because I think we will probably have vaccine on time next fall.

CHAIRPERSON FERRIERI: Thank you very We can now adjourn the meeting. Well, let me continue. We will start with H1N1. For those of you in the audience who have been here past years, year in and year out, I think this panel has been very prudent, appropriately cautious when necessary, and very sensitive to the needs of industry. It has not always permitted us to give you all your answers at once, as you know. And FDA and CDC and other regulatory bodies, I think are similarly prudent. And to move in and make some rash decision would be certainly not in keeping with our past performance and record here.

So with H1N1, let me summarize just a tiny bit what we have heard then. The current strain, the A/Beijing/262/95 induces very broadly cross-reactive antibody that is able to interact with a number of other strains. The beauty of the current strain, the the current vaccine, is it is well characterized and we certainly have a lot information about it. We have no information that is substantive on other strains. So if we could just

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1	focus on this now, the H1N1. I would like to open it
2	up now to our advisory panel for a reaction and a
3	motion and then we will come to a resolution on H1N1.
4	To start, Dr. Estes and then Dr. Greenberg.
5	DR. ESTES: Well, I actually recommend
6	that we keep the current vaccine strain.
7	CHAIRPERSON FERRIERI: Thank you, Mary.
8	That is one of the most beautiful and succinct
9	sentences that I have heard today. Dr. Greenberg?
10	DR. GREENBERG: I second the motion.
11	CHAIRPERSON FERRIERI: Beautiful. We are
12	into discussion of the motion that has been seconded.
13	Any comments? Ms. Cox, do you wish to add anything?
14	Ms. Cole, sorry. Rebecca, do you have any comment on
15	the motion?
16	MS. COLE: No, Pat, I agree with it.
17	CHAIRPERSON FERRIERI: Okay. Thank you.
18	Any further discussion? Then we will have a formal
19	vote, yes or no in favor of the motion to retain
20	A/Beijing/262/95 in the new vaccine.
21	DR. DAUM: I was intrigued by one of the
22	options that Dr. Cox put forward, which would be to
23	update to a more recent virus in the Beijing lineage,
24	but then dismayed that there is no good candidate to
25	do that updating with. And I guess that therefore I

1	am coming around to the same conclusion, which it
2	sounds like others have expressed. But if such a
3	candidate could be developed, it might be a time to
4	reconsider my view on this.
5	CHAIRPERSON FERRIERI: Nancy, do you have
6	any comment on that? She may not be in the room right
7	now. Well, there is a motion here. I call for the
8	questions. We will start with Dr. Greenberg, yes or
9	no in favor of the motion.
10	DR. GREENBERG: I vote yes.
11	CHAIRPERSON FERRIERI: Okay. Dr. Daum?
12	DR. DAUM: Also yes. I hope that comment
13	would be noted.
14	CHAIRPERSON FERRIERI: Dr. Huang?
15	DR. HUANG: Yes.
16	CHAIRPERSON FERRIERI: Dr. Kohl?
17	DR. KOHL: Yes.
18	CHAIRPERSON FERRIERI: Dr. Snider? Is he
19	in the room?
20	DR. SNIDER: I pass.
21	CHAIRPERSON FERRIERI: Pardon me?
22	DR. SNIDER: I pass Madam Chairman. I
23	just got back from lunch.
24	CHAIRPERSON FERRIERI: Thank you.
25	Abstention. Dr. Estes?

1	DR. ESTES: Yes.
2	CHAIRPERSON FERRIERI: And Dr. Edwards?
3	DR. EDWARDS: Yes.
4	CHAIRPERSON FERRIERI: Dr. Kim, I think,
5	had to leave for his plane. Dr. Eickhoff?
6	DR. EICKHOFF: Yes.
7	CHAIRPERSON FERRIERI: Dr. Hall?
8	DR. HALL: Yes.
9	CHAIRPERSON FERRIERI: Dr. Hoke?
10	DR. HOKE: Yes.
11	CHAIRPERSON FERRIERI: Dr. Poland?
12	DR. POLAND: Yes, with the one concern to
13	note that if I read it right, the only U.S. isolate so
14	far would not be covered well by this vaccine strain.
15	CHAIRPERSON FERRIERI: Dr. Breiman?
16	DR. BREIMAN: Yes.
17	CHAIRPERSON FERRIERI: Dr. Kilbourne?
18	DR. KILBOURNE: Aye.
19	CHAIRPERSON FERRIERI: Aye, great.
20	CHAIRPERSON FERRIERI: I think I have
21	covered and my vote is yes, Nancy, for the record.
22	Okay. I wanted to start with the easiest. That gives
23	us more inspiration to tackle the others. I would
24	like to move to B now, so that we separate the A's
25	from the B's, and then we will tackle H3N2 last. So

the current strain, the B/Harbin/7/94, this past several years has been included in the vaccine, four years or so. For the record, I want to be accurate. Roland, how many years has the B/Harbin been in the vaccine? Four?

DR. LEVANDOWSKI: Since 1995, so I think this is coming on to the fifth season it would be -- the fourth or fifth.

CHAIRPERSON FERRIERI: Okay.

DR. LEVANDOWSKI: One of those.

CHAIRPERSON FERRIERI: Fine. We have heard that in Asia we have some B/Victoria-like strains and B/Yamagada, and we have also heard that there are lower titers reacting with the newer United States viruses with decreased inhibitory activity of ferret sera. So among the possibilities today would naturally be, number one, to keep the current one, and there are other candidate strains that have been studied a little bit -- the B/Shangdong/7/97 and B/Foshan/396/98. The former, the Shangdong, has been studied to a certain extent and apparently has a moderate yield. But there are unknowns about Foshan. But we heard that among the possibilities also would be updating B/Harbin of the same lineage or update the B/Vic lineage. We will start some discussion on it,

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1	but I do think that I have concerns, grave concerns,
2	about continuing with B/Harbin, and there has been
3	considerable B activity here and there around the
4	world and we might be in for another B year next year.
5	We haven't been hit hard by B for a little while, for
6	a few years. Who would like to launch a little more
7	analysis and moving us closer to some decision making?
8	Dr. Poland?
9	DR. POLAND: I guess from review that we
10	heard this morning and looking at the data, and I
11	can't recall what the yield was for this, but the
12	B/Beijing/184 strain looked to me to be the most
13	appropriate given the isolates that we have so far.
14	CHAIRPERSON FERRIERI: Which one, Greg?
15	DR. POLAND: B/Beijing/184. But Roland,
16	could you remind us, was that one that we could grow
17	in moderate or better yield?
18	MS. COLE: Pat? Pat, it is Rebecca.
19	MS. CHERRY: Hold on, Rebecca.
20	DR. LEVANDOWSKI: That particular strain,
21	the B/Beijing/184/93 was the strain that was
22	recommended. It was chosen for the reasons that have
23	been commented on already, but it was a strain that
24	did not grow at all. It would not have been
25	appropriate for manufacturing. Maybe I should comment

that it was a situation that put the manufacturers in 1 somewhat of an awkward situation because it was a late 2 Nevertheless, it was possible to find an 3 alternate strain that 4 seemed to be appropriate antigenically with the information that was available 5 6 at the time. DR. POLAND: And is that the strain that 7 8 WHO is using? 9 DR. LEVANDOWSKI: Everybody in the world is using the B/Harbin/7/94 strain for vaccine. Nobody 10 in the world is using B/Beijing/184/93, at least not 11 12 to anyone's knowledge here. 13 CHAIRPERSON FERRIERI: Nancy, would you 14 mind -- this has been a huge amount of data, as usual, and it has been hard to retain all of it. But could 15 16 you give us some notion of how big a deal it would be to update the current B/Harbin, so we would keep this 17 18 lineage rather than go back to the B/Vic lineage. And then maybe Dr. Slusaw would like to comment on my 19 20 question. I see him nodding his head. So updating, 21 how big a deal? And how good will it be then? 22 DR. COX: I think we have evidence using a number of antisera for viruses that are related to 23 Beijing 184, which is a little -- it is a sublineage 24

separate from viruses related to B/Harbin.

evidence that antisera to those strains tend to cover well, just as the Beijing/184 antisera tends to cover better. We have -- the viruses that we have now that are egg isolates are the B/Yamanashi/166/98, B/Bucharest/311, there is a Romania strain, and then of course we have the very recent B/Georgia/4/98 strain. And so what we would like to do is some additional serologies and further explore some of those strains.

CHAIRPERSON FERRIERI: Dr. Slusaw, do you have a comment on this aspect of updating? The hardships? The pros and cons?

DR. SLUSAW: My only concern about the B is that as of this point to consider other B/Harbin-like B candidates, the manufacturers don't have alternate B strains in our hands yet to begin working with to make working seed for production. So given the time tables I have shown, it would be a number of weeks or perhaps a month or a month and a half until we would have a working seed. So that is our concern.

CHAIRPERSON FERRIERI: Last year, of course, we made two major changes, two different components. Both A's changed and you coped very well even though there might have been some ultimate delay.

Dr. Kohl? And then I will have Ms. Cole on the line.

DR. KOHL: I guess I want to get back to Bob Daum's question, I think, and plus a question by Caroline Hall. I would like some more reassurance that the B/Vic is going to stay where it is. What I have heard so far is that it has been there for 9 years or so and hasn't moved and I should be happy about that. Not being a flu expert, is that good enough?

CHAIRPERSON FERRIERI: Dr. Cox?

DR. COX: Well, its been good enough for us for the past five or six or however many number of years it has been. I think we -- our feeling is that we really need to keep close tabs on the B/Vic-like viruses. The Australians certainly are very nervous about the B/Victoria strains because they are right on their doorstep being in Thailand and Singapore. But we have faced very much the same situation that we have seen now for the past number of years and so far we have been okay going with the B/Harbin lineage.

DR. KOHL: And what is going to trip the switch? What do you have to see before you advise us to go with B/Vic?

DR. COX: We would be looking for a pattern similar to what we for the saw H1N1 A/Beijing/262 virus, which moved to additional

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continents. Last year we had detected it in Africa, 1 2 Europe and North America. 3 CHAIRPERSON FERRIERI: Rebecca Cole, unrelated to Steve Kohl here. Ms. Cole? 4 5 I was going to ask the same MS. COLE: question that Dr. Poland did. 6 7 CHAIRPERSON FERRIERI: Okay. Did you get 8 a sufficient answer, Rebecca? 9 MS. COLE: Yes. Thank you. 10 CHAIRPERSON FERRIERI: Thanks. Dr. Hall and then Dr. Kilbourne. 11 12 DR. HALL: I could think that probably the consensus thus far would be that we would like to 13 obviously recommend potentially an update on the B 14 15 antigen such that it would give better coverage for the B/Beijing/184. The question being obviously that 16 17 there is no really good candidate. But, Nancy, I 18 thought that you had mentioned B/Georgia/4/98 as potentially good. It is at least an egg isolate. 19 20 you know more about that? Is it a candidate, even if 21 it is not quite in the hands of the manufacturers yet? 22 DR. COX: We would actually like to send 23 it out because we just put it into ferrets. We just 24 got the egg isolate a week ago or so and have just put

it into one test. But given the time constraints that

we now have, we would like to get it sent out right 1 away. We will have a cross test in ten days or so and 2 we will have the sequence analysis as well. So I think 3 this would be a potential candidate. 4 5 CHAIRPERSON FERRIERI: Dr. Snider? sorry, Dr. Kilbourne, forgive me, and then Dr. Snider. 6 7 DR. KILBOURNE: Yes. It is relevant to this because I think that on the table here should be 8 the consideration that Roland introduced earlier, and 9 that is that the A and B viruses are different. 10 11 are different not only structurally to some extent, the size and so forth, but I think that they are 12 13 epidemiologically different in the sense that we don't 14 always have the continuous sequential antigenic drift, unidirectional drift that we have seen with the A 15 You may get pockets of these strains that 16 are sort of isolated like the Victoria seems to be, 17 18 and I think we can be less secure about predicting the future with that. So that I think that ought to be on 19 20 the table in the discussion. 21 CHAIRPERSON FERRIERI: Dr. Snider? 22 DR. SNIDER: Yes. I quess I just want to 23 reiterate what several people have said. I have a 24 great deal of concern about Influenza B for next year

given the fact that we haven't had that much activity

It seems possible that given the fact in the past. that it was almost 20 percent in some places this year, it could be even more dominant next year. So I am very concerned that we have coverage and I am concerned about the drift that we have seen and would like to see a better match. I think what is difficult for us at the present time is that we have just a small amount of data. It seems to me that what we would have to do if we want to make a change is make it contingent on the availability of a strain that would be able of appropriate levels of replication in eggs as well as elicit the appropriate antibody titers or immunologic responses we are looking for, and we are working in a very tight time frame. And I think we are talking about, although we haven't gotten to it yet, a potential change in two of three components. And one of the things we may have to do at the end of our discussion is give some indication of the priority of each of the two changes. Because for a lot of practical reasons, it may or may not be possible to make both of those changes this year.

CHAIRPERSON FERRIERI: I appreciate your comments very much on that point, Dixie. When we have finished later with H3N2, I think we can then address the prioritization. All of you have heard many people

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speak here. There is unrest here on the ranch. We don't feel comfortable moving forward with the current B. Dr. Greenberg?

DR. GREENBERG: I am still not clear -since once before, I guess, a B was picked as ideal
but then had poor growth characteristics, I would hope
-- how many candidates are moving forward now of the
new Harbin subtype? I don't know what you would call
it. How many are moving forward in eggs so that the
likelihood will be that one of them will have the
correct serology and the correct egg phenotype? And
ideally when will that emerge?

DR. LEVANDOWSKI: Me? Oh, thanks.

CHAIRPERSON FERRIERI: Roland.

DR. LEVANDOWSKI: Well, obviously Nancy Cox said that there were several strains that were possibilities. Some of these we have already. Some of these were discussed last fall but had not been distributed to manufacturers yet. The only strains that we have distributed to manufacturers are the ones that Dan indicated. We have not sent out a new B/Harbin-like strain in the last several months. So we would be at some what -- the manufacturers would be at somewhat of a disadvantage even at this time trying to produce a seed virus for a new strain. Having said

that, I think they are pretty good at handling things very expeditiously. And although I don't think I want to put them on the spot either, I think they expect us to do more than we can sometimes also.

