UNITED STATES DEPARTMENT OF JUSTICE

The Science: ANTHRAX PRESS BRIEFING

Monday, August 18, 2008

Federal Bureau of Investigations
J. Edgar Hoover Building
William H. Webster Conference Room
935 Pennsylvania Avenue, NW
Washington, D.C. 20535-0001

BACKGROUND OFFICIAL: Thanks, everybody, for coming today. It's great to see so many Justice regulars flanked by their best science friend. As advertised, today's briefing will be designed to shed more light on the scientific aspects of the investigation into the Anthrax mailings. And what we said before, and I'll say today, it's difficult to separate the investigation from the intelligence from the science, we are, in fact, going to attempt to do that today because we're limited.

At the same time that the DOJ and FBI are moving toward making more documents available, it's still an open investigation and we remain limited today what we can discuss, which will be emphasized, I'm sure, time and time again; and that for a number of reasons. And when that status changes, obviously, there'll be more information available to you.

As stated on the advisory, today's briefing is on the record with respect to the individuals who are identified here. At the same time, we have a number of investigators, prosecutors, and other scientists who are going to be available to clarify points, or, in some cases, make sure we stay within the boundaries we need to stay today.

Leading today's discussion is Dr. Vahid Majidi and Dr. Chris Hassell of the FBI. Dr. Majidi is our Assistant Director for the Weapons of Mass Destruction Directorate. He comes to us from the Los Alamos National Laboratory. Dr. Hassell is even newer to us. He heads the FBI laboratory. He came from Oklahoma State University as well as Los Alamos. And our format today will be Dr. Majidi will open the program, give a brief overview; Dr. Hassell will introduce

the other panel members.

DR. MAJIDI: Thank you. Good afternoon, ladies and gentlemen. I am Vahid Majidi, the assistant director responsible for the FBI's Weapons of Mass Destruction Directorate. I would like to start today's session with a brief opening statement and define the scope of our roundtable discussion.

After nearly seven years of investigation, we have developed a body of powerful evidence that allows us to conclude that we have identified the origin and the perpetrator of the 2001 Bacillus Anthracis mailing. The attribution process and identification of the specific perpetrator relies on the confluence of intelligence, investigations, and forensic information.

It is the forensic information that determined the source of the 2001 Bacillus Anthracis mailing to be derived from a unique pool of spore proporation known as RMR-1029 that was maintained at U.S. Army Medical Research Institute for Infectious Disease, Fort Detrick, Maryland. From now on I will refer to that USAMRIID.

While there were countless investigative hours spent narrowing the field of suspects, we are here today to focus on the scientific aspects of this case.

First of all, let me dispel some frequently repeated erroneous information. For example, there were no additional additives combined with the Bacillus Anthracis to make them any more dispersible. The purity of samples obtained from the four letters was sufficiently different, which allowed us to conclude that at least two different Bacillus Anthracis batches were prepared from the original RMR-1029. This indicates that alloquots of RMR-1029 were removed and cultured in at least two separate batches to produce the materials used in the mailings.

The FBI began this complex investigation by coordinating analysis of the spore powders contained in the 2001 Bacillus Anthracis mailing. We enlisted the help of more biodefense experts to assist our examination, including those who have previously developed and tested strains of Bacillus Anthracis to identify the spores in the letters of the Ames strain.

Other strategies were employed to target the chemical and elemental profiles of the spore powders. Specific techniques included scanning and transmission electron microscopy, energy-dispersive x-ray analysis, carbon dating by accelerator mass

spectrometry, and plasma optical illusion and mass spectrometry.

Additional scientists under the Department of Defense and the Center for Disease Control examined the spore materials and it was determined that there were many phenotypic variants within the samples. The general support that both the National Institutes of Health, the National Science Convention, and other government agencies, FBI scientists worked with the Institute for Genetic Research to determine if genetic mutations were responsible for the altered appearance of the variant found in the Bacillus Anthracis letter. Several genetic mutants were discovered in these studies.

FBI microbiologists contracted the assistance of several laboratories to develop highly specific assays to detect four specific genetic mutations found in a Bacillus Anthracis letter. The mutation detection assay were validated and used by the FBI laboratory to examine the repository of Bacillus Anthracis Ames that was collected through the course of this investigation. And we'll give you more information on that repository. This unprecedented scientific approach allowed the FBI to identify potential sources of the Bacillus Anthracis used to produce the 2001 spore powder.

For a comprehensive analytical approach the investigators were provided with validated scientific data which linked the materials in the 2001 attacks to materials from USAMRIID identified as RMR-1029. It is important to emphasize that the science used in this case is highly validated and well accepted throughout the scientific community. The novelty is in the application of these techniques for forensic microbiology.

Today I'm very confident that the significant lessons learned from the 2001 Bacillus Anthracis case have been rigorously evaluated by the FBI and appropriate actions have been taken to safeguard the American public. The FBI laboratory has revolutionized the approach to non-traditional forensic samples and developed robust capabilities to collect and examine evidence containing biological, chemical, radiological, or nuclear materials. We have developed a strong partnership with the U.S. Government Laboratory Complex, Public Health System, private industry and academia to significantly enhance our capabilities dealing with future investigations.

The creation of the Weapons of the Mass Destruction Directorate is another example of FBI's progressive approach focusing on prevention, as well as investigations of all issues involving chemical, biological, and radiological as well

as nuclear materials.

Please note that there were many dedicated individuals including prosecutors, scientists, investigators, analysts, and support personnel that have worked on this case. For the purpose of this meeting, the science and technology community within the Bureau has a lead, and if individuals from the sidelines are asked to provide additional background to any of your questions, please make sure to attribute all answers to the FBI Laboratory Director, Dr. Hassell. You can also use "FBI scientist" as a notation as well.

Finally, I'm asking you to understand that this is the first step toward broader dissemination of the scientific information surrounding this case. Additional information will be available through peer review publications, and I ask you to please respect the integrity of that process.

In fact, several research projects related to the FBI's investigation have already resulted in peer review publications and we will provide you with that list. Additional publications will be available for peer review as more information from the investigation is released.

Before we open the floor for question and answer, we would like to introduce you to our distinguished panel. Today we have with us a small group of individuals representing a large cadre of non-bureau scientists that helped us chart and navigate our scientific path through this unprecedented case.

In the near future, after we work through each non-disclosure agreement and privacy issues, we will release the names of those key individuals who tirelessly worked with us on the 2001 Bacillus Anthracis mailings.

To my left is the current FBI laboratory director, Dr. Chris Hassell. Dr. Hassell will introduce our panel members.

DR. HASSELL: Thank you. I'll start on my right. On the far right is Professor Paul Keim. He's a Regents professor of biology and he holds the Cowden Endowed Chair in Microbiology at Northern Arizona University. He's also director of the Pathogen Genomics division at the Translational Genomics Research Institute.

His research focuses on molecular genetics for a wide variety of organisms, including bacteria, plants, and animals. His work in support of the FBI included identification of the spore powders as the Ames strain of the Bacillus Anthracis.

Next -- to his left -- is Dr. James Burans, who's currently the associate laboratory director of the National Bioforensic Analysis Center. He has been in the forefront of the development of diagnostic assay techniques to identify and characterize biological threat agents. He led several of the scientific working groups that were assembled from the National Academy of Sciences, National Laboratories, and other federal R&D facilities in support of this investigation.

To his left is Dr. Rita Colwell. She is currently a distinguished professor both at the University of Maryland, College Park as well as at the Johns Hopkins University Bloomberg School of Public Health. She's also senior advisor to Canon U.S. Life Science Incorporated.

From 1998 to 2004 she served as director of the National Science Foundation, which provided funding for much of the genetic sequencing efforts in support of the FBI investigation. She has served as president of American Association for the Advancement of Science, the American Society for Microbiology, and she is a member of the National Academy of Sciences. In July of 2007, she received the National Medal of Science.

To my left -- immediate left -- is Professor Claire Fraser-Liggett. She's a professor of medicine and director of the newly created Institute for Genome Sciences at the School of Medicine, University of Maryland in Baltimore, Maryland. She was previously the president director of the Institute for Genomic Research, sometimes referred to as TIGR, where she led teams that sequenced the genomes of several microbial organisms including important human and animal pathogens. TIGR performed genetic sequence analysis in support of this investigation.

To her left is Professor Jacques Ravel, who is also at the same institute. He's an associate professor of microbiology and a member of the Institute for Genome Sciences at the University of Maryland School of Medicine. He also was formerly with the Institute for Genomic Research. His research focuses on the application of microbial genomics to several key areas including microbial genomes, sequence, comparative analysis, to the special emphasis on human microbial pathogens including Bacillus Anthracis. His work included genetic sequence analysis and characterization of genetic mutants in support of this investigation.

And finally, to my far left, is Dr. Joseph Michael. He is the distinguished member of the technical staff Sandia National Laboratories in Albuquerque, New Mexico. He currently works in the materials characterization department of the Materials Science Center there, where he develops and applies electron and ion microscopy to the characterization of materials. He is co-author of the leading textbook on scanning electron microscopy. He assisted mineral analysis, electron microscopy of the samples and with development of the strategies for analysis for analysis of chemical and physical properties of the spore powders.

The next step we'd like to actually go through the panel and have each member of the panel talk in a little bit more detail about their specific participation in this investigation. So if I could start with Dr. Keim.

DR. KEIM: So as Chris mentioned I'm a professor of microbiology at Northern Arizona University and director of the Pathogen Genomics division of TGEN. I'm also an affiliate at Los Alamos National Laboratory in the biosciences. My laboratory began studying Bacillus Anthracis prior to 9-11 and the Anthrax letter attacks by developing methods for precisely identifying -- what we considered precisely identifying at the time -- different strains of Bacillus Anthracis and it was those relatively crude pre-genomics type technologies that we employed in October 2001 to identify the Ames strain from the letters.

After that, we continued to analyze populations of Bacillus Anthracis around the world to try to understand exactly what the Ames strain is and what it isn't. And in the post-genomic era and at a period of time after we had whole genome sequences generated by TIGR, we were able to develop more sophisticated, more sensitive methods for identifying what the Ames strain is and what it isn't. And so my laboratory worked on that aspect.

We worked on the repository that the FBI established for Ames strain, which was collected from around the country, and indeed around the world, providing biosafety support for the Bureau early on in the investigation as they began to stand up their own facilities in that area.

DR. BURANS: My name is Jim Burans. I'm a pathogenic microbiologist. I'm a retired naval officer and come from the U.S. Naval biodefense community. In the early ‘90s I provided bioforensic support to several biocrime investigations for the FBI as well as supporting bioforensic analysis for the U.N. Special Commission to

Iraq.

In the November time frame of 2001 I became a scientific consultant to the FBI in the early stages of the Anthrax investigation, and in 2003, I helped to establish the National Bioforensic Analysis Center to deal with the analytical investigative challenges in bioforensic analysis to support homeland security and the FBI. And since that time we have supported the FBI in analyzing evidentiary samples from biocrime investigations.

DR. COLWELL: -- microbial systemitist, microbial ecologist, and I've worked my entire career on cholera in many countries, as well as the few cases that occur in the U.S. and its ecology. I've been long interested in the molecular systematics and evolution of microorganisms. I was director of the National Science Foundation when the Anthrax event occurred. The National Science Foundation received a proposal which we were able to fund under the program of small grants for innovative or exploratory research. This permitted us to act very swiftly and to have the sequencing done rapidly. The work was done by TIGR, about which you will hear in a moment. We, at that time, a consortium of agencies worked together. The NIH, the NSF, Department of Energy, Homeland Security, the intelligence community, Department of Justice, the FBI, the USDA, DOD, including USAMRIID. We met on a regular basis and we served as a source of advice and advisory for the FBI, but also to establish the capacity to expand the few sequences that were available at the time. And so from the work, as you will learn this morning, has emerged a legitimate new discipline, namely microbial forensics.

DR. FRASER-LIGGETT: I'm Claire Fraser-Liggett. I'm currently a professor of medicine and director of the Institute for Genome Sciences at the University of Maryland School of Medicine. Prior to last year I was the president and director of the Institute for Genome Sciences that was involved in essentially all of the genome sequencing work related to the Amerithrax investigation. I've been involved in the field of comparative microbial genomics since 1995, with the sequencing of the first microbial genome and out of that work have come an interest on my part in using these techniques to better understand microbial evolution and diversity.

At the time of the Anthrax letter mailings in October 2001, we were finishing up the first project to sequence Bacillus Anthracis Ames. It was a strain that was

unrelated to the Anthrax letter mailings, but as soon as this news broke, as Dr. Colwell mentioned, we quickly put together a proposal to the National Science Foundation to ask the question as to whether or not genomics-based technologies could be used to identify polymorphisms, that is DNA sequence variance, in different samples of the same isolate of Bacillus Anthracis. The isolate that we were working on for genome analysis also happened to be Bacillus Anthracis Ames as was reported in a paper published in Science in 2002. Indeed, that initial comparative study identified a small number of high-quality snips and we were very encouraged by that initial finding that, indeed, this might be a very useful approach as one part of a large toolbox to be brought to bear on the Amerithrax investigation.

