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>> Welcome everyone and thank you for joining the American Brain Tumor Association's webinar series and thank you for participating in today's free educational webinar of the third webinar offered in May during brain tumor awareness month.

>> Our webinar today will do that --address genomics and bring tumors. Directed by Dr. Will Parsons. All lines during the webinar today are muted . If you have a question you would like to ask please type and submit it using the question box in the webinar panel on your screen. Dr. Parsons will answer as many questions as possible at the end of the presentation. Tomorrow you will receive an invitation to complete a brief feedback survey. Please take a few minutes to share your comments about today's webinar. Your feedback is really important to us as we developed future webinars that we are recording today's webinar and will post to the ABTA website. Let's pause for a moment so we can begin the webinar recording.

>> --The American Brain Tumor Association is pleased to welcome you to our webinar series, our webinar today is genomic implications for brain tumors. My name is Jillann Demes, Senior program manager at the American Brain Tumor Association. I am delighted to introduce our speaker today, Dr. Will Parsons. He is a pediatric neuropsychologist and codirector of the neuro-oncology program at the Cancer genetics into gnomic program at Texas children's Cancer Center. Baylor College of medicine, his research focuses on the clinical application of genomic technologies and pediatric cancer care. He was fortunate to receive a ABTA Fellowship in 2007 which supported his early research on the genomics of glioblastoma. Thank you so much for joining us Dr. Parsons. You may begin your presentation

>> Thank you for the very nice introduction, I am excited to be here. I am going to give my talk today specifically on the topic of genomics and Brain tumors. Before we get into it I thought it would be good to give an overview of some of the topics we are looking at, some of the objectives for the call.

>> The overall goal as I said is to learn about how to use genomic testing specifically talking about gene sequencing, and those new technologies that I will elaborate on for the patients with brain tumors. Both children and adults.

>> A number of specific questions we hope to cover, first of all how can we use these types of generally test to study the biology of brain tumors and the soup --the researcher been my --arena. And secondly how can we start to use these test in the clinic. We talk a lot about personalized medicine approaches, but the question is how can we actually go about doing that. It's an entirely new area for everybody.

>> The third is what types of findings are potentially clinically actionable for patients. Trying to find things with these test that we can use to help provide information for patients or oncologist, or help decide about what treatments might make sense.

>> And finally what are some of the practical and ethical considerations in using these test. By nature they are very broad test that can provide a whole bunch of different types of information, that's clinically potentially relevant information. --Related to cancer. So the question is how do we go about doing that for our patients. Those other things we will be talking about.

>> So we still have another --a number of progress and oncology. There are still a number of challenges. I can summarize those in terms of examples with a pediatric patients in three different ways.

>> The first is there are still a number of the specific cancers that are very hard to your. Some we do a better job of and some words, but some are really difficult to cure.

>> And the second is even those treatments that can be effective at treating, can obviously very challenging for our patients in terms of toxicity source side effects they have at the time of the tumor, but also later on. This is an example of a pendulum I. Enhancing this tumor you can see that. The tumor itself. That is the tumor that's in theory curable with a surgical section and radiation therapy. You can imagine how it would be challenging and difficult to take this out. It can be done but it comes at a decent cost.

>> The third is we would really like to know about these tumors earlier, before they grow and cause the symptoms so we can work on preventative. In summary, we still have a long way to go. We were hoping to use genetics to learn about how to use or inform neurobiology as a way of approaching this.

>> This is a summary slide recently showing schematically an example of how we think of cancers forming. When we say cancer as a genetic, I don't mean in all cases or most cases, inherited directly through the genes. What we do mean is there is a sequence of events or mutations are changes that take place in the normal cell of the body that eventually leads to having a capacity to become a tumor and metastasize as well with all sorts of problems.

>> This diagram shows on the left, the best example of what we have --it's really clearly delineated in: cancers. In this case we start with the normal epithelial cell or normal cell of the body. And each of these items on the block --on the top, the APC, the cave rats, different genetic changes that happens in that particular tumor cell allowing it to go from normal biology onto a cancer. So what I say cancer is a genetic disease that the disease of the genes. To talk about terms, genetics and genomics are two different terms. They really just refer to the scale of things work genetics are the study of genes or individual genes. And genomics are the study of all of them or many of them. And relevant to recent years a number of technologies that allow us to test huge numbers of genes in tumors or patients brought to us, not just one or several but hundreds. That's what we have been working towards. The type of information we are trying to use.

>> So there's a couple of other points I would make about cancers. One is of the disease of mutations in genes and this is quite complicated. It's not the case that each tumor of a different our specific type as the same mutation or the same genes or same biology, but different tumors in different patients with tumors are different in some ways. What we tried to do is learn about how to make the differences or understand what that means for individual patients.

>> The slide shows an example of a representation of all of the mutations in different genes that are found in a particular type of cancer. Each one of these dots represents a different gene. The height of the peak or mountain on those genes is representative of how common that particular gene is and how relevant it is for the tumor study.

>> And then you line up the chromosomes which are --going to all of a person's DNA to the end. As you can see here in this picture, there are several of these genes, the mountains that we know are really important to cancers and they occur in a large portion of cancers, and those are obviously areas of research.

>> What we see is although some of those, there are many of more smaller, where an individual gene might just be mutated in a small percentage of patients with brain tumors for example. 1% or 3%, or a couple of cases.

>> What we need to learn is not to how to use the common things like the mountains but also the less common. That's where we hope to find individual patient tumors.

>> The way we try to make sense of this in terms of treatment, we try to simplify it. Instead of a particular mutation we are often talking about a particular type of biology we think is important to the cancer, then we can design a drug.

