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DEPARTMENT OF HEALTH AND HUMAN SERVICES FOOD AND DRUG ADMINISTRATION CENTER FOR BIOLOGICS EVALUATION AND RESEARCH

BLOOD PRODUCTS ADVISORY COMMITTEE 64TH MEETING

VOLUME II

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> Bethesda Ramada Inn 8400 Wisconsin Avenue Bethesda, Maryland

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CONTENTS

	PAGE
Opening Remarks	3
IV. Medical Device Panel Reclassification of HIV Drug Sensitivity Assays	
Introduction and Background: Andrew Dayton, M.D., Ph.D.	6
Overview of Device Reclassification: Leonard Wilson	9
Presentation: Douglas Mayers, M.D.	58
CDER Perspective: Jeff Murray, M.D., MPH	101
Open Public Hearing Curtis Scribner, Visible Genetics Michael Ussery, Innogenetics Tony Lam, Applied Biosystems Brendan Lardner, VIRCO	141 146 151 155
Charge to the Committee: Linda A. Smallwood, Ph.D.	164
Committee Discussion and Recommendations	168

PROCEEDINGS

Introductory Remarks

DR. SMALLWOOD: Good morning and welcome to the second day of the 64th meeting of the Blood Products

Advisory Committee. I am Linda Smallwood, the Executive Secretary. Yesterday, I read the conflict of interest statement. It also applies to today's meeting.

This morning, the Blood Products Advisory

Committee will be sitting as a medical-device panel. You will hear presentations that will describe the role of a medical-device panel. For this purpose, we have asked consultants to join us today in this deliberation who will be sitting as temporary voting members.

I will introduce those consultants to you. They are Dr. Carmelita Tuazon. Would you please raise your hand, Dr. Tuazon. Dr. Paul Edelstein. And Dr. Roy Gulick. We understand that, because of the weather, that some individuals have had difficulty in getting here. We are assuming that they will be coming since we have not heard that they are not.

We also were to have join us, as a guest of the committee, Dr. D'Aquila who advised me that he was unable to attend today.

The Chairman of our committee is Dr. Blaine Hollinger. Dr. Hollinger, would you raise your hand,

please. For those of you who were not here yesterday, I will just quickly run through the committee and give myself a memory check here. 3 Dr. Gail Macik, Dr. Richard Kagan, Dr. Mary 4 Chamberland, Dr. John Boyle, Dr. Norig Ellison, Dr. Michael 5 Fitzpatrick, Ms. Katherine Knowles, Dr. Donald Buchholz, Dr. 6 7 Joel Verter, Dr. Mark Mitchell, Dr. Jeanne Linden, Dr. Paul McCurdy. We also have Mr. Corey Dubin. I don't see him 8 here this morning but I assume he will appear. 9 Are there any declarations that would need to be 10 made before we proceed with this meeting concerning any 11 12 conflict of interest or any perception thereof? Hearing none, then we will follow the agenda as 13 closely as we can. We have a lot today. We will try to 14 meet the time frame that has been established if everyone 15 16 will cooperate accordingly. At this time, I will turn our meeting over to our 17 Chairperson, Dr. Blaine Hollinger. 18 DR. HOLLINGER: Thank you, Linda. We will stick 19 within our time frame, hopefully, today. This is, I think, 20 an important meeting today as we sit as a medical-device 21 panel for reclassification of HIV drug sensitivity assays. 22 This is, of course, an important issue, also. 23 I think it is going to be an interesting morning. 24

I hope you have all looked at these forms. Mary Chamberland

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said that she has been in government a long time and she
said it took her six hours to fill it out. OMB says one to
two hours, butI told someone that that means that we all
get a royalty of about 5 percent on anything that is
produced.

So, we are going to start this morning with an introduction and background. Andy Dayton is going to start us off today and then we will go to an overview of the device reclassification. Then we will have a presentation of the problems and issues associated with this.

Medical Device Panel Reclassification of HIV Drug Sensitivity Assays

DR. DAYTON: Good morning.

[Slide.]

Today, you are going to be asked for your recommendations as to whether or not HIV drug resistance genotype assays should be reclassified as class II medical devices rather than class III medical devices.

This is a timely issue because downclassification would foster rapid and simplified regulation of numerous, currently diverse, HIV genotype assays and this would facilitate antiviral drug studies and, ultimately, accelerate physician access to information useful in the management of individual HIV-infected patients.

I am going to give a very short presentation of

the regulatory considerations. My presentation, in general, will give you a general overview of basic regulatory and technical issues involved today. Following my short presentation, Len Wilson will present a more detailed and comprehensive review of the regulatory issues.

[Slide.]

After that, I will give a brief overview of the scientific and clinical issues and then Jeff Murray and Doug Mayers will present more-detailed summaries of the relevant clinical and scientific literature. After the presentations on regulatory and technical issues, there will be an open public session and then a session for committee discussion following which you will be asked to make a recommendation on the classification.

I want to emphasize at this time, as you have already been told, you are sitting as a classification panel. We are not requesting you to vote on approving or clearing or licensing any product. We are asking you to decide at what level we should regulate HIV drug resistance genotype assays. What I mean by this will be explained during the course of this session and I believe you have also had an introduction yesterday as to the various classifications available.

[Slide.]

Currently, there are no FDA-approved or cleared

assays for the assays for the determination of HIV drug resistance. Given this, HIV drug genotype drug resistance assays, by default, are class III medical devices requiring premarket approval.

An option exists, however, to classify such devices into class II, or 510(k), when general controls and special controls exist to insure the safety and effectiveness of the device. It is FDA's view that adequate special controls can be provided by adherence to a guidance document containing recommendations for study designs, reagent characterization and performance characteristics—for instance, reportable range, sensitivity, precision, specificity, stability, et cetera—and by completion of postmarketing surveillance studies designed to evaluate the correlation between predicted and observed viral phenotypes in a clinical setting.

[Slide.]

These are the questions that we are going to asking you at the end of the presentation and, of course, you are welcome to alter them as you see fit. Does the committee support the reclassification of HIV drug resistance assays from class III medical devices to class II medical devices? If the answer to No. 1 is yes, what additional special controls or requirements, if any, does the committee recommend?

If the answer to No. 1 is no, what additional specific criteria does the committee recommend to allow future reclassification as class II devices?

[Slide.]

The science involved can be quite complex and, certainly, much desired information is incomplete. However, we urge you to remember that the key issue is not whether or not all the scientific information is complex or whether all the scientific questions have been answered. The key issue is whether or not you believe we can identify special controls which will guarantee reasonable efficacy without requiring the completion of full-blown, traditional clinical trials before marketing.

In the next presentation, Len Wilson will focus on this issue from a regulatory perspective.

Len?

Overview of Device Regulation

MR. WILSON: My presentation today is to take the committee through the regulatory pathway to classify medical devices. Why do we do this? Because the law says we must classify medical devices. So we go through this exercise periodically as new products come up or we want to change the regulatory classification of existing products.

In the past five or so years that I have been engaging in reclassifying devices, this committee has voted

on a number of them, sometimes classifying up from a I to a II, sometimes classifying down from a II to a I, et cetera. So there are no surprises in this process.

With that, what I would like to do is have the first slide and essentially start out.

[Slide.]

What we are trying to reclassify here an HIV mutation test. An essential proposal is that the HIV mutation test can have a reasonable assurance of safety and effectiveness when regulated as a class II medical device.

Class II medical devices, as I will discuss later, have some requirements associated with them. One of the requirements is having a special control.

The proposal here today is that the FDA would develop a guidance document for the content of the 510(k) filing, the class II medical-device filing, which we would review and we would clear if the manufacturer provided sufficient information to assure the safety and effectiveness of the device.

And then there is an additional special control that we are proposing, postmarketing surveillance. This would be used, as Dr. Dayton described, to do some follow up. I want to emphasize that the postmarketing surveillance component of a special control here is not intended to be the basis for the approval of the product, approval or

1 clearance of the product.

The postmarketing surveillance is intended to answer some unanswered questions or some prospective concerns.

[Slide.]

What I will be talking about are, basically, three topics. Is the product a medical device? If so, who regulates it within the Food and Drug Administration? And, into which regulatory class should it be assigned?

[Slide.]

Is the product a medical device? According to the law, if a product is labeled, promoted or used in a manner that meets the following definition in Section 201(h) of the FD&C Act, it will be regulated by FDA as a medical device subject to premarketing and postmarketing controls.

[Slide.]

A device, by definition, is an instrument, apparatus, implement, machine, contrivance, implant, in vitro reagent or other similar or related article including a component part or accessory which is--

[Slide.]

--recognized in the official National Formulary or U.S. Pharmacopeia or any supplement to them, intended for use in the diagnosis of disease or other conditions, or in the cure, mitigation, treatment or prevention of disease in

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man or animals or--

[Slide.]

--intended to affect the structure or any function of the body of man or other animals and which does not achieve any of its primary intended purposes through chemical action within or on the body of man or other animals and which is not dependent on being metabolized for the achievement of any of its primary intended purposes.

[Slide.]

So now we have established that this type of a product would be a medical device. The next question is how would it be regulated by the FDA, either by the Center for Biologics or the Center for Devices, the Center for Biologics Evaluation and Research, the Center for Devices and Radiologic Health.

The Center for Devices and Radiologic Health regulates most of the medical devices that are in commercial distribution in the United States. In 1991, there was an intercenter agreement which was issues between the two centers. In general, CBER has the lead for regulating medical devices used or indicated for the collection, processing, storage or administration of blood products, blood components or other analogous products.

So, for example, this empowers the Center for Biologics to regulate those test kits which are used to

screen blood donors.

[Slide.]

But it also states that CBER also regulates in vitro tests including diagnostic tests and any other medical devices intended for use in dealing with retroviral products. So this particular product that we are talking about today is a retroviral product, so the Center for Biologics has jurisdiction.

[Slide.]

I wanted to underscore, also, even though we have jurisdiction over this product, we use the same sets of regulatory requirements that are dictated by the Food, Drug and Cosmetic Act which the Center for Devices uses. So we are using the same sets of rules, here.

[Slide.]

Devices are classifying as required by law into one or more of three categories, or classes, depending on the regulatory controls needed to provide reasonable assurance of safety and effectiveness. This would be class I, class II or class III.

[Slide.]

A device is automatically, by law, in class III if it was not on the market before May 28, 1976. This was the date at which the Medical Device Amendments to the Food, Drug and Cosmetic Act were passed establishing medical-

device law and regulations. Or if no predicate device exists; in other words, FDA has not cleared a 510(k) for the same device. So a predicate would mean, in this particular situation, has the Food and Drug Administration cleared an HIV mutation test or viral-resistance test before. Is there something that we can compare against?

And the answer is no. So, by default, as we move down, it would be in class III in the absence of formal classification. However, there is an option where the FDA can classify products into some other medical-device classification.

[Slide.]

So the steps, in general, to classify a medical device are found in the regulations, 21 CFR 800 through 899. It can be initiated by FDA or a sponsor. In this particular instance, FDA is bringing it to the committee. A sponsor would mean someone who was petitioning the FDA who would be trying to get a test kit approved or cleared. They can petition the FDA and say, "Gee; I would like to have this regulated as such-and-such as class." And then we would go through this same type of a cycle except it is coming externally.

We would obtain a recommendation from an advisory committee, this committee. Based on that recommendation, we would publish, in the Federal Register, for comment, the

outcome of the committee's deliberations and vote and then get some comments, make potentially some changes, and then publish a final rule.