As you've also heard in the opening statements, we were then subsequently asked to work with the Bureau to process a large number of samples. This gave us an opportunity to further develop a number of both experimental and computational approaches that had utility not only in the investigation, but I think will also have broader utility of microbial forensics. Many of those approaches were developed by my colleague sitting to my left, Dr. Jacques Ravel.

DR. RAVEL: My name is Jacques Ravel. I'm an associate professor at the University of Maryland School of Maryland at the Institute for Genome Sciences, which Claire is the director of. My laboratory is focusing on several things, but to this matter today the part of my laboratory is the one that studied human pathogens, so we're applying comparative genomics to study human pathogen and what leads a non-pathogen to become a pathogen. So the part that the team that I led at TIGR back in 2002 took in the investigation were sequencing the genomes, some of the variant we'll be talking about later, and using comparative genomic approaches to identify specific polymorphism, DNA sequence differences in those variants, to develop a specific assay to query those for the presence of those variants in other samples.

DR. MICHAEL: Good afternoon. My name is Joe Michael. I work at Sandia National Laboratories. My background is material science, and specifically I use electron and ion microscopies to characterize materials over range of length scales expanding from millimeters down to the nanometer scale.

In this case, I got involved back in January of 2002, when we first started to

receive samples from the investigation, and our interest was to determine if there were or were not any additives added to the samples as far as weaponization.

DR. HASSELL: As was mentioned earlier, many people are seated behind us that all work for Bureau -- many for the laboratory itself -- have done a tremendous amount of work on this whole investigation. To start out, since a lot of the questions we kind of anticipate, it might be helpful to just give an introduction on some of the work that went on to led us up this point. So I've asked one of our chief scientists, actually, to sort of open that introduction.

BACKGROUND OFFICIAL: I'm going to give you in a nutshell --

QUESTION: Can we get a name, please?

BACKGROUND OFFICIAL: -- my statements are not for attribution. They're for background only. Thank you. To give you a little bit of a background as to the process that was followed for the scientific part of the investigation. The investigators early on worked very hard to try and identify the source of the Anthrax, but the first job was to identify which strain was used, and Dr. Keim, his work was really a central work in identifying it as the Ames strain. So the investigators had to then identify what laboratories had the Ames strain. That was a process that took a lot of work, and over the course of several years through the process of subpoenas and the execution of warrants for search, a collection that we call the FBI repository, was collected. This amounted to well over a thousand samples of the Bacillus Anthracis Ames that was collected both domestically and internationally. That repository is the evidence that we used, that we screened, for forensic signatures to assist the investigation. It was noted early on in the examination of the Anthrax powders that there were some unusual characteristics of the Anthrax in those powders. There were many different variants of the Ames strain that were noted in the Anthrax powders that had a different appearance.

Those colonies with different appearance had their DNA purified by Dr. Keim's lab and that DNA was sent to the Institute for Genomic Research, for sequencing of the entire genome. And through those efforts it was noted that many of those variants had mutations that were most likely associated with the change in the characteristics. Some of those mutations were further exploited in the

development of very specific assays, genetic assays, to identify those mutations in an overwhelming background of wild-type Ames. And it was those scientific assays that were used to examine that repository of over a thousand Ames strains that were collected throughout the course of the investigation. The results of that scientific work and the screening of the repository resulted in the identification of eight samples that had the combination of four genetic markers that were all characteristic of the Anthrax in the letters. And that's the background for what you've been hearing of the genetic screening of the Anthrax.

DR. MAJIDI: All right. We'll open the floor for questions. I will moderate the question and answers. The majority of the questions will be answered by myself or Dr. Hassell. If you have specific question for any of our panel members, please voice them and we'll get that answered appropriately. There are areas that are clearly not within our expertise. So if you ask a question that falls within one of our panelists' expertise we will defer those questions to them.

QUESTION: It would be helpful to know, especially for the background, some timeline or some understanding of when certain things were done. You know, if you would, the scientist who just gave us the background, could give us a little bit of an idea when certain identifications were made. That would be helpful.

BACKGROUND OFFICIAL: In 2002, or early on in the investigation, it was noted that there were variants of Ames that were detected from the Anthrax powders. And it took some time because each one of those had to be confirmed to make sure that we didn't have a mixed culture, that it was, in fact, still Bacillus Anthracis, and it was still, in fact, Ames. And that's what Dr. Keim was very instrumental in doing for us. Once they were identified as Ames then it fell to TIGR to help us identify what those mutations were. Most of that was completed between 2002 and late 2003. Then subsequent to that we contracted the assistance of other scientists, experts in the biodefense arena who have experience with Anthrax, and contracted them to assist us in developing those assays. We felt there were a number of assays that needed to be developed. If the FBI laboratory took on that responsibility itself it would have taken a long time so we contracted the help of the biodefense community to help us build those assays. We validated those assays and then over the many years of this investigation, the repository was also being built. So from roughly 2003 to 2006 is when we completed the repository and the screening of the material in that repository.

QUESTION: Could I ask a little more about the timeline? I saw in the paper that colleagues published in 2002 in Science describing a large number of markers. Did you not have sufficient information there to select the four markers and thereby match the source to the strain; and if not, what was missing and when did you acquire those missing pieces?

BACKGROUND OFFICIAL: What was the reference you quoted?

DR. FRASER-LIGGETT: That was the comparison of the Porton strain that we had sequenced initially with the Florida strain; and that was just -- I think to answer your question, Nick, that was a comparison of one sample that had been collected as part of the investigation and I think what's been made clear is that in the interest of being thorough what was essential to do was to look at as many different samples as possible that had been collected from the multiple letters in order to get a broader sense of whether the markers that had been identified initially were seen in all samples from the investigation.

QUESTION: In the 2002 paper, there are a large number of markers described. It does include the four markers that were --

DR. FRASER-LIGGETT: Some of them turned out to be found in other samples, but not all of them.

QUESTION: So you --

DR. FRASER-LIGGETT: Correct.

QUESTION: When were the final four markers --

BACKGROUND OFFICIAL: In the 2002 paper we had not yet fully characterized the mutants that were isolated from the letters, so those four genetic

markers were not referenced in that paper.

QUESTION: -- what the markers were --

DR. FRASER-LIGGETT: No, ultimately, no.

DR. KEIM: Do you understand that those markers are not relevant to the four? Those markers in the 2002 paper were only relevant to the Porton Down strain of Ames versus the Florida strain; and those did not exist within the core lineage of the Ames strain so they're not relevant to the current investigation. What they were important for was demonstrating that we could discover these small number of markers. There weren't a large number, it was a small number of markers, and so we knew -- and TIGR knew -- that this is a strategy that was going to be used.

QUESTION: So when you characterize the attack strain in the 2002 paper, so again, what needed to happen then to make the match to the source? Could you describe the sequence itself -- events, the logic tree you went through to get to the June 2002 paper to the match of the attack strain?

BACKGROUND OFFICIAL: One thing that's important to note is that when you look at wild-type Ames, when you have a sample that dates back to 1981, which is the probably the closest sample that we have to the isolations from the cow. And this was provided to a scientist in 1981; and that is what we referred to as the wild-type Ames. That sequence was published in --

DR. RAVEL: It's not published. It's available in GenBank.

BACKGROUND OFFICIAL: -- right, but it is identical to the published sequence, I believe.

DR. RAVEL: That's exactly the point to make here is that this paper referred to the comparison to the Florida isolate to Porton. Porton is a highly modified Ames isolate. It was cured of its plasma so it doesn't have any plasma. It underwent mitogenesis to get rid of the plasma, so the mutation you're actually looking at are actually more looking at what happened to Porton instead of Florida. And when you only have one strain like this, if you start using those polymorphisms and discover you're looking polymorphisms that Porton has and try to tie them under the Anthrax from the attack would not make any sense. We needed more isolates

from the attack to make the comparison to and comparing to the Ames ancestor, not the Ames Porton, to discover the real polymorphism.

DR. FRASER-LIGGETT: And I think another important point is that the Florida strain which was related to the Anthrax attacks was a sample that came from the first individual to die of inhalation Anthrax. This was not a sample that came from the spore powders. This was a sample that was obtained from either the blood or the CSFs, I don't remember, the spinal fluid of the first Anthrax victim. So in that sense, this was a sample, if you will, that was yet one step removed from the powder in the envelope.

The importance of the paper that you're referring to is the point that Dr. Keim made just a few moments ago; that this was really a proof of principle demonstration that in fact using whole genome sequencing at a sufficient level of coverage, it was possible to identify high-quality polymorphisms. Had we not found any differences whatsoever, that would have put the potential to use these approaches in a whole different light.

DR. MAJIDI: Paul, did you want to make a comment?

DR. KEIM: No, I was just going to say exactly what Claire said was, this was coming out of a victim, and so this is a very purifying process, and many of these variants will not come through a victim or through a host.

BACKGROUND OFFICIAL: Okay, so getting back to the timeline, the Anthrax powders, themselves, were investigated. And I'm going to give you a little background with Ames. If you look at the 1981 Ames isolate and what was isolated from the victims from their samples, there's virtually no difference. So that is -- the genome sequencing of those samples gave us an idea of what Bacillus Anthracis Ames is supposed to look like, what it looks like.

Naturally, as you mentioned, the Porton Down strain looked quite different from that and that was explained by the fact that they did manipulate it a lot and were trying to mutate it in their laboratory. But when we looked at the examination of the Anthrax powders, what we noticed was something that we don't normally see with Ames, and that is a large amount of colony variation within those samples. It's very unusual for Anthrax, not just Ames. So we exploited the findings of those phenotypic variants, things that looked different, first identified that they were

Ames and then TIGR, using their genome sequencing capabilities were able to compare those strains to the wild-type sequence just as they did the Porton strain, and determined that there were significant mutations in many of these colony variants that were from the letter powder.

The FBI then decided that we would exploit those genetic differences for forensic purposes and develop assays to detect those mutations and screen the entire repository of samples that we collected to try to identify possible sources for the production of the Anthrax letters.

QUESTION: How many of the samples in your database match three of the markers?

BACKGROUND OFFICIAL: None.

QUESTION: None of them matched three?

BACKGROUND OFFICIAL: None.

QUESTION: Okay. And what level were the mutants present at? Was it 1%?

BACKGROUND OFFICIAL: Yes, very low percentages.

QUESTION: Do you have a number?

BACKGROUND OFFICIAL: You mean percentage --

QUESTION: Yeah, I mean, I assume most of them are one type of Ames and there are some small mixture of these mutants in there. What level is --

BACKGROUND OFFICIAL: Oh, yes, in many of the samples, the mutant was well below 1%.

QUESTION: Was there one mutant or four mutants, one with each --

BACKGROUND OFFICIAL: We used four in the --

DR. MAJIDI: There are more than four mutants. Four was used specifically --

QUESTION: -- but each of those are for a separate mutant. It's not four the

identify
one --

DR. MAJIDI: Exactly.

QUESTION: Okay.

QUESTION: What's the level of confidence? If something hits, matches all four mutations, what's the level of confidence that's a real match and not a random chance?

DR. HASSELL: Well, it's very high because since there were eight of the thousand that matched, that gives us a high degree of confidence, and then also the way that the investigation side of this kicked in, we found those eight out of the thousand. We were able to trace those back. The investigation in this whole exercise shows that they were traced back to a single flask.

DR. MAJIDI: So from 1,000-plus material that we have in our repository, roughly eight of them had the four markers, and then when you add the investigative approach, you find out where those samples came from. They were all daughters, or directly driven, from the RMR-1029.

QUESTION: Where were those samples taken from? I understand that you are saying they all came from one flask.

DR. MAJIDI: Right.

QUESTION: What victims or other areas did you get them from?

DR. MAJIDI: To help me understand the question again, I'm not sure exactly what you're asking.

QUESTION: So you pooled the samples from labs and then compared them; right? And then were able to match them back to USAMRIID; correct?

DR. MAJIDI: Right.

QUESTION: Okay, so those eight that matched; where did they come from?

DR. MAJIDI: Those locations -- it is not eight laboratories. I got to be clear about that. They came from different locations. A good number of them came

from USAMRIID itself. And we're not disclosing the location.

QUESTION: How many were outside of the United States, and how many were non-governmental labs?

DR. MAJIDI: None outside the United States.

QUESTION: Were they all government labs?

DR. MAJIDI: There's a fine distinction there and I don't know really what we call government and what we call quasi-governmental, so we're going just going to leave that as is.

QUESTION: When you said that eight have them had four markers --

DR. MAJIDI: Roughly eight of them had four markers.