However, having said that, there are some strains. As Dan mentioned, we are prepared to send out the Foshan strain. We do have the Romania strain in our repository. Some of these other strains could be sent directly from CDC to the manufacturers. So all these things could be in the pipeline immediately if not sooner.

the panel is not going to be able to make a recommendation on what the substitution could be, but we could come up with a recommendation that very expeditiously strains should be provided of the ones that have just been cited -- Romania/318/98, is that one of them, Roland? And then the Foshan/396/98. And maybe Nancy Cox, the Georgia strain as well? At least those three? And try to rev up and see what kind of growth characteristics we might have. But I think that we are at a point where we can make a motion that is along the lines of what I have stated and that includes a provision for fall-back if they should fail. Who would like to make such a motion? Steve

1	Kohl, please?
2	DR. KOHL: Yes. I would like to make a
3	motion that appropriate updated seed stock or whatever
4	you call it appropriate updated B virus be
5	forwarded to the manufacturers for initializing the
6	vaccine for an update of the Harbin/B.
7	CHAIRPERSON FERRIERI: And the provision
8	that if it fails
9	DR. KOHL: I guess I am being prompted?
10	And the provision that if it fails, we would I guess
11	have to fall back on the current isolate.
12	CHAIRPERSON FERRIERI: Yes. A second on
13	that? Who seconded that? It is multiples. For the
14	record, Dr. Daum seconded it. We are open for
15	discussion now. Excuse me, we are open for discussion
16	now. Dr. Daum?
17	DR. DAUM: Excuse me, Dr. Ferrieri. I
18	wondered whether Dr. Kohl might like to specify the
19	lineage in his motion?
20	DR. KOHL: I would think that the people
21	from the CDC and the FDA would be better at that than
22	me than I.
23	CHAIRPERSON FERRIERI: Well, they are
24	DR. KOHL: The non-Victoria group is what
25	we are talking about.

1	CHAIRPERSON FERRIERI: They are Beijing
2	lineage. They are Beijing lineage.
3	DR. KOHL: Fine, Beijing lineage.
4	CHAIRPERSON FERRIERI: Other discussion
5	before we have a vote on the motion?
6	DR. BREIMAN: Pat?
7	CHAIRPERSON FERRIERI: Yes, Dr. Breiman?
8	DR. BREIMAN: Is failure well enough
9	defined? Do we have to define what failure is?
10	CHAIRPERSON FERRIERI: Well, as a non-
11	virologist but someone who has worked with
12	bacteriophage, failure would be inability to propagate
13	the virus and to have a low yield. Is that a good
14	enough one for industry? Inability to prepare
15	reassortants. I mean, that would be part of it.
16	DR. LEVANDOWSKI: Currently there aren't
17	any reassortants being made for Influenza B viruses,
18	so the manufacturers are really stuck using whatever
19	they get from nature at this point.
20	CHAIRPERSON FERRIERI: Okay.
21	DR. BREIMAN: I am sorry, the level of
22	immunologic response is not part of the measurement of
23	failure?
24	CHAIRPERSON FERRIERI: Well, they wouldn't
25	have that information except empirically based on

ferret cross reactivity with the strains and human reactions -- human sera from last year's component from the classic B/Harbin. It would be based on that immunologic data unless there is something that is being stashed away that we haven't heard about. Okay. Now further comments? Dr. Edwards and then Dr. Estes.

DR. EDWARDS: I have a question. What if one manufacturer is capable of generating a high yield product and another is not? Would we have two different kinds of vaccines made by two different companies or is there some sharing of these stocks from the manufacturers?

DR. LEVANDOWSKI: Manufacturers each make their own seed virus. We actually don't use the term seed virus to describe what we send to them. reference strain that is distributed to the manufacturers and they each make their individual seed based on their experience and capabilities knowledge of how to handle the viruses. I shouldn't speak for the manufacturers again, but I suspect that there probably are differences in the yield of the strain for different manufacturers because something as simple as a half a degree Centigrade of temperature can have a significant effect on how much is recovered and duration and the process

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1	itself. Actually, some of this doesn't even relate to
2	we are getting into things that don't relate just
3	to the virus itself but the capabilities of the
4	manufacturing process to tolerate differences in the
5	strains. It is a little bit unpredictable which way
6	that would go. But I guess the short answer is that
7	there could be differences in yield for different
8	manufacturers and their probably are differences in
9	yield for different manufacturers for the same strain.
10	DR. KILBOURNE: Each so-called virus
11	strain is in fact a quasi-species, so a new mutant may
12	pop up in one lab that isn't present in the other.
13	Even though you think you are all dealing with the
14	same thing. So even at that level, they may be even
15	slightly different antigenically.
16	CHAIRPERSON FERRIERI: Dr. Estes?
17	DR. ESTES: I wondered this actually
18	relates to Dixie's earlier comment. Do we need to set
19	an outside time frame for this decision to be made?
20	Because the manufacturers will have H1N1, but they
21	will need a second strain to get started with. And
22	because of the issues we are going to discuss about
23	the third component.
24	CHAIRPERSON FERRIERI: I am not
25	comfortable with our setting a time limit on it here.

I think that would be unwise. I think that the regulatory agencies should be working, as we move forward now, very, very closely, and we will be hearing an update on this within 8 weeks. So we will have information, Mary. That would be my goal. I don't want that to be a rigid rule. I think there has to be active communication and information and then we move forward based on the preliminary data from the attempts to propagate the virus. Dr. Greenberg?

DR. GREENBERG: I would like a little clarification on the B/Victoria. I find myself in agreement with the analysis that it has stayed where it is and so that is the best data you have. I would like to know whether that picture could change in the next three or four months, and if it could, are you prepared for that? Should you have an egg isolated strain that is ready to go sort of in the bank?

DR. COX: I can answer that. I take the easy questions. We do have a strain. It is the Shangdong/7 strain, which is actually being used in an experimental vaccine trial in Australia. We previously used the Beijing/243 Victoria-like virus in an experimental trial. So we would have both of those strains, potential vaccine strains, that had already been put into humans.

And those have been distributed to manufacturers as well. 2 So everybody should have that in their repository now. 3 CHAIRPERSON FERRIERI: We have a motion to 4 5 deal with now. think Ι we have discussed sufficiently and we have a lot of discussion that we 6 7 need to apply to H3N2. So if someone would please call the question and we will vote on the motion, 8 which is to provide at least these three strains we 9 have heard about, the Foshan, Romania and Georgia of 10 the Beijing lineage to industry as soon as possible 11 and to find out their characteristics for propagation 12 and yield. And if all fails, then the contingency 13 fall-back plan is to retain the B/Harbin strain that 14 is in the current vaccine. So we will start voting on 15 the opposite side of the room today. Dr. Kilbourne? 16 17 DR. KILBOURNE: Is this a vote? 18 CHAIRPERSON FERRIERI: Yes. 19 DR. KILBOURNE: Yes. 20 CHAIRPERSON FERRIERI: Thank you. Dr. Breiman? 21 22 DR. BREIMAN: Yes. 23 CHAIRPERSON FERRIERI: Dr. Poland? 24 DR. POLAND: Yes. 25 CHAIRPERSON FERRIERI: Dr. Hoke?

DR. LEVANDOWSKI:

1	DR. HOKE: Yes.
2	CHAIRPERSON FERRIERI: Dr. Hall?
3	DR. HALL: Yes.
4	CHAIRPERSON FERRIERI: Ms. Cole?
5	MS. COLE: Pat, my vote is yes.
6	CHAIRPERSON FERRIERI: Yes?
7	MS. COLE: Yes.
8	CHAIRPERSON FERRIERI: Thank you, Rebecca.
9	Dr. Eickhoff?
10	DR. EICKHOFF: Yes.
11	CHAIRPERSON FERRIERI: Dr. Edwards?
12	DR. EDWARDS: Yes.
13	CHAIRPERSON FERRIERI: Dr. Estes?
14	DR. ESTES: Yes.
15	CHAIRPERSON FERRIERI: Dr. Snider?
16	DR. SNIDER: Yes.
17	CHAIRPERSON FERRIERI: Dr. Kohl?
18	DR. KOHL: Yes.
19	CHAIRPERSON FERRIERI: Dr. Huang?
20	DR. HUANG: Yes.
21	CHAIRPERSON FERRIERI: Dr. Daum? Sorry,
22	Bob?
23	DR. DAUM: Yes.
24	CHAIRPERSON FERRIERI: And Dr. Greenberg.
25	DR. GREENBERG: Yes.

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CHAIRPERSON FERRIERI: And my vote is yes.

Thank you all very much. We will move on then to the H3N2. We have heard a lot of data on this. There has been a lot of activity and there are many, many strains -- a couple of hundred -- 200 Chinese strains that have arrived for study in CDC. So there has been expressed up to now grave concerns about possibility of retaining the current H3N2 strain. we have various candidates that have been mentioned. A couple of Sichuan strains, 436 and 418/98, and we have some information on their yield even -- moderate yield. But we need, perhaps, more data. We don't have the serologic data that is very vast to address this specifically. But now having stated sort of the briefest summary of the problem, I would like very much for the panel to share their assessment analysis of this issue, H3N2. The problems and could we work a solution or not? Who would like to start? Dr. Eickhoff, thank you.

DR. EICKHOFF: Excuse me. I recall Dr. Kilbourne last year at this meeting, when we selected the A/Sydney variant, after we had gotten through the selection process and we agreed to do it, he allowed as how maybe we are locking the barn door after the horse is out. And indeed the same comment would apply

even more so this year. As Nancy has pointed out, the A/Sydney H3N2 variant has circulated widely for two years now. I think we would be pushing our luck to expect that to be a stable situation for this coming year. I don't think we are at a stage yet where we can pick and choose individual strains, but I would think it would be time to move on in the direction of one or more of the A/Sydney variants that are currently being isolated and would hope that we wind up with a motion to do very similar to what we just did with influenza B, namely to ask for further data regarding growth characteristics of some of these variant strains and defer a decision for the time being.

CHAIRPERSON FERRIERI: Dr. Snider and then Dr. Huang.

DR. SNIDER: I just wanted to be reminded of how many strains that are available yet to be characterized and get some idea of how long it will take to get, if not all, a substantial proportion of those strains characterized. Because clearly the season this time has been mentioned late, so we are just now in many parts of this country in the midst of the outbreak and we don't really have as good a handle on it as we would like. It sounds like we have got to

make a decision by March on the last component of this vaccine, so it is really a question for me of how much information we can get between now and the time the last component has to be decided upon. And it may very well be that given a lot of other considerations about Influenza A and so forth, that the H3N2 ought to be the last component to go in so that we can get the maximum data about it. But if Nancy and others could tell us where we stand with regard to how much is outstanding in the way of isolates.

CHAIRPERSON FERRIERI: Nancy?

We did a quick check yesterday DR. COX: and have another 200 strains that had already been logged into the computer and another 7 packages had arrived just yesterday that contained viruses that hadn't been logged in yet. So I have no idea how many were in there. But some of the viruses are newly arrived and haven't gone into tissue culture, but have gone into tissue culture ordepending on their substrate of origin. So we can actually test as many as 75 antigens in a test. providing they are growing well, which they have been doing pretty well this season, we can crack through quite a few viruses in a two to three week time period. So we could have another 150 tested if they

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are growing well in another three weeks.

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2 CHAIRPERSON FERRIERI: I hope that is maximum. Actually, Dr. Estes, we will be rediscussing 3 this issue in approximately 41 to 42 days, not 8 weeks in order to come up with very firm recommendations on B and H3N2. So I am hoping that everything goes well. Someone in my lab asked me what we were going to be deciding today, and I said, well, I didn't know yet, but a lot of information was very contingent on what comes out of China. And she said, but why China? And I said, well, historically a lot of trends antigenic changes have emerged from strains from China and similar parts of the world. Would either of you like to say something a little more sophisticated than Or Dr. Kilbourne, if you would like to say something on that point.

DR. KILBOURNE: Something sophisticated? CHAIRPERSON FERRIERI: As you wish. Our definition here is very broad. We have a lot of leeway.

DR. KILBOURNE: The conventional wisdom -and I have some unconventional wisdom -- is that China is an area where you have a combination of both enormous population, particularly in urban centers and the opportunity for many generations of virus and

therefore many mutants to be thrown off. You also 1 2 have rural areas where there is exposure to animals, whence some of these come. And the other question I 3 4 think is really the chicken and the egg business of 5 where did it all start eventually, and this may have 6 to go back to the origins of man. So I don't know what 7 you can say than that, sophisticated 8 unsophisticated. 9 CHAIRPERSON FERRIERI: Thank you. Ι 10 wanted us to have a little levity here because it 11 doesn't get any lighter. 12 DR. KILBOURNE: This is as good as it 13 gets. 14 CHAIRPERSON FERRIERI: It is as good as it 15 gets. Yes, Dr. Hoke? 16 DR. HOKE: Well, it seems to me there are 17 two bits of information that we need. One 18 regarding any possible strains that are on the menu here that might be better. 19 And I think that the 20 A/Sichuan/346/98 was mentioned as a possibility. So I 21 guess there is information regarding whether that is 22 ready to go as well as information on this new 23 collection that CDC has and whether there are any 24 surprises in the isolates to be made. But is this

strain one that would do the job and is it ready to go

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CHAIRPERSON FERRIERI: Well, we have some information on it. We know that the yield has been moderate with that one as well as with 418/98. Is that correct, Nancy? On one of the slides that you showed or someone showed it -- Roland did.

DR. LEVANDOWSKI: Well, these are strains that we were able to get out to manufacturers and they were able to get at least some minimal amount of information back to us. I guess I would say that moderate is probably a generous description for these strains, the Sichuan/418 and Sichuan/346, and they are not equivalent. The Sichuan/418 inherently seems to grow better, and other people have found this besides our lab, than the Sichuan/346. The Sichuan/346 is one of those that could be a problematic strain just because it yields relatively poorly to begin with. probably on its own would not be a strain that would be useful for manufacturing and even a high growth reassortant could be somewhat lower yielding than some of the other high growth reassortants are. not all equivalent. So we have just that kind of information.

CHAIRPERSON FERRIERI: And could you clarify for me again, either you or perhaps Dr. Cox,

the difference serologically? It was my impression that the current antisera against A/Sydney and from immunized individuals and ferret sera have better neutralization or reactivity with 418 than with 346, Nancy? And so that we have more information that makes it a superior strain than simply its growth characteristics. But again, there may be something better out there. Would you want to comment on that? Everyone wants to feel secure that we are not holding back and denying industry a go-ahead on something like Sichuan 418/98.