Once that final rule is published, into the CFR would appear, once the administrative processes are completed, a section that would be entitled, for example, HIV Mutation Test. It would have a number and then any sponsor who comes to the Food and Drug Administration to get a test approved or cleared, they could cite that as a predicate and they could file, in our proposal, a class II--it would be regulated as a class II and they can file a 510(k).

[Slide.]

In the regulations, the committee should consider, in determining safety and effectiveness—and this is something that you may want to tag on the slides that I gave you—you should consider the persons for whose use the device is intended, its conditions for us, probable benefit to health weighed against risk of us, and the reliability of the device.

[Slide.]

Which regulatory classification are we attempting to vote on here? Well, all medical devices, as stated earlier, are classified into three classes. Class I, general controls are sufficient to assure the safety and

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effectiveness of the device. Class II, general controls are insufficient to insure safety and effectiveness of the device so special controls are added on top of the general controls in order to insure safety and effectiveness of the device.

Class III devices are those where general controls and special controls are insufficient to insure the safety and effectiveness of the device and premarket approval is required. That would be a PMA, a class III. In general, a premarket approval application, which I will touch on later, essentially, there would be clinical trials associated with it because the answers for the safety and effectiveness of device could not be assured by general controls and special controls.

I will walk through what these controls are.

16 [Slide.]

What are general controls? General controls, which apply to all medical devices, are registration of the manufacturing facilities. We need to know, at FDA, where the product is being manufacturing. The manufacturer is required to have a medical device listing, what products are being manufactured there.

These two bits of information are used so that FDA knows where to inspect on its periodic inspections. These products are routinely inspected on a periodic basis for

their compliance with good manufacturing practices or what we now call QSRs.

There was a revision to the good manufacturing practices. Good manufacturing practices are those sets of rules by which manufacturers produce products in a clean environment, have quality control, et cetera, et cetera.

Again, these are listed in 21 CFR 800.

Recently, within the last two years, the good manufacturing practices section has been revised and upgraded. They are now termed QSR, quality system regulations. The important point here to consider is that they have been strengthened considerably. However, in class I products, design controls, which I will explain in a moment, are not required, in general.

Class I general controls also include labeling requirements to make sure that there are adequate instructions for use, et cetera. For a class I, a submission of a premarket notification also known as a 510(k) is required. It is also important to note that certain general controls can be exempted, also. That could be done by the Food and Drug Administration as well as by a committee vote.

For example, some products we may exempt the need to file a $510\,(k)$. This committee voted on such a situation several years ago where we dropped the requirement for a

510(k) for copper sulfate for use in determining hemoglobin in blood donors.

[Slide.]

Some more general controls; record keeping and requirement for repair, replacement and refund when defects are found.

[Slide.]

Some examples of class I devices; heat-sealing devices to crimp blood collection tubing; alanine aminotransferase tests. This is a clinical-chemistry test and you can see the it has an asterisk. This, in fact, has been exempted from filing a 510(k). So all the other general controls apply, but they are not required to file a 510(k) to get premarket clearance. An ammonia test system; iron-binding-capacity test systems.

The 21 CFR 862 is that section which is listed in the regulations and I will show you an example of what you would have in this particular situation for HIV mutation tests as we move towards it.

[Slide.]

Class II; general controls are insufficient so, therefore, you would need special controls. Now, special controls consist of, for example, a guidance document. And I have bolded that because that is what FDA is proposing. A guidance document would basically have the content of the

510(k) submission spelled out. There would be some clinical data if indicated. There would be contraindications, warnings, adverse effects, et cetera.

Now, I want to draw attention to the committee that, in August of 1989, FDA issued what we called then a points-to-consider document. But it is essentially a guideline for manufacturers as to what to submit for a product-license application for a blood screen. This is, conceptually, what we are looking to produce here for this particular product. Dr. Dayton will go into that in more detail.

Another special control can be a performance standard. Are there voluntary standards or international standards that can be applied to this type of product. What FDA would do, then, is we would recognize it by rulemaking, notice, comment and rule, and that would be the special control for that particular device if voted on by the committee.

[Slide.]

There could be special labeling, some restrictions, some additional information that would be imbedded into the labeling that wouldn't normally occur in a medical device because there is some greater concern that has to be mitigated.

Patient registries; sometimes, patient registries

are necessary to track particular devices, how they are used, because there could be a problem with them that we would have to get back and notify the patient. Again, I am bolding here postmarking surveillance to answer unanswered questions once the product does get into the marketplace.

It is important to note, going back to the GMP part, the QSR, design controls are required for class II medical devices. Now, what are design controls? The short answer is that design controls are part of the manufacturing process where each product has a set of controls placed on top of it where design input, design output, verification and validation of all the manufacturing processes are tightly controlled.

This is a new concept because FDA has determined, over the last decade, that failures of medical devices consists basically of two types. They weren't manufactured according to the instructions. The other type is they were manufactured according to the instructions but there was a design flaw and the product didn't work.

The objective here of design controls is to insure that the design of the product has been adequately challenged and it insures that the manufacturing process, as well, can be conducted with integrity.

[Slide.]

Examples of class II devices; an empty container

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for the collection and processing of blood, transfer bags, a 1 quality-control kit for blood-banking reagents. controls that are used relative to CLIA, positive and negative controls for HIV tests, hepatitis tests, are regulated under this regulation. And they are classified as class IIs.

CMV serological reagents; the CMV test kits which are used electively to screen donors are regulated as class IIs. Lectins and prolectins used in blood banking are regulated as class IIs. However, we have recently exempted them from filing 510(k)s because the safety and effectiveness could still be assured without doing that.

[Slide.]

Class III; general controls and special controls are insufficient to insure the safety of the device, so premarket approval, also known as a PMA, must be filed. There is an alternative to a PMA called a PDP, a productdevelopment protocol, but it gets you to the same place.

The main issue here is that clinical trials are required to insure the safety and effectiveness of the device.

[Slide.]

Some examples of class III devices are HIV homecollection test systems which are sold over the counter in pharmacies; HIV tests for prognosis; and HIV tests for

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monitoring. These would be the viral-load types of tests.
[Slide.]

I tried to put together a compare-and-contrast chart for class II versus class III. This is not all-inclusive, but I think this hits the major points. Class II, general controls; class III, general controls. Class II, special controls; class III, special controls, if necessary. Class II, clinical data not always required. We do have the authority to ask for clinical data in a class II medical device. It is generally not done, but we do have the authority. With a class III, clinical data is always required.

QSR design controls are required in both. We have a postmarketing order option. In other words, we can say to manufacturers, "You need to do some follow up to answer some unanswered questions." Both classes are required to report, under medical-device reporting, if there is a failure that could cause serious injury. They have to report that to the Food and Drug Administration.

A difference with the class II is that there is a 90-day review cycle. 510(k)s have a 90-day review cycle. PMAs or class IIIs have a 180-day review cycle. The reason for that is that the content of the class III PMA is generally more detailed so FDA is allowed more time to conduct the review.

As I stated earlier, class II products have periodic QSR inspections which are conducted by the field investigators. For a class III device, there is a difference. There is a preapproval inspection and then periodic QSR inspections are conducted. So, with the class III, there is basically a GMP inspection of the plant or QSR inspection of the plant prior to the approval.

[Slide.]

So, which regulatory classification are we looking at here? Well, in the regulations, Chapter 1, 12 CFR 866, immunology and microbiology devices, subpart D, serological reagents. The proposal would be that, in Section 866, and a number would be assigned, there would appear an HIV mutation test.

[Slide.]

This is what it would look like, actually, in the regs. Mutation-detection reagents; a, identification, HIV mutation-detection reagents are devices that consist of ligands use to identify mutations in the HIV genome in infected individuals. The identification of mutations aids in the clinical management of HIV-infected individuals.

We used the term "ligands" because we wanted to have flexibility whereby this could be done by nucleic-acid testing or, potentially, by other means, serological and the like. So we would have the regulatory designation that we

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would be able to use for some variance on the same theme.
[Slide.]

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The next part of the regulation would basically be which classification is it. It would stated that it is a class II and special controls are required.

[Slide.]

So the FDA proposal is that an HIV mutation test can have a reasonable assurance of safety and effectiveness when regulated as a class II medical device and the special controls proposed consist of a guidance for the content of a 510(k) and postmarketing surveillance.

With that, I would ask Dr. Dayton to resume to spell out the concepts associated with the guidance document and the postmarketing surveillance.

DR. DAYTON: Do you want to take some questions now because we are going to on to the sort of technical and scientific issues.

DR. BUCHHOLZ: I wonder if, for the committee, you could indicate the actual time for the review as opposed to the statutory or guidance times for a 510(k), for a PMA and for a supplement to a PMA, say, an average over the last couple of years, just to give us a feel for how long it takes if, for example, one wanted to make a change in a product that was a PMA product, how long it would take to make that change as opposed to a product that was a 510(k)

1 | product.

MR. WILSON: You have asked a number of questions there. I will do my best and, if I slip on one, please--I don't have the actual review times with me, but let me try to help answer that question. For a 510(k), when the manufacturer supplies that submission, we are obligated to review it within 90 days.

There is a device action plan that CBER is now fully engaged in and the effort is to make that date on all medical devices that are filed under 510(k). If the manufacturer does not provide sufficient information to allow us to make a determination of substantial equivalency to a predicate, we would write a "more information" letter.

Now, it is up to the manufacturer how long the manufacturer responds. There is a statutory requirement of 30 days an we have the option of actually withdrawing it if they don't respond. I can tell you that many manufacturers have taken a lot more time than 30 days to respond.

We try to be reasonable and flexible, particularly when products that we think are a benefit to public health, are valuable to the market. When the manufacturer does respond to the additional information with the 510(k), the time clock is reset. It is another 90-day review cycle. Now, we do our very best to review those products as efficiently as possible, but we do have the authority to do

that.

I think, to try to answer your first question, a fair number, maybe half or more of the 510(k)s that CBER reviews, take more than one review cycle to get clearance. So you are talking approximately six months beyond. The regulatory requirements for making changes in a 510(k) are somewhat different from those for a class III medical device. And we spell that out in guidance. CDRH has done a great job of articulating it.

It leaves the decision to the manufacturer. It is essentially if there is a new intended use or if there is technicologic change, they are required to file an additional 510(k). In other words, they would have to wait to make those changes. So that is the 510(k) side of it.

PMAs, we have a statutory requirement of doing the review within 180 days. Depending on the type of response that we get, we can reset the clock on a deficiency letter to an additional 180 days. I would say, in most instances, in CBER-regulated products, we do not have many products that we have approved under class III under one review cycle.

Making changes to a PMA product, more stringent rules are required. So, therefore, a supplement would need to be filed in many instances. The supplement would have a 180-day review clock on it.

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Did I capture all your concerns?

DR. BUCHHOLZ: Thank you.

DR. HOLLINGER: The real asset here, somewhat, is the assurance of safety and efficacy between these two classes, II and III. Can you give us some more information about what you really mean by safety and efficacy, how these really differ between II and III in terms of classifying something? Maybe some examples, even.

MR. WILSON: I think the best example would be where we have apheresis equipment. Apheresis equipment, in fact, has two regulatory levels associated with it, a II and a III. Class IIs are those which the technology is by centrifugation. Class IIIs, which are intending to downclassify to II but, to try to answer your question, is by filtration. So separation of the blood components are performed by a different technology.

The centrifugation has less of a concern relative to the product produced—the platelets, for example—than the filtration. The concern with the filtration was that there would be membranes that would potentially capable of activation platelets, so there were additional issues of safety and effectiveness that would be of scientific concern so that, at the time when those products were—back, approximately ten years ago, when they first came to the marketplace, they were class IIIs.