QUESTION: -- so what were the four markers? Were they snips? Were they tandem repeats? What are the four markers and what is the statistical confidence in the uniqueness of these four markers as some type of Ames Anthrax?

DR. HASSELL: There are actually more than four that were found, but because, for example, there were issues and less confidence in the snips being used in this, so those were not used.

QUESTION: You didn't use any snips?

DR. HASSELL: No.

DR. MAJIDI: They're all --

QUESTION: So they're insertions?

DR. HASSELL: Insertions or deletions.

QUESTION: I'm sorry, I couldn't hear you.

DR. HASSELL: They're all insertions or deletions.

QUESTION: And do you have a statistical confidence number? I mean, you said you were able to generate something for the uniqueness for these four markers.

DR. MAJIDI: Well, the question of statistics is tough because the processes I'm going with this, roughly about 1,000 sample, eight of them had the markers but all eight were driven from the same source, so if you're going to do the statistical validation, it's really skewed because the source is a similar source. Now, the fact that from the universe of the 1,000-plus samples that we analyzed, we found these four markers in eight and we were able to drive the eight samples back to a single source through validation -- investigative validations, it's really difficult to assess the statistical value, but that's what it is.

QUESTION: How did you tie it back to that source? I mean, just by --

DR. COLWELL: If I may, I think it's important to note that the samples were all blind samples. In other words, those being tested didn't know where they came from.

QUESTION: So where I see we're getting to is a whole idea of an error rate. How many eyes were doing this and you've got people like Frances Kohn saying why don't you just make all this public so that scientists outside of your cadre can say, look --

DR. HASSELL: So let me actually pull on that string a little bit. I'm going to answer a couple of questions. Number one, we have had a large body of scientists, very well-known scientists, working with us and helping us throughout this process. You see a handful here today, but the universe of folks that were really expert in this area and helped us, it exceeds 60-plus and we'll provide those as soon as we get their okay to release their names. So the fact that we have had peer review Red Team validation, rigorous validation of our data throughout the process by external scientists, that has happened.

Number two, we've had a number of peer review publications, and that list is available and you can see it. So the fact that those have already been published in a peer review journal outside the context of Anthrax, that is once those papers were out we didn't advertise that these were directly related to our case, but there were many methodologies that was actually used to go into the analysis of our case. So we have done many of those things, and the answer is -- today is another example of we're trying to provide as much information as possible to help you identify some of these methodologies.

One other aspect of this is that we're trying to preserve the peer reviewed scientific

publishing process, so we've identified a number of papers that will come out of this also, so again, these are multiple layers of validation. We talked about the various ways that -- we had the working groups that advised on the approach, how we develop the process; we had many people work on the actual samples themselves and on the repository. There were so many people involved in this that participated we want allow them another layer of validation, which is the peer review process. So this will be made public. We have more than 10 papers that we have tentatively identified to be published on this. We're just preserving the ability to do that. If we disclose everything here then we will not be able to publish those papers.

QUESTION: I guess the big question then is, once you have the one set of eyes, the one lab that said okay, it's these eight and we trace it back, how many other sets of eyes -- how many other independent science labs went and retraced everything and said you're right, and did any lab retrace those and say wait a minute, they have a problem?

DR. MAJIDI: To the best of my knowledge we've had nobody telling us that they had a problem with it. We've had many discussions that actually helped us fine-tune our approach to many of these methodologies. And, again, I've got to say, it's not a new science. It's not a new technique. It's the application of well agreed-upon set of standards that's used in human genome factored into microbial forensics.

QUESTION: So how many groups verified your technique and your results?

BACKGROUND OFFICIAL: Let me interject here a little bit. As I said, when we developed these assays, we did not do this -- you know, without the participation of several laboratories. So there were, in fact, there were four laboratories that independently developed assays and actually looked at several of the genetic mutations that we had and took a crack at developing assays. Of course at the end of all that, we chose the four best that were the most sensitive and the most specific for identifying those mutations in our evidence. Those were all blindly validated before they were applied to the evidence and over the course of the analysis we called in expert scientists from throughout the community, and we conducted reviews. We had scientific working groups. The FBI laboratory always had scientific working groups that participate in all of its forensic disciplines.

We had to create a new scientific working group in this area of forensic microbiology. In addition, when all the data came in, we invited a cadre of scientists to conduct a Red Team review of the science that we performed; and we took their suggestions, we made additional experiments and the data available to those Red Team at their suggestion. And so all of the science that went behind this was well-reviewed.

QUESTION: I'd like to ask a question about the chemical and physical analysis, elemental analysis. Can I actually ask a question unburdened by an advanced degree here? Can you explain something to me about -- as I understand it, every time there's a generation, every time you take a spore and culture it and make a new spore, you create the possibility for a mutation. So if you think of the flask, it's one generation of the powder and then I guess another generation that comes out of the victim in Florida, Dr. Stevens. That's what, two generations removed from the flask? Is that as far away as you got with the Anthrax attack material that you looked at; and was the specific four things you were looking for present in every generation?

DR. MAJIDI: Go ahead, Paul.

DR. KEIM: We've done a lot of work on mutations and how they occur in Bacillus Anthracis. In fact, there are many more generations than you've just described. Even in a very small colony on a plate, there's probably a billion -- almost a billion generations, and so because of that --

QUESTION: From the flask, you mean?

DR. KEIM: -- no, the flask --

QUESTION: Or this goes back before that?

DR. KEIM: -- the flask, itself, contains a very large number of spores, perhaps 10 to the 12th.

QUESTION: Generations?

DR. KEIM: Spores.

QUESTION: Oh, I'm sorry.

DR. KEIM: Okay? And if you have 10 to the 12th spores, it turns out that you have almost 10 to the 12th generations. It's actually 10 to the 12th minus one. So that's a very large number of generations, and so mutations, while they're rare, and that's an important part of biology, a part of life, is that you're progeny don't totally mutate like crazy otherwise your kids won't look like you do; so mutations tend to be rare but when you're working with very large numbers, like a trillion, something that only happens once in a billion, happens. So that means when you end up with that many spores you have the possibility of having these mutations occur and then an astute microbiologist perhaps can see the evidence of those in the way they look. So when you're describing the generation of a spore batch out of the original stock, that's not a single generation. That's a single amplification and there's many generations going on there.

QUESTION: All right, but the point is that every time that you find this Anthrax that came from the flask, whether it's from Dr. Stevens, the victim in Florida, or from the letters, the buoyant letters or the granular letters in the early mailings, you find these markers in all of these samples?

DR. MAJIDI: Well, let me correct that. The sample that's obtained from victims, when you sequence that you find the wild-type genome information because the predominant concentration of the material is the wild-type so the mutants don't have a opportunity to outgrow the wild number. It's only when we look at the letters and only when we look at the RMR-1029 is that when we see that ensemble variation of mutation within those samples.

DR. KEIM: And I think in response to David's question a moment ago, he mentioned that these variants are at a low percentage, like 1% or below. Those are very rare. And so if you look at the mass it will look like the progenitor and you won't see those variants. You have to go in and pick out the morphological variants and concentrate on those to find these mutations.

QUESTION: Okay. On the elemental and chemical analysis, what extra stuff was there in the spores? For example, we've heard about silicon. Was there material from the growth media? And also, were you able to tell something about the water that was used to develop the growth media? Did it come through into the spores?

DR. MICHAEL: First of all, we did find we did find that the spores contained

silicon and oxygen. Our quick SEM analysis, that's Scanning Electron Microscopy, we detected silicon and oxygen within the spores. Later when we had thin sections for high resolution microanalysis in the scanning transmission electron microscope we then could localize that silicon and oxygen to the spore coat, which is a layer on the spore that's within the spore itself.

QUESTION: I'm having trouble hearing what you're saying.

DR. MICHAEL: The spore coat is a layer, as I understand it, that's within the spore and it's not the outermost layer of the spore. So the spore had sequestered silicon and oxygen in the same location on the spore coat. We found no additives; no exogenous material on the outside of the spores. We did have the opportunity to look at weaponized material to compare it to the letter material and they were very different. And the weaponized material the additives appear on the outside of the spore. Again, in the letter materials the silicon and oxygen were co-located on the spore coat, within the spore. In fact, we found some vegetative cells that were going through the sporulation process and the spore within the mother cell had this same signature.

QUESTION: Did you develop a theory as to how each of those two additives came into contact --

QUESTION: I'm sorry, can I just --

QUESTION: -- sure.

QUESTION: Did you develop any theories on where the silicon and oxygen came from, and do you think it played any role in making the spores super buoyant?

DR. MAJIDI: If I can actually pass that question to Dr. Burans, because he's our expert on processing.

DR. BURANS: In essence, as Dr. Michael described, the silicon associated with oxygen that was found within the spore, not on the surface of the spore, being present within the spore coat, which is covered by something called an exosporia, the silicon would not have contributed to the fluid-like qualities of the Anthrax powders.

QUESTION: And as to where it came from?

DR. BURANS: It's known that Bacilli are capable of mineralizing different types of elements including silicon, so as early as 1982 Bacilli species Bacilli species have been shown to localize silica within their spore coat.

QUESTION: Can I ask a follow-up?

DR. MAJIDI: It could have been within the growth media. It could have been within --

DR. BURANS: It was a natural occurrence.

DR. MAJIDI: -- natural occurrence, yes.

QUESTION: Dr. Peter Jarling and Dr. Tom Geiserd of USAMRIID said that they both saw silica on the exosporium, and Dr. Frank Johnson and Dr. Florabel Mullick of the Armed Forces Institute of Pathology both said that they found silica, not -- you know, in their elemental analysis at APHID. I went back to them several times and they both -- all these scientists insisted it was silica on the surface of these spores. So I was wondering what --

Can you please account for the discrepancy between your findings and those of two U.S. Army laboratories?

BACKGROUND OFFICIAL: I can answer that for you. They did not have the technology to make those statements. They would not have been able to give an elemental analysis using the technology --

QUESTION: You're telling me energy-dispersive x-ray fluorescence spectrometry is not capable --

BACKGROUND OFFICIAL: -- I'm not aware that they --

QUESTION: -- of doing elemental analysis?

BACKGROUND OFFICIAL: -- performed that.

DR. HASSELL: It's not capable of locating where it is. It could -- if there is bulk silica in there, but x-ray fluorescence is not capable of doing location.

BACKGROUND OFFICIAL: The Armed Forces Institute of Pathology used scanning electron microscopy to do a gross examination of the spore preps to see if there was exogenous material mixed with the spores. So it's Dr. Michael who did the x-ray analysis on the spores and showed that --

QUESTION: Wait, wait, wait. APHID published a newsletter saying that they did energy-dispersive x-ray fluorescence spectrometry on the spores.

BACKGROUND OFFICIAL: Right, they did a bulk analysis of it. They could not tell where the presence of the elemental signature was coming from. They couldn't tell whether it was coming from the outside of the spores or the inside of the spores. The type of analysis they did was a bulk elemental analysis.

QUESTION: Can you tell us what the dry weight percentage was on the silicon and the oxygen?

BACKGROUND OFFICIAL: There was no exogenous silicon in the spores.

QUESTION: I appreciate that, but can you please tell me what the dry weight percentage was of the silicon?

BACKGROUND OFFICIAL: It was high.

QUESTION: It was high?

BACKGROUND OFFICIAL: Yes.

QUESTION: Which was, according to Dr. Frank Johnson of APHID, consistent with the silica signature, because they did a reference sample of silica before they examined the spores.

BACKGROUND OFFICIAL: Nobody is saying that there was no silicon, elemental silicon.

QUESTION: But he said they were silica.

BACKGROUND OFFICIAL: Okay, we're going to get to that. We're going to let Dr. Michael answer that. But I'm telling you what APHID did was a bulk analysis. They would be able to tell that there was silicon and oxygen present in the prep, which would be hypothesized as silica. But their gross examinations did

not show any exogenous silica --

QUESTION: I appreciate that but obviously what Dr. Jarling and Dr. Geiserd said they actually saw the silica on the surface of the spores.

DR. MICHAEL: But that's just not possible. It's not possible.

QUESTION: You're saying they're mistaken?

BACKGROUND OFFICIAL: Yes, they are mistaken.

BACKGROUND OFFICIAL: -- and there have been presentations at the American Society for Microbiology where some of those photographs were presented and --

QUESTION: Can you tell me what they saw then? How did they make such a mistake?

BACKGROUND OFFICIAL: -- I don't know that. I don't know where their statements came from.

DR. MAJIDI: What we can do is we can stay within the scope of what we know. Telling you what other people say on our samples, based on our knowledge of what they have done is -- this is the list of methodologies that we have; it's unlikely with the methods that they used they were able to actually derive that conclusion that silica was added. And again, it becomes very critical to look at those electron microscopies with energy-dispersive x-ray to be able to do the spatial location identification of the silicon signal you see.

QUESTION: May I say something? Manufacturers of the EDX machine, ThermoNORAN, disagree with you. They say that they can detect -- they can differentiate a silica signal.