DR. COX: Right. I think the complicating factor is that we do know that there are some sequence differences between these two strains which probably account for the difference in reactivity that you see on two of the tables. And we noted that in the human serologic studies, the responses to Sichuan/346 were lower than to 418. So this strain is more different and therefore possibly a strain that should be given greater consideration. Unfortunately, it is not the strain that grows well, so we have both sides of the coin that we are trying to look at.

CHAIRPERSON FERRIERI: And what you will be doing with these roughly 200 strains or so is to characterize them and see how close they may be to

this. Will one of them emerge as being broadly very 1 well neutralized by antisera that we have available, 2 human and ferret and so on? 3 Trying to come up, again, with best choice that covers all ground. 4 5 DR. KILBOURNE: Nancy, can we really say 6 at this point that there is any significant difference 7 between the two viruses, the 418 and the 346? Because it may just be a matter of antibody affinity at this 8 9 point, isn't that correct? In terms of judging the 10 reactivity when you talk about lower titer? Just because they have a lower titer with the original 11 12 immunizing strain doesn't necessarily mean that they are antigenically dissimilar in an important way. 13 14 DR. COX: They are not really terribly different from each other. 15 They are not terribly different from each other. So you are right in that 16 17 There could be a difference in avidity. sense. 18 we do see some sequence differences between them that could account for -- some four-fold differences that 19 we see on some of these tables. 20 21 CHAIRPERSON FERRIERI: For the record, I 22 have been -- I wrote it down as 346 and then somewhere 23 else I saw it as 436/98. 24 DR. COX: I apologize. 25 CHAIRPERSON FERRIERI: Is it 346?

1 DR. COX: 346. 2 CHAIRPERSON FERRIERI: Thank you. For the record, we have been talking about Sichuan/346/98 and 3 contrasting it with 418/98. Further comments from the 4 5 audience? Yes, Dr. Huang? 6 DR. HUANG: I would like to second everything that Dr. Eickhoff said much earlier, which 7 summarized basically, in that we don't have enough 8 information right now to really specify strain. 9 However, I think most of us feel that we should not go 10 ahead with the current A/Sydney. And if it is at all 11 helpful, we may perhaps vote on that and then delay 12 the decision until we get more information on the 13 14 Sichuan strains. 15 CHAIRPERSON FERRIERI: Thank you, Alice. Would you be so kind as to make that a motion that we 16 do not support the use of the current A/Sydney and 17 want to encourage further study of these other strains 18 before -- with data to be presented to us as soon as 19 20 possible so we finalize the decision. 21 DR. HUANG: So moved. 22 CHAIRPERSON FERRIERI: Second on that? 23 DR. EICKHOFF: Second. 24 CHAIRPERSON FERRIERI: Thank you, Ted.

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Now we can have discussion on the motion. We don't

1	want anyone to feel swept away. We are not being
2	I hardly think this is being impetuous today, but I
3	think we have to for FDA and for everyone in the
4	audience, permit them to understand our thinking.
5	This is not a surprise, what we have arrived at.
6	Other comments on the motion? Yes, Dr. Poland?
7	DR. POLAND: I guess my only concern,
8	while I sympathize with the intent of the motion, is
9	that what if these 200-some odd viruses yet to be
10	characterized turn out to either be uncharacterizable
11	or worse, A/Sydney?
12	CHAIRPERSON FERRIERI: Well, I could
13	answer that, but I would like the pros here to do that
14	the influenza pros. Who would like to tackle that
15	question?
16	DR. POLAND: Because now I guess the
17	idea I am getting at is now the numerator for non-
18	A/Sydney viruses becomes much smaller. And I don't
19	I guess in part it may be a question of is it
20	unprecedented to have the same strain of H3N2
21	circulate three years in a row?
22	CHAIRPERSON FERRIERI: It is highly
23	unlikely, but has it ever happened before?
24	DR. KILBOURNE: It is highly unlikely, but
25	I am not myself persuaded of a need for change just on

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the basis of something never happened before. 1 one hand, if you look at the ferret data, the strains 2 are 50 percent unrelated. If you look at the human 3 data, they are 50 percent related. So we are really 4 at that hinge point, I think. And I think we always 5 6 forget how much overlapping, inter-heterovariant immunity there is. I think that is a point that Ted 7 Eickhoff established years ago working with the early 8 9 H2N3 variants. 10 CHAIRPERSON FERRIERI: Other comments on 11 the motion? Yes, Steve Kohl? 12 DR. KOHL: A question. Am I reading the data wrong? It looks to me like the Sichuan strains 13 effectively neutralize the A/Sydney. 14 So even if A/Sydney continued to be a problem, the Sichuan 15 strains would still be a reasonable answer, is that 16 17 correct, Dr. Cox? 18 DR. COX: If you look at Yes. the homologous titers, they do. And if you compare the 19 20 titers that you get with homologous strains to the 21 titers that you get with Sydney-like viruses, you see that they do a good job in an HI test. So you are 22 23 reading it correctly. 24 CHAIRPERSON FERRIERI: But how poorly is

the reverse, though? Is the reverse sufficiently poor

to warrant going with one of the A/Sichuan's rather 1 than staying with A/Sydney? Will that -- do you feel 2 it will be based on the study of all the new isolates 3 4 that have come in? 5 DR. COX: I think that is one of the things that we are going to be looking very carefully 6 for is how well do these two new Sichuan antisera 7 inhibit the most recently isolated strains. 8 one of the key pieces to the puzzle. 9 10 CHAIRPERSON FERRIERI: Okay. Dr. 11 Greenberg, and then we are going to vote. 12 DR. GREENBERG: Is 418 not acceptable? Or if your data shows that the antisera to 418 works well 13 with your new isolates in HI, do you have to -- is 14 15 another isolate needed? Because I heard that 346 was a poor grower, but I couldn't quite figure out the 16 17 other one. 18 DR. COX: Well, it is a little bit difficult to explain all the nuances. And, of course, 19 I am sure you all realize that we are trying to work 20 21 very closely with WHO. There is really no scientific reason to have different vaccines in North America and 22 23 in Europe. The strains that circulate are very, very 24 similar. And there are sort of -- the criteria that are used for making the recommendations at WHO are

similar, but we sort of talk about things slightly different way. And when you look at the human serologies, you see that the titers to Sichuan 346 are reduced to a greater extent than they are to 418, and that sort of moves one towards thinking that this is strain that has greater antigenic differences when it comes to the way human beings respond to these strains. So it is just unfortunate that the 418 -- the 418 strain does grow better. I think we just need to gain more experience with these two strains and the antisera to them and really weigh all the different components of the decision making and see what works and what the experience is of the vaccine manufacturers. Because sometimes a strain that initially grows poorly, once there is a high growth reassortant, it does behave satisfactorily for the manufacturers. So I think it is sort of a wait and see kind of situation.

CHAIRPERSON FERRIERI: I'd like to restate the motion that the committee seconded. We do not recommend retention of the current A/Sydney/5/97. There is insufficient evidence or data to recommend a substitute strain at this time. And we recommend expeditious study of the approximately 200 Chinese strains and submission of further data in the very

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near future for us to make a final recommendation as 1 2 a panel. Will start the vote. The discussion ended. 3 Is there something that is vital? Dr. Eickhoff? 4 DR. EICKHOFF: Do we wish to include a 5 fall-back position? 6 CHAIRPERSON FERRIERI: Well, the original 7 motion did not have a fall-back. The Chair entertains 8 a revision or whatever you would like to have as an 9 add-on to the motion. 10 DR. KILBOURNE: My problem with your 11 motion, Madam Chairman, has to do with the statement 12 that we do not recommend. Because I don't think that 13 we have enough information. I think it becomes sort 14 of self-contradictory in the rest of the motion. 15 I am not sure that we want to say -- maybe some would 16 to recommend Sydney. Ι would have 17 reservations about whether or not the ensuing data we 18 are going to get might reverse our position on that. Also, I would like to bring up a point that Dr. Cox 19 20 brought up with me over the phone the other day and 21 remind her of it. It was my understanding, Nancy, that as yet the leading candidate strains to replace 22 23 this have not been epidemiologically very significant. Is that right in China? The Sichuan viruses? 24

DR. COX: That is right. I mean, we have

a cluster of these viruses from Sichuan, and actually there was fairly extensive activity from May to September. But we don't have Sichuan-like strains identified yet in this current package from China. But we are working -- as we work our way through, we will see what we see.

CHAIRPERSON FERRIERI: Would you like me to the restate motion? We are not strict parliamentarians here. But the sense of what was earlier moved and seconded was that we do recommend retention of the current A/Sydney strain and based on the data we have, we have no recommendation for a substitute. And part of the motion was that we expeditiously study these additional strains and gather more data. That is as benign as the motion gets.

DR. BREIMAN: It could be a little bit more benign and just say we are concerned about it or something. Because it seems to me that once you are on record saying that you do not recommend use of that particular antigen, that if the other ones turn out not to work or they have problems, I believe you have closed the door.

CHAIRPERSON FERRIERI: If we insert the phrase based on the information that we have at this

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185 1 time, then Ι think that it might accommodate everyone's ideas and it leaves it completely open. 2 be more specific than that I think would be unwise. 3 4 Because we need more information. Dr. Kohl? 5 DR. KOHL: Again, Dr. Cox, clarify this 6 It looks like there are strains 7 California from Sichuan, from again California from Korea that are low HI with the A/Sydney. 8 9 DR. COX: That is correct. 10 DR. KOHL: So there actually has been --I don't know if the word widespread is correct, but 11 there has been multiple sites of isolation of H3N2's 12 that are not covered -- not well covered by the Sydney 13 isolate. 14 15 DR. COX: That is correct. And I made a comment, which I went over very quickly. We were sent 16 17

DR. COX: That is correct. And I made a comment, which I went over very quickly. We were sent quite a bit of information from the WHO collaborating center in Melbourne, and they have a fairly substantial proportion of strains which are reacting -- which are four-fold down or more -- actually, 30 percent of their viruses are four-fold or greater reduced with the Sydney antiserum. And of some recent viruses from Thailand which they had analyzed, approximately 50 percent of those strains were reduced four-fold or greater. So I think we can say that

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there is a wide geographic distribution of strains which are reduced in titer to the Sydney.

DR. KOHL: And I think we are starting to get widespread, albeit anecdotal reports, of immunized individuals in this country who are having documented Influenza A not further characterized. So I am not convinced that the A/Sydney is a solution to next year under any situation.

CHAIRPERSON FERRIERI: Thank you, Steve. think this is a very important point that you unearthed in the data presented earlier and we didn't go back and reemphasize that. This is why the motion was presented originally as it was. There was great unrest about accepting the adequacy of the A/Sydney in the new vaccine to come on board. Is it relatively rare that we are going to get boxed into a corner, Roland, and end up with nothing better? I mean, we have other strategies. We always can pray and do -and I mean that very seriously. There are other things that can be done in the laboratory hopefully that will solve this problem. We will have something We are determined there will be something better. better.

DR. BREIMAN: Can I ask one more question?

CHAIRPERSON FERRIERI: Yes, and then we

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will vote. DR. BREIMAN: Those strains that Steve referred to, though, if you look at the ferret antisera data, and maybe I am reading these wrong, but for several of those strains, the dilution was not that impressive for 418 either. So that I guess I am a little confused as to why we think that that would be the solution. Am I reading it wrong? DR. LEVANDOWSKI: Are you asking me? DR. BREIMAN: Well, anybody. CHAIRPERSON FERRIERI: Yes. Do you wish, Roland, to start answering it? DR. LEVANDOWSKI: I am not sure I even heard it because I was thinking about your comments and wondering if I was supposed to respond to those things. CHAIRPERSON FERRIERI: No. waxing philosophical. Sorry, Roland. What is going through my mind is that of course we don't have anything really in hand at the moment for any of these things. And just as we were talking about for Influenza B, the same situation applies here.

is the vaccine strain that we have. It may not be

ideal, but at least we know quite a lot about it and

how it works and how it can be handled.

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would hope that part of the fall-back position would be that if everything else falls through, at least we still have Sydney to use.

CHAIRPERSON FERRIERI: That is not part of our motion, but I think we must keep that in mind that that may be the only thing that we will be able to fall back on. I like to think of things as having partial immunity. A little bit of the antibody goes a long way and may be better than having no antibody. So a modified illness to me is a positive strike in any disease. If you can modify illness not so extreme that you don't have a superimposed staphyloccal or pneumococcal pneumonia and die in a nursing home. There is a full spectrum of influenza clinically from having at the most minimal, mild myalgias, no fever or very low grade fever and a little sore throat and you get better over three or four days and you may even be going to work and even spreading it all around, but it responds to mild anti-inflammatory agents. At the very middle of the spectrum, you stay home in bed for a week and you have high fever and full blown systemic symptoms. At the very far end of the spectrum, you are 80 years of age and you were unimmunized and you come down with influenza and succumb to a superimposed bacterial pneumonia. But in-between, in all of those

1	three spots, a little bit of antibody could make you
2	go from third phase into the middle or the low end in
3	terms of clinical severity of disease. So we are not
4	considering that in any of our thinking or discussion.
5	We are trying to be pristine in what we are invoking
6	immunologically, and that may not always be possible.
7	So I agree. If we can't have a perfect strain here,
8	then I would say let's go with A/Sydney. But that is
9	not part of the motion. We will have a chance to come
10	back to it in six weeks, I hope. Does anyone feel
11	differently about the clinical activity? Okay. Let
12	us vote then. We will start with Dr. Greenberg. The
13	motion in its most simple is that we do not recommend
14	retention of the current A/Sydney/5/97 at this time
15	based on the data presented and that we have
16	insufficient data to recommend a substitute strain and
17	that further studies will be done on the 200 Chinese
18	strains to gather more data.
19	DR. GREENBERG: I would ask whether saying
20	rather than we do not recommend, saying we have
21	substantial reservation would be just almost as strong
22	and give us slightly more of a back door. I am sorry.
23	CHAIRPERSON FERRIERI: A revision to the
24	motion has been accepted. Is there a second?

Second.