It was found that, with the data presented to a committee back in the 1980s, that those instruments by centrifugation were found to have sufficient safety and effectiveness regulated at the class II level.

Recently, some data has been presented to the committee whereby we have got enough information now. What is enough information? It has been out on the marketplace for a period of time. We have looked at the MDR reports, the medical-device reporting, and found that the problems are not serious and, therefore, we feel that the lower regulatory controls would provide us safety and effectiveness.

There are some advantages and disadvantages to which regulatory class a product is in. There are some requirements that manufacturers have to follow--annual reports, for example--with a PMA and the like.

Am I helping you here? That would be, for example, where we had safety. Effectiveness, I am stuck here. If I could try to roll the two of them together where the platelet is performing, when separated by filtration, as well as when separated by centrifugation.

As you can imagine, there was a lot of detailed analysis to determine platelet function and the like. And it was determined that yes, the platelets were not compromised and the equipment could be felt to be

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substantially equivalent.

DR. HOLLINGER: You have placed HIV tests for monitoring and for prognosis, the NAT test, as a class III device. I think that has something to do with what we are talking about here. I would like to know, if you can, in the short term, tell me a little bit about why you decided that that should be a class III device for both prognosis and monitoring.

Some of those systems are very much maybe what we are going to be discussing here today with this test.

MR. WILSON: I can give you the short answer. The short answer is that when we first were reviewing HIV monitoring, viral-load type tests, we did not have anywhere near the kind of information and knowledge base that we have today for genotype testing. Again, that would be the short answer.

I think that Dr. Dayton will be providing you those distinctions as he continues with his talk.

DR. MACIK: You talk about if you are going to make it a class II that you would look, perhaps, at putting on postmarketing surveillance. What does that mean an what weight does that carry if you take it out into the market and you are watching it and something comes up. I did not go clinical trials as a phase III. You put it out as a phase II.

You are really allowing your postmarketing surveillance to be your clinical trials. How can you bring it back? How do you get it if we let it out there ahead of time?

MR. WILSON: Very good question. First of all, the postmarketing-surveillance order can have a number of different requirements, not necessarily those constituting a clinical trial. Again, the idea here is that the postmarketing surveillance is not intended to be the basis for approval. That would be backwards; we clear the product and then we will find out if it works.

No; that is not what we are trying to do here. What we are saying is the product is clearable with what is provided to us. And then there are some logical additional unanswered questions that, from a public-health point of view, probably should be evaluated. So the postmarketing order would be structured on that.

Again, Dr. Dayton would be providing you with where we are headed with that.

Let's say something goes terribly wrong. We have several regulatory options here. One is an inspection of the facility to determine problems with--complaint handling, to see if there are a number of problems there. We also have some, by law, ways of dealing with products that are not performing; they are either adulterated or misbranded.

So there are compliance mechanisms to control that. I think that, if, over a period of time, it becomes evident that a product has problems that were not foreseen, it could be brought back to the committee and we could present a proposal to upclassify it to the III.

Also, as I said earlier, FDA could propose to the

Also, as I said earlier, FDA could propose to the committee. Sponsors could also do the same thing. So there are some regulatory remedies. You are not in II forever, if you vote for a II. But we are trying to look at our knowledge base of dealing with guidance documents, dealing with what we already know about these types of tests and the technology and we feel, at least at this point, that a class II would give us reasonable assurance—the law says "reasonable assurance of safety and effectiveness."

DR. FITZPATRICK: You mentioned that you don't have to do full-blown clinical trials. So that implies to me that FDA would, then, open the door for the manufacturer to submit data from clinical use that was not part of a clinical trial, which they don't do in some other instances. Is that what you are saying?

MR. WILSON: That could be a part of the postmarketing-surveillance order. Again, I think Dr. Dayton would be able to frame out where we are, what we are proposing with that.

MS. KNOWLES: I think that I recall that even FDA

recalled a home-collection test kit for HIV that was in III at one point in time in the last two years; isn't that correct--because it did not perform?

MR. WILSON: There was a home-collection test which was classified as III that there was a problem associated with some labeling and it got relabeled on the pharmacy shelves and FDA took action, basically, because there was a violation. That got corrected.

MR. DUBIN: Early on in the year, our organization had met with Commissioner Henney. One of the things we discussed was postmarketing surveillance in terms of AIDS drugs because we had concerns. We had all supported fast track but we thought fast track was getting a little out of hand.

What was conveyed back to us was a resource issue, that what we were talking about would involve a lot of FDA resource in terms of both people power and dollars, and there were some questions. So I think my question is, in terms of undertaking this and managing it in a postmarket climate, does FDA have the resources and the people power to be able to do that and stay on top of it close enough to insure that we don't have some of the problems we are seeing with AIDS drugs.

MR. WILSON: I can't always predict the future, but I think that the tools that we have are structured to

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enable us to assure these types of orders and maintain the integrity. For example, for postmarket studies, it would be a postmarketing order, the obligation of the manufacturer to do X, Y and Z.

A lot of times, we will have reporting requirements periodically over a period of time. I can tell you first-hand, if we don't get the report, we call them up and say, "Where is the report? You are obligated." We put it in writing. We send it out and, if we don't get it, then we have several other options. Directed inspection; the reviewer can propose, because the manufacturer has not responded to the Office of Compliance, we would like to have a directed inspection to the firm. This can be done on a priority basis depending on the particular product involved or health issue.

In many instances, and I have triggered them myself, within a week or two or three or sometimes overnight, we can have inspectors into the plant. They know what the problem or the concern is and the headquarters is often on the phone on a daily basis with the inspectors because they are not the headquarters reviews and they will need a little bit insight. We have got a very good working relationship in that regard.

Does the help to answer some of the concerns?

MR. DUBIN: Yes.

1	DR. TUAZON: I know that the genotyping and
2	phenotyping assays are being used clinically right now.
3	What regulatory measures do we have on those used at the
4	moment?
5	MR. WILSON: There are no cleared or approved
6	tests by FDA. The products I assume you are talking about
7	are those that would be generically identified as "home
8	brew?"
9	DR. TUAZON: They are really done by the labs do
10	our routine testing for HIV patients.
11	MR. WILSON: Right. But the actual reagents,
12	themselves? They build the test themselves?
13	DR. TUAZON: These labs that we sent through the
14	medical centers are sent through diagnostic labs like LabCor
15	or Quest Diagnostics.
16	MR. WILSON: There isand this can get a little
17	bit complicated so I am going to try to give a short answer
18	but there is a regulation called the ASR Rule, analyzed
19	specific reagents, which has requirements for some home-brew
20	types of products. I guess I can say that, with the outcome
21	of this vote here, that may have some effect on the
22	regulation of those types of tests.
23	But the objective of that would be to level the
24	playing field. I think it is important to bear in mind
25	thatI think all want good-quality tests of high integrity

that have the reliability, et cetera. Whether it is a home brew or whether it is regulated by FDA as a normally distributed commercial product, it should work well.

So we have got two arms for regulation, one for the home brew and the other for traditionally commercially distributed products.

DR. HOLLINGER: Thank you, Mr. Wilson.

Dr. Tabor?

DR. TABOR: Just in further answer to Mr. Dubin's question; provided there is no negative impact on the public safety, the use of the 510(k) mechanism is resource saving for FDA because a lot more FDA human resources have to go into the review of a class III device than a class II device.

DR. DAYTON: Let me elaborate on some of the questions that Len just answered and, in particular, let me start with Dr. Hollinger's question about special controls and how you would choose between class II and class III.

Let, of course, gave a very accurate answer but the way I wanted to elaborate on it was to portray to you how we feel this decision should be viewed for this particular product today.

Imagine--you don't have to imagine. Take a mutation which gives you well-documented resistance to a certain drug. Let's assume that there is a long history in

the literature studying that mutation. You see it appear in patients when they are on that drug. If you switch to another drug, it disappears, they do better, et cetera, et cetera, et cetera, et cetera.

This would be the kind of data that we would consider adequate to let this product be regulated under class II. In other words, there is a lot of data in the literature. It is well-done. It is well-known. It is well-characterized. And we don't see a particular need for clinical trials, premarket.

Take, by comparison, another mutation. Let's say there is one study which shows that it appears when patients are on a particular drug. We would want to see more data for that second type of mutation.

The way we would like to handle this is we would like to--the postmarketing surveillance, essentially, is claim specific. So the way that we would handle this is we would like to let a product under class II regulation go to market for the first type of mutation to back a claim for the first type of mutation.

So, in other words, the assay could claim to pick up that particular mutation which is well characterized and that would be of benefit to the patient. If they wanted to have an additional claim for the second type of mutation, the one which isn't so well characterized, they would have

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to submit additional data in the postmarket period to get that claim.

We feel that, by splitting it up like that, we can get these products out there fairly quickly and we can also control them very effectively. The whole issue of claims is very important because that is what the postmarketing surveillance will address. Postmarketing surveillance will, in part, be largely claim-specific. It will address additional claims.

In terms of FDA mission, even if there is one mutation out there and it is clinically relevant and an assay can pick it up and can redirect therapy, that is benefit. That is clinical benefit.

In the real world, we believe that there are mutations which are fairly well characterized. There are a lot of mutations which are less well characterized. In fact, Dr. Mayers and Jeff Murray will be presenting data to show that, actually, these assays are clinically beneficial. We believe that the reason for that is because the mutations—there are mutations that are correctly characterized.

I think that those were the key issues that I wanted to address before I sort of give the introductory talk to the next two speakers.

[Slide.]

The highly-active antiretroviral therapy has been a tremendously successful approach for treating HIV infections. Unfortunately, it is not perfect and it is still plagued by therapeutic failures. Mostly, therapeutic failure is heralded by falling levels of CD4-positive lymphocytes and rising levels of circulating HIV.

However, these two parameters are not always inversely correlated and they are, at best, indirectly measurement of therapeutic failure. Consequently, there is an increasing need for more accurate and more direct measures of therapeutic failure, particularly measures which identify the mechanism of therapeutic failure.

[Slide.]

HIV drug resistance assays promise to fill this need. One of the most common, but by no means only, causes of treatment failure is the existence or emergence of virus species resistant to the drugs included in the regimen.

Various categories of assays exist to measure HIV drug resistance.

As general examples, in one approach, virus is isolated from a patient, expanded, titered and tested in replication assays in the presence of antiretroviral drugs. In another approach, the reverse transcriptase and/or protease regions of the infecting virus are isolated and subcloned into well-characterized laboratory strains.

These derivative viruses are then expanded, titered and tested for drug sensitivity and resistance. Dr Murray will go into more detail on the types of assays currently available, but these assays are time-consuming, laborious and ill-suited for use in general clinical laboratories.

[Slide.]

HIV genotype assays have been developed as a relatively simple, cost-effective measure for determining the drug resistance sensitivity profile of HIV in infected patients. These assays can either be based on direct sequencing technologies or on hybridization technologies. The information they produce is the nucleic-acid sequence or genotype at critical codons of reverse transcriptase and protease which are known to be critical for determining drug resistance and sensitivity.

In other words, genotype assays determine the viral genotype and use this information to predict viral phenotype which, for our purposes today, is the clinical phenotype which, in this case, is the drug resistance sensitivity profile of the circulating virus or the expected response of circulating virus to clinical intervention.

[Slide.]

The predicted phenotypes are then used to guide treatment choices for patients identifying to which drugs

the predominant viral species is resistant. This information is used with information about the patient's previous viral regimens and it can be useful in choosing new regimens in patients experiencing therapeutic failure.