BACKGROUND OFFICIAL: Let me ask Dr. Michael to address that. He did the analysis.

DR. MICHAEL: The first thing you have to understand is the scanning electron microscope is not a surface-sensitive technique. When we use an energetic electron beam on the order of 20 kv, which I believe is what they used in that study, we are sampling over a micron deep into the sample. Now, the average

spore size that I have seen is on the order of a micron to a micron and a half --

DR. MICHAEL: They have no indication of exactly where that silica or that silicon oxygen signal -- I hesitate to call it silica, because we don't know how it's bound together, and EDS does not tell us how it's bound together. So when they sample they're sampling through a thickness of a micron or so. And again, the average spore size is a micron and a half or so. So they're sampling a large fraction of that spore. Now, what we did was after we looked at it in the SEM and said, "Yes. We see silicant oxygen signal here," using our ThermoNORAN system, by the way, since you brought it up, we then went and made thin sections of these materials. And then we took them to a scanning transmission electron microscope. Now, the stem -- or the TEM that you may be familiar with --

QUESTION: Yes.

DR. MICHAEL: allows us to focus our probes down to the nanometer scale. And if we look at a thin section, we now are looking at spatial resolutions on the order of a few nanometers. In those samples we can localize the silicant and the oxygen signal to the spore code.

QUESTION: And can you tell us what the dry rate percentage was of your analysis?

DR. MICHAEL: My analysis does not --

QUESTION: Of the silicant -- that gentleman over there, who has not identified himself, said that it was a very significant spike, which is what Maj. Gen. John S. Parker, the commander, former commander, of USAMRMC said upon seeing the APHID analysis.

DR. MICHAEL: It was a significant peak in the x-ray spectra. Yes.

QUESTION: Right. But can you translate that into a number for us, please?

DR. MICHAEL: I would not translate that into a number from an SEM identification. There are significant pitfalls and problems of doing quantitative analysis --

QUESTION: The EDS would have given you that. What was the number?

DR. MICHAEL: No. The EDS cannot give you a quantitative number from a rough surface of particles. The EDS can tell you relative amounts of chemical species, but it cannot give you quantitative answers from a rough surface. If you gave me a perfectly polished surface of a metal or an alloy or a ceramic, I could tell you the quantification with EDS. With a rough surface? No. That's not possible.

DR. MAJIDI: We have a question in the back.

QUESTION: I'm going to go back to grammar school for a second.

DR. MAJIDI: Sure.

QUESTION: Can you explain -- did you develop a working theory as to how each of the 22 victims actually came into contact with the attack strains? And in particular, I'm thinking of the elderly woman in Connecticut was a bit of a mystery. What was your working theory as to how the dispersals happened?

DR. MAJIDI: You know, that again, you know, it's really --the answer is we -- some are just, you know, truly unknown to us. We have never found the Florida letter, for example. So we don't know how that -- what was the genesis of that particular contact. Others, through the mail-sorting machines, and we have the U.S. Postal Service here with us that can talk about that a little bit later. But some was through the dispersal of material as they go through the rapid sorters. Others -- potentially cross-contamination of the mail.

QUESTION: Dr. Michael, if the average spore size was one to one-and-a-half microns did you ever look at how big the pores are in an envelope?

DR. MAJIDI: That's exactly --

QUESTION: And how -- do you have any sense of how much of the stuff fell out before it ever got delivered?

DR. MICHAEL: I have -- I have not looked at envelopes. That wasn't part of our charge in this study.

DR. MAJIDI: We have looked at the envelopes. And in fact the envelopes, when you do the comparison of pore size, are porous. They allow the material to do --

QUESTION: Bigger than one-and-a-half microns?

DR. MAJIDI: Yeah. It depends on obviously the type, but yes. And we were afraid that some of the material through the mail-sorting machines, as they were going, literally left the envelope through those pores.

QUESTION: Did you ever make in the course of your investigation something as small -- some sort of inert -- to study physical properties -- something like the anthrax, that small, one to one-and-a-half microns and look at what would happen when you sent a letter through the mail with it or anything like that to study how -- I'm just trying to get a sense of how much of it must have fallen out of the envelope in the course of the mailing?

DR. MAJIDI: Yeah.

BACKGROUND OFFICIAL: Yes. This was done by both U.S. Postal Inspection Service -- they used a simulant and put it in envelopes and put it through the automated facer cancellers used in postal system as well as the delivery barcode sorters. And to answer your question on the epidemiology of the victims, a lot of that has been published by the CDC in Emerging Infectious Diseases Journal, including the mapping of the facilities. And you will notice in those publications that anthrax plumes were detected over the sorting equipment as high as 30-some-odd feet into the rafters of those facilities. So all of that clearly indicates that the envelopes were definitely porous, and the energy of the mail-sorting equipment was sufficient to expel a lot of their material throughout the facilities. There are videos that were made by both U.S. Postal and the British Postal System and their studies of them.

QUESTION: Follow up to the previous question. Two out of three of those purported the scientists at the FBI have not been able to replicate this actual powder. Have you been able to, and can you tell us what you were able to find out in terms of what the news and if any of that is available to Dr. Ivins, for example, standard off the shelf, 600 --

BACKGROUND OFFICIAL: Well, one of the -- one of the interesting things is that if we can get -- along that same question, but if we can get back, related to the silicant signature, there is literature going back 30 years that show that biological or some sort of phenomenon incorporation of minerals into bacillus pores.

QUESTION: That's true. The scientists who first published that paper in a related bacilli species -- bacillus subtilies -- said they could not account of that silicant --

BACKGROUND OFFICIAL: Exactly.

QUESTION: They even thought it was a possible laboratory error resulting from the silicone antifoaming agent. So they never -- they never sufficiently accounted --

BACKGROUND OFFICIAL: Let me finish my statement, and I'll clear up all that for us.

QUESTION: Okay.

BACKGROUND OFFICIAL: Fortunately for the FBI we went to Mrs. Somlio, one of the authors on that paper, and were able to retrieve her husband's samples from 30 years ago. She had them on the shelf in her office at the University of Virginia. The samples were provided to Dr. Michael, who looked at them. And he confirmed their results of 30 years ago. It was not an anomaly, and in fact the silicant incorporation was very similar to what we saw in the anthrax letters. So we now have documented proof that with bacillus, the genus bacillus, that mineralization -- including mineralization of silicant -- below the exosporian, because the strain that they used, the bacillus series T strain, did have an exosporian similar to anthrax.

QUESTION: But we still need to know the weight, because that tells you how this stuff was weaponized.

DR. MAJIDI: Just wait a second. Wait a second. You know, there is -- this -- I don't understand what -- you are using the term, “weaponized” -- no one -- when you look at weaponization, there is a clear definition. That is you have an anthrax spore; you do specific preparation to make it suitable for us a biological weapon. The material that we recovered did not have any additives added to it to make it in any more easily dispersible. They material we have is pure spores --

QUESTION: But we have information to the contrary. That there was ten times more silica in the media powder sent to New York than there was in the powder

sent to Senators Daschle and Leahy.

DR. MAJIDI: Well, the water in New Mexico has ten times more silicant in it then the water in some other states. That --

QUESTION: Dr. Majidi, that gets me back to the question I was wondering earlier. In your looking at the elemental and chemical properties, could you tell anything about the water that was used to filter this anthrax, and did that do you any good?

DR. MICHAEL: No. No.

QUESTION: And if I could just follow up on your question. Would it be fair to say then that the silica and oxygen presence in these spores was, for want of a better term, accidental or not intentional or put there by God or something, but it just happened? And did that -- a) is that correct? It just was sort of accidental or serendipitous if you want.

BACKGROUND OFFICIAL: Well, there are scientific reasons behind it. I mean, you know, bacillus species often produce proteins that are -- whose sole purpose is to chellate metals and other minerals. And the theory behind it is that it makes the spore heartier. That if the spore mineralizes they're more -- so that's a scientific theory.

QUESTION: But that's something the anthrax did, not man?

BACKGROUND OFFICIAL: The understanding of that process is not well understood.

QUESTION: Okay. And secondly, is that -- did that -- the presence of that material inside the spore make it more buoyant? Did that -- do you know why -- what is it about these spores that make them so buoyant?

BACKGROUND OFFICIAL: What do you mean, “buoyant”?

QUESTION: Well, the fact that they would hang in the air for such a -- “fluidized,” I think is the way you all put it.

DR. MAJIDI: No. No. So let me again go across that one, because number one, these were -- these were what many would consider our dried sample from a

suspension. In fact, many biological single-cell organisms when you dry them, like algae, they -- they're very buoyant, for a lack of a better term, as you said it. That is, you know, you open the contained, they do fly all over. These samples -- they had a combination of not only single-cell spores but also agglomerates -- larger agglomerates. So it was by no means --

QUESTION: Uniform?

DR. MAJIDI: Uniform. And the comparison of two different letter sets that we've done, the comparison, one preparation was more refined than the other one. So --

QUESTION: Were those the two Senate letters?

DR. MAJIDI: The two Senate letters versus the two New York letters.

QUESTION: Oh. Right.

DR. MAJIDI: Right. One preparation was more refined then the other one.

QUESTION: Which one?

QUESTION: Senate letters.

DR. MAJIDI: I think those were the ones. Yeah.

QUESTION: Substantially so; right?

DR. HASSELL: Observably so. You could see the difference. There was difference in the color. There were --

QUESTION: Could you duplicate that?

QUESTION: Do you believe they were milled?

DR. MAJIDI: Again, I don't want to speculate, you know, if there were -- if they had extraordinary efforts put to crush these things, because of a couple of reasons. Number one, we saw larger agglomerates. Number two, if you haven't done so, I suggest take a tour of the U.S. Postal Service and look at how those letters handled through the metal -- through the letter-sorting machines. It's a very, very, rigorous process.

QUESTION: The machine --

DR. MAJIDI: The machines will do a very good job taking care of the envelopes.

QUESTION: Dr. Majidi, the paper published in the Journal of the American Medical Association in 2002 said the 80 -- the larger 80-micron agglomerates tended to disintegrate just on disturbance.

DR. MAJIDI: Well, here's the thing. You know, if --

QUESTION: So if they were treated --

DR. MAJIDI: Let's put it this way. If 80 agglomerates – 80-micron agglomerates were tended to disintegrate, how did they survive the mail machine?

QUESTION: The particles disintegrated into the smaller particles.

DR. MAJIDI: So it takes --

QUESTION: Small particles?

DR. MAJIDI: So it takes the energy of a thought process to blow them apart, but they stay long-range through the mail machine?

QUESTION: Well, I guess what I'm getting back to here, Dr. Majidi, is what you're saying then, the fact that this stuff was so --

BACKGROUND OFFICIAL: Friable.

QUESTION: The word -- "friable." Thank you. The fact that it was so easily hang in the air.

DR. MAJIDI: Sure.

QUESTION: We were told for example that when they went in to clean up the Senate offices, it was only on the horizontal surfaces. It didn't stick to the wall, for example. It was not on the vertical surfaces, and that they found that unusual. In other words, that it was not attracted to other things. Is that not true, by the way?

DR. MAJIDI: You know, I don't have that level of detail on the clean up, but --

QUESTION: It's not? Okay. Well, all right. So in any event is it possible then -- you're saying that it just -- this is just -- it was a natural process to get this.

DR. MAJIDI: Is it a natural process that makes it that way.

QUESTION: Can I ask a question about the equipment and what was used to make this, potentially, and whether it was at Fort Detrick? Was it just a lyopholizer or something more sophisticated?

DR. MAJIDI: You know we really -- we really don't have the -- we don't really have any answers for what process was used to grow additional spores or what methodology was used to dry them. I think that a lot of folks focus on the issue of lyopholizer. You can ask any of the folks and the panel members, and they will tell you that you can dry biological samples in one of dozens of ways. Lyopholizer is one of them. You can let the samples heat-dry. You can let the samples -- the water evaporate. You can --

QUESTION: Do speed vac.

QUESTION: What was that?

QUESTION: Use a speed vac.

DR. MAJIDI: So again, I don't want to get wrapped around the issue of how was a sample processed. The critical issue --

QUESTION: Isn't that part -- an important part of the evidence, though?

DR. MAJIDI: Well, no. The important part of the evidence is that the materials of the letter with the genetic mutations could exclusively be related only to RMR-1029.

QUESTION: I have a quick question about that.

DR. MAJIDI: Yes?

QUESTION: The eight mutations were all from RMR-1029. I just wanted to distinguish between sample and source.

DR. MAJIDI: Sure.

QUESTION: Were there any samples from RMR-1029 that did not have the eight mutations? And when you have a thousand samples in your pool, are those coming from only 20 labs or a thousand different places? Clear that up.