DR. EDWARDS:

1	CHAIRPERSON FERRIERI: Very good. I am
2	not sure if that is parliamentarily acceptable.
3	DR. GREENBERG: I am sure it is not, but
4	it works.
5	CHAIRPERSON FERRIERI: It will be fine.
6	None of us is a lawyer or parliamentarian at this
7	table that I know of. Thank you very much, Harry. I
8	think that is quite acceptable to me.
9	DR. GREENBERG: I vote yes.
10	DR. DAUM: I vote yes.
11	DR. HUANG: Yes.
12	DR. KOHL: Yes.
13	CHAIRPERSON FERRIERI: Dr. Snider?
14	DR. SNIDER: Yes.
15	CHAIRPERSON FERRIERI: Dr. Estes?
16	DR. ESTES: Yes.
17	CHAIRPERSON FERRIERI: Dr. Edwards?
18	DR. EDWARDS: Yes.
19	CHAIRPERSON FERRIERI: Dr. Eickhoff?
20	DR. EICKHOFF: Yes, with the provision
21	that I would not limit consideration of variant
22	strains to the 200 strains that most recently arrived
23	from China.
24	CHAIRPERSON FERRIERI: Dr. Hall?
25	DR. HALL: Yes.

1	CHAIRPERSON FERRIERI: Dr. Hoke?
2	DR. HOKE: I is it fair for me to ask
3	to hear what it is that we are voting on? I mean it
4	was changed but
5	CHAIRPERSON FERRIERI: It was the motion
6	that we have grave reservations it has been
7	reworded so that instead of saying that we do not
8	recommend retention of the current Sydney/5/97, it has
9	been reworded that we have grave reservations about
10	retaining the strain.
11	DR. HOKE: I actually would be opposed to
12	that.
13	CHAIRPERSON FERRIERI: Well, you have a
14	choice at this point of voting against the motion then
15	or abstaining.
16	DR. HOKE: I vote against it.
17	CHAIRPERSON FERRIERI: Fine. We have a
18	no.
19	DR. POLAND: Would you accept a friendly
20	amendment to remove the word grave?
21	CHAIRPERSON FERRIERI: Was that
22	DR. GREENBERG: I said substantial rather
23	than grave.
24	CHAIRPERSON FERRIERI: I am sorry, Harry,
25	I thought you said grave.

1	DR. POLAND: Could we just
2	DR. GREENBERG: I actually like
3	substantial more than grave.
4	DR. POLAND: Could we even then remove
5.	substantial? We just have reservations.
6	DR. GREENBERG: Reservations is fine.
7	CHAIRPERSON FERRIERI: You accept that,
8	Harry?
9	DR. POLAND: In that case, I can vote yes.
10	CHAIRPERSON FERRIERI: Fine. Dr. Breiman?
11	DR. BREIMAN: Yes.
12	CHAIRPERSON FERRIERI: Dr. Kilbourne?
13	DR. KILBOURNE: Yes.
14	CHAIRPERSON FERRIERI: And I vote yes.
15	Dr. Hoke, I do want Mrs. Cole?
16	MS. COLE: I vote yes.
17	CHAIRPERSON FERRIERI: Thank you. I would
18	like for the record for us to understand your
19	objections, though, Dr. Hoke. We went through so many
20	revisions of it that I thought it would be a step back
21	to start over. But I want to know what the objection
22	was.
23	DR. HOKE: I agreed with the comment that
24	someone made earlier that if we made an excessively
25	negative comment about the current vaccine strain and

we are left with nothing else, then we would have a 1 difficult time rationalizing why in the final analysis 2 3 we might go back to that. And so, I mean, we have a bird in the hand and we have no bird in the bush in a 4 5 sense. 6 DR. KILBOURNE: Charlie, the motion was 7 modified. 8 Well, yes. Well, I just grew DR. HOKE: confused by the multiple modifications. 9 10 CHAIRPERSON FERRIERI: Yes. I sympathize. 11 DR. HOKE: I felt that it would be better to have a motion that reflected that really there is 12 nothing wrong with this as a vaccine strain. 13 the only thing that is wrong is that we have used it 14 for a couple of years and the strain is now dominant 15 16 and it is not likely to be -- or there 17 possibility that it won't be the dominant strain in 18 the next year. So that there is nothing -- I wanted 19 to leave us a comfortable position in case we are left 20 with nothing else. 21 CHAIRPERSON FERRIERI: I understand. 22 actually it is a very serious issue that we have been using it for all of these years and that there may be 23 sufficient drift that has taken place that this isn't 24

adequate and that this has occurred in past years here

in these deliberations as well. It would be nice if 1 we had something more substantial to say this looks 2 like this is our trump card that is in the wings now 3 and we are just going to refine it. But we don't 4 5 today. 6 DR. KILBOURNE: Perhaps if the motion as modified could be read back to Dr. Hoke, it would be 7 reassuring to him. 8 9 DR. HOKE: Okay. 10 CHAIRPERSON FERRIERI: Dr. Eickhoff? Do you have a point? We have voted on the motion as part 11 12 of the record and so we also have on record Dr. Hoke's 13 reservations about the motion and I think all of that will be taken into account. I have no doubt that the 14 15 right thing will be done eventually, Dr. Hoke. 16 DR. HOKE: Neither do I. 17 CHAIRPERSON FERRIERI: Thank you. That is part of the public record too. Dr. Eickhoff? 18 19 DR. EICKHOFF: Well, I hesitate to say this now, but I think the committee is almost surely 20 unanimous in what its sense is and I think some artful 2.1 wordsmithing of the motion or editing of the motion 22 23 might be appropriate. 24 CHAIRPERSON FERRIERI: Other comments? I 25 propose we take a break because we are moving into the

next session, which is also an open session on update of H5N1. I know some of you may have to leave early. And for members of the committee whom I have been working with for the past several years, I want to thank you all. It has been a great joy intellectually and personally for me to have served with you all, and I hope we will see each other again.

(Whereupon, at 2:58 p.m. off the record until 3:17 p.m.)

CHAIRPERSON FERRIERI: I'd like everyone to take a seat now. If the panel could return to the table. We would like to start as soon as possible this afternoon. I want to really thank everyone who plans to stay all afternoon. Some members of the advisory panel have an unavoidable early flight because of commitments back at their own institution. But as we move into this session, the speakers are going to have to be extremely strict with their time. Any ability to condense your presentations will be appreciated. The reason I say this is that there are individuals who are speaking today who have asked to leave early. So that has complicated things.

on time. And I am going to be here quite late because my flight was canceled. So I have no urgency. But I

don't want everyone else to have to be inconvenienced with traffic problems and getting to the airport and so on. So Dr. Roland Levandowski will start. We need the intro and I hope that the reorganization that we were just asked to do will not be confusing to those of you who know nothing about H5N1 viruses. Roland? DR. LEVANDOWSKI: Okay. Great. Thanks very much. I thank you for indulging us some. Ι It is actually not the fault of the speakers. It is really my fault that there is some confusion about the timing for the meeting and how I

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12 had instructed people. So I guess you have to blame me

13 for that gap. But we will get started and we will try

14 to be expeditious and stay on time.

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just want to give a very brief introduction. We wanted to take the opportunity to let the committee know about activities that have been going on since the H5N1 viruses became apparent in Hong Kong. As you know, there really has not been any H5N1 activity in people that we know about to this point since December of 1997. In spite of that, we have many activities that are ongoing in terms of design and production of vaccines, and we did want to have an opportunity to let you know some of the things that are going on.

Just briefly, you are familiar with the fact that there are a number of Influenza A subtypes.

I put this slide up here to simply illustrate that if we use the H1N1 virus as the root virus for people, in the past there have been events where reassortment has occurred in nature that has resulted in pandemics and widespread of new Influenza A subtypes. And what I am showing here in one instance is the H3N2 strain, that has mostly human gene segments. And since influenza

is a segmented virus, it can exchange freely these

gene segments. And the H3N2 virus that is in people

today actually seems to have acquired three of the

gene segments from an Avian strain at some time in the

past.

Now there is plenty of information that has been published about the H5 strains, and I only wanted to point out to you here that the difference between the H5N1 strains and other strains that have been in people relates to the fact that these strains truly are avian in nature and all the internal genes really derive from an avian source and do not represent a humanized strain. That may be some explanation for why these strains have not gone any further than they have.

The activities that are related to the

vaccines and investigations have really been global in Just as everything else for influenza is and nature. must be, the understanding of how to deal with the new subtypes as they appear, how to identify them, and how to do manufacturing is a very complex situation. partly it is complex because as you know from today there is something going on related to producing influenza vaccines all the time for the licensed manufacturers. and there are some verv active manufacturers who will be seeking licenses no doubt for other types of vaccines.

But what I am showing here is that much information stems from the organization of international centers that have been backed by the World Health Organization and also many national laboratories that collaborate to supply information, not the least of which have been the laboratories in Hong Kong during this last year in relation to the H5. Industry also has had a large part to play investigations. And as we will discuss, you will see that there are collaborations that are going on government and industry to evaluate vaccines and candidate strains. And finally, within the United States here, of course all the different arms of the Public Health Service in collaboration

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with USDA and the Department of Defense have been actively involved in identifying ways that we can complete some evaluation of vaccines that are in the process now.

Now obviously there are lots of issues that could be addressed, and I don't intend to address many of them here. There are, of course, a number of strains that could be considered for use in vaccines in the classical sense for the inactivated vaccines. prototype strains from Hong Kong were nomenclature of the Hong Kong/156/97 as one prototype of one variant, and Hong Kong/483/97 as the prototype for another variant of what is really the same virus but were easily distinguished antigenically. Thev both share in common that they were highly pathogenic for birds, and there are strains that came out of birds that are probably the direct precursors for the human strains. But that pathogenicity is something that has made work with these strains a little bit difficult. Because we know from the clinical experience in Hong Kong that these strains can be very severe in terms of morbidity and mortality in people. You will hear about activities that have been going on to make use of molecular techniques to bypass that sort of problem.

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Finally, there always may be other strains that could serve the purpose and there have been at least one strain that may be a non-pathogenic surrogate that could be used for production of vaccines, the A/duck/Singapore/97. It has a problem on its own in that it has a neuraminidase that is different from the prototype strains that we are mostly interested in, but there are ways to handle this, including reassorting techniques and other things.

Now the kind of vaccines that could be contemplated, of course, are the whole panoply of vaccines that have been discussed in various forums over quite some time. Obviously a plasma DNA vaccine sounds like it might be a good idea because of the simplicity of production of the vaccine and delivery. Nevertheless, that is not something that is really in the works at the moment except in animal studies. purified hemagglutinin vaccine, you all are aware that there are companies that are interested in producing these vaccines. One in particular, Protein Sciences, has been very active in clinical trials over the past several years with not only the H5 subtype but also with the more typical H1 and H3 subtypes and have a substantial body of clinical information that has been

published.

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Not to belittle the inactivated vaccines, they of course have a very important role to play, but the inactivated vaccines require, as we have been talking about earlier in the previous session, a seed virus that is adequate to support manufacturing. This is not always a simple thing to get a virus that can grow in eggs well or grow in tissue cultures well and that has all the characteristics that you would like it to have.

And finally, last but certainly not least, live attenuated vaccines are possible candidates for And what we are going to hear from the speakers who come next are bits of information for all of these. Now just by way of background, and this information won't be necessary until some speakers, but I just want to mention that there are some clinical trials that have been made very great progress over the last year, and have been in not only Phase I but Phase II trials. The CDC, of course, produced a plasmid from the original Hong Kong/156/97 prototype strain and provided that to Protein Sciences, who made a purified hemagglutinin vaccine that was suitable for doing clinical trials. Those clinical trials were sponsored by NIAID, and I would

like to take credit at FDA as being one of volunteers for the study, since that may be my only way to take credit for being in this. studies -- there were Phase I studies that were done to evaluate the utility of the purified hemagglutinin vaccine in laboratory workers to give the possibility of some protection at a time when it was not really possible to produce in that very limited space of time an inactivated vaccine or any other kind of vaccine. Those studies have now gone on, and we will hear more about them from later speakers. The

studies -- we will also hear something about the Phase II studies, which have been pursued to try to identify exactly what the dose of the vaccine of inactivated vaccines should be and to glean some information that could be useful for other studies of inactivated vaccines. I think I should stop there and turn it back to you, Dr. Ferrieri.

CHAIRPERSON FERRIERI: Thank you very much, Roland. The order has been reversed. So the European vaccine's trial scheduled for 4:00 by Dr. Wood from the UK will be presented now.

DR. WOOD: Thank you very much. Most of my talk will be about European vaccine -- attempts to produce an H5 vaccine and plans to do clinical trials

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of this vaccine. But I will talk about some more general issues at the beginning.

If we can go back to December of 1997, what were our objectives at that time in terms of vaccine? I have identified three main objectives here. To identify a safe, practical vaccine strain. To develop reagents to measure the potency of any of those vaccines. And to evaluate those vaccines by animal studies and if we have time to do limited clinical studies.

Roland has alluded to some of the strategies that could have been followed, but at that time there were three main strategies that were followed. First of all, to attenuate the Hong Kong/97 virus, this pathogenic virus, by genetically modifying the hemagglutinin so the virus would not be pathogenic for chickens and hopefully not for people as well. To identify a surrogate H5N1 virus that resembled the Hong Kong virus yet was not pathogenic. And thirdly, to express the H5 hemagglutinin in a expression system such as a baculovirus system. And we will hear about these two, the attenuation and the baculovirus system in later talks.

I am really going to concentrate on the surrogate H5N1 virus from now on. This is a

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phylogenetic tree of the HA1 region of the H5 hemagglutinin provided by Jill Banks of the Central Veterinary Laboratory at Weybridge in the UK. Here we have the chicken Hong Kong virus and the human Hong Kong virus, and quite closely related to this is Duck/Singapore that Roland just mentioned. In fact, its HA shares about 93 percent sequence homology.

When we look at the Duck/Singapore virus antigenically and compare it with the Hong Kong viruses, we see it also is antigenically quite closely related. This is an HI test with post-infection ferret sera to two Hong Kong viruses, Group I virus and Group II virus and Duck Singapore virus. And you see although these HI titers are not identical, they are quite close, showing that the Duck/Singapore virus is quite closely related antigenically.

So this was in fact one of the leading vaccine candidates back in about January of 1998. It had advantages and it had some disadvantages. The advantages I have listed here are that first of all it was non-pathogenic. So a vaccine manufacturer could work with this virus in safety. The hemagglutinin was similar. A conventional vaccine could be made from Duck/Singapore virus and there would be no licensing issues.

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the downside, it had On the wrong neuraminidase. It has N3 neuraminidase and it grows extremely poorly in hens eggs. So to try and rectify both of these disadvantages, a number throughout the world tried to produce reassortants to increase the growth and substitute the N1The basic strategy was quite similar neuraminidase. in most of the labs that tried. It was to reassort Duck/Singapore with PR8 or a virus with PR8 internal And to try and substitute the N1 either from PR8 or from another virus such as a swine virus isolate in Ireland which had an even more closely related N1 neuraminidase.