So it is an important point to realize that these are not stand-alone assays. These are used in the context of the entire clinical picture of the patient. In fact, as you will learn later, these assays often will not detect minor species and there can be minor species of resistant mutants left over from previous antiretroviral therapy.

[Slide.]

The motivation for FDA's desire to downclassify these genotypes is that we feel it would be an overall benefit to the public health. Downclassification would allow enhanced physician access to these assays by allowing sponsors to go to market with premarket clinical sensitivity and specificity data, allowing postmarket clinical-trial data to further correlate assay prediction with clinical responses.

This would significantly facilitate clinical trials for new drugs and therapeutic regimens. As I said, the relevant science can be complex and incomplete but it is FDA's opinion that sufficient information exists to insure a significant level of efficacy of these assays by formulating an appropriate set of special controls.

In other words, we feel that, although we are not perfect, there is enough science out there that we can sit down and say, this is what needs to be done. We can identify these studies and they will tell us whether or not these assays are going to be beneficial.

It is also FDA's opinion that postmarketing studies can be designed to further improve the efficacy of these assays as increasing scientific knowledge is obtained.

[Slide.]

We are drafting a guidance document outline requirements anticipated for regulation of HIV drug resistance assays as class II medical devices. Obviously, we won't go very far with that document. If you decide to regulate it a class III, we will just recast it as a class III document and change the ideas.

This document, as it stands now, addresses issues pertaining to assay precision, reproducibility and accuracy, quality control of reagents, laboratory testing and pre- and postmarket clinical data requirements. FDA's current thinking about the contents of this guidance document is contained in a September, 1999 concept memo which covers highlights of the guidance document and which has been included with your pre-meeting materials.

What we gave you in the pre-meeting materials doesn't cover all of the details in the guidance document

such as the manufacturing controls. We tried to limit it to the critical issues which are relevant to your decision here today.

Over the course of the next few minutes, I will review these highlights with you.

[Slide.]

First, we start with the nonclinical laboratory data and we focus on validation of phenotypes predicted by genotyping. I will start out by saying that in this part of the guidance document, we expect to attract a lot of comment, a lot of discussion. The guidance document will be put out in draft form for public comment after we have cleared it in-house and there will be a lot of scientific input to it at that point.

What we are thinking about now, as an example, is that, in general, sponsors will be expected to validate claims that certain genotypes predict certain phenotypes.

We expect that validation studies will include in vitro viral-replication assays and determination of the effect of a given genotype on the 50 percent or 90 percent inhibitory concentrations of the drugs in question.

We are also entertaining the concept that when non-clinical validation studies demonstrate an eight-fold or greater increase in the IC50 or IC90 associated with a given resistance mutation, validation may or may not also include

certain types of clinical validation studies of individual mutants.

We also expect that when nonclinical validation studies demonstrate a less than eight-fold increase in the IC50 or IC90 levels associated with the mutation that validation will require clinical validation studies.

[Slide.]

We have requirements for analytical sensitivity.

We assume that we will ask sponsors to perform sensitivity,

precision and reproducibility studies on spiked samples and

anticipate that sponsors will submit sensitivity data for

all single and multiple mutations for which a claim is

sought. Basically, what we are saying here is if it is

there in the tube, can you measure it? Can you sequence it?

The sensitivity studies should determine and validate both the minimum viral level and the minimum mutant proportions reliably detected by the assay. So we want to know can you pick this up if your viral load is down at 1,000 copies per ml, or does it have to be up at 10,000 copies per ml.

If the resistant mutant is present as 5 percent or 10 percent or 25 percent of the infecting population, can you detect it? We assume, but it may not necessarily be true that the assays will demonstrate in these studies sensitivity at viral levels which are clinically relevant.

Certainly, that is our preference.

FDA also anticipates requiring accurate titration of sensitivity through and below the minimum detectable levels and proportions. Basically, we want to know how quickly does assay performance deteriorate with decreasing levels or proportions of the analyte.

[Slide.]

clinical data. A key issue here is going to be validation of the phenotypes predicted by genotyping because that is the key question. Our current thinking is that validation studies should, optimally, include determinations of the existence or appearance of a given phenotype in patients subject to antiretroviral therapy as well as correlation of the disappearance of a given mutation with changes in antiretroviral therapy.

Throughout these studies, FDA will probably want to see data on overall viral burden, as well. We are considering the possibility that viral burden may be an adequate indicator of response to therapy for particular drugs. FDA may variably recommend or require clinical studies to validate the phenotypes of individual mutations according to the changes in IC50 and IC90 determined by in vitro viral replication studies.

Basically, what we are saying is, let's see how good your in vitro data is and then we will decide whether

or not we will need additional studies. Certainly, we will be interested in seeing data in the literature as well as data done specifically at our request.

[Slide.]

For clinical sensitivity, one of the things that has been proposed to be done is to do sensitivity and reproducibility studies on a panel of unspiked specimens whose genetic makeup is known. Basically, somebody is going to have to, presumably, sponsor, or industry, is going to have to take a bunch of patients, get specimens on them, determine what the distribution of the viral swarm, or the quasi-species, is and then show that they can always pick up the mutations that they are looking for, or can pick them up with a certain sensitivity. These would be unspiked samples.

On this particular issue, of course, and, as on all the others, further discussions will determine whether or not the panel must include representatives of all genotypes to which a claim is sought.

[Slide.]

The FDA is also considering requiring traditional clinical trials in which assay phenotype predictions based on genotype correlate with changes in viral burden and/or mutant representation in response to antiretroviral therapy. FDA may also allow these studies to be prospective or

retrospective on archived specimens.

[Slide.]

To facilitate these things coming to market, we are giving serious consideration to the concept of requiring either the panel-type clinical studies or the traditional clinical trials but not both to be submitted premarket.

Now, certainly, a manufacturer could submit both premarket if they wanted to, but we feel that there is a likelihood that we will be willing to say, "Well, look; if you have got the clinical-trial data, you can do the panel-type data postmarket." Or, "If you have the panel data and you want to go ahead, you can get some of the clinical-trial data postmarket."

In this case, FDA would anticipate requiring the alternative studies to be submitted postmarket, as I have just said.

[Slide.]

As we have discussed here, we are almost surely relying on extensive postmarket studies to further support claims made during the approval or clearance process as well as additional efficacy claims; for instance, new correlations between phenotype and genotype.

[Slide.]

In being asked to classify HIV drug resistance genotype assays as class II medical devices, you are being

technically asked to vote on the classification and on the adequacy of special controls. This presents a little bit of a quandary for you because the special controls are outlined in the guidance document and we have only given you highlights of that guidance document, and it hasn't been finished.

Although the special controls are in a guidance document which is currently in draft format only, we feel that the information presented today will convince you that the clinical and scientific data in the literature are such that our expertise, together with the expertise of all of the scientists, clinicians and members of the general public who choose to contribute to the final document will be sufficient to formulate adequate special controls to insure efficacy and safety.

So, in the upcoming presentations, what you need to look for is does it look like the field is at a point where the field can sit down and identify adequate special controls for at least some mutations which would allow these kits to go to market with such identified special controls.

With that, we have some presentations. Who is up first? Doug? We have going to have Doug Mayers talk. We will entertain questions, but one thing I did want to say in response to Dr. Hollinger's question about class III regulation of viral-load tests. Len was really quite

accurate. We know a lot more now with these tests that are coming to market, or are coming up, the genotyping tests than we knew in the early days of viral-load testing.

There are going to be a lot of questions. I am certainly happy to entertain questions now. You are just about to get two talks that go into the scientific and clinical literature in much more detail than I have described it. So I am certainly willing to answer questions, but if you think it might be answered in the next two talks, you are certainly welcome to wait.

DR. HOLLINGER: It doesn't look like the committee thinks they can wait.

DR. VERTER: It's a good try, though. In trying to read some of the documents last night and listening to the two presentations this morning, I wonder if you could clarify--I am still having trouble understanding the II/III issue. From what you just described, it seems to me almost like a very fine line. In fact, it almost came down to the statement, "Considering the concept of requiring either the panel-type clinical studies or the traditional clinical trials, but not both," whereas, in a III, do you require both and in the II only one? Can you give me some feel about that?

DR. DAYTON: We are kind of skirting the issue a little bit there. And it is confusing. I think one key

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1	point to make is we can make class II regulation as
2	stringent as we want it, if we really want to. So we can
3	make it as stringent as class III, basically.
4	What was the second part of your question?
5	DR. VERTER: I was just trying to clarify in my
6	mind, and maybe in some others, as to where the fine line
7	is. I understood what you just said and I thank you for
8	that comment.
9	DR. DAYTON: The real question is, as I said, does
10	it look like we can identify special controls or studies
11	that are going to make this thing effective, even partially
12	effective. The critical issue is not so much whether we
13	require one pre and one post. That is something that we are
14	thinking of.
15	The real issue is does the science say, "Look; the
16	field is far enough along that some mutations can be fairly
17	well guaranteed to be relevant in measuring them and,
18	therefore, be effective. That is the key issue.
19	Have I answered your question? Have I addressed
20	it?
21	DR. VERTER: You have addressed it.
22	DR. MITCHELL: Can you tell me what do you mean by
23	panel-type clinical studies? Is that presenting panels of
24	known
25	DR. DAYTON: It would bebasically, as the

proposal stands now, we somebody would assemble a panel of 50 unspiked patient specimens. Presumably, they would take each one and they would make multiple clones from them by standard microbiological techniques, sequence them in the regions that we are interested in, and come up with a description of the distribution of quasi-species in the viral swarm.

So, for instance, if there is a particular mutation you are looking for, it might be there 10 percent or 1 percent or 25 percent. Then you would take a panel of these and you would challenge them. You would put them through your assay as opposed to subcloning and sequencing and everything. You would put them through your one-shot assay and you would see how well you pick up the mutations that are there and at what concentration.

In a way, it is like the spiked panel studies except that it is unspiked. It is a more natural environment. And it is a tougher challenge. Does that explain it?

DR. MITCHELL: Yes. Thank you.

DR. BOYLE: I think I am grappling with the same thing everybody else is, but let me see if I understand correctly. In a class III, you would normally require clinical trials before it be approved for use in the marketplace whereas, in a class II, you might require

clinical-trial data but it could be done postmarketing?

DR. DAYTON: Well, no. In a class II, we actually could require clinical trials premarket if we had to. That is an option. But what we would be doing in a class II situation, in the situation we would like to do, is looking at clinical data in the literature and be able to say, "Look; these mutations here are really quite well established so we are quite confident that they deserve a claim for that."

But there are this whole set of other mutations over here that we know a lot less about. So, if you want to claim them, you come back postmarket. You can go to market but you only get a claim for the first set of mutations and you only get the second set of mutations when you come back and prove it.

But, again, it could be data in the literature, not necessarily clinical-trial data. We could also specify clinical-trial data in postmarketing, which we may do.

Len, did you want to comment on that question?

MR. WILSON: Maybe I can help out a little bit. I

am going to use an example of something that already exists,

CMV assays, class II medical device. The intended-use

statement goes on the line of to detect antibody to CMV in

the serum of blood donors, or some such. It doesn't say,

for the prevention of CMV transmission. It doesn't say

that.

If it said for the prevention of CMV transmission, you would have to run a clinical trial to show that it does that. But since it is limited to for the detection of CMV antibody--all right; what is the content of the 510(k) class II. Many of the concepts that Pr. Dayton has described are just, simply, reproduced in the class II.

We have analytical sensitivity data, analytical specificity data. Because it is used for the blood supply, we run a study that is in blood donors to check specificity because you can't check specificity in a blood-donor population any other way than running it. And why would we do that? Because we don't want to have too many units of blood tossed out because of false positives.