DR. MAJIDI: Well, the answer is that many labs provided multiple samples. As you can expect when you go through a scientific laboratory, they're working on a particular strain, there are many samples of that strain. So, clearly, the thousand samples that we have comes from a much smaller universe of laboratories.

QUESTION: Approximately how many? Fewer than a hundred?

DR. MAJIDI: Yes. It's fewer than a hundred. And then when you look at the -- I'm sorry. I missed the second part of your question.

QUESTION: Just did any of the RMR-1029 samples not have the eight mutations? Were the eight that were there, the form of mutations -- were the eight samples all of the ones from RMR-1029?

DR. MAJIDI: RMR-1029? Yes. Yes.

QUESTION: And then along those lines, was the subtilies contamination that was in the post --

DR. MAJIDI: Yeah.

QUESTION: Is that found in any of the other -- anything else?

DR. MAJIDI: No. Again, you know, the bacillus contamination showed up in one batch, not in the other one, and it really didn't drive us any place specific.

QUESTION: It didn't show up in any of the eight matches, any of those samples?

DR. MAJIDI: Pardon?

QUESTION: So the stuff from the letter that matched eight samples -- none of those had bacillus --

DR. MAJIDI: No. No.

QUESTION: So early on Dr. Ivins provided a sample to you guys that was

somehow tainted or different or unusable. Can you explain what was wrong with that particular sample?

DR. MAJIDI: Sure. We have a series of -- let me start this way. We spoke with many people and scientists at RID as we were trying to start working on this case. Clearly, did --the world experts who were in RID as well as a few other places. So we asked for their advice on some of these issues. Initially, as we were going through the process of developing a plan to subpoena the sample, we received two -- we received a sample from Dr. Ivins. And as we were working on our subpoena everybody then submitted sample based on a subpoena. Subpoena specifically listed a very rigorous methodology of how we expected a sample to be collected. The first sample that Dr. Ivins provided to us prior to the subpoena did not meet the requirements of the subpoena for submission.

QUESTION: In 2002.

DR. MAJIDI: That's right.

QUESTION: In what way did they not match?

DR. MAJIDI: They didn't follow the protocol that we had on the subpoena for sample submission.

QUESTION: But that was prior to the subpoena?

QUESTION: He was doing it of his own initiative?

DR. MAJIDI: That's exactly -- that's right. So that is the very first sample that we have from Dr. Ivins. He submitted the samples ad hoc, and it was -- because the subpoena came after his submission, his submissions didn't meet our requirements for the sample. So that sample to the FBI repository was destroyed because it didn't meet our requirements.

QUESTION: In what way didn't it meet it?

DR. MAJIDI: Well, it didn't follow the protocol.

QUESTION: What protocol?

BACKGROUND OFFICIAL: He didn't comply with the subpoena in terms of the instructions -- the very specific instructions that were in the subpoena. He didn't use the proper medium and, with slants, there was no guarantee that he prepared it in the way that the instructions directed.

QUESTION: I thought you just said that the first sample was given before there was a subpoena.

BACKGROUND OFFICIAL: Exactly.

QUESTION: So how could he have not followed the procedures if --

DR. MAJIDI: Well, that's the thing. So, he ad hoc submitted a sample --

QUESTION: So it's not true that he didn't follow procedures.

DR. MAJIDI: Well --

BACKGROUND OFFICIAL: He didn't know the procedures. He was provided information as to what was going to be in the subpoena --

DR. MAJIDI: Right.

BACKGROUND OFFICIAL: And he submitted those samples before the subpoena came out. But he knew what the protocol was.

DR. MAJIDI: Yes.

QUESTION: Can you make that clear on the record, please?

DR. MAJIDI: Yes. Yes.

QUESTION: It's important.

DR. MAJIDI: Yes.

QUESTION: So he did know what the protocols were and did not follow them?

DR. MAJIDI: Yes. That's true.

BACKGROUND OFFICIAL: Yes.

QUESTION: Was he the only person submitted before the subpoena was sent out?

BACKGROUND OFFICIAL: Yes. He was the only one.

QUESTION: Did you say "yes"?

BACKGROUND OFFICIAL: He was the only person who submitted before the subpoena.

QUESTION: Okay. And what about the second submission on the subpoena? Did he follow the protocols on that?

DR. MAJIDI: So we basically got a sample from RID that not only contained RMR-1029, but was not submitted based on the required submission protocols in the subpoena. Now, at the same time, while the subpoena had not been issued, Dr. Ivins was aware of the protocol in the subpoena.

QUESTION: How was he aware of it?

DR. MAJIDI: We had discussed with him as to what the protocol was going to be.

QUESTION: Did he help you develop the protocol?

DR. MAJIDI: Yes.

QUESTION: Thank you.

QUESTION: So what did he specifically do about the mediums and format -- What does that mean? What did he do not to follow the protocol?

DR. MAJIDI: Well, again, it wasn't the right medium and it wasn't the right type of slant that he submitted the samples.

QUESTION: Is this something that could've been accidental or do you think that he intentionally did not follow the protocol?

DR. MAJIDI: Well, again, this is not the -- this is not the court of law. I'm just here to discuss with you the facts of the case as it relates to science and

technology. So I won't speculate on why, I'm just telling you what.

QUESTION: What would that do to the court of law? You know, as you guys were doing this, you're obviously doing it to prepare a criminal case. It's not science for the sake of science. So how are you protecting these samples? How are you maintaining the chain of custody?

DR. MAJIDI: So that's another issue. The first sample we received didn't really meet our requirements for the chains of custody issue, either.

QUESTION: So what happened? Well, continue the narrative. So, it's the first sample, second sample; can you take us through that?

QUESTION: I'm just wondering if because of the medium issues, that would have made it difficult to identify. Wouldn't -- you know, because it was not using the right medium --

BACKGROUND OFFICIAL: Well, you know, let me just say from the scientific point of view, if you don't follow the procedure, the result is ambiguous.

DR. MAJIDI: So after the first sample, Dr. Ivins received the subpoena --

QUESTION: When?

DR. MAJIDI: April 2002?

BACKGROUND OFFICIAL: Just to clarify the timeline, the first subpoena was dated February 22, 2002. Dr. Ivins submitted his first samples February 27th of 2002. We have reason to believe, based on conversations with other scientists -- other FBI scientists -- that he actually submitted them in response to the subpoena, based on notations of the conversation that he had, that a scientist had with Dr. Ivins, that he actually did comply. You know, he had the subpoena in hand and he submitted the first samples. They were rejected because they were submitted on the wrong type of slant. He was told to resubmit them in April of 2002. That he did, according to the protocol on the appropriate commercially available slant, though that second sample lacked all four genetic mutations.

QUESTION: Thank you. Can you identify yourself?

BACKGROUND OFFICIAL: I'm one of the prosecutors on the case.

QUESTION: Unless I'm mistaken here, I was told, in fact it turned out, that that second sample was the RMR-1029. How did that get screwed up? You didn't realize for three years that he had submitted the correct sample that you were looking for; right?

DR. MAJIDI: No. Okay, so -- well, let me repeat this again. The first sample we got, which was submitted ad hoc prior to the issuance of subpoena, that sample, because it was on a wrong slant --

QUESTION: She just said it was after the subpoena --

DR. MAJIDI: The very first sample that was submitted --

BACKGROUND OFFICIAL: And just so -- I know it's kind of confusing, but we had reason to believe that there was something wrong with the April submission. It didn't have these mutations, and so that caused the investigative team to say that it might be something more to this. And so that's when, a number of years later, I think in 2006, they consulted with Dr. Keim out of Northern Arizona University, who actually retained his duplicate slant of the original February 2002 submission. He actually had retained that. He hadn't destroyed his. The repository destroyed their February sample because it was on the wrong slant. Dr. Keim, thankfully, had kept his February 2002 identical submission.

So, in other words, every researcher submitted two identical slants of the same material. One went to Dr. Keim for strain typing, one went to the repository for the comparison. It turned out, many years later, that actually Dr. Keim had retained his from the February -- the initial submission. That initial submission had the mutations. And so --

QUESTION: And so the first one was destroyed because of the wrong slant and run through the repository without being tested. So had he tested it at the time, do you think he would have been, perhaps, five years -- six years ahead of where we are now?

DR. MAJIDI: Well, no, not really. Because remember the science for genotyping, those specific mutations were developed over the next few years.

QUESTION: My understanding was -- my understanding, tell me if I'm wrong, from the briefings that you gave to Congress last week, was that the second sample of your subpoena, you originally thought was not the RMR-1029/Dougway sample and you thought that Dr. Ivins was being deceptive. And you did not realize for three years, until further testing, that in fact, he'd given you exactly what you'd asked for. Is that right or wrong?

DR. MAJIDI: The second sample -- the second sample that we received from Dr. Ivins did not have the genetic mutations.

QUESTION: Therefore, it could not have been RMR-1029?

DR. MAJIDI: Well, again, I don't want to speculate that far. What I'm saying to you is that every sample we have had of RMR-1029, and the letter samples, they all have the genetic mutations. The daughters of RMR-1029, which we were able to trace back to understand that they were, in fact, coming from RMR-1029, they have the genetic --

QUESTION: By records? How did you trace it back?

DR. MAJIDI: We did that investigatively. You know, we looked at many, many, many lab reports. We looked at lab notebooks. We looked at transaction forms and we were able to identify and trace the genealogy of all samples.

QUESTION: Was the second sample from an isolate that was in his control? A separate one? I mean, can you type it to a different flask in his lab?

DR. MAJIDI: But -- I don't --

QUESTION: So you don't know where that came from.

QUESTION: Let's put it another way. His question, was it the sample that you had requested? Did he comply with the subpoena?

DR. MAJIDI: We asked for all samples. So the answer was, we asked for all Ames samples, and in fact he had submitted an Ames sample. But the second submission, the Ames samples that were received from him, did not -- if it was all sample in his laboratory, did not include any of the genetic markers.

QUESTION: But did he give you what you had asked for? The sample from his lab, from --

DR. MAJIDI: Clearly not. Because RMR-1029 was in his laboratory and this sample was not directly traceable back to RMR-1029.

QUESTION: But it was at least enough to say it is questionable.

BACKGROUND OFFICIAL: Let me clarify something first here. The first sample that he submitted was rejected because it was outside of the subpoena process. It didn't comply with the full instructions of the subpoena.

QUESTION: Right. Right.

BACKGROUND OFFICIAL: In the subpoena process, you have to remember that slants were sent to two different places. One, to Paul Keim and one for the FBI repository submission.

It was the FBI repository submission that was rejected and disposed of. Dr. Keim saved his sample of that first submission that was rejected. Dr. Ivins then submitted correct samples under compliance of the subpoena, and those went into the repository process and also went to Dr. Keim's lab for typing.

Remember, the duplicates were always sent to Dr. Keim to insure that it was Ames and not some other anthrax facility. And then, by 2004, we had brought two assays online. Two of the genetic assays online to begin screening the repository. The repository was not complete at that time, but we had two assays that had been validated and we started to screen the repository.

In the early screening of the repository, it started to become evident that the two genetic markers that we had in our repertoire at the time were pointing towards USAMRIID. At that point, the focus was put on the samples that were testing positive at USAMRIID, and the FBI went back in, seized additional samples, including 1029, showed that 1029 tested positive.

And since the repository -- second repository sample submitted by Dr. Ivins did not, but was allegedly 1029, that raised some suspicion. At that time, the FBI went back, contacted Dr. Keim, several years later, and found out that he had retained the two original submissions. We seized those, brought them back, and they tested positive for both of those assays.

QUESTION: Okay. But if the first submission tested positive, yet it was submitted outside the four corners of the subpoena, didn't you just say that makes the results ambiguous?

BACKGROUND OFFICIAL: It doesn't make the results ambiguous. It's a question of, when talking about the science in a court of law, we would want every sample treated equally.

QUESTION: So you're saying it's a legal issue, not a science --

Scientifically, there was no problem with the first one -- the first sample that Dr. Ivins gave you. Yes, it was in the wrong medium; yes, it was on the wrong slant, but scientifically, had you had the ability then and actually investigated then, you would've not been able to tell, so it was more legal chain-of-custody-type of thing.

BACKGROUND OFFICIAL: Any results on that sample could have been questioned because it was not obtained in the same manner that all of the other repository samples --

QUESTION: But it could have pointed you to him, it just couldn't have been used well, and it wouldn't have stood up in court. Is that fair to say it that way?

BACKGROUND OFFICIAL: Well, it may have pointed to him, but what I said was, that when we began screening the repository, there were additional samples that pointed us in that direction. So it wasn't like that -- by not testing that sample, that we did not have an early lead as to the source of -- of possible source of the anthrax material. We had other samples coming from USAMRIID that were testing positive.

QUESTION: When was that raid, did you say?

BACKGROUND OFFICIAL: Pardon?

QUESTION: Didn't you say that the FBI raided the lab, or, what was --

BACKGROUND OFFICIAL: Well, we went back and conducted a search.