The first virus -- I should say first of all that no one has been successful. All of these attempts have yielded H5N3 virus in using conventional techniques in eggs. The first virus that was produced was produced in my lab in May of 1998, NIB-40. It had a growth advantage. It was not a reassortant. It had all the genes from Duck/Singapore. So it was probably a high growth variant we just selected out in the process. Alan Hampson in Melbourne produced ARIV-1, which grew much better than both the Duck/Singapore parent and NIB-40. I don't know whether this is a I haven't been able to find this out. reassortant.

And then we have two viruses which were derived, one in Roland Levandowski's laboratory here and one in Ed Kilbourne's laboratory. And these are still being characterized.

But it has shown how difficult it was to produce reassortants from the Duck/Singapore virus. Now you can speculate as to the reasons for this. There may be that there is a basic incompatibility between the human PR8 virus genome and the avian virus genome. It may be that the selection process in eggs wasn't efficient or our antiserum reagents weren't good enough to do the selection. But whatever the reason is, we weren't very successful.

NIB-40 was the virus that in fact was chosen in Europe to do some limited clinical studies with. As well as having a seed virus, we also need reagents to measure the vaccine potency. The test that is used worldwide is a single radial diffusion And we have developed antigen -- you need a reagents, a calibrated antigen and an of antiserum against the hemagglutinin. We have made antigen reagents to Hong Kong/489 and Duck/Singapore and three different antiserum reagents. One was produced a long time ago against Chick/Scotland/59, an H5N1 virus. The other two were more recently

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produced. One against the baculovirus HA. This was the Hong Kong/156 virus. And the other against purified HA from Hong Kong/489. We evaluated these three sera in the test with these antigens, and by far the best was this old antiserum, Chick/Scotland. And I must say that delighted by director, Geoffrey Schild, because at the time this was produced, he was actually working in the lab. So he produced this serum. So he is delighted that one of his old serum has come good.

The next thing we did was to evaluate the Duck/Singapore virus as a vaccine in mouse efficacy studies. We produced inactivated whole virus vaccines from Hong Kong/156, from 489, from NIB-40, which is Duck Singapore here, from an irrelevant H3N2 vaccine, Shanghai/90, and we had an unvaccinated group. There were groups of 10 mice and they each received two shots of 15 mcg, a human dose. And on this left-hand side of the slide, we see the antibody response as measured by HI test. In red, we have the antibody responses to H5 measured using the Hong Kong/489 virus, and in yellow we have antibody to H3 measured with a Shanghai virus. So you see the Shanghai virus was just as immunogenic as the H5 viruses. want to comment on the fact that the Duck/Singapore

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vaccine was maybe not so immunogenic. But I think this is probably due to antigenic differences between the Hong Kong/489 virus and Duck/Singapore. Because if we use Duck/Singapore virus in the HI test, we have equivalent antibody levels. So I think we can quite safely say that each of these vaccines was equivalent in terms of immunogenicity.

Two weeks after the second shot, we went on to challenge these mice with a lethal challenge dose of Hong Kong/156 virus. And then we monitored survival of the mice. In both of the control groups, the unvaccinated group and the H3N2 vaccine group, there was no survival at all. The mice died within 8 days. Yet complete survival in each of the H5 vaccine groups. So this is very encouraging that the Duck/Singapore vaccine had some potential to protect against the pathogenic Hong Kong virus. I have since seen quite similar data from Jacquie Katz using the Hong Kong/489 -- or is it 483 -- the Hong Kong/483 as a challenge virus. So it protects against the other group of the Hong Kong viruses as well.

So we now move into plans for clinical studies. In the UK, Carol Nicholson and I have been interested in doing clinical studies in naive populations to ask the question what would happen if

you put a vaccine into naive populations in a pandemic situation. And we have been thinking about different models, such as an H7N7 vaccine or an H2N2 vaccine. But then H5N1 came along and we had an ideal model and we could also use this to evaluate the Duck/Singapore as a candidate vaccine.

But these were some of the questions that we thought we should try and answer. What is the minimum immunogenic dose of the three types of vaccine, whole virus, split and surface antigen Is one better than the other? vaccine? There is a school of thought that says the whole virus vaccine would be actually more immunogenic in naive populations, but it has never been satisfactorily answered. Past studies -- the vaccines have not been standardized as efficiently as the vaccines are standardized now. So you would always question the actual dose that was administered back in 1957 or 1968 or 1976 or 1977, when similar studies were done. There is no consistent agreement from trial to trial on the results as far as I could see, and there was also no direct comparison of each of these three vaccines.

Another question you might want to ask is does a PR8 reassortant induce antibody more

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effectively than a completely foreign avian virus with no human influenza genes at all? So that may be an issue for the future. How effective are adjuvants? We know that a variety of adjuvants have been tested in animal models and some of them have shown to be very effective. Yet, when we go into clinical trials, some are less effective. It may be that in naive populations in human trials, the adjuvant would behave more like it does in an animal model. And it may actually be very useful. It may be antigen sparing, where an antigen is a precious commodity in a pandemic situation. And finally, would alternative strategies be better in a pandemic -- DNA vaccines, vaccines, et cetera.

Two companies in Europe have made vaccines from Duck/Singapore, from NIB-40. Chiron, Italy have made 14,000 doses of surface antigen vaccine. This is at a level of 15 mcg. Medeva in the UK have made 7,000 doses of surface antigen vaccine and 1500 doses of whole virus vaccine. And these are intended to be clinically evaluated.

The plan for the UK trial as it existed back in January of 1998 was to do a direct comparison between a vaccine made from Hong Kong/489 virus, a pathogenic virus, and vaccine made from

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Duck/Singapore to compare their immune responses. And to have three different dose levels, 7.5, 15 and 30 mcg., and to give the subjects two shots and then evaluate the immune response. And to compare their response with the Duck/Singapore whole virus vaccine. There will be Phase I and followed very quickly by Phase II, should the Phase I have been shown to be that the vaccines were safe.

This was -- to put this together, we had a consortium of a number of organizations. CAMAR down in the UK, NIBSC, Medeva, Maria Zambon at the PHLS, and Carol Nicholson, the clinician at Leicester Royal Infirmary. The biggest challenge, as you can imagine, was to produce this arm of the study. The virus was produced in containment under conditions which were as close as possible to good manufacturing practice. And a limited amount of inactivated allantoic fluid was made in containment. The big problem was when we came to process this at the site of manufacture. normally, as many of you know in the audience, you deal with hundreds of liters or thousands of liters. Yet here in containment, I think we produced about 30 liters of inactivated fluid. So there is a big scale difference between what we produced and what normally processed by a manufacturer, with the result

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that we lost most of this. It was a big disappointment, but we lost it. It just didn't survive the processing to produce the surface antigen vaccine. So that meant we had to drastically change our plans.

So the current plan is that we will look at the Medeva surface antigen Duck/Singapore vaccine compared with the Medeva whole virus vaccine at these three dose levels. And also taking place in the UK is a collaboration between Chiron and Carol Nicholson to evaluate their Duck/Singapore vaccine. This time the comparison will be surface antigen versus adjuvant at surface antigen to compare the effect of the MF-59 adjuvant in naive populations.

One problem in evaluating the immune responses is that the HI test, which is the gold standard for serology, has been shown not to be very sensitive in measuring antibody to H5 in human sera. This is one reason that we are not relying on this test. We are going to use the virus neutralization test that Maria Zambon has developed. But we are also going to evaluate another test, the single radial hemolysis test. And for those of you not familiar with this test, this is an agarose gel containing erythrocytes -- sheep or turkey erythrocytes -- to

which is bound the virus of interest, in this case Duck/Singapore virus. Also in the gel is incorporated guinea pig complement. And then if we introduce serum containing antibodies to Duck/Singapore in the wells. the antibody binds to the virus and initiates the complement mediated lysis of the cells. So you have a zone of lysis and the size of that zone depends on how much antibody was in that particular serum. This test is used routinely in Europe for evaluating vaccines. It is allowed by the regulatory authorities. So we have a lot of experience with this test.

Duck/Singapore. These are two ferret sera, post-infection ferret sera to Hong Kong/483 and to Duck/Singapore. And you see very big zones of lysis here. We also looked at a range of human sera, pre and post-conventional vaccine, 1997 trivalent vaccine no zones. But unfortunately we saw two very faint zones with random human sera. And what we think is happening there is that these sera contain some antibody to nuclear protein, Influenza A nuclear protein, which Duck/Singapore is recognizing. So it does initiate a faint, non-specific zone of lysis. We can remove this entirely by adsorption with another

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Influenza A virus. So these along the bottom line here are the sera adsorbed with Influenza A viruses. No non-specific zones, but the specific H5 zones are left intact. So with just one extra step, adding an Influenza A virus, I think we have a test which is worthy of evaluation in our clinical studies.

This is my last slide, and I think many of us view the Hong Kong episode as really a rehearsal for what will come in the future. And I think at this stage it is very useful to look back. It hasn't been an easy year for quite a few of us. And to ask ourselves how could we prevent some of these problems happening in the future? What lessons can we learn? And the first one, I have put up here is a dialogue with veterinary authorities. This was one of the first hurdles we had to overcome. We had to have approval in the UK from the Ministry of Agriculture, and I am sure this was the same here with the USDA. They had to grant us a permit and they had to inspect our facilities. And I think it is important that this dialogue continues for the future and veterinarians are involved in many aspects of pandemic planning.

We had to work in containment laboratories for the Hong Kong virus. For some of us, we already had containment laboratories. For others, they had to

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either find a colleague who did have a containment laboratory or actually build one. So there problems with actually getting funding to build containment laboratories. There were problems in writing codes of practice for a new virus, in getting stocks of antivirals, and getting approval from safety and veterinary authorities. All kinds of hurdles we had to overcome to actually get up and running and working with the pathogenic virus.

Now we have containment laboratories in quite a few laboratories throughout the world and it is really important that these are maintained. possibility that we may want to consider is that we have at least one or two containment laboratories within a site of manufacture. So that without any change at all, a completely novel possibly even pathogenic virus can be grown and produce a few thousand doses of vaccine that could be used for people in surveillance laboratories and for other vaccine manufacturers and for the staff in those laboratories. And we have learned that if we are going to do this, we certainly need small scale production plans.

We have had problems in producing reassortants. Normally this process is very

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efficient. We produce them more or less to order with the normal Influenza A strains. But with the H5 virus, we have problems. So maybe it is time to reflect and ask ourselves are we doing this the right way. Are there other methods we could look at such as using plaquing in mammalian cells or maybe using reverse genetics to produce the reassortants in the future.

Rob Webster has, for a number of years, put forward the idea that we should be working up banks of seed viruses for likely pandemic strains. I think with our recent experience, I really believe it is time to start working with this. H5's and H9's and H4's and maybe other possible subtypes -- H2's. And start to build up banks of reassortments and SRD reagents to measure the vaccine potencies.

Fast track regulatory systems. We never actually got the marketplace with H5 vaccines. There was no need for it. So there were no licensing problems. But you can envisage that with some of the strategies that were being followed to make H5 vaccines, there would have been problems. Because some of those were genetically modified products, which are not currently licensed. We have had preliminary discussion in Europe, a brainstorming

session back in March of last year, to try and think of methods to fast track novel vaccines in a pandemic situation, and also to fast track the mandatory testing of those vaccines. And I think that is something that should be encouraged.

And finally, we should continue developing alternative technologies to produce vaccines. We shouldn't rely on the whims of a chicken laying eggs. We should keenly pursue cell culture vaccines, adjuvanted vaccines and DNA vaccines, just to name few. Thank you very much.

CHAIRPERSON FERRIERI: Thank you, I don't know, Roland, if you had built in time for questions from the panel. How do you feel about the afternoon? The ones who have stayed are to be congratulated, but I guess we could have some room for at least a question. I understand the next presenters have to leave at 4:30. So we will keep that in mind in the time we take for any questions. But if you have questions for Dr. Wood at this point? I quess not. So we have another presentation called additional vaccine activities by T. Mabrouk from Biochem Pharma in Canada and Dr. Li from Aviron. Will both of you be presenting? Only one presentation, okay.

DR. LEVANDOWSKI: Dr. Ferrieri, there are

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actually two separate presentations. 1 CHAIRPERSON FERRIERI: So there will be 2 3 two presentations. Dr. Mabrouk? 4 DR. MABROUK: Thank you very much. 5 CHAIRPERSON FERRIERI: Thank you. I would 6 advise then that we keep it with two thirty minutes 7 maximum total for the two of you. 8 DR. MABROUK: Sure. First of all, I am 9 very pleased to be here to present some results regarding the H5N1 project. This study was done at 10 Biochem Vaccines, which is a subsidiary of Biochem 11 Pharma. First of all, I have to thank very much Dr. 12 13 Levandowski to give this opportunity to Biochem 14 Vaccines to present some results regarding this 15 project. 16 So we have talked today about the H5N1 17 project, and this is the plan of my presentation. 18 First of all, I will do a very small introduction because I think the most important things was done by 19 Dr. Levandowski and Dr. John Wood. The second one, 20 21 the objective of the study. And after that, what is 22 the strategy to do that and the results. 23 So as you see, the results is divided into three parts. The first, how we assess the identity of 24

the clone H5N1, and the second one, how we assess the

purity of the clone and some immunogenicity data that we have already now.

So I have to clarify one point before I start the presentation. Biochem Vaccines is developing now with our new partner, which is Smith-Kline Beecham, a new technology for the production of the vaccine using cell technology. At Biochem vaccine, we have now a new clone, which the name is It is MTCK derived cell line, but this cell BV5F2. line is not a mutagenic cell line. So during all these studies, I will talk about BV5F1 and the clone was isolated using this BV5F1, which is, as I said, not a tumorigenic cell line.

So as you know, H5N1 is subdivided into two groups, 156-like virus and 413-like virus. It is the first time that we showed a direct transmission from the poultry to humans. We had 18 cases of infection reported and we have 6 persons who died. So the virulence of this H5N1 is associated with a stretch of basic amino acids as the cleavage site between H1 and H2. And the other particularity of this clone is that we have deletion of 19 amino acids on the neuraminidase protein.

So the objective of this study is to develop a non-pathogenic H5N1 in order to produce

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split H5N1 vaccines using the cell technology and without using PC facility. That is the objective of this study. And as you know and as it has been mentioned, Protein Sciences has good results regarding the complement H5 proteins and Aviron is working on the itinerary to H5N1.