We do have, and I think along the lines of where Dr. Dayton is going, some known positive samples that we would test--the manufacturers would use the test to determine whether or not, in fact, they truly detect a true positive. But it is not in clinical-trial format in that sense.

So, therefore, that enables FDA to clear the product with claims or labeling limited to what the thing has been documented to do. So, in terms of this particular assay, there are a lot more questions and we know that, because of viral resistance and mutations, things are going

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to change and the logical issue is that there are going to be new mutations and how does this correlate and the like. That could be done in a postmarketing surveillance type of order.

I hope that helps.

DR. DAYTON: If I can continue on; what I think you will see in the later presentations is that there are quite good laboratory studies for the significance of various mutations. There is data for the appearance and disappearance of these mutations in the literature and there are also studies coming out showing that use of these types of assays has clinical benefit.

So, if you put all of that together, that is really telling you a very strong message; hey, these things work. What we would be saying is, "Okay; these things work but we want to see more in the postmarket."

Does that answer your question?

DR. BOYLE: Yes.

DR. FITZPATRICK: You said the panels have not been developed yet. When we began HIV testing, there were difficulties developing reliable panels in enough source to be provided to all the laboratories doing testing to get similar results. Is your expectation that this is much easier now?

DR. DAYTON: We are leaving that up to sponsors at

the moment. We are certainly open minded about how to actually approach this. It should be reasonable for a sponsor to assemble his own panel which might be the quickest way to do it, but it is quite laborious.

It would be also possible to have a centralized panel set up. Also a sponsor has the alternative of coming forward with the clinical-trial data while he waits--and doing the panel postmarket. We are trying to make it flexible so that it can go either way.

I think Ed wants to comment on this.

DR. TABOR: I think the discussion is confusing the issue tremendously.

MR. DUBIN: We have done that before.

DR. TABOR: I think part of it is that it is focussing on constructing panels and focussing on postmarketing surveillance. The issue is between whether this should be a class III device or a class II device. The discussion should have nothing to do with blood screening because a test that is used for blood screening usually is a licensed product for which a PLA is filed.

What we should be focussing on is is the clinical impact of this assay so great and, perhaps, so unknown that you need clinical trials and to file a PMA and have an 180-day review clock which really translates into more than a year of review time with resubmissions or is the clinical

significance of this so clear and is the impact on the patients' health more an issue of management than of life and death such that the manufacturer can file a 510(k), have a 90-day review clock, and have minimal or no clinical data.

Postmarketing surveillance is another issue, I think, here. It is not totally divorced from this but you shouldn't be focussing on something that you want clinical data and you are going to wait and get it after marketing. If you want clinical data, it should be a PMA and a class III device.

The question here is are the manufacturers going to have to go through a longer review cycle with more clinical data up front or are they going to be able to file a 510(k) with only special controls and any clinical data, really, as icing on the cake.

DR. DAYTON: Let me just elaborate on Ed's response. It is absolutely correct. Again, don't feel that you are having to judge a particular product. You are asked to judge, is the science such that we can judge a product, or that a product can be judged.

DR. HOLLINGER: I think probably we ought to listen. I think that the next step should probably be to listen and see what the data is out there and see what it means. Let's have one more and then let's go to some of the data.

MR. DUBIN: I was going kind of towards where you were going, Dr. Tabor. Here is how we frame the question. I think, from our perspective, the big plus is if this is going to give clinicians who are actually, at the grass-roots level, treating patients and dealing with resistance problems, then that is going to give the clinicians more freedom and more ability to move.

I think, from our perspective, that is clearly a good thing because, certainly, in hemophilia, this is a big problem in the infected hemophilia community. We are having a lot of problems with the resistant strains and a lot of our guys are in trouble.

Our only concern, and the way I was trying to frame it, was we have had concerns about how fast-track has gone, things that have happened and have caught our attention and concerned us. But I think, in this instance, the issue is, and I agree with you, if we can do this in a way that provides the freedom to the clinicians and the ability to track it, then it seems like a no-brainer on one level from our perspective.

DR. STRONCEK: I have a couple of comments. There are a number of HLA tests where genotyping is used to determine phenotype which are marketed so I presume they are regulated. Are those regulated as class II--class II, I would presume.

1	The other question is are the current NAT tests
2	being done on blood, are they regulated as class III? Ed
3	seemed to suggest that it is something different. Then, if
4	that is true, I am really confused.
5	DR. TABOR: Let me answer your second question.
6	The NAT test to be done on blood, or for blood screening,
7	they will be required to file a PLA or BLA for licensure the
8	same as for any of the other required or recommended tests
9	for screening blood. There was a very big regulatory issue
10	about two years ago when the manufacturers wanted to just go
11	ahead and do the testing. And we said, "No; there are a
12	number of issues that make this a blood-screening assay."
13	So those will be PLA tests that are being done
14	under IND now, and they are totally separate from what we
15	are talking about here.
16	With regard to the HLA test, I think someone from
17	Devices will have to answer that. I am not familiar with
18	that.
19	DR. DAYTON: I don't know the answer to that.
20	MR. WILSON: Those HLA tests which are used that
21	are labeled for the detection of the antigens are
22	predominantly class I. There are some which are class II.
23	I am talking about the ones that are non-diagnostic.
24	DR. BUCHHOLZ: Just having watched this from an

industry perspective for a number of years, I wonder if I

1	could try simplifying a little bit this class II and class
2	III.
3	I think, back in 1976 when this device legislation
4	took place, there was an effort to kind of establish risk
5	categories associated with a device. A device, class I, not
6	much risk if something goes wrong; class III, a lot of risk
7	if something goes wrong.
8	I think, in some of the original language, there
9	was the concept of life-sustaining device for a class III
10	device, like an implanted pacemaker. I think the thing that
11	is probably confusing the committee is that there are now
12	some things that are, by fiat, put in class III because
13	there was no predicate device; by that, there was no device
14	like what we have today because the problem didn't exist.
15	So those devices end up being bumped in this
16	class III category until they can get dispersed into,
17	perhaps, a more appropriate category.
18	Does that help a little bit?
19	DR. HOLLINGER: Thank you, Don.
20	Why don't we go ahead, Andy.
21	DR. DAYTON: I guess we are ready for Doug Mayers.
22	Presentation
23	DR. MAYERS: I want to thank the FDA for making
24	drug resistance interpretation seem simple.
25	[Slide.]

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what I would like to do in the next forty minutes or so is go over the background of HIV resistance testing, a little bit about the biology of HIV resistance and then overview the current clinical data both retrospective and prospective. By nature, this is going to be a survey and not exhaustive because there are far too many studies today than the time I have to present them.

I just want to make a caveat that I will occasionally use a company slide in this talk because I didn't have a slide to illustrate the point, but those slides are made to illustrate a biological point and not the support any company and, where possible, I have used every company in the area's slides, one of each, so they don't feel like they have been slighted.

[Slide.]

It is important to recognize of HIV that the replication of the virus is very rapid in a patient such that patients make up to a billion particles each day with a half life of about one day.

[Slide.]

The reason this is important from an HIV resistance point of view is that the virus, as a replication strategy, makes, on average, one error per each progeny virus. So, if a billion viruses are produced and you have a 10,000 base virus making, on average, one error, that means

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you have 100,000 of every single-base variant and about ten copies of every double-base variant in your patient.

So when you have these discussions of do drugresistant viruses exist at some level, yes, in all of our patients, they exist and they are spontaneously produced every day in the patient. This is the virus' strategy to escape immune pressure and it also uses it to escape drug pressure.

[Slide.]

In 1989, two years after AZT was introduced into clinical practice, Doug Richmond and Brendan Larder had a paper that came out in Science. What they showed was that viruses were produced in our patients that were 100-fold less susceptible to AZT than when they started therapy.

This shows the phenotype assay results from that paper. What you have on the vertical axis of this is the amount of virus replication relative to a no-drug control. On the horizontal axis is drug levels. What you can see in the upper left-hand panel, C, is that for the virus in light blue that the virus is susceptible to AZT and it takes about 0.03 micromolar of drug to suppress it.

Then, as you watch the viruses over time, you can see that you move out to the yellow virus which is obtained a number of months later and now the virus is 100-fold less susceptible to AZT and it takes about 3 micromolar of drug

to suppress it.

We were very lucky with AZT. You have an 100-fold difference between sensitive and resistant virus so it is fairly easy to pick out what resistance was. This is the standard type of phenotypic test that would be reported out to the clinician.

[Slide.]

About six months later, Brendan Larder and Sharon Kemp took paired isolates from that original study. They took studies from before the patients had seen drug and a sample of virus when the patient had highly drug-resistant virus. With six pairs, they were able to show that there were four mutations associated with AZT resistance at positions 67, 70, 215 and 219.

Over the years after that, two more mutations were associated with AZT resistance but most of the story was well explained with six paired isolates. This would be the resistance-associated mutations or a genotypic assay. So you can either grow the virus in the presence of drug or you can look for mutations associated with resistance.

[Slide.]

Once we had these assays available, we were fairly quickly able to show what was associated with the development of resistance; host factors, either advance disease or low CD4-cell counts, virus factors such as very

high levels of HIV RNA in the blood, baseline drug susceptibility and antiviral drug activities, the virologist's paradigm being that if you don't have a drug, you don't have drug resistance.

[Slide.]

Looking at the emergence of resistance, there are three patterns that we see in the clinic. There are some drugs in which you see very rapid emergence of very high-level resistance. These are drugs such as 3TC and the non-nucleoside agents. The reason you see very high-level resistance emerge quickly is that a single-point mutation will produce a hundred- to a thousand-fold resistance to these drugs.

So these viruses preexist in the patient and if you do the calculation, you expect it would take about fifteen days for them to emerge under drug pressure. In monotherapy studies, it took about fifteen days for these drugs to produce high-level resistance. So these are the drugs in which it has very clearly been associated with the loss of activity is associated with single-point mutation.

The next drugs take a moderate amount of time, usually three months or more, to get high levels of resistance. And these would be drugs such as zidovudine, abacavir and the protease inhibitors. The reason these drugs take a bit longer to get high levels of resistance is

you have to have a number of mutations. So it takes the accumulation of three, four or five mutations to get high-level resistance and it takes the virus a period of time in the presence of drug to get to those high levels. But it is fairly easy to describe what resistance is in them because they do get the high levels of resistance.

The last group of drugs, ddI, ddC and d4T are really where much of the controversy of interpretation of resistance assays comes from. From these drugs, you never really get very high levels of resistance in the clinic with the drugs. You get four- to five-fold resistance which is almost within the assay variability of a phenotypic assay. So there always a fair amount of debate as to what ddI, ddC or d4T resistance is. This leads to some of the variability in the reports that the clinicians receive from the laboratories.

[Slide.]

Looking at a crystal structure of the reverse transcriptase, what you can see is that along a loop between about bases 65 and 75, there is a whole string of mutations associated with nucleoside resistance with multiple different agents. And so it wouldn't be surprising that resistance to one drug might be associated with cross-resistance to other drugs in the class.

[Slide.]

This has clearly been shown. For zidovudine, it produces low levels of resistant to ddI and ddC as you get high levels of zidovudine resistance. But, more importantly, it has been shown that once you have high-level zidovudine resistance, combinations of AZT-ddI and AZT-ddC did not lead to clinical benefit.

For 3TC, abacavir, ddI and ddC, these drugs all have overlapping mutations. Clearly, one drug will produce mutations at some level of decreased susceptibility to the other drugs. And d4T hangs out by itself because we really, even in 1999, don't understand d4T resistance very well.