QUESTION: Yes, and so what was the date of that?

BACKGROUND OFFICIAL: The RMR? April.

BACKGROUND OFFICIAL: April 2004?

QUESTION: Yes.

QUESTION: And then when you go back to Keim for -- Dr. Keim for --

DR. MAJIDI: 2006. Was when we collected, we went back to the slant from the first go around. The improper submission was collected from Dr. Keim in 2006.

BACKGROUND OFFICIAL: So I just want to make sure that's clear. Are we clear as to why, number one, it was rejected because it didn't comply with the process and we wanted to make sure that we had an even process in collecting samples from everyone.

But then, fortunately, it was saved. And we went back. And it's not that we -- you know, that the result is questionable, I mean, obviously we found the markers in that sample, eventually all the markers in that sample. However, it's possible that it could've been argued that that sample was not collected the same way all of the other samples were collected.

QUESTION: How many others were destroyed --

QUESTION: Obviously, he gave you two samples and one of them appeared to have the genetic marker. The other didn't. Why would he have -- why wouldn't he have given you the wrong sample both times? Had something changed in terms of your methodology, or your leads, or --

BACKGROUND OFFICIAL: We're here to discuss the science. We can't speculate --

QUESTION: Well, can you tell me if there'd been some change in the direction or the technology being used that would have led him to believe that it would have been advisable to change his sample the second time out?

BACKGROUND OFFICIAL: Well, we can't speculate on that.

QUESTION: If you didn't have Dr. Keim's sample, would this case have been able to be brought? I mean, would this still be a strong case, in your view, if you

didn't have the sample from --

DR. MAJIDI: Okay. So let me say that we're here today -- and this is really extraordinary for the FBI and the Department of Justice to talk about a case that hasn't gone to trial or hasn't gone through its complete due process. We opened the discussion for a number of reasons. Clearly, for a closure for victims' families as well as a tremendous public interest.

We're -- clearly, we understand the victims' families as well as Dr. Ivins' family, as well as the Bureau and Justice Department, we really would have liked to do this in a proper manner; gone through a court of law and presented our evidence in their entirety and been able to discuss it. Obviously, from our point of view the investigative and scientific evidence are strong enough that we are disclosing the material to you today.

So what would have happened, the next step, I think that's a bit of a moot point.

QUESTION: What's a slant?

DR. MAJIDI: "Slant"?

QUESTION: Sorry.

BACKGROUND OFFICIAL: It's a test tube of auger --

QUESTION: It's a what?

BACKGROUND OFFICIAL: It's a test tube of a solid medium, auger, that when you fill the tube with the media, if you lay it on a slant, it will form a flat surface on -- diagonally across the tube.

QUESTION: Okay. Thank you.

And when you're talking about these samples that are collected. It's not just one sample. These people are submitting multiple samples of everything they had in their lab. So it wasn't that he gave you one thing from RMR-1029. He was giving you multiple samples from -- you know, multiple tubes of anthrax that are all --

Is that correct?

DR. MAJIDI: We at least got two copies of every material.

QUESTION: How many different strengths of anthrax did he have in has lab?

DR. MAJIDI: As far as I know --

BACKGROUND OFFICIAL: Multiple strains.

DR. MAJIDI: Yeah -- you know, multiple strains, but remember, the issue here is that --always go back to what was in the letters. Ames. So we -- as we look at the universe of anthrax, there are many, many different strains. What were the victims affected by? It was Ames. What was in the envelopes? It was Ames, plus the specific mutations that interest us. What was in RMR-1029? It was the Ames, plus those four specific mutations.

QUESTION: So how many Ames did he have?

QUESTION: What's that -- the second strain that he submitted in response to the subpoena, was that available in his lab? Where would he have gotten it from? Where did it come from?

DR. MAJIDI: Yeah, it was available in his lab.

QUESTION: So there were -- you know, you've got 1029. You've also got 1030, 1031. There are different test tubes full of Ames in his lab that he would have submitted samples of. Is that correct?

BACKGROUND OFFICIAL: Correct.

DR. MAJIDI: That's possible.

QUESTION: How many?

BACKGROUND OFFICIAL: Do you mean anthrax strains other than Ames?

QUESTION: How many Ames strains of anthrax, in your, experience did they do? Not just 1029, but whatever.

BACKGROUND OFFICIAL: All right, let me clarify a couple things on the collection of the material standpoint. It's that the subpoena process said pretty much in the world of Ames. Everybody knew that we were looking for the Ames

strain.

Now, remember based on the information that you got from Dr. Ravel, Dr. Liggett, Dr. Keim, the mutations that we were discovering were coming on-line simultaneously to the subpoena process; okay? So it was almost going like this, if you want to think about how our knowledge of what exactly we were finding for.

In late 2004 is when we started to get some of the results of some of the very first assays that we have brought on-line that were from the mutations that were linked to the letter material. Now, from that, we started to be able to -- the investigators were able to start now to get valued information about what they should start looking for.

Now, the whole question about submissions, that's what led us to start the investigation -- to start collecting samples. So once these samples coming on-line from the subpoenas, it was clear there were discrepancies between what was provided by some and what was coming up in some markers based on what the investigators learned and some of the genealogy.

That led to massive collections of hundreds and hundreds and hundreds of samples. So that's why you get the thousands of samples that we have in the repository.

And that's why it's a good collection of the Ames strain, is that every tube of anthrax was collected. Dr. Keim was screening it for the Ames strain. Everything that was the Ames strain then flowed into the genetic assay test. But it wasn't until late 2005/2006, that RMR-1029 was the focal point of our investigation as far as from a genetic standpoint. So I hope that clears up some of the confusion about subpoenas and samples, and what was what. I mean that is the timeline.

That is when the genetics caught up with the investigation in identifying what sample went with what submission, because the laboratory will blind it. We would get a repository number. We provided that number back to the investigators, who then went and did a detailed investigation into all the things that you talked about before, but it's not particularly relevant to the science of what we did, which that timeline is accurate for.

QUESTION: How many besides Dr. Ivins' first submission to the FBI lab, which was destroyed -- how many other samples were destroyed? Or was that the only

one destroyed?

BACKGROUND OFFICIAL: But remember that --

QUESTION: I understand that. I just want to know how many were destroyed.

BACKGROUND OFFICIAL: Once the genetics started coming on-line in 2004, searches were conducted by the investigators, and material was directly sampled. All material. All anthrax.

QUESTION: I understand that, but the question is just how many were destroyed.

BACKGROUND OFFICIAL: Remember, the only sample received outside the space of subpoena was that one sample. So that's the only sample we destroyed.

QUESTION: So -- okay. Of the --

How many samples were sent as a result of the subpoena as opposed to the searches? So -- I mean, would you say 500 samples, a thousand samples were sent, and the only one destroyed happened to be the one that was it?

BACKGROUND OFFICIAL: No. The only sample that was destroyed was not the one that was it. Remember, as I told you as we were screening the repository, there were other samples from USAMRIID which did test positive. So you are wrong in that statement. It was not the only sample. It's not like that was the sample and we destroyed it.

QUESTION: No, no, no, but I'm saying it was the only sample that was destroyed happened to be it.

BACKGROUND OFFICIAL: That was the only sample that was destroyed, and, yes, it was positive, but there were other positive samples.

QUESTION: Is it a violation of your protocol to destroy a sample just because it doesn't meet the formatting requirements? Should that have happened? Should that sample have been destroyed?

DR. MAJIDI: You know, looking at it -- hindsight, obviously, we would do things differently today, but let me just go back and say in the days that we started this process, microbial forensics was completely unknown to us. In fact, that's a

science we helped usher with the rest of the community. So what we tried to do was initially stay as closely to the protocol as possible.

And the amazing thing about this case that I would like to additionally point out is the amount of lessons learned. Were we perfect? Absolutely not. We've had missteps and those are the lessons learned that we have incorporated into today's approach to have sample that involves now pathogens, chemicals, radiological and nuclear material.

So it was only the past few years that we were able to incorporate all of the lessons learned that we had throughout this investigation.

QUESTION: Dr. Majidi?

DR. HASSELL: Let me clarify one thing first, too, because it goes back to your question that I don't believe it was answered very well earlier about chain of custody, and what's going on now.

A tremendous amount of work and budget and everything else at the FBI laboratory goes in towards quality control; quality assurance; maintaining the chain of custody; just maintaining the integrity of that whole system. It's an accredited system. So things that fall outside of the normal operations -- you know, it doesn't fit very well within our -- the way we work. So the fact that that was destroyed is not really unusual. It's just -- you know -- it --

You're right -- like Dr. Majidi said, in hindsight, it would have been useful just to have saved it, probably, but having destroyed it, that's not unusual, because if it didn't match the protocols that we had set for the investigation, then it would always be questioned. If it came up one way or the other later on, it could always come into question.

QUESTION: Can you just clarify what initially turned suspicion to Ivins? Was it that the sample was negative and he should have had a positive sample because all of these other positive samples were derived from RMR-029, so you expected him to have that and he didn't?

DR. HASSELL: Well, again, we're getting close to the investigation side of this, but the --

DR. MAJIDI: I'll answer that. Sorry, Chris, I'll answer that.

Investigatively, after we saw various mutations outside the RMR-029, it all pointed back to RMR-1029, so the question became "Why are we seeing these mutations in these samples, and we know where they're coming from and why are we not seeing it in their origin?"

The other thing I've got to just point out is on a destroyed sample, I just want to leave you with this one last note, that from an evidentiary point of view, if we request a standard so we can do a comparison, if it doesn't meet the basic quality assurance guidelines, that is useless to us. Now, could it be a forensic sample that we could have used? Yes. Was it good as a standard that we could have included it in our repository? No.

QUESTION: Dr. Majidi, may I go back again to the unusual quality of the letters -- Anthrax sent to the Senate, whatever word we're using to describe how powdery it was.

DR. MAJIDI: Yeah.

QUESTION: If -- what I hear you all saying today is it was that way just because that sometimes happens when you dry an organism like anthrax. If that's the case, why did it surprise the experts so much in how buoyant it was? Wouldn't this have been seen before?

DR. MAJIDI: So I'm just going to go out of school here and just tell you about some of the ways that you deal with single-cell organisms and culturing. If you look at the experts in the country, a lot of them have worked with solutions and auger plate. You'll find very few true experts that they know anything about powders.

That's just a bottom line, that the true experts in this area as we discussed this with them, by no means they're surprised that this is so dispersible. In fact, as we discussed these with subject matter experts, the idea of putting these things in a letter and mailing it, because of the porosity of the envelopes; because of the size of the spores, were all questionable actions. So is the material being so easily dispersible really unusual? The answer is "no."

QUESTION: It just doesn't happen very often.

DR. MAJIDI: Well, no. But there's no testing on it. So -- you know, Anthrax by and large -- I'm going to ask Jim Burans to help me out with this one.

Go ahead, Jim.

DR. BURANS: We in our laboratories, and even investigators at USAMRIID, avoid ever working with anthrax in a dried form. All laboratories endeavor to work with these back trail pathogens that can cause significant disease in liquid form because they're far easier to handle. You can manage aerosolization and prevent infection of your coworkers by handling them in liquid form. We have biosafety hoods to work under, which are very capable of dealing with aerosols.

They are less capable of dealing with aerosolized powders. One of the unique characteristics of the dried anthrax spores that hasn't been referred to is that they're very --very easily take on charge; and many of the types of evidence, sample bags and plastic tubes and things of that sort that these types of materials are put into tend to add charge to a powder such as this. And so it sticks to everything when you --

QUESTION: It sticks? I thought this stuff was different because it didn't.

DR. BURANS: No. In plastic it did stick to walls.

QUESTION: Ah.

DR. BURANS: And in fact, as you would open a tube, people have described it as having a mind of its own. It could fly, but it was flying based on charge forces, or repelling of charges. So to this day in our laboratories, we avoid at all costs working with materials in dried form. There's no reason to.

QUESTION: Okay. Thank you. That's very helpful.

Dr. Majidi, is it correct that you all tried to reverse-engineer this? And were you successful in coming up with something that behaved the same way?

Sorry. I'll repeat the question.

DR. MAJIDI: Thank you.

QUESTION: You were just talking about the fact that this stuff was not -- it wasn't as we heard, that it would not react to a static charge. It would. But we had thought that you tried to reverse-engineer this, that you tried to come up with your own stuff like this. And when you did, did it act the same way?

DR. MAJIDI: You know, as far as our preparation goes, we were able to repeat almost everything except the silicant signal.

QUESTION: Except the what?

DR. MAJIDI: The SI signal that we see within the spore. And, again, that's not unusual, because that's the material that's mineralized and it's endogenous to the spore and different recipes will give different results. And really, that wasn't something we were focused on trying to exactly replicate that. Can we make the same spore purity? Yes. Can we make the spore dry? Yes.

QUESTION: And without the silica signature, did it behave the same way?