So here in our strategy we used the Duck/
Singapore virus and the swine virus. And as it had
been mentioned by Dr. John Wood, we used the Singapore
virus because the H5 of this virus is very close with
the H5 of Hong Kong and the N1 of swine virus is very
close to the N1 of the Hong Kong virus.

So what we did is we infect the virus by these two viruses and after that we purified the clones by using the technology of plaques technology. So here the first step is the plaque purification. And after that, we do the immunoselection using the antibody against a New Jersey/876 to neutralize H1 of the swine virus. So we isolate some clones here. In this case, we have 50 clones. And we grow these clones and after that we select only the clones that show very high growth on the cell lines.

So after that, the first step is to be sure that our clones is H5N1, and we do that by PCR. So we have four clones positive for H5 and positive

for N1 segments. And the second step is to do the same selection using the same antisera. After that, we have to do the exercise of plaque. I mean, to make another selection, and we have to analyze by PCR and we have to be sure that at the first passage, we do not have any contamination -- I mean H1 and N3.

After the first passage, we have to do five passages on the cell line to be sure that our virus is not contaminated. So we do the same exercise after the five passage. We do identity. We look for the H5N1. We assess the purity by looking for the contaminant H1N3. So in this case here, we have the clone 1A, 1B, 5A, 10B, and 27A positive. When I say positive, that means that H5 and N1, and we do not have any contaminant, N3 and H1.

So I don't think that I have to go through all these techniques. I think that you know the techniques. The first step is to do the reverse transcription for cDNA and after that we have to amplify the segment hemagglutinin or neuraminidase, and this depends on the kind of primer that you use.

So this primer is used for the identify. So to assess the purity of the clones, we have to do the first PCR. And then the second time, we have to do the nested PCR. So we use two microliters of the

first PCR reaction to do another PCR to be sure that we do not have any contaminations. So this is the primer that has been used for the nested PCR.

So here are the conditions of the first reverse transcription. So as usual, you know it very And we did only one cycle to amplify and to synthesize cDNA. Here are the conditions of the PCR reactions. So we use two primers, 5 prime and 3 prime, depending on the segment. And we did 30 seconds, 55 degrees for 30 seconds and 70 degrees for one minute. All of these conditions I think is already published on the papers. So here is the nested PCRs that I did. As I mentioned before, we used only 2 microliters from the first PCR and we do the same reaction of PCR, 30 seconds.

So here we show you the results that we had. So for the passage 1 and for the identify, we have here the results of the PCR reactions. We put here all the positive clones and all the counter swine virus, the dog virus, and the negative as a mark. And we amplify the segment by using primers, which normally does give to us a fragment of 295bp. So as you see here, only for the H5 we detected that for the dog. We do not detect anything for the swine. And we have 1A, 1B, 5A, and 10B and 27A positive for H5. And

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for the N1, we have all these clones are positive for neuraminidase. So we pursue these studies using only the clones which are positive for H5.

So this is after passage 5. We get the same reactions using the same primers. And we do see that we have the same positive results for the clones 1A, 1B, 5A, 10B and 27 A, and we have nothing for the negative and we have nothing for the swine virus. And for the neuraminidase, we have the same pattern of results.

Now it shows here that after passage #10, we have the same kind of results after passage #1. So this is to be sure that our clone is H5N1 by doing PCR. Now to be sure, we present a lot of veracity to support the idea and to support the results that it is H5N1 and not another clone. So the first is the PCR and the second is the sequence. So we sent the sequence to another lab and after that we sent the sequence to the Internet, and we have here as you see 93 percent of identity between our clones and the Hong Kong sequence. And we did that for the hemagglutinin molecule and for the neuraminidase protein.

So this is the nucleotide sequence. It doesn't mean that for the amino acid sequence we will have the same percentage of identity. Maybe we could

have higher than that. But we did not have these results now.

So here is some serological results where we used post-infection ferret. sera against Duck/Singapore H5N3. This is lot number 1, if I can say, and Duck/Singapore #2 and A/Texas and Nanchang. And after that, we react these post-infection ferret serum against these viruses and these clones. So here, as you see, all the clones are very -- they give us a high titer when we use the Duck/Singapore postinfection ferret serum. But we do not understand why when we use the A/Texas and the Nanchang, we have a very high titer here in this case. This was repeated many times and we have almost the same kind of results.

So now to be sure that our clone is pure and is not contaminated, so we have to assess the purity of the clones at passage #1 and passage #5. So here I am showing the results of the purity after passage #1. This is for the hemagglutinin H5. So here we detect H1 only for the swine, but we do not detect anything for the other clones. This is the nested PCR, and we have the same pattern even after the second PCR. So it does mean that our clones, 1A, 1B, 5A, 10B and 27 A are pure at passage #1.

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did the same thing the neuraminidase and we see that here we have one for the Duck/Singapore, but it is not clear here on the photo. But on the gel, we have it. It is very hard to convince you. And we did the same thing for the neuraminidase here at the second PCR, what we call nested PCR, and we detect only one band here for the Duck virus. And we have the same results after passage #5. So we have no contamination with our clone.

So based on these results, we can say that the clones that we have -- clones 1A, 1B, 5A, 10B and 27A -- are H5N1-like virus, and we cannot find any contaminant on these clones. So we have the same results.

So we did some immunogenicity activity testing by doing hemagglutination inhibition tests. So we used post-infection sera against Hong Kong viruses. We have here the lot number. This is against the 156-like virus and this is against 483 and this is against 491. So actually you can see here for the clone 1B, we have a high titer with all these postinfection ferret sera. And for the B/Harbin, we detect the titer was less than 20.

We could not really do -- I mean, to

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complete these experiments, we have to use the postinfection ferret sera against our clone, but we do not
have that antisera now. So we administer this
recombinant to the mice and here we have the results.
This is the number of the mice -- 1, 2, 3, 4, 5, 6.
Mice #'s 1, 2 and 3 received PBS and the mice #'s 4,
5, 6, 7, 8, 9, and 10 received the H5N1 vaccine. So
here as you see for our recombinant 1B, we have some
mice, #5, who has some immune response against H5N1
vaccine. For the A/Singapore, you have only two mice
who showed some immune response. But for the swine,
the level is very, very low and for B/Harbin.

So if I can summarize all of these results, we can say that for the identity, we can say that our clones are H5N1 based on the results of PCR sequencing and immunoreactivity. And we can say that our clones are pure based on the results of nested PCR. And we can say that these clones are immunogenic based on the results of immunogenicity in mice.

So I have to thank Dr. Janique Forget and Francine Allard, who did this work, and I have to thank very much Dr. John Wood from the NIBSC, and Dr. Nancy Cox. Dr. John Wood sent to us all the Singapore and swine virus, and Dr. Nancy Cox sent to us all the reagents to assess the immunogenicity of these

+	viruses. Inank you very much.
2	CHAIRPERSON FERRIERI: Thank you, Dr.
3	Mabrouk. Roland, did you have any questions for him?
4	DR. LEVANDOWSKI: I guess maybe I would
5	make just a comment that it is remarkable considering
6	what the rest of us have been trying to do working in
7	eggs to make reassortants. It seems that there was no
8	problem at all using this technique of picking out the
9	clones and then working with them separately rather
10	than having to work with a complete mixture. And
11	actually, this is something that Dr. Kilbourne has
12	been talking about for years already, and it seems
13	like a technique that we should be moving toward
14	adopting. I don't know if Dr. Kilbourne has some
15	thoughts on that.
16	DR. KILBOURNE: You have expressed them
17	well.
18	CHAIRPERSON FERRIERI: Other comments from
19	the panel here? Otherwise, we will move on then to
20	Dr. Li from Aviron. And then when he is through, we
21	will go back to the purified HA vaccine trials
22	originally slated for 3:15.
23	DR. LI: We have been working very closely
24	with the CDC, NIH and FDA to develop vaccine
25	candidates against the HEN1 influence viruses. I am

going to summarize the preparation and the pathogenetic testing of two candidates which can be used to prepare live attenuated vaccines and which can also be used as a substrate for manufacture of inactivated vaccine.

We know from the previous introduction by Dr. Levandowski, we started the vaccine development approach in January of 1998. We know from work done at the CDC and by others that there were highly pathogenic viruses. We knew that all genes of the H5N1 isolate are of avian influenza origin. We knew there were two antigenic subgroups coexisting with 156 and 483, the prototypes respectively. We knew that the HA cleavage site contained much of the basic amino acids which might contribute to the pathogenesis seen in chicken and possibly in humans.

Based on this information, we needed to find a vaccine approach which not only can result in a safe, efficacious vaccine for human use, but also is safe for personal immune development and the protection of the vaccine. You already heard about a vaccine approach by using baculovirus system or by using apathogenic antigenic strain. I am going to present to you a vaccine strategy which is illustrated here by applying genetics.

The strategy is to modify the HA cleavage site by deleting most of the basic amino acids and then to produce a recombinant 6:2 reassortant virus which contains the genetic modified HA agent and an unmodified NA agent from the H5N1 Hong Kong isolates and the remaining genes for a very long life itinerary of ours, the ca A/Ann Arbor/6/60 strain which was developed many years ago by Dr. Massab for the University of Michigan.

For this purpose, we have cloned the HA and NA gene ofboth the 156 and the 483 strain. In the HA construct of our vaccine candidates, we deleted the five basic amino acids at the HA cleavage site you can see here. In addition, we inserted a 1 sera reduce bag to mimic the low pathogenic HA or NA gene. The remaining arginine codon of the vaccine construct was changed to appear medium codon to increase the stability of the construct.

Then we applied the recombinant technology to introduce the cloned HA and NA genes into the coded WR spectrum. To prepare candidates in 483, we were forced the transfect the modified 458 HA and NA gene into the coded WR spectrum to generate the 7:1 intermediate. Subsequently, we have transfected the wild type unmodified 483 NA gene into the 7:1

intermediate to generate the 6:2 vaccine candidates.

Candidate MVS/156 was generated in a slightly different way in which we explore possibility of transfecting HAand NA genes simultaneously but in two different reactions. In fact, we were able to generate two intermediates, one bearing the HA gene and one bearing the NA gene. Subsequently, we applied this classical reassortant technique to generate the 6:2 MVS/156. I should have mentioned that we also use a condition similar or very close to the GMT condition to produce the vaccine strain, including a useful for doing the transfection of for vaccine production.

Here our colleagues at the CDC test the antigenicity of the vaccine candidates by using ferret sera risked against 12 different H5N1 Hong Kong isolates, including against the wild type 156 strain and the 483 strain. Overall, we can see that the antigenicity of the MVS/156 were similar to the wild type of 156, and the MVS/483 is antigenically more similar to the wild type 483 virus.

We did some of the original characterization of the vaccine candidates. We show here both candidates reduplicated a reasonable titer in eggs with the MVS/156 up to $10^{9.4}$ EID 50 per ml.

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This is an important finding because the production capacity of the vaccine is largely dependent on the replication of the worst titer in eggs, currently the only substrate approved for production of the influenza virus vaccine.

Duck/Singapore/97, as you know from the previous speaker, is another potential vaccine candidate. However, it doesn't replicate unless in In addition, we have shown here that both candidates vaccine replicate at a 25 degree temperature. So they are cold adapted. They are also temperature sensitive with a shut-off temperature of 39 degrees. Also, they are parenteral cold adapted Ann Arbor/60 strain.

As we know, the virus has much of its basic amino acids at the HA cleavage site. They require trypsin for every replication in many cells. Whereas viruses with single basic amino acid HA can require trypsin for efficient replication. Here we show that the vaccine candidates, after depleting most of the basic amino acids, now require trypsin for efficient replication. In CEF and MDBK cells, we can see the vaccine candidates, like the cold adapted parenteral virus and like the apathogenic or low pathogenic Duck/Singapore strain, form plaque in the

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presence of trypsin, but in the absence of trypsin, no plaque was detected.

We know that type H5N1 viruses are highly pathogenic in chickens and kill them more quickly. We did two experiments in chickens to test how safe are our vaccine candidates. We used two different chicken The first experiment was done exactly species. according to USDA guidelines. We show that like the cold adapted parenteral virus and like the Duck/Singapore/97 strain, the vaccine candidates did not kill any chickens. So they are low pathogenic in chickens.

In the second experiment, we increased the inoculation dose by 10-fold. We had other different inoculation routes including the intranasal intratracheal route. Again we show that like the cold adapted parenteral virus, the vaccine candidates did not kill any chickens. In contrast, the wild type 156 and 483 strains killed chickens within two to three days after inoculation.

Here we show the vaccine candidates, when distributed in live attenuated form, are capable of inducing protective immunity in chickens. I should tell you at the beginning that a chicken is not a very good model for testing the immunogenicity of the cold

two

adapted virus presumably because of the high body temperature or the temperature sensitive phenotype of the cold adapted viruses. And this I should mention to you that the sample size of this study is very small, each group represented four chickens only. However, we can say here that three of four chickens which were inoculated with MVS/156 were protected from wild type 156 challenge. All four chickens which were inoculated with MVS/483 were protected from wild type 483 challenge. Now two out of the four chickens which were inoculated with MVS/156 were protected from wild type 483 challenge, and the two of the four chickens immunized with 483 were protected from wild type 156 challenge. However, because of the small sample size, we cannot draw much of a conclusion about whether this caused protective immunity between these subgroups. And as I expected, cold-adapted parenteral virus did not initiate any protective immunity against both the 156 and the 483 strains. Recently, Dr. Perdue from USDA did one more experiment by using inactivated preparation for the MVS/156. What was shown here is that all chickens inoculated with this inactivated preparation were protected from either wild type 156 or 483 challenge.

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This clearly indicated the vaccine candidate is immunogenic and caused protection in this animal system.

The ferret is an excellent model for mimicking the human influenza virus infection. We did two experiments in ferrets to assess the safety characteristics of the vaccine candidates. We show that none of the inoculated ferrets developed flu-like symptoms. In addition, the replication of the vaccine candidates are mostly restricted in the upper respiratory tract. We also cannot detect any virus replication in the lung.

Notably, in the second experiment, we didn't observe any replication of MVS/156 in both the turbinate and lung. In terms of immunogenicity, we did a preliminary study in ferrets. Again, because of the limitations which we have to do to conduct the animal trial, we used a single ferret for each of the groups only. We show in the first experiment that the single ferret which was inoculated with MVS/483 shows the same HI antibody response to both wild type 156 and 483. whereas the singular ferrets which were inoculated with MVS/156 did not show the same HI response. However, when we repeated the study in the second experiment, we showed that both groups show the

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same HI response.