[Slide.]

An aspect that has been very interesting to virologists but it has complicated things for the clinician is that the virus can take numerous routes to get the high levels of resistance. The good news from a clinical point of view is that the vast majority of isolets do it the way you would expect. They get AZT resistance. They get 3TC resistance. They add the classical mutations together to produce a high-level resistant virus.

But, in the last year or two, we have discovered that a small number of patients can go down a different pathway of a 151 mutation and, even more fascinating, the virus can actually add six bases into that loop I showed you and produce high-level resistance by an insertional mutation

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which we never expected to see, but it can be easily identified.

[Slide.]

From a clinical management point of view, though, the vast majority of our patients are failing with 215 and 184 with associated other nucleoside mutations. So, from a clinical point of view, the overwhelming majority of patients fail with known mutations and known resistance patterns.

[Slide.]

Moving to the non-nucleoside drugs, the non-nucleoside drugs have a totally different pocket from the ones of the nucleosides. The picture has actually become relative simple in 1999 because of the use of the non-nucleosides in combination with either AZT or d4T. The vast majority of the non-nucleoside agents right now are failing with a mutation at position 103, a single-point mutation called K103N. This mutation, essentially, inactivates all of the non-nucleoside drugs.

[Slide.]

This just shows, in a number of clinical isolates, that isolates that only had the 103N mutation with non-nucleoside resistance had developed significant decreases in susceptibility to efavirenz, nelvirapine and delavirdine.

[Slide.]

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Moving to the protease enzyme, the protease enzyme has sort of a bewildering assay of mutations that you can see but, in all honestly, only about five or six of them are really critically important to high-level resistance. Those are shown in this model by the red balls. They are the mutations that tend to occur in the active site of the enzyme and produce resistance.

There are a number of other mutations that are associated, in this figure with the yellow or white balls, and these are compensatory mutations. What you see the virus doing in patients is the virus will develop a critical-site mutation, a red-ball mutation, and get some level of resistance. But then it doesn't grow very well. It doesn't cut proteins as well as a protease so it adds in two or so of the compensatory mutations. Then it adds back in another resistance mutation and it works its way through fitness base.

But, for the practicing clinician, what you really need to do is just count how many critical-site mutations were there.

[Slide.]

This shows the critical-site mutations for the drugs that are currently available. For saquinavir, it is 90 and 48. For indinavir, it is 82, 46, 84. Nelfinavir, it has been the D30N, usually L90M, occasionally. And for

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amprenavir, it appears to be a 50 mutation.

[Slide.]

An issue that has caused real concern of resistance was initially data from indinavir where they showed that if you had high-level phenotypic resistance to indinavir, there was a loss across the class of resistance. For ritonavir, it is 100 percent. For saquinavir, it is 60 percent. Nelfinavir, it is about 75 percent. And, with the newer data for amprenavir, it is probably closer to 55 to 60 percent of these isolates would be resistant.

This is one place, as we will see later, where genotyping hasn't been as useful as we might have liked and phenotyping actually has been very useful to help find which of the lucky patients has sensitivity to one of the proteases that remains.

[Slide.]

For nelfinavir, this appeared to be different and amprenavir it appears to be different in that initial resistance to one drug does not produce cross-resistance to the rest of the class. A concern that has come up has been that, even though they don't have primary mutations that are cross resistant, they share a lot of the background polymorphisms and the compensatory mutations and so, are you one mutation short of disaster.

[Slide.]

It appears that may actually be the case for these drugs so that you can get a good response with the next agent but you have to totally suppress the virus or you can rapidly see broad class resistance emerge after that type of protease inhibitor.

This just shows that the addition of a single V82A mutation took a virus from totally ritonavir-susceptible to highly ritonavir-resistant.

[Slide.]

The slide illustrates the point that in the management of patients on protease-containing regimens that a single-point mutation will lead to the initial loss of antiviral activity but if you leave the patient on the protease inhibitor for any extended period of time, you will see the sequential additional of multiple mutations.

The reason this is important is that is important is that, in most instances, there is low-level resistance associated with single-point mutation and not very broad cross resistance. But once you get to five and six mutations in the virus, you have a virus that is highly likely to be both highly resistant and relatively broadly cross-resistant.

[Slide.]

This is just some data that came out of a recent meeting in which they looked at patients who had had several

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PI regimens. They looked at ten-fold decreased susceptibility to any of the available agents and showed that about three-quarters of the isolates had decreased susceptibility to all of the agents by the time they got there.

[Slide.]

Switching over to susceptibility testing, the sort of gold standard for susceptibility testing was an assay developed in 1990 between the ACTC and the Department of Defense in which we took patient isolates, we grew them and expanded them, titered them and assayed them for drug susceptibility on patient-donor lymphocytes.

[Slide.]

This assay allowed us to look at roughly

95 percent of the patients and look at how they were failing
on drugs. This just shows the susceptibility pattern. The
green and the yellow are pre-therapy isolets--the white and
the red are post-therapy isolets--that were obtained from
that original study the Doug Richmond did back in 1989.

[Slide.]

The nice aspect about this assay was we had reasonably good quality control. You could note susceptibility within about three-fold. Sort of a standard of thumb has been that if the decrease in susceptibility is less than three-fold for these types of assays, you are not

1 | really sure if it is resistance or just assay variability.

The newer assays may be able to get down to the two-fold, two-and-a-half-fold, but I think the two- to three-fold is about as close as you can know a phenotype on a virus.

[Slide.]

We were able to actually set reasonable cut points for sensitive, partially resistant and resistant that actually had clinically validated meaning. The sensitive of less than 0.2 micromolar was based on patients' isolates who had never seen drug and the range of susceptibilities in wild-type virus. Resistant was associated with loss of clinical activity and clinical disease progression.

[Slide.]

The problem with this assay is illustrated in this chart. Times 0 on the bottom is the time at which phenotypic resistance emerged in these patients. This was a study done in about 1993. What we showed was that patients who always remain sensitive had good stable CD4 counts. The unfortunate news was that, by the time we saw phenotypic resistance from a co-cultured virus from the cells, the patient was already failing by enough--had had about a 50 percent CD4 decline and so the clinicians didn't need our assay to tell them that they were not doing well.

[Slide.]

About this same time, data began to emerge from 3TC and also some of the AZT studies that, if we took the plasma virus and looked at that for mutations or susceptibility that we could actually detect resistance very nicely at the beginning of the rise in the viral load as opposed to the PBMCs where it took a bit longer to show up.

So most of the focus on resistance testing has moved from trying to take cells in coculturing virus to looking at the virus that is circulating in the plasma in an individual patient.

[Slide.]

Currently, all of the assays available, either genotypic of phenotypic, basically PCR a segment of the virus that includes the protease gene and the early 250 to 300 bases of the polymerase gene which is where we have identified resistance mutations. So, basically, you lift out from the plasma the protease and part of the RT gene and then, for phenotypic assays, you clip it into a vector and grow it up. For genotypic assays, you sequence it.

[Slide.]

This just points out that we have to PCR amplify for all the assays we use on that segment of the genome.

[Slide.]

This just shows what a sequence looks like that we are actually doing. The sequence with the arrow over it

shows the detection of the emergence of a subpopulation of virus. So, basically, you either have a peak by itself which can be described as a single amino acid or you have a peak where there is a mixture. Those can be associated with minority populations of virus.

For all the assays we use for genotyping right now, they all use population sequencing and we basically can pick up somewhere between 30 and 50 percent minority populations. So these assays clearly do not pick up minority populations well. We are not picking up 5, 10 percent virus. We are picking what the predominant circulating virus is in all of these assays.

One of the difficulties with doing these assays is also illustrated by the arrow in the second row because the mutation they are pointing out isn't associated with resistance.

[Slide.]

For the common viruses, we take that same segment of the genome. We PCR amplify it, put it into a deleted vector, grow it up and then test it against drugs. The reason that this has been, I think, very useful in the development of resistance testing is that this allows us to not have the alterations in the virus associated with growing it up for long periods of times in cells. It also speeds up the process so, instead of taking six to eight

weeks to get a phenotype back to the clinic, the new RVA assays can turn a result around in about three weeks back to the clinic.

So it has been a significant increase in speed and it looks like there has also been an increase in quality control such that their variability appears to be less than the variability we had with the PBMC-based assays.

[Slide.]

This just shows the types of susceptibility curves that they can get. What you see here is the blue curve on all these figures is a control virus that they put on the plate, and the yellow curve is the clinical isolate. As you can see for 3TC, the virus has essentially no susceptibility to 3TC. As the curves shift toward the right, you are seeing increasing resistance. So these are the types of assays that the companies are doing for phenotypic testing right now.

[Slide.]

At this point, I would like to switch over to clinical relevance. This has always been a somewhat contentious topic.

[Slide.]

For clinical significance, zidovudine is the only drug for which we have data for clinical progression and death. I honestly believe that we will probably never have

any other single drug for which we will be able to show clinical progression and death because of the use of combinations.

But, for AZT, we could clearly show with greater than 1.0 micromolar resistance at baseline if this was the associated progression and death in both the ACTG 116B, 117 study and a prospective study in the Department of Defense with about a two-and-a-half to three-fold risk of disease progression. This was independent of the other baseline parameters available to us at that time.

[Slide.]

For the pediatricians, this is a similar study looking at the 215 mutation in plasma virus. What they did was, the yellow dots are the children who had no disease progression and were doing quite clinically well. The orange dots are the children who were progressing and having disease progression.

What you can see is that the children who had no disease progression also had no evidence of the 215 mutation and the children who were progressing developed increasing amounts of the 215 mutation in their plasma virus and it was strongly associated with disease progression in this cohort.

[Slide.]

The companies have been doing a very good job recently with the new drugs in defining the phenotypes and

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genotypes associated with loss of activity of their drugs. This is illustrated in this slide from abacavir where the company looked at abacavir in its clinical trials and found out that, if clinical isolates had less than an eight-fold decrease in susceptibility from a wild-type isolate that they could get a good clinical response and if it was more than eight-fold above the wild-type virus that they were not getting good activity.

They also were able to find the genotypes associated with lack of activity of abacavir. As you notice, they are the genotypes that are associated with a multi-drug-resistant, multi-nucleoside-resistant, virus.

[Slide.]

Similarly, for nelfinavir, they were able to, in expanded access, look at the major mutations associated with resistance and were able to show that—they could literally count major mutations and response was related to how many major mutations were present, or they could look at phenotypic susceptibility as broken by four—to ten—fold and show, again, a very nice association with decreased drug susceptibility phenotypically or presence of resistance mutations predicted who would respond or not respond to nelfinavir.

[Slide.]

Similarly, for ritonavir and saquinavir, they were

able to look at phenotypic and genotypic resistance. What they showed very nicely was that the predictors of failure were the same as we had seen previously for zidovudine, CD4 count, disease stage, HIV RNA, but also either phenotypic resistance or genotypic resistance predicted lack of response to saquinavir and ritonavir.

[Slide.]

Moving into broader-based clinical studies, Andy Zolopa and the group at Stanford looked at patients who received ritonavir and saquinavir who were all PI experienced. They looked at short-term virologic responses, and the clinical predictors were the same as we had seen previously.

Of note, drug history, number and prior duration of drugs predicted poor response and simply counting the major protease mutations, the red-ball mutations, I showed you earlier. If you simply counted them, the number of mutations in the virus predicted response to ritonavir and saquinavir. The more you had, the worse you did.

[Slide.]

Steve Deeks presented data at the same meeting which, I think, gave us a great deal of insight into what you need to get a good response in an experienced patient.