DR. MAJIDI: Yeah.

QUESTION: It did?

DR. MAJIDI: Yeah, absolutely.

QUESTION: Getting back to when you're going to make this, you talked about in a peer review you're going to put this up to the actual full sequence is up to peer review. What's the timeline for that? Because -- you know, there are so many suspicions about the way it's been handled. Is that going to be within a month or a year?

DR. MAJIDI: I don't think, number one, we were ever going to put the suspicions to bed. There is always going to be a spore on the grassy knoll --

[Laughter.]

DR. MAJIDI: -- and we will follow the procedures for peer review and just to kind of manage your expectations, as I have published a number of articles in a peer review journal. You submit. You wait for reviews. You make corrections. You resubmit; and, at that point, it may get accepted for publication. It may get rejected.

And then from there on there is a lead time to a press, so that process can be as short as -- you know, half a dozen months to as long as a year and a half or two. The Human Genome Project, the last gene that was sequenced was in 2003. The paper that came out of it was in 2006.

QUESTION: So where are you in the process? Have you submitted? You haven't submitted yet?

DR. MAJIDI: We have many papers that are currently in publications. They are already published.

QUESTION: But the full sequence here?

DR. MAJIDI: We have prepared some that are ready to be submitted and we will prepare the rest depending on -- you know, as we get more material ready.

QUESTION: The full sequence, is it ready to be submitted?

DR. MAJIDI: Eventually, yes.

QUESTION: These people are free of secrecy agreements to talk about their scientific results?

DR. MAJIDI: Yeah, that's one of the things I mention actually in the beginning, that number one, we are waiving the non-disclosure agreements, so people can talk about their scientific results.

QUESTION: So if I want to talk to Dr. Keim, he doesn't have to worry about the FBI coming after him if he wants to discuss it.?

DR. MAJIDI: Not on this topic.

[Laughter.]

QUESTION: Can you tell me in your preparations how long it took you to make a spore like this as of the SI enhancer or whatever -- the drying, et cetera? How long did that take?

DR. BURANS: Basically, it would take somewhere between three and seven days.

QUESTION: That's all? How many people did it take to do that to that; to --

DR. BURANS: One person can perform the operation.

QUESTION: Just two more quick questions on the 1029. So I've seen different estimates. How many people at Detrick or anyone else actually have access to RMR-1029?

DR. MAJIDI: The total body -- the total universe of people at some point were associated with RMR-029 -- I'll qualify that. Roughly, about 100-plus.

QUESTION: Hundred-plus. Were those all at Detrick, or other labs --

DR. MAJIDI: No, they were at Detrick and other labs.

QUESTION: Okay, and then just to follow up, the 1029 strain that Ivins was working with, this was particular to his vaccine research, I assume. Was there something distinctive about 1029 that made it useful for his legitimate research?

DR. MAJIDI: Yeah, because the 1029 was basically the gold standard that was used at RID for -- you know, the vaccine as well as the inhalation challenge studies that were done.

QUESTION: What made it the gold standard?

DR. MAJIDI: There were lots of spores in this container. It was a high concentration.

DR. HASSELL: It was just a high-quality preparation. It wasn't necessarily that it was, you know --

DR. MAJIDI: There were scientific publications on it. It had a very well-defined pedigree.

QUESTION: “High-quality” means “high-purity;” just anthrax and not a lot of other stuff?

DR. MAJIDI: Yeah.

QUESTION: Now, the four mutations --

QUESTION: Okay. How many people at USAMRIID had access to the four mutations?

DR. MAJIDI: Well, I'm just going to stay back with roughly about a body of -- a universe of a hundred people had access/association with -- this is not at -- just at RID. The total body of people that were in the Ames RMR-029 universe were about a hundred people.

QUESTION: Can anybody speak to the flask itself? How many people at USAMRIID had access over whatever period of years to that flask?

DR. MAJIDI: Yeah, that's -- yeah. Yeah, I think -- you know, I think what I can tell you is that everyone who was in the universe of RMR-1029 was investigated.

QUESTION: Okay. In terms of the four specific mutations, is it fair to say they were natural mutations, or were --

They weren't engineered mutations?

DR. MAJIDI: There is no sign for engineer.

QUESTION: Any idea -- I mean, the mutations don't do anything specific that you could tell us?

DR. MAJIDI: No. That's not a particularly –

It's a natural selection.

QUESTION: -- behind you was doing so much of the talking, and this was billed as an on-the-record meeting, can we please have his name?

DR. MAJIDI: Well, you can -- you know, you can use either "the FBI scientist," or if you're really dying for an attribution, you can just call all Dr. Hassell's attributions.

QUESTION: Yeah. We can't do that. You can't do that, that's not accurate --

[Simultaneous discussion.]

BACKGROUND OFFICIAL: That violates their protocol.

DR. MAJIDI: Pardon?

BACKGROUND OFFICIAL: That violates their protocol.

[Laughter.]

DR. MAJIDI: I understand. Well, maybe we should destroy --

[Simultaneous discussion.]

QUESTION: Prosecutors and scientists would not be identified, and that's how it was billed when we started this.

QUESTION: Can you talk about the carbon dating?

DR. MAJIDI: Sure.

QUESTION: And how confident you are that that pinpoints the period in which this --

DR. MAJIDI: Well, you know, I'll do a ten-minute chemistry lecture, if you guys can bear with me.

BACKGROUND OFFICIAL: Oh, we don't have ten minutes.

QUESTION: Uh-oh.

DR. MAJIDI: All right. I'll do a two-minute chemistry lecture.

[Laughter.]

DR. MAJIDI: I don't mind it.

QUESTION: We don't mind it. We don't get this chance very often.

DR. MAJIDI: Okay. Carbon dating is used in different contexts. The particular kind of carbon dating we used was based on the principle that during the early days of atomic testing, there was a lot of atmospheric nuclear testing done. As a consequence of this atmospheric nuclear testing, the concentration of carbon-14, a

specific isotope of carbon, was skewed in the atmosphere to a particular spike, that a concentration of that spike is incredibly well known, and that carbon-14 decays as a function of years. As the years go by, the concentration of that carbon-14 that was the spike generated to the atomic testing, goes away.

The error band associated with the measurement is a couple of years -- plus or minus two years. When we did our testing, it showed that the Bacillus Anthracis sample that was used in the letters was of modern age. Modern age is with a grain of salt, plus or minus that two years. So it wasn't prepared 30 years ago; it wasn't prepared ten years ago. It was within that two-year time window.

QUESTION: And that was in 2004; right? What's that? When you did the carbon, the C-14 dating? What year was that?

DR. MAJIDI: But let me go back. Let me go back. The carbon dating is specific of the time that the organism ceases to replicate. So whenever that spore had stopped its sporulation form, that is the locked date for that organism, because we had obtained those samples in 2001, the carbon-14 concentration is 2001, plus or minus two years.

QUESTION: It could only be minus, obviously.

DR. MAJIDI: Well, no -- you know, I'm talking strictly from a scientific point of view. It could have been, you know, theoretically from 2003. It's from a strictly scientific point of view.

QUESTION: Yes.

BACKGROUND OFFICIAL: Dr. Majidi, can you take one more question?

DR. MAJIDI: Absolutely. Actually -- you know, let me just ask, how many more of you would like to ask questions? Can I see show of hands? Okay, we're going to take three more questions. Okay.

Can we start right up here?

QUESTION: Go ahead, please.

QUESTION: How did you rule out -- you said you had about a hundred people --

have the same positive samples -- how did you rule out --

DR. MAJIDI: Okay, so you're mixing apples and oranges there. A hundred people did not have positive samples. There were only eight samples that showed positive --

QUESTION: But a hundred people had access to those.

DR. MAJIDI: So a hundred people are within the universe of this RMR-1029 sample, and everyone was investigated. We looked a number of different factors that go into the investigation, and we were able to include and exclude specific individuals in that list.

QUESTION: So the forensic evidence narrowed you down to about a hundred people and then other types of evidence --

DR. MAJIDI: Forensic data -- to RMR-1029, looking at people who have had access to RMR-1029 reduced that universe to a hundred-plus people, and then as we investigated every individual, we narrowed down our focus.

QUESTION: The second sample that Dr. Ivins submitted; am I correct, it wasn't RMR-1029?

DR. MAJIDI: It did not have the four genetic markings.

QUESTION: Did you have a designation for that sample, and were you able to trace it to a different flask in a different part of the laboratory?

DR. MAJIDI: Basically, yeah. You know, the best I can tell you is that it didn't match RMR-1029.

QUESTION: But you don't know where it came from, is what I'm asking.

DR. MAJIDI: You know, I don't – unfortunately. It came from USAMRIID. That's all I can tell you.

QUESTION: Can I get some more specific numbers, actually?

DR. MAJIDI: Sure.

QUESTION: You talked about at least, more than 1,000 samples submitted that

you had looked at.

DR. MAJIDI: Right.

QUESTION: And then sometimes you said "thousands," and you know, there's a difference --

DR. MAJIDI: A thousand seventy.

QUESTION: A thousand seventy. And then the other is just a rough estimate on how many different scientists outside the FBI confirmed --

DR. MAJIDI: Sixty --

QUESTION: Confirmed that, you know, RMR-1029 matched here. In other words -- you know, your peer review, how many sets of eyes here?

DR. MAJIDI: Sure. I've got to really get that number for you, because --

QUESTION: Would you say dozens, scores?

DR. MAJIDI: You know, the panels that I recall, there was at least a dozen people in the room. At least.

QUESTION: So at least a dozen different scientists confirmed this? The connections.

DR. MAJIDI: Well, let me just say, when we release the names of scientists, you can clearly go and talk with them -- but there's a body of scientists, more than 60, that were involved with this case at some point, and we have had very extensive both scientific working group as well as panels that helped us throughout this process.

QUESTION: So it would be fair to say at least a dozen different scientists confirmed the connections that you --

DR. MAJIDI: Well, no. Let me just put it this way. The scientists worked on the scientific aspects. In many cases, they were blind in investigative clues that was going in there. So did scientists know that this sample came from RID? No, probably not.

So the answer is: Did scientists match these genetic markers to USAMRIID? No. They matched it to a sample, and then as you un-blind the submissions, you realize that it is --

QUESTION: But that's what I'm saying.

DR. MAJIDI: Yes --

QUESTION: You say those matches. Once you un-blind, that's fine.

DR. MAJIDI: Right.

QUESTION: But the version of peer review as in a scientific journal saying, "Yes, we could re-create what you did." At least a dozen different scientists were able to recreate what you did?

DR. MAJIDI: Yes.

QUESTION: Can you just tell us, of the eight samples that the letters matched to, how many places were they at? You were sort of vague earlier.

DR. MAJIDI: Sure. Let's just say they're definitely not at eight places.

QUESTION: But can you just give us the number? Why can't you give us the number?

DR. MAJIDI: Because if I provide you with the exact number -- well, there's a number of reasons, I'll just give you a generic one. We don't want you to bug those laboratories.

QUESTION: Well, don't give us the names, just tell us how many.

[Laughter.]

QUESTION: You've already told us a hundred people; right? So --

DR. MAJIDI: Yeah.

QUESTION: -- how many labs?

DR. MAJIDI: Hmm --

QUESTION: Is it one?

DR. MAJIDI: It's more than one.

[Laughter.]

DR. MAJIDI: Hmm --

QUESTION: Can we keep guessing?

[Laughter.]

QUESTION: Two?

QUESTION: Is it ten?

DR. MAJIDI: Okay, it's total two laboratories.

QUESTION: Total two. Including USAMRIID? Or --

BACKGROUND OFFICIAL: Two institutions.

DR. MAJIDI: Two institutions.

BACKGROUND OFFICIAL: Because when you say "laboratories," you got to figure, remember --

QUESTION: Yeah.

DR. MAJIDI: Two institutions --

QUESTION: So that means USAMRIID and two other institutions?

DR. MAJIDI: No, that means USAMRIID and one other institution.

QUESTION: USAMRIID and one other institution?

DR. MAJIDI: Yes.

QUESTION: Okay. Thank you very much.

BACKGROUND OFFICIAL: I'd like to clarify for the record, too. Your question was: How many people have -- you said "reproduced this in peer review."

DR. MAJIDI: Yes.

BACKGROUND OFFICIAL: This science has not been made available to anybody to reproduce. Remember, we're still talking about analysis of evidentiary samples, and nobody will be able to reproduce these assays until evidence is releasable, and I can't tell you when that will be, as long as the investigation is ongoing. So the peer review was that they were presented the science and the validation data behind it --

QUESTION: Okay.

BACKGROUND OFFICIAL: -- and they agreed that it was conducted properly and valid.

QUESTION: But no one else outside of the FBI and your group has actually replicated the work because of --

DR. MAJIDI: Well, by "outside of the FBI," are you talking about we have to include FBI and all the laboratories in academia and industry that were associated with the FBI in this process. So outside of that whole universe of people that worked on this project, no, no one else outside that has verified this.