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In summary, we have applied the recombinant technology to generate a vaccine candidate against the H5N1 virus. The candidates contain genetically modified HA and unmodified NA gene from the wild type H5N1 viruses and the remaining gene from live attenuated cold adapted strain. We show that the vaccine candidates are temperature sensitive, they are cold-adapted, they are dependent on trypsin in some in vitro cell lines, and they grow to very good titer in chicken eggs. In addition, the recombinants are nonpathogenic in chickens and safe in ferrets. are capable of inducing protective immunity in chicken in both the live attenuated form and in the activated form. And finally, we believe that the H5N1 vaccine candidates have satisfied the preclinical material and should be considered for further characterization in humans.

who contributed tremendously to this development on pathogenic studies. Drs. Klimov, Subbarao and Cox from CDC, Dr. Perdue from USDA, Dr. Hietala from U.C. Davis, Dr. Liu from Aviron, and Dr. Bryant, who was formally associated with Aviron. Thank you.

CHAIRPERSON FERRIERI: Thank you for a

very interesting presentation, Dr. Li. Any questions 1 2 His approaches have great promise for for Dr. Li? 3 other related viruses. I guess not. Dr. Kilbourne, 4 comments or questions? 5 Well, the comment is one DR. KILBOURNE: of admiration for the accomplishment. 6 But I would 7 like to know specifically, when you say this is high 8 yield in eggs, what does that mean in terms of 9 relation to PR8, for example? DR. LI: You made a very good comment. 10 11 I said high yield, I should take it back. I tried to say it is a reasonable titer. And certainly we didn't 12 13 have a comparison. Maybe the inactive manufacture 14 could comment on this much better. We think -- I 15 don't have any idea how -- normally the high yield reassortants, what kind of titer you achieve in the 16 17 eggs, but the titer, of one of the candidates of 10 to 18 the 9.4 ETD per ml, I thought that was reasonable. 19 DR. KILBOURNE: Okay. I hope you could 20 put some quantitative figure on it, but that is okay. 21 CHAIRPERSON FERRIERI: Yes, Dr. Breiman? 22 DR. BREIMAN: You mentioned removing the 23 5 basic amino acids to produce virulence and then a couple of steps to increase stability of the strain. 24

With your live attenuated form, do you have any way of

evaluating the reversion?

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That is a very good question DR. LI: because why the H5 always have the pathogenic viruses whereas the other sub types don't. Maybe it has something to do with the HA structure itself. What we did basically is, as I also mentioned before, we changed the arginine codon to increase the stability. In addition, we did a sera passaging of CEF cells in the absence of trypsin to see if the phenotype changed. In fact, after three to four passages, there was still a requirement of trypsin for replication, indicating that the modification didn't change. DR. KILBOURNE: Does the neuraminidase

clone retain the deletion?

DR. LI: Yes. You are absolutely right. The deletion, which is a characteristic of the neuraminidase. At this time, we didn't see a direct correlation of pathogenesis -- of this deletion to any pathogenesis. We didn't do any. In the meantime, we tried to generate mutants, which help to repair to say what kind of phenotype we might have there.

CHAIRPERSON FERRIERI: Thank you very Now we will move back up to the top. And we will hear presentations on purified HA vaccine trials from Dr. J. Katz, CDC first. The two presentations

were originally designed for 45 minutes, but I understand that one or both of you volunteered to contract your talks a bit.

DR. KATZ: I guess that is me. I have just removed about five overheads. So hopefully we can keep things shortened. This is just an outline of what I was going to talk about, and I will just give only one overhead as an introduction now. And then I will move straight into a description of the serologic assays that we have been using to evaluate antibody to H5 avian viruses in humans, and then how we have used those assays to determine the serologic results from the Phase I trial that Dr. Levandowski introduced, and then also I will give preliminary results of the Phase II trial being conducted at the University of Rochester.

This is my only introduction. Everything else so far has been said by the other speakers. So I just wanted to remind the audience that the 16 H5N1 viruses that were isolated out of 17 cases fell into two antigenic groups. And just to remind you of the severity of the disease in humans, with 6 fatalities and two other severe cases, and both groups were fairly equally represented in the fatal and severe cases as you can see by this timeline of the case

distribution in May, November and December.

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So I am going to move on right now into looking at the different serologic methods. It became very evident early on in the outbreak investigation from the H5N1 outbreak in Hong Kong that the traditional hemagglutination inhibition assay was not going to be terribly useful for detecting antibody to H5 viruses in humans, and I will show you a bit of data about that in a minute.

at the time the first case was recognized, we went into development microneutralization assay to detect antibodies to H5 in human sera, and it is just basically an overnight assay looking at the ability of antibodies to inhibit about 100 TCIB 50 of virus, and we have recently had a publication accepted which describes this assay and its useful detection of antibody in human sera. it also relates to the other assays that we were setting up concurrently. We also looked at the H5 indirect ELISA, and this was using the recombinant HA protein prepared by Protein Sciences and expressed in the baculovirus system. And we found that the ELISA was useful and specific for sera from children, but we had so grave limitations in using an IgG ELISA for adult sera, and I will show you why in a moment.

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So we also -- we wanted some sort of confirmatory assay because the microneutralization assay was new and being used for the first time in this way. So we again used the Protein Science recombinant HA as an antigen in Western blot, and we used this confirm to results in the either microneutralization assay for positive results from adult sera or the ELISA in children.

This just an overview of the microneutralization assay. Basically two-fold dilutions of serum are added to a 96 well plate and then the virus. In our hands, we have been using Hong Kong/156, which means we have been doing these in a BSL-3+ containment facility. It is added and then allowed to incubate for a couple of hours, after which time a relatively low number of low passage MDCK cells are added to the plates and the plates are incubated overnight for 18 to 20 hours. The next day, the cells monolayer is washed and fixed, and the readout is an ELISA detecting the presence of the Influenza A nuclear protein using a specific monoclonal antibody. And the readout, the way we express the titers, is a 50 percent endpoint based on control positive and negative wells.

So once we had identified several

cases confirmed that were confirmed by virus isolation, we had S1 sera that were collected within about 7 days of the symptom onset of the individuals, and in some cases, we also got S2 sera, which were collected about 14 days later. And so we wished to compare the hemagglutination inhibition assay with our microneutralization assay using -- this was Hong Kong/156 H5N1 virus. And you can see for these first two cases, we couldn't detect any sero conversion by HI, but we could detect a nice 8-fold rise from the S1 to the S2 by the microneutralization assay. And this was true for other single serum that we got at a substantial time point after infection. And only in situations where we had neutralization titers of over 1,000 could we detect any significant HI activity. So we decided that we probably would go ahead and use the microneutralization assay.

And this is just characterizing now the primary antibody response to H5N1 infection in 16 individuals. This is a combination of all the serum that we could obtain at different time points from different infected individuals. And some of these were just single time points and our ability to collect sera at adequate time points was compromised by the severity of the illness in a lot of individuals. But

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you can see that the best fit curve pretty much defines a very typical primary response to a primary infection and this dotted line -- this is actually a log scale, but this dotted line represents a titer of 80. And we could see that after about 14 days after symptom onset, most individuals were making an antibody response of 80 or more, and we decided to use this as a cutoff for a level of positivity for the presence of H5 specific antibody in human serum. And you can see actually that out by day 20 or so onwards, titers were actually as high as 640 to about 1280. So they were making quite a substantial antibody response.

So we could now go ahead and test the sensitivity and specificity of the microneutralization assay using these known confirmed cases of H5N1 infection, and we could use these to detect the sensitivity of the assay by just seeing how many of these we could detect antibody in. And then we also used a fairly large number of controls which were collected from individuals age-matched, either adults or children, that were non-exposed, and these were individuals that had come from Hong Kong blood donors or other children's groups in Hong Kong and also in dividuals in the U.S.

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And we actually compared each of these three serologic assays we had developed separately, but we were really interested in a combination of assays, since we didn't really consider the Western blot was a feasible serologic test to be doing on thousands and thousands of serum, which is what we were looking at when we were doing the outbreak investigation. So you could see -- and we broke this down into children and adults, and it was mainly based on the results we were getting with the ELISA. But I will just go ahead and go through the results with You can see that the ELISA was very sensitive in detecting specific antibody to H5 children and also quite specific. And when we actually combined either the neut or the Western blot, the ELISA was slightly better in both cases. However, this wasn't true in adults and we found that the neutralization assay was superior, and the main reason was the fairly significant reduction in specificity that we found in the IgG ELISA in adult human sera. And you will see more examples of that when we look at the responses of individuals in the clinical trial. So a combination of neutralization and Western blot turned out to be the most specific and sensitive assay

that we could use to detect antibody to H5 in adult populations.

So I will move on now to some results we have obtained in the Phase I trial that Dr. Levandowski introduced, which was organized by a number of groups and used two doses of the Protein Science baculovirus expressed HA from the Hong Kong/156 virus. We used two fairly low doses, and there were a lot of reasons for choosing these doses at the time. And one of those was just the sheer limitation of the amount of protein that was available. So the decision was made to start out with relatively low doses. So either a 10 or 20 mcg dose were delivered. There were two doses delivered intramuscularly at day zero and then at day 21. I will be showing you antibody responses detected at pre-vaccination and at various time points postvaccination. We used all of these assays. I am not going to show you the Western blot, but just to say we have done Western blot results on all of these sera.

So the first Phase I trial so far has been conducted at five sites for a total of 56 adult volunteers with an age range of 28 to 66. The first two sites received two doses of 10 mcg of the recombinant H5 protein, 28 volunteers with a mean age

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of 43. And I believe that this group has subsequently been offered a third dose at the 20 mcg level, although I won't be presenting any of those results today. Then three other sites received 2 doses of 20 mcg, and again, there were 28 volunteers with a mean age of 41.

And what I have done here is just compare the different assays that we were using to evaluate the immune response to the vaccine and the top is the neutralization. And I have just marked with the arrows the two individuals here that are by our criteria making a response to the vaccine. that they needed to have at least a three-fold rise and at least achieve a titer of 80. Now you can see these two individuals actually have high antibody, but they started out with high pre-existing titers. what I forgot to mention with the sensitivity and specificity of the microneutralization is that we have noticed when we were setting up that in individuals around 60 years of age and older, that we start to see a lack of specificity. And we are presently working to try and determine what this lack of specificity is, but at least in some of these individuals, this is an age-related effect.

Interestingly, we also went back to the HI

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just to see if in this group of individuals, we could detect antibody by the HI. And you can see that we do small amount of antibody in these individuals that are reacting by neutralization. in this case, it is basically going from less than 10 to 20 and from here it is going from less than 10 to So it is not really a terribly robust response. And then we also looked at the ELISA, using again the recombinant protein. And again, although we could see many sort of four-fold increases after vaccination, we were again starting out with very high levels, if you look at this ELISA endpoint antibody titer here. We are up in the range of thousands and millions of And so in some cases, we really -- we just titer. couldn't distinguish significant any antibody responses over and above the background.

So we did the same sort of comparison with a site that now received a 20 mcg dose, and here again we have 2 individuals out of 12 in this situation that were making a significant neutralizing antibody response. And this time, the HA was -- the hemagglutination inhibition test was absolutely flat. We could not even detect these antibody responses by HI. And because of the very high backgrounds we were seeing with the ELISA, we decided to try something

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1	different here. We thought that one of the problems
2	with the ELISA not being H5 specific was that we were
3	probably picking up some cross-reactive epitopes that
4	cross-reacted with other subtypes of Influenza A,
5	which as H3 or H1, which most individuals would have
6	antibodies to. But perhaps these were not very high
7	affinity antibodies for binding to H5. So we went to
8	the method of using various doses of urea, which is a
9	common method for looking at high affinity antibodies.
10	And we found that when we used 8 molar urea as a
11	washing stick in the ELISA, that we could dramatically
12	reduce the background. The scale is now about 10 to
13	100 fold lower. And that we could still see the same
14	sorts of relative increases in post-vaccination serum
15	that we were seeing without the urea in place.
16	However, when you look at these results on a one to
17	one level, you can see that these two individuals that
18	show neutralizing antibody also show a four-fold rise
19	in ELISA, but there are other individuals such as this
20	one which isn't giving any significant neutralizing
21	antibody response but is showing a whopping ELISA
22	antibody titer and there is a couple of other examples
23	of that down here.

So the feeling from our lab is that we prefer the neutralization assay still as the most

specific assay and sensitive assay in the detection of antibody to H5.

And this is a summary now of the sera that we have tested so far from the Phase I trial. As I said, there were five sites, and these are the numbers of individuals in each of those sites. The 10 mcg dose, ultimately only 2 out of 28 individuals gave a greater than three-fold rise and achieved a titer of 80 or more for a total of 7 percent of the individuals responding. And as we doubled the dose, we also improved the response somewhat such that a total of 6 out of 28 individuals receiving the higher dose or 21 percent were showing a response. But that was still far below what we had hoped, and it was somewhat disappointing.

Before I go on to a more hopeful end to the talk, I just wanted to briefly mention some of the results we are trying to get now and also looking at the lymphocyte proliferation response in individuals who have received a 20 mcg dose. This was an individual who didn't have an antibody response. This individual did. And you can see when we look at their proliferative response to the recombinant HA's, we get a very nice -- this is just post-vaccination at this point. We get a nice response to either the Hong

Kong/156 or the 483 recombinant protein, and that that response is much higher than the background to other recombinants such as the H3 or the H7.

This was just really a preliminary assay for us to define the system, and we are going to go back now and look at pre and post-vaccination responses.

This is the more hopeful end to the talk. Just a few days ago, we were able to get very preliminary results from John Treanor's Phase II trial, and I think he is going to speak about that and give you a little more detail of that. But that was a dose escalation trial, and we decided to start with the highest dose and work our way down. Sort of rationalizing that if we weren't going to get anything at the highest dose, we could just forget about it. But we have, in fact, gotten some very nice results, this is the preliminary results What I am showing here is zero time individuals. point at the first vaccination and then 14 days after the first vaccination. Zero time point at the second vaccination and then 14 days after that. But the way the clinical trial has been set up, there are three different intervals between the first and second vaccine, and John will explain a bit more than that.

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But the encouraging thing is the number of responses we are getting above this line. And in fact, you can see that except for these two individuals, we are getting quite substantial response and even the height of the neutralizing antibody mean titer that we are getting is upwards of 200 to 400, which is very encouraging. You can see that some individuals are responding right after the first vaccination, whereas other individuals seem to require the two doses.