They took eighteen patients who had received abacavir, saquinavir, nelfinavir and nelvirapine. These were all four

new drugs these patients had never seen. So they took four drugs that the patients were naive to. They looked at a phenotypic assay.

[Slide.]

What they showed was that seven of the patients had only zero or one active drug in the regimen by susceptibility testing. In those patients, none of them got a response. It was only very transient and none of them went below the limits of detection of the assay.

So this was showing the impact of cross-resistance in this population. Eleven patients had two or three active drugs. They all had a sustained response and eight of ten went undetectable. None of them had all four drugs in the combination active. What this basically told us was if you are going to get a good response in a regimen for heavily pre-exposed patients, you are going to need to find two or three active drugs to give that patient.

[Slide.]

That is the retrospective data. I am now going to move to the two prospective trials that have been done on genotyping. The first trial is the GART trial, GART standing for genotypic antiretroviral resistance testing.

It was a trial done by the CPCRA in patients who had had a good response to protease-containing regimen and then lost that response.

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The patients had plasma virus, had plasma sent in. The virus was sequenced. It was reviewed by a panel of three virologists; myself, Tom Merigan and John Baxter. We gave the clinicians back a report of susceptibility and we 4 also gave them some recommendations for treatment at that 5 6 time.

You have got to remember this trial started in 1996. The community docs really were not comfortable that they could take the sequence data and use it in clinical management at that time. So the test was a test of getting the sequence data with some suggestions versus using your own clinical judgment in the management of these patients.

It had a short-term virologic endpoint of 4, 8 and 12 weeks of follow up. The reason the data was chopped after 12 weeks was that the patients and their physicians were allowed to switch drug regimens if they hadn't had a good response during that time period. So the test was only relevant during that short period of time.

[Slide.]

Looking at the randomization, patients had about 230 CD4 cells, about 30,000 copies of HIV RNA. The majority of the patients had received nelfinavir for indinavir which was common to the community at that time. About half of them were failing on their first protease-inhibitorcontaining regimen and the other half were on their second

or third regimen.

[Slide.]

Looking at the baseline resistance mutations, as we had shown previously, in this population, about three-quarters of them had both RT and protease mutations. About 20 percent had RT mutations alone. And 5 percent had absolutely no mutations in their virus. It is the impression of the clinicians and the virologists in the study that that 5 percent was probably not actually on drug at the time that these susceptibility tests were done.

Looking at the mutations, we saw, again, 184 and 215 were the overwhelmingly common human-failure mutations with only 1 or 3 percent of patients getting the insertion in the 151 mutation. And we had a variety of protease-inhibitor mutations.

[Slide.]

The bottom line was that if you use genotyping to assist in the management of the patient, we could get about a half-log better virologic response at the 4- and 8-week time point than we could by clinical judgment alone. And this was a highly significant p-value.

[Slide.]

This just shows the response over time and shows that, actually, the best response was, unfortunately, at four weeks and there was some paling off of response during

the 8- and 12-week time period as some patients got a transient response to drug and then resistance reemerged.

[Slide.]

But it should be noted that, at all time points, about twice as many patients were undetectable using resistance testing as they were if you just used clinical judgment alone. Even at the 12-week time point, about 28 percent of our patients were undetectable with genotyping and about 15 percent were undetectable with clinical judgment alone.

[Slide.]

A point of contention in this study has been that the patients who were getting the genotyping also received, on average, one more drug than the patients who were getting phenotyping based potentially on the fact that their docs could see the resistance data available.

[Slide.]

But we have actually gone back and reanalyzed the data. If you look for patients who got three drugs, four drugs or five drugs, at every number of drugs, the patients did better if they had genetic data to assist in the management than if they guessed with clinical judgment alone.

We think this actually explains the results of this trial. The green curve is the viral-load response that

you see in these patients. The blue bars show you how many active drugs were present in the no-GART arm and the yellow bars show you how many active drugs were present in the GART arm.

What you can see is that, on average, patients who got the genotypic testing were able to get one more active drug in their regimen than they could get by clinical judgment alone. The response the patients got was clearly associated with the number of active drugs they received. And so it appears that the genotyping allowed us to find, on average, one more active drug to give in a salvage regimen than you could give by clinical judgment alone.

[Slide.]

So the conclusion was that GART, with expert advice in patients failing antiretroviral therapy, was superior to no-GART as measured by short-term viral-load responses. In a greater viral-load response, reduction in GART was attributed to the greater number of active drugs prescribed.

I'm sorry I didn't bring the slides, but one of the truly impressive findings for us in the trial has been the robustness of this finding. This half-a-log difference held up over CD4 ranges, over viral-load ranges, over resistance profiles, over first failure, second failure, third failure.

Basically, any cell that had more than eight patients in the cell had a significant difference with genotyping.

[Slide.]

The second prospective study was the VIRADAPT study which was conducted in France. This was a bit different study in that there were basically a number of French clinicians at about three French medical centers who followed a series of patients and did genotpying and then would meet and discuss the results either with genotyping or without genotyping for the manufacturer of individual patients.

[Slide.]

It is a little bit smaller study. There were 43 patients in the control arm and 65 patients in the genotyping arm.

[Slide.]

The patients in the study were a bit more advanced than the GART patients. They had, on average, a plasma HIV RNA of about 150,000. The CD4 cells were about 200 to 220, and quite a few of them had actually had symptomatic HIV disease.

[Slide.]

If you look at their prior exposure, they were very heavily exposed. They had seen, on average, one-and-a-

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half to two PIs when they came into the trial. They had had, on average, about four nucleoside agents and, again, about half of them were first-time failures and the other half were second- and third-line-failure patients.

[Slide.]

The results in this trial show that they actually got a sustained benefit to six months. The difference between this trial and the GART trial was that if you hadn't gotten a good response at three months, you could retest the patient at three months and go to six months. And so, in GART, you got one test, we followed you. In this trial, you got a test every three months.

The data went out to six months in a randomized fashion. As you can see, there is about a half-log difference between the two arms out to six months that persisted. They subsequently extended the analysis out to a year and they have had a stable reduction in RNA out to a year in these patients who could get repeated testing.

The trial was no longer randomized after six months because, once the GART results were released, the French unblinded the trial and took everyone over to genotypic testing.

[Slide.]

Of note, and very similar to the GART results, you can see that roughly 30 percent of patients were

undetectable in the GART arm and about 14, 15 percent of the patients were undetectable in the no-GART arm so, again, about a two-fold difference between genotypic testing versus clinical judgment alone.

These results have been remarkably consistent across these two trials that had somewhat different methodologies.

Also of interest, both trials used the same algorithm to interpret the data for genotyping. The algorithm is actually contained in table 8 of the Stanford Guide for the Management of HIV-Infected Patients. It is a little pocket guide.

[Slide.]

So in choosing an effective salvage regimen for patients who are failing on combination therapy, I think we have a number of clinical parameters available; number and duration of prior antiretroviral drugs, knowledge of cross-resistance patterns between the drugs.

This data can be supplemented with resistance testing. I think the bottom line is to have an effective salvage therapy in patients who fail combination regimens. You need to be able to find two or three drugs that remain active against the patient's circulating virus.

[Slide.]

The current dilemma is even with the availability

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of repeated genotypic testing, we can only get 30 percent of patients suppressed below 500 copies per ml. This just emphasizes the need for us to continue to get salvage drugs available for these patients.

[Slide.]

In the last few minutes, I would like to go over the public-health data looking at resistance. This is the percent of patients with AZT resistance by year. Before 1987, we never actually saw an AZT-resistant virus in an untreated patient. In 1987, the drug entered clinical practice. It was available to about 20 percent of patients because you had to have late-stage disease to get access to the drug.

So, from 1987 to 1990, about 20 percent of our patients had access to AZT and there was about a 1 percent level of transmission of drug-resistant virus. In 1990, because of the 116, 119 results of the ACTG, there was an expansion of the use of AZT to patients with less than 500 CD4 cells. Two years after the increased indications for AZT usage, the transmission rate jumped to 7.5 percent and then actually moved to between about 8 and 10 percent for the next five years.

[Slide.]

So AZT resistance was seen at about an 8 to 10 percent level in new seroconverters from 1993 through

about 1996. In 1996, 3TC became available within a year.

Because of a single-point mutation, 3TC-resistant

transmissions were seen. The most recent data, as we have

moved to a very broadened use of combination therapy, is

that we are seeing an even increased risk of transmission of

drug resistance. This is data from both the military and a

What they showed was that, looking for resistance by phenotype and genotype, they found a level of somewhere between 20 and 30 percent of new infections were infected with drug-resistant virus in 1999. What has become a bit scary to the practicing clinician is an increasing number of these patients actually have multi-drug-resistant virus with both nucleoside- and either protease- or non-nucleoside-associated mutations.

[Slide.]

cohort led by the group at San Diego.

So I think we can actually categorize a number of high-risk populations for drug resistance; patients who have lost virologic control on a combination antiretroviral regimen, new HIV seroconverters, HIV-infected infants of HAART-experienced mothers--we don't have very many of them but when they occur, these children are at very high risk for drug resistance--and occupational HIV exposure of healthcare workers. These are four categories of individuals who are at high risk of drug-resistant virus.

[Slide.]

Some unresolved issues. For genotypic testing, I think the companies--I am not aware of any company that has actually brought a technical-validation panel to the FDA. I know the panels are being developed. I think this is probably one of the big issues for the companies is to prove that they have a kit where three different techs and four different labs can get the same result with the same sample

I think that is coming and I think you will see that type of data very soon. Interpretation of complex genotypes is difficult in these patients. The ultimate clinical utility, if you want to go to long-term durability or clinical outcomes, has not been proven but at least at time frames of three months to year, there is a clear benefit of using genotypic testing to get better virologic suppression.

[Slide.]

From our studies, and in the CPCRA, it has become clear that there are a number of instances where phenotyping does have significant utility, potentially more utility than the genotyping assays. One is in patients who are failing with indinavir resistance because we can tell you, from a genotype, that you are likely to be cross-resistant to the other agents but can't tell you which ones you are likely to be sensitive to, whereas the phenotyping can actually

identify the individual drugs to which the virus remains susceptible and then complex genotypes of apparent multi-drug-resistant phenotype where, in a potential of mutational interactions, you can find a drug or two by phenotyping that you won't be able to detect with our knowledge of genotyping.

[Slide.]

For phenotypic resistance testing, I think technical validation remains an issue as well. Of bigger concern are the current susceptibility breakpoints where they are actually set somewhat arbitrarily not related to either clinical progression or to loss of virologic control. I think there is going to be a major effort by the companies to get these breakpoints better established.

A concern is, right now, that it appears that the non-nucleoside susceptibility breakpoints from all the current assays may be set a little bit too low for sensitive virus and they are calling a few false positives for low levels of resistance.

Clinical-utility data is clearly coming from these types of assays but there are no prospective trials available to report at this time.

[Slide.]

So, where are we? I think, for biologic plausibility, this is a slide similar to the slide I

presented in 1996 to this committee for viral-load measurements. I think, for biologic plausibility, we certainly have that for both genotypic and phenotypic resistance. There is good retrospective data for quite a few drugs that both genotypes and phenotypes can predict response to drug and can predict loss of activity to the drug.

For prospective data, the short-term data of three months to twelve months for genotyping from two trials, ongoing trials for phenotypes. There are long-term trials going on for both types of assays at this time.

I point out to the committee that, when it was presented with the decision for viral-load measurements, an approval of viral-load measurements, there were no prospective studies available to the committee when they had to make this decision. At this point, there are two prospective studies for resistance measurements.