QUESTION: There's one other thing I think we've been asking around, and I feel like I haven't quite gotten an answer to --

DR. MAJIDI: Sure --

QUESTION: -- which is: Did you try and duplicate the process? And how close did you get to making something like, you know -- the finer preparation that appeared?

DR. MAJIDI: We were able to get those spores minus the silicon signal. I think I was pretty clear on that.

QUESTION: Okay. I'm sorry. It may have been when I was outside. And what did you have to use? What were the specific machines? Did it have to be milled?

DR. MAJIDI: No.

QUESTION: Did not have to be milled?

DR. MAJIDI: No.

QUESTION: Just dried and then it just -- you crumble it somehow? How do you --

DR. HASSELL: You got to understand, there are some national security implications if we give you all the details of the many possible ways to do this. So if we're hedging a little bit, that's --

QUESTION: Were the things available to Dr. Ivins? All the devices, were they in his lab, that would have been required to do this?

DR. MAJIDI: It would have been easy to make these samples at RID.

QUESTION: You said a couple times that this was a novel application. Were you concerned, as you were going through your work here that that had this case gone to trial, that the science itself -- the method -- might have not been admissible? After all, 20 years ago, DNA was still controversial.

DR. MAJIDI: Absolutely. And what I have to just point out is that -- you know, we are under a lot of criticism that why didn't we come up with the data sooner; why didn't we find the perpetrator sooner; why didn't we have this case buttoned up quicker? And the answer is: As we were going through the genetic analysis, as we developing this analytical technology, we had to validate at every step. And that was a painstaking process to go through this entire validation and peer review to make sure that, in fact, the information we were getting were of evidentiary quality, so we could then push them forward.

And actually, the science by the time we really look at when was the science finally put together that could unequivocally say what we're saying, was early 2007 time frame. And a lot of it has to do with the validation.

QUESTION: Just to clarify something you just said. You said you were able to get -- replicate the spores minus the silicon signal.

DR. MAJIDI: Right.

QUESTION: Does that also mean you're able to replicate the powder -- the aerosol?

DR. MAJIDI: Well, we never aerosolized it; you know?

QUESTION: I just -- sorry?

DR. MAJIDI: We never --

BACKGROUND OFFICIAL: There is a misconception going around this room that very simple spore preparation, simply spores washed in water, when dried, are not dangerous and friable. That is a misconception. We have seen many biological preparations that when just washed with water and dried are extremely friable.

QUESTION: All right. But were you --

The reason I'm asking is because of 2004, a Michael Mason, who was the head of, I believe, the Washington Office of the FBI, went on the record and said that the FBI attempt to reverse-engineer the powders at Dugway failed --

DR. MAJIDI: Yeah. He was exclusively talking about the silicon signal.

QUESTION: So -- he was exclusively talking a about the silicon signal, not the powders?

DR. MAJIDI: That's right.

QUESTION: Not the powders?

DR. MAJIDI: No.

QUESTION: Okay. So during that reverse-engineering process -- at Dugway is where you did it?

DR. MAJIDI: It doesn't matter really where we did it. Let's just say we were able to reproduce parts.

QUESTION: Did you say that --

DR. MAJIDI: Before we conclude, there is really two clarifications I'd like to put on the table, because I don't want have you folks leave with a misconception. Number one, that I've ducked any of your questions. Number two is the statements that both Dr. Hassell is going to make -- and we have one additional statement on top of that; correct?

DR. HASSELL: Hmm, no.

DR. MAJIDI: Okay.

DR. HASSELL: I just want to make a statement, because I think there's just been misunderstanding. Hopefully this will clarify. Dr. Ivins was an advisor on the repository process, that is the process for gathering all the samples. He submitted a sample. This first sample was not collected under the protocol, the QA -- QC protocols which we established. He was told that it violated that protocol. He was resubmitted and attested that this -- he resubmitted and attested that this second submission would count as his official repository submission.

Now, as has been pointed out, the genetics really weren't on-line at that time, so there was no way to determine at that time that this was a deception or not. So we've use the word "questionable," rather than "this was a deception." That's about as far as we can go.

Finally, he was the only one to violate the protocol.

QUESTION: If it's not clear if it was a deception, why did the affidavit label this as a failure to cooperate?

DR. HASSELL: Affidavit is a snapshot in time of what the investigative picture brings to bear. And this should really be looked at only as that. As we develop the case throughout, we may find information post-affidavit that may either support or nullify what's in an affidavit.

QUESTION: So the --

QUESTION: If the affidavit was filed in October of 2007, that was repeated in that --

DR. MAJIDI: Right.

QUESTION: And by that point, how do you determine that he -- he submitted a sample that was later --

DR. MAJIDI: So -- so – so, obviously, that's one of the assertions that we were making, that the sample that we received, not being of RMR-1029 origin, is highly questionable. Why wasn't that sample from RMR-1029?

QUESTION: Well, why would he have given -- if he was trying to deceive you, why would he have given you something other than RMR-1029 the second time, but given you the real thing the first time?

DR. MAJIDI: The full gene sequencing that we used in RMR-1029 was not available back when the first submission was made.

QUESTION: You're saying --

[Simultaneous discussion.]

QUESTION: -- when the second submission was made either --

[Simultaneous discussion.]

DR. HASSELL: The real answer is we don't know. There's just no way to know. We're as puzzled by it as you.

DR. MAJIDI: If you could clarify that you did -- in the affidavit it does say that the eight samples were directly related to this single-strain batch. But then did you just say it was actually two institutions that they matched; AMRID and one other?

DR. MAJIDI: Two institutions had the eight samples.

QUESTION: But did two have RMR-1029?

DR. MAJIDI: RMR-1029 in its flask form is only at RID. The other eight samples were daughters of RMR-1029's.

QUESTION: RMR-1029 is a mixture of isolates? Is that correct?

DR. MAJIDI: That's right. It's a mixture of a number of different batches.

BACKGROUND OFFICIAL: If I can clarify that for the record. RMR-1029 is a

conglomeration of 13 production runs of spores by Dugway, for USAMRIID, and an additional 22 production runs of spore preparations at USAMRIID that were all pooled into this mixture. It is a total of over 164 liters of spore production, concentrated down to about a liter.

So this is quite an unusual prep. This is not a single culture. So when we looked at the number of mutations that were found, the phenotypic variance in the anthrax letters, we thought it odd, because if you take anthrax -- a culture of anthrax -- and you culture it over night and plate it out and look at it, you will be hard-pressed to find any kind of phenotypic variation in anthrax.

And you can do multiple passages and still not find -- be hard-pressed to find a phenotypic variation in anthrax. That's the nature of anthrax. So it was noted to be unusual that a number of mutations -- well over a dozen mutations, were easily found by their appearance in the anthrax powders. This seemed unusual right from the beginning.

When we started to conduct the genetic tests of the repository and zero in on the samples that were positive for these genetic markers that we found in the anthrax letters, it started to zero in on 1029 -- many mutations in it, when we learned about 1029, and the fact that it is over 30 productions of spores pulled together, then it starts to make sense as to why so many mutations were found in 1029.

BACKGROUND OFFICIAL: Okay. Before we wind this down, I just want to give a little more chance to the members of the distinguished panel -- because we don't know when they are all going to be together again -- to add anything to this discussion before --

DR. KEIM: I guess I would just say that a lot of the questions missed one of the most powerful points of this, and that is in general, when we analyze pathogens, we take the isolate and we identify it very precisely, using these methods that we've talked about.

In this case, the investigation went inside of a culture and identified minor variants. And those minor variants then became the signature. This is a very unique investigative approach, using methods that we've had before that are now becoming very inexpensive and possible to --

That perhaps, is one of the most interesting and innovative things that ever

occurred in this investigation.

BACKGROUND OFFICIAL: Comments?

DR. BURANS: Yeah, I think I'd just like to add that the Anthrax investigation helped to really found the science of microbial forensics, or bio-forensics, and led to development now of the National Bio-Forensic Analysis Center, which is -- was mandated by Homeland Security Presidential Directive Number 10 to support the FBI in biocrime and bioterror investigations. And we now have dedicated laboratories, dedicated staff, dedicated protocols for conducting these types of analysis.

DR. COLWELL: I would also like to reiterate the inter-agency cooperation in the many, many meetings that were held in the advisory capacity to the FBI, that indeed, there were many, many distinguished scientists who gave a large number of hours, voluntarily, to serve as advisors, and to do that on a regular basis over the last seven years.

DR. FRASER-LIGGETT: And I would just like to add, as has been brought up already, that clearly, this was a situation where we were, in many instances, learning as we went along. And I think it's important to leave all of you with the idea that the lessons that we learned from this several-year investigation are ones that we can take forward as we think about national security from the point of view not only of another bioterror event, but also in a much broader context in terms of national security related to food- and water-borne illnesses, and even outbreaks of illness in the hospital setting.

BACKGROUND OFFICIAL: Okay. Thank you for that.

QUESTION: What does the flask look like? Is it a little, glass thing with --

DR. MAJIDI: It's called an Erlenmeyer flask. Check it out on the web. It's a triangular flask.

QUESTION: With a glass stopper at the top? Is it a --

DR. MAJIDI: Well, this particular one did not have a glass stopper. It had a --

QUESTION: Piece of Saran Wrap over it?

[Laughter.]

DR. MAJIDI: I think it was a cheesecloth, or cotton.

QUESTION: How do you spell that, “Erlenmeyer”?

DR. MAJIDI: Erlenmeyer?

QUESTION: How do you spell it?

DR. MAJIDI: Erlenmeyer.

QUESTION: How did they look different when they were cultured?

DR. MAJIDI: E-r --

DR. COLWELL: E-h-r, it’s named after a German -- E-h-r-l-e-n-m-e-y-e-r.

QUESTION: Thank you.

QUESTION: About how big is it? Is it --

DR. MAJIDI: Well, the flask was a thousand-milliliter flask, but the total sample was not a thousand milliliters. It was only a few hundred milliliters.

QUESTION: Could you just describe how the mutant looked different?

DR. MAJIDI: Two one-liter flasks, sorry.

QUESTION: -- one-liter flask was just --

DR. MAJIDI: Two one-liter flasks, total volume of one liter.

QUESTION: This was Ivins’s stuff?

DR. MAJIDI: Yes.

QUESTION: So they were each about half-full.

QUESTION: The markers you keep referring to, are they nucleotides?

QUESTION: Can you just tell me what the mutants looked like? You said they looked different when they grew up; you could tell that there was something funny going on.

DR. MAJIDI: Yeah, just different colors --

QUESTION: Different colors.

DR. MAJIDI: -- different textures on the surface.

QUESTION: Shape?

DR. MAJIDI: Yeah, the shape. You know, some of them are going to be round, others are kind of fuzzy-looking.

DR. COLWELL: Right. But this is very classic microbiology. When you play it out with culture, some of the colonies will be smooth, and very perfectly round. And others will be rugose -- that's the term we use, meaning "rough and wrinkled." And some may have a pigment, some may not. So you look for these variants, and you pick them.

QUESTION: Were the spores round and like little pellets? Or were they long, like little rods?

DR. HASSELL: They were just typical Anthracis -- again, if you --

QUESTION: -- anthrax?

DR. HASSELL: Yes.

QUESTION: Oh, okay.

DR. HASSELL: Let me, let me, let me -- let me correct the flask question, just so there is no confusion there. Originally, it was divided into two one-liter Erlenmeyer flasks, more or less equally. When we seized it, by that time it had been reduced into one flask -- one-liter flask of several hundred milliliters. So there's not two flasks in evidence, there's just one.

QUESTION: A center which has grown 160 production strains, isn't it surprising they all have the same four mutations?

DR. KEIM: No, no, no, no, they all don't have the same four mutations. The mixture contains four mutations.

QUESTION: So in the attack strain --

DR. MAJIDI: Here is -- here is -- here is my -- here is my explanation to my daughter. So help me here. You've got a bag of mixed M&M's. You have a bag of blue M&M's. You take the blue M&M, which is wild-type. You get a little bit of mixed M&M's. You got blue. You got a couple of reds in there, a couple of yellows in there. The predominant blue is the wild, and then different colors are the mutations in that giant batch.

QUESTION: So does each mutation appear with a characteristic frequency in this mixture, because it seems -- if it were this mixture scenario, everything would --

DR. MAJIDI: Not only that it gives the complexity of this mutation set, it also gives you the exact fingerprint.

QUESTION: So --

DR. MAJIDI: That's why it drives us back to 1029.

QUESTION: You mean what you are looking for is each of the four mutations in a specific percentage

DR. MAJIDI: No. We are looking for the presence of each of the mutations.

QUESTION: Does the presence of them characterize --

DR. MAJIDI: Yes, absolutely.

QUESTION: Well, that's --

DR. MAJIDI: Thank you very much.