So just to put that in perspective with the earlier study now, we can see that, again, for only a very limited number so far examined, for 10 individuals we have 8 of them responding and we have a very nice pre to post -- or at least a post-vaccination GMT rise in the neutralizing antibody response. So of course we will be working in the future to go backwards now and look at the lower doses and see what the minimal dose is that will give satisfactory immunogenicity.

So in summary, I just wanted to remind you that in a naturally infected individual, by 14 days post infection, we can see titers of 80. And after 20 days or so, the typical neutralizing antibody titers were as high as 640. The results I just showed you are somewhere in-between that, and that would suggest

to me a pretty satisfactory response to a vaccine. 1 So we have used the microneutralization 2 assay with confirmation by Western blot. I should say 3 4 the last set of results I showed you have not yet been 5 confirmed by Western blot, but I am confident that 6 that is just a formality. And we have used it to 7 adequately detect antibody to H5N1 in adult sera. 8 When we vaccinated individuals at the 10 or 20 mcg dose using the recombinant HA, we show 9 10 fairly low antibody responses in only 7 of 21 who 11 responded respectively. However, I will leave it to 12 John Treanor now to spend a bit more time on his dose 13 escalation study, and I think the results from that 14 will be far more promising. Thank you. 15 CHAIRPERSON FERRIERI: Thank you, 16 Why don't we move on to Dr. Treanor. While he 17 is coming up front, if anyone at the table has a 18 comment or question for Dr. Katz. Dr. Hoke? DR. 19 HOKE: Do you have any 20 characterization of the confirmation of the antigen? It is folded correctly 21 DR. KATZ: Yes. think Dr. Wilkenson, who is from Protein 22 23 Sciences, can probably address that. But it actually has HA activity, so it has correct 3-dimensional 24

structure as far as we can tell, and actually forms

sort of a rosette that they can look at under the BM, 1 2 is that correct? 3 DR. WILKINSON: Bethanie Wilkinson from Protein Sciences. And I didn't hear the question, but 4 5 I think it is about the structure of the protein and whether it forms chimers? Is that correct? 6 7 DR. HOKE: I was -- you know, it Yes. seems as though there is a specific activity -- there 8 9 is activity, but the specific activity is suggesting that there are lots of -- there is a lot of 10 11 poorly formed protein. 12 WILKINSON: I am sorry, I don't 13 understand where you would get that from. 14 DR. HOKE: Well, the dose is so much -- is 15 -- well --16 DR. KATZ: One thing that we probably 17 should say is that this is on just a mcg of protein basis, and I don't think you can exactly correlate 18 that to the 15 mcg of hemagglutinin that is used in 19 20 traditional vaccines which is measured by a different 21 method. And the point has been made in the past that 22 at some point we probably should compare those 23 directly. But I think the assumption was that if you 24 use the method that is used by the FDA, that 10 mcg

dose may actually be a little bit lower.

DR. WILKINSON: Actually, we have measured the specific activity and it is very good. The doses were too low and you do need a higher dose. But with a vaccine where people aren't naive, you can use a 15 mcg dose and you get equivalent to what you get in a current vaccine. So we think it is -- it is probably just as biologically active. There are slight differences in the glycosolation which may account for some of the differences that we see.

CHAIRPERSON FERRIERI: Thank you. Dr. Treanor, University of Rochester.

DR. TREANOR: I'm going to guess that anybody who is still here probably missed their flight, so I can just talk for as long as I want. But we will try and go through this briefly.

We have been working with the recombinant baculovirus for several years through the vaccine evaluation units. And a number of years ago, just by way of background, we did some very preliminary immunogenicity studies which are shown here. This is just a comparison of the HAI responses to various doses of recombinant either H3 or H1 hemagglutinin or bivalent vaccine. And I just want to show you that the various doses of the Beijing, which is the H3, or the Texas, which is the H1, did induce levels of HAI

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antibody, which is a functional antibody, which were comparable to those induced by sub virion vaccine in that there was a dose response with relatively higher doses of the recombinant hemagglutinin resulting in progressively higher levels of post-vaccination antibody, much more striking for the H3 responses than the H1 responses in healthy adults.

Now the next slide. Those HAI responses also were associated with the development neutralizing responses against H3 and H1 measured by microneutralization tests very similar to the one that Dr. Katz just described. In one of the studies, and these studies were done in collaboration with Doug Powers at St. Louis University and also with Peter Wright at Vanderbilt. And in one of the studies, although not designed as a formal efficacy trial, we did follow the subjects during the flu season and we did suggestion see some that the vaccine had protective efficacy. This was one of the dose-ranging studies in which individuals received 15 mcg or 15 mcg with alum or 90 mcg, or received a trivalent vaccine or placebo in a randomized double blind fashion, and what you can see is that the rate of laboratory confirmed influenza illness was 13 percent in the in the placebo recipients and it was 1 percent

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combined 77 subjects who had received recombinant hemagglutinin in any dose, which is suggestive that there would be some protective efficacy here, although clearly this is not a definitive test of efficacy.

When the Н5 situation arose. the recombinant H5 product was ready very early, and so it was available for testing. And we designed a study which involved with was mostly objectives determining the minimum effective dose with the idea that the strategy would be to try and stretch the available quantities of vaccine as far as possible, and also to try and determine what type of schedule of administration would induce antibody the most rapidly, believing that possibly this would necessary if a pandemic were eminent. So that the study was designed look at dose-related antibody responses, effectiveness of low-dose boosting, the optimal interval for boosting, and the kinetics of antibody following the second dose.

This had results in a somewhat complicated study design, but we looked at doses of 25, 45, 90 mcg for an initial dose followed by boosting with either 25, 45, 90, or 10 mcg. And we randomly assigned people to either a 21 day interval between doses, 28 days, or 42 days, with a corresponding placebo group

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in each cohort so that people were, of course, unblinded as to interval but were blinded as to dose assignment.

The vaccine was administered in a total of 1 ml intramuscularly. Individuals filled out a diary card for 7 days, and serum for antibody was drawn before and 14 days after dose one and then before, at 7, 14, 21 and 28 days after dose 2. A lot of sera. lot of stuff is a to handle in the microneutralization lab. The sera was tested by an IgG ELISA against baculovirus expressed antiqen, which was done in protein sciences, and then in heroic efforts at CDC by microneutralization against the Hong Kong virus.

Now very briefly, the results of the formal safety analysis has not been completed, but there were no serious adverse events. There was one, I guess significant event. One of the subjects became pregnant after the first dose. This was a woman who had had a tubal ligation and became pregnant anyway. We don't know whether this was a vaccine-related effect or something else. There were no complaints of severe arm pain or swelling in any dose group. No individuals had fever following vaccination, and generally the vaccine was extremely well tolerated as

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had been seen with the recombinant H1 and H3 products.

Now these are antibody responses in the 21-day interval group assessed by ELISA. And this ELISA is done at a single dilution of 1:1000. This is just sort of screening preliminary information. As Jacquie mentioned, there is some background even in these subjects who clearly have never been exposed --well, I shouldn't say clearly, but probably have never been exposed to H5 viruses before -- at a single 1:1000 dilution, OD readings in the pre-vaccination sera ranged from undetectable to 0.6. And to clean this up a little bit, what we have done is actually subtract the first sera's value from all subsequent sera to try to adjust everything down to a single baseline.

And what you can see is that 14 days after a single dose, there is a significant increase in the amount of OD reactivity at 1:1000, and that with the boost at 21 days, there is not much of an additional increase. But the striking thing here was that particularly at 45 and 90 mcg doses, there is a very significant increase in reactivity against the baculovirus expressed H5 antigen by ELISA.

Now the next slide shows the results from

the 28-day interval group, which are very similar. Again, at the higher doses, 90 mcg and 45 mcg, there is a very significant increase in OD reactivity. This is a placebo group in which there is no increase, and the 20 mcg dose in which there is a trivial increase in OD reactivity. At 28 days, the antibody has drifted down a little bit and there does appear to possibly be a response to boosting. And then the next slide shows the 42-day interval. Again, a response to the initial vaccine, which is dose dependent, and then possibly a response to boosting. Now I should point out that this is preliminary and only has been completed for about half the subjects in the trial. And so it is really premature to draw conclusions about the effect of boosting. But strikingly, there is an increase in antibody, at least as measured by even after a single dose, and summarized on the next graph.

This shows the pooled results for all individuals who received any dose, regardless of interval, and just looks at the OD reactivity 14 days after the first dose. And you can see that there is a dose related effect in terms of the amount of antibody as measured by ELISA at 14 days, with the highest levels at 90 and 45 mcg. These are the plus

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and minus, the standard area. The results in terms of OD, total increase in OD. is statistically significantly different in the 45 and 90 mcg doses than it is in placebo or 20 mcg, using as a crude criteria an increase in antibody of 0.4 units or greater. There were a total of 8 out of individuals who appeared to have responded at 20 mcg, 10 out of 16 at 45, and 25 out of 30 at 90. This is obviously a completely arbitrary criteria, but is beyond the amount of variability from assay to assay when assaying the same sera by several standard deviations.

Now as Jacquie alluded to, we have very preliminary data regarding neutralizing antibody responses which are shown here. What we elected to do to try and cut the work load down is to simply assay the sera from individuals who had received 90 mcg or placebo. These assays were done by Dr. Katz in blinded fashion without knowing either the order in which the sera were obtained or whether the volunteers had received vaccine or placebo. And this looks at the serum results just in the vaccinees. This is the log 2 titer of neutralizing antibody plus or minus the standard error. And what you can see is that there is an increase, a significant increase, in antibody level

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14 days after receiving 90 mcg, and another increase after receiving a booster dose of 90 mcg. Unfortunately, I can't count. This is really 10. Using that criteria of a three-fold increase to a level of over 80, there were 4 out of the 10 individuals who had responded by the pre-dose 2 sera and 8 out of 10 individuals who had manifested a neutralizing antibody response following two doses.

So the preliminary conclusions of this study are that the recombinant H5 is well tolerated at doses as high as 90 mcg. Serum binding and neutralizing antibody were detected as early as 14 days following a single 90 mcg dose. Serum binding antibody was detected after a single dose of 45 or 90 mcg, but was infrequent after 20 mcg, which is similar to what was seen in the Phase I study. And the rapid responses to a single dose may suggest that normal U.S. adults are partially primed for responses by a previous exposure to H1 or H3 influenza, although that is really very speculative. But it is interesting to see those very high responses to a single dose.

The study was sponsored by NIAID, Gina Rabinovich and Bill Blackwelder played a major role in the study design, especially Bill with the statistical approach. Bethanie Wilkinson and Gale Smith are at

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Protein Sciences. Bethanie has done the ELISA's.

Jacquie Katz and Nancy Cox from the CDC influenza

branch, and at the University of Rochester, the study

coordinator, Diane O'Brien.

CHAIRPERSON FERRIERI: Thank you very much, Dr. Treanor. This is open now for comments or questions. Dr. Levandowski?

DR. LEVANDOWSKI: I have got a question. Thinking back to the data that you showed for the H1 and the H3, where there was, I guess, a pretty evident difference in what could be called the dose response curve, can we draw any conclusions from that for other Influenza A subtypes or hemagglutinin subtypes? Do you think that there is any validity to that difference that you were seeing with the H1 and the H3, and should we plan to -- or should we expect more of that for other subtypes?

DR. TREANOR: My own opinion is that at least in the way that the vaccine is currently being vialed and delivered that it is likely that responses to 45 mcg doses or in that range will be better than to 10 or 15 mcg for the recombinant hemagglutinin. And there are multiple possible reasons for that that you could speculate about. But just in terms of the practical observations, it seems to be fairly

consistent that 45 mcg doses are better just in our experience.

CHAIRPERSON FERRIERI: Yes, Dr. Hoke?

DR. HOKE: Well, I would just like to commend your whole group for their persistence, and it really looks like you've got something. I did some work some years ago in another system where there was HAI and neut and it was Japanese encephalitis, and it was very curious as to how ELISA and HAI and neutralizing antibody responses to vaccine worked out sometimes in rather paradoxical ways, but that the neutralizing tests somehow always seemed to be the one that was most clear in spite of the difficulty of doing a biological assay.

I am puzzled a little bit by some suggestion early on that there was -- that there is some background antibody that you had to adjust for? This is H5 and no one is supposed to have been exposed to that.

DR. TREANOR: By ELISA, I think that looking at the health laboratory workers in the Phase I study and even in our healthy adults, there is a certain amount of binding of that very highly purified H5 antigen by sera from individuals who would not be expected to have had prior exposure. And this may

reflect antibody which cross reacts with -- or which 1 is directed against cross-reactive epitopes. 2 a very interesting question which could be approached, 3 but right now I don't know what the answer to it is. 4 And even at higher doses, I 5 DR. HOKE: don't remember if you said, but was there ever any HAI 6 7 antibody? DR. TREANOR: We didn't test it. Now that, 8 as Jacquie was explaining, is subject to a degree of 9 10 technical issues related to affinity with 11 assay, I don't think we have done HAI testing. 12 13 14 15 16

hemagglutinin and red cells and whatnot. But in this is something that will be done. As far as the other thing is concerned, someone mentioned earlier, I think actually John Wood, that some of this cross-reactivity can be eliminated by adsorption of the sera with H3 antigen. Now one possibility is that it is directed against the common antigens. But because you can also eliminate it in the ELISA to a certain extent by adsorption with purified Н3 hemagglutinin, suspicious is that at least some of it is directed against cross-reactive epitopes on the hemagglutinin itself.

CHAIRPERSON FERRIERI: Thank you very It is now time for the open public hearing.

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1	This is an official part of our posted program in the
2	Federal Register. Is there anyone in the audience who
3	would like to come forward and say anything? If not,
4	I would like to thank all the remaining members in the
5	room for staying. I thought the program was very
6	interesting and I want to thank you, Roland, for
7	organizing everything today. Thank you.
8	(Whereupon, at 5:07 p.m., the meeting was
9	concluded.)
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CERTIFICATE

This is to certify that the foregoing transcript in the matter of:

MEETING

Before:

VACCINES AND RELATED BIOLOGICAL PRODUCTS

ADVISORY COMMITTEE

Date:

JANUARY 29, 1999

Place:

BETHESDA, MD

represents the full and complete proceedings of the aforementioned matter, as reported and reduced to typewriting.

_ June Gay