Technical validation is ongoing for both types of assays and standardized interpretation in getting the standards out there is also ongoing for both types of assays.

I thank you.

DR. HOLLINGER: Thank you, Doug.

Andy, do you want to go on to Dr Murray?

DR. DAYTON: I will leave it up to you.

1	DR. HOLLINGER: Let's see if there are some							
2	questions here of Dr. Mayers.							
3	DR. CHAMBERLAND: In the packet of information							
4	that we got, there was a recent Lancet publication on the							
5	results of the VIRADAPT study. Has the GART trial been							
6	published?							
7	DR. MAYERS: The GART trial has been in submission							
8	to JAMA for over eleven weeks right now so that if they ever							
9	release it, we hope they will publish it.							
10	DR. CHAMBERLAND: Because one of these papers, I							
11	think, referenced an abstract for the GART study. Could you							
12	just clarify, in the GART study, in the methodology, in the							
13	GART arm, physicians got results of genotypic testing. In							
14	the non-GART arm, what informationI wasn't clear, exactly.							
15	It looks like they got the recommendation from							
16	DR. MAYERS: No.							
17	DR. CHAMBERLAND: No; they didn't get anything?							
18	What did the non-GART get?							
19	DR. MAYERS: What the non-GART got was that the							
20	team gave them the current recommendations and they gave							
21	them regular updates from the ongoing meetings for salvage							
22	regimens in that population. So, basically, we sent out to							
23	themafter each meeting, we would send out to them an							
24	update; "Here is what we are seeing with these drugs in							
25	these types of patients."							

So we did an educational component, but we did not give them direct recommendations.

DR. CHAMBERLAND: So they just got general guidance about current thinking for salvage therapy--okay.

But even in the non-GART arm, would you feel that clinicians were probably getting more information than the average treater gets because--

DR. MAYERS: I think that is fair. I think the thing that has encouraged us that this was not biased in a significant way is the French study where there was no expert advice given at all and all they got was the genotype given back to them. And the fact that GART and VIRADAPT essentially lie on top of each other at similar time points suggest that there was, probably, not a huge bias in that.

DR. CHAMBERLAND: Can you tell us more who the physicians were who participated in the GART and the non-GART arm? Where I am going is that I think there is a spectrum of treaters out there who treat HIV patients. At one end of the spectrum, we have folks like yourself, very knowledgeable, involved in research and, at the other end, are treaters who--and I think they may constitute the majority of treaters--who really are trying very hard to keep up with a moving target.

They have these publications from the Public

Health Service and from these advisory committees about what

1	to do, but they are not really well-educated about							
2	genotypic, phenotypic, information, et cetera and they get							
3	these very complicated reports from these laboratories.							
4	They are tough to interpret. I do very limited clinical							
5	work and it is tough.							
6	DR. MAYERS: I have the same problem, myself,							
7	getting some of these reports.							
8	DR. CHAMBERLAND: So I kind of wanted to know,							
9	because we don't have a publication, unfortunately, who was							
10	in the GART trial, where to they fall in this spectrum of							
11	treaters because I think this is important to the committee							
12	ultimately having to vote on this issue, to have a kind of							
13	an understanding of what information is going to be							
14	DR. HOLLINGER: Yes; and how was it determined who							
15	was non-GART and GART?							
16	DR. CHAMBERLAND: Exactly.							
17	DR. MAYERS: Basically, I want to apologize to the							
18	committee for giving you the GART study but the rules that							
19	the FDA operates under are if I give it to you, I have to							
20	put it out on the table out front. Since it is still in							
21	submission to JAMA, I could not give it to the committee.							
22	The clinicians throughout the CPCRAthese were							
23	the community docs in the CPCRA system, so they were at all							
24	the sites in the CPCRA, randomly out there. Any doc who							
1								

sent a sample in could participate from the CPCRA.

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	93								
1	The randomization was done in such a way that the								
2	patient's provider would send a sample into the team, the								
3	group of virologists would look at the sample, interpret it								
4	and get the report done, submit that report to that stat								
5	center not knowing if they were going to randomized or not,								
6	and then the stat center would roll the dice and randomize								
7	them after they had received the report from the virologist								
8	back to the field.								
9	So, basically, this was a large group of community								
10	physicians throughout the United States and the reports were								
11	done the same if you got the report or didn't get the report								
12	as far as the virologists were concerned. We didn't know								
13	who was going to get a report when it went out.								
14	MR. DUBIN: So any one physician who has seen								
15	multiple patients, sometimes he is going to get GART and								
16	sometimes not?								
17	DR. NELSON: Yes; there were some physicians who								
18	treated a few patients with the genotyping and a few								
19	patients without it. That's correct.								
20	DR. HOLLINGER: And decisions for changes by the								

non-GART was based on CD4s and HIV concentrations that they received back?

DR. MAYERS: The clinicians and the virologists in the study knew CD4s, viral loads, and they also knew the treatment history of each individual patient. So you knew

how	man	y di	rugs	they	got	and	what	drug	gs t	they	had	had	tox	cicity
or	not	had	tox	icity	on.	So	it w	as tl	he d	data	that	wo.	ıld	be
con	vent	iona	ally	avai:	lable	e to	a do	ctor	tre	eatir	ng ar	THI	7-	
inf	ecte	d pa	atie	nt.										

DR. HOLLINGER: And he would make a decision, or she would make a decision, based upon the results that came back to that person.

DR. MAYERS: When the patient came back to the clinic for their randomization visit, the doctor would either get a GART report and have to tell us how it impacted his decision making or her decision making, or they would not get a GART report and have to use the data that they had had available to them prior to make a decision as to which drug to switch to.

DR. TUAZON: In terms of having--once this test had been approved, where do you see the clinical utility of both assays? I think, for the experienced, PI-experienced patients, you probably would just go ahead with the phenotypic. Accounting for the cost of both of the assays, what are the practical uses of this?

DR. MAYERS: I think one of the real surprises that we have seen across both studies has been that the relative benefit has been the same across rounds of therapy. But that is relative benefit in the face of a shrinking response.

What I see happening at this point is going to be in newly infected patients who you know are newly infected, not patients who walk in with PCP but newly infected, that they are at fairly high risk and I think there is going to be a move to take this testing to look for newly infecteds fairly soon because the rates are clearly above 10 percent in that population right now.

For other patients, I think we will use CD4 and viral load like we currently do. A person who is below 50 copies and is doing well without a genotype, I don't need the test. I think, on early rounds of failure, you will probably see genotypic testing used on those patients because it has a fairly quick turnaround time which will probably start to drop to less than a week as market forces develop and it is less expensive.

I think that, for people, as they get to the point where the genotype becomes different to interpret and they can't find the drugs they need, you are going to see a shift toward phenotypic testing because it can find holes that you can't find with the genotype testing in these individuals. That current assessment is based on cost and turnaround times.

If the phenotypic companies can get their cost down in the same range and the turnaround time in the same range, I really don't see a great deal of difference in

early failures between either methodology. They can both show you where there are potential holes to get active drugs and they can both show you were resistance exists.

So a lot of it is going to be how fast they turn them around and how much they charge you. I think the interpretations are clearly improving a lot recently. The reports clinicians used to get back a year ago, and even with some companies, as was stated, get now can be difficult to interpret.

I know they are difficult to interpret when one of my docs brings it in to me and I look at it and scratch my head and try and figure out what they are saying so that I can tell him what to do. I think that this is an area where there really does need to be some work by industry to develop a standardized reporting format.

I can tell you that there are some groups that develop computerized algorithms that give a very nice report that says, sensitive, partially resistant, resistant, just like you would get from your microlab for a bacteria. And you can do it for both phenotype and genotype if the companies want to.

DR. NELSON: Again, back to the GART trial. You gave the randomized physicians recommendations for which drugs to use. Did you also measure how the recommendations were followed by the patients and the physicians? Was that

done?

DR. MAYERS: Yes; we did. Actually, the scariest comment from my first IRB was when the head of the DSME asked me did I actually think the docs were following my recommendations. The honest answer is that some did and some didn't. Some used the data in their own way--

DR. NELSON: It is not only the doc. It is the patient.

DR. MAYERS: Yes; I understand. The bottom line was that for docs who took the advice regularly and consistently, the difference actually increased to almost a log difference between the GART and the non-GART arms. For the docs who didn't use the advice given, it narrowed down considerably. I think that this is one of the things that is going to drive HIV care, especially for the experienced patient, into the special provider and take it out of the primary-care realm.

This is just too complicated to deal with the cross-resistance issues and try and deal with the drug interactions to select an effective non-toxic regimen for these patients.

DR. HOLLINGER: Doug, along those same lines, you obviously have patients who are receiving information that you are imparting to them in the GART test and I presume the same thing was true in the other study.

So what was the compliance? we now know that					
probably the greatest challenge is making patients					
compliant. Those patients who are not compliant with their					
medications are the ones who different resistance the					
fastest. So the issue would be is that in the group that					
was not getting this information, did you measure					
compliance, other than just asking the patient. Were there					
any other basic measurements to be sure that these patients					
were taking their medication as were the ones who were on					
the GART trial					

DR. MAYERS: We are currently going back into the trial. This trial, when it was originally done, was done as a pilot study that Tom Merigan and I and John funded off our laboratory internal budgets. So there was a certain limit as to how much testing we could do for free.

But what has happened is those restored samples done at every time point on these patients and we are now going back into these samples doing genotyping, phenotyping and drug-level measurements at every time point for every patient with support from a number of the companies. And we will have that data to bring back.

We did not have timing so I won't be able to tell you high/low. But I will be able to tell you, yes, they had drug or no, they did not have drug, of a very sensitive assay. The data from the French trial that was recently

completed with de-escalation of therapy suggests that this is adequate data to at least predict were they taking drug at all or not taking drug.

And so we are looking at that but it is not available at this time.

DR. McCURDY: It appears that even though there are certain mutations where it is pretty well established that either alone, or in combination, they confer resistance. The question that I have is suppose a new mutation or a new group of mutations seems to correlate with resistance, perhaps, to a new drug or something like that.

How is the decision made as to how this new work is interpreted? Is this based on limited data and then you follow along?

DR. MAYERS: Basically, I can tell you how we do it in the CPCRA where I have a little control. Basically, if the mutation associated with loss of viral activity of a drug or is associated with a clear change in phenotype, we will add it into the algorithm fairly early on and then look for its impact prospectively.

I think what is developing over time is a number of groups, the CPCRA, a number of industrial groups, the ACTG, are developing very large databases that include mutation's response to the next round of therapy. So what is going to happen fairly quickly is that as soon as a

mutation is detected, or what we think is a polymorphism today is shown to be a true resistance mutation, you are going to be able to have two or three groups very rapidly tell you, yes, we see this to be true or no, this appears to have been an artifact.

So I think the ability to actually confirm or rule out these mutations in a very rapid fashion is actually getting much better almost by the day.

DR. McCURDY: Dr. Stroncek made the analogy to HLA typing. For a number of years, there were workshops that got together that developed--wet workshops and others that got together to define new types. Is this sort of thing happening? Are the databases getting together or is this an individual entrepreneurial activity?

DR. MAYERS: The honest answer is it is not happening as much as it should. One of the problems is that each of the major commercial sponsors have developed a proprietary algorithm which they are trademarking and patenting as quickly as they can so that we don't have sort of your blue-collar framework everyone agrees to at this point for either breakpoints for phenotyping or genotypic interpretation.

I think this is an area where we can do better and this is an area where I think there could be some useful work to develop NCCLES type of standards for genotypic and