>> This is an example of what we call in the diagram showing a molecular pathway, a signal pathway. This is the pathway the cell uses telling it to grow or whatever. So this cell line is the membrane on on top is the outside the signal cold --some signals come from the outside and it goes to each of these different genes and they activate each other in the downstream signal. And then it causes the cell to have an action such as divide, grow or do something

>> What we found is we don't necessarily need to think about mutations or any particular mutation but in this case the mutation of any of a number of different genes all in this one pathway that could have a similar biological affect of turning on the cells and so forth. So we don't have to design a drug for each one of these individual targets so to speak, but if we design something that shuts down a circular pathway in general that might be effective.

>> So were trying to take what is, --quite complex, and make it into something simpler. That is the big challenge

>> The other thing I would say is although in most cases cancers are not inherited. Meeting there wasn't something inherited from a parent that caused that cancer to occur. It does happen in some cases. Obviously we know about it happening in an adult, sometimes in ovarian cancer gene. But it can also happen in children. This is an example of the case where a single patient had a pediatric cancer and each of these circles or squares represent other family members and anywhere there is color it means there is a cancer.

>> What we try to make the point, were trying to learn about the changes present in the tumors and not, and also inherited changes that might produce those cancers.

>> So how do we look at these types of changes in genes and mutations to figure out what they mean. There is a number of methods in recent years to identify for gene sequencing rDNA sequencing, RNA sequencing. Genome sequencing or etc. Genome sequencing or etc. What with a are referring to is different ways to figure out what is the sequence of the DNA or the RNA of the genetic material in a particular patient or tumor.

>> 25 years ago or even 10 years ago, this would be a fishing expedition. Is roughly 20,000 genes and if we were interested in anyone you could spend a career studying that one gene, looking at the mutations that trying to figure out what it means in terms of biology. The biology part takes a long time.

>> So you don't --you have a candidate and use am interested in this particular one. Now that there are differences in technology that allow tens or thousands or the entire genome meeting the entire

DNA to be looked at, we can do this in a much higher throughput way. We can actually do it on a much larger plane.

>> This a number of different methods and test. This is just an example of some of them. The details are not specified. A single gene sequence see --sequencing is what we have done in the past. A targeted panel sequencing our test that might studied 50 genes are 100 genes. Let as test used clinically sometimes. A number of genes for particular disease

>> Been you can do the whole Excel --XM sequencing exome sequencing . And then there's whole genome sequencing which is all of the DNA card not just the parts --. The list goes on and on. The basic that the polls are we will try to learn about how to use all of these to take care of patients.

>> So this is not drawn to scale because if it was the red line would go way off the slide. This shows the progress that has changed over the last 10 to 15 years. Before 2003 in these new methods, as I said looking at one gene or analyzing one gene in a patient would be quite a challenge. And now in the earlier to thousands, you can look at families of genes concept of genes. And in 2006, this is where exome sequencing came into play.

>> And more recently the genome sequencing.

>> So the general point is we now have technology to identify far more interest is information than we ever have before.

>> The challenges what to do with the information.

>> These are methods that have been used to analyze all sorts of tumors and identify new genes that are occurring in particular to lead to a logical studies and how those genes might be used. There are 1 million cases of that and I show this one for a type of tumor I have studied in the past, major low-price stoma -- Medulloblastoma. This is one that has been funded by the ABTA and I'm very grateful.

>> This is a picture of the patient with a Medulloblastoma and the tumor back here is the right thing, this is what it looks like under a microscope. And each one of these is a different gene we current in mutated in patients more than once. Some of these are ones that we knew and some like the red ones are a particular function of have a structure DNA and how they allow gene regulation to occur. --They were not known to have anything to do with cancer and specifically brain tumors. But now I pointed out in area we have gone on to study to utilize this information not just for diagnosis but to design better drugs.

>> And these are methods that have been used for a long time.

>> What were interested in doing now is how to take the same sorts of test and use them in the clinic. There are a number of ways these might be useful.

>> The first is beyond the histology or what the tumor looks like under a microscope, we can actually define what the diagnosis is. The individual tumor types, if there's confusion between the different cancer, based on what it looks like under the microscope. And in addition we know there are many subtypes to these tumors. Not just one biology of Medulloblastoma Medulloblastoma that different types of that have different --and the theory might be treated in different ways. This allows us to find that and we can use and hopefully to provide better information about prognosis and expected outcome and responses to therapy for a patient. Then we can decide what the best treatment might be or whether more or less treatment for a particular type of medicine might work for both patients

>> And we can use this information to figure out in terms of clinical trials and pry toward ties -- prioritize the findings for further study in our patients and using better treatments and how we go about doing that.

>> There are many types of clinical applications to be used.

>> Going back to the example of Medulloblastoma , this is one example of us comedic --a schematic for how this can be used. This was published years ago by Michael Taylor. What this shows essentially is at the top is an analysis of molecular analysis expression for a certain type of genomic study. For a number of patients it can be used to categorize them in different groups. These are all patients of Medulloblastoma. Each of the columns here is a different patient and the red and the blue shows what genes are turned on and turned off. The point is by doing this analysis, instead of one disease of Medulloblastoma , which has a certain characteristic, there are specific biologic subgroups, the blue and purple called the --particular biologic pathway. Or the hedgehog pathway or these others that are not as named we are still figuring out what they do. The important point is we can figure out these tumors in different biology's so that not all Medulloblastoma are the same . It's not just for designing treatments for these groups but also in terms of information and provide strategies.

>> This for example, this curve the why access, probability of survival for a patient. And the other axis from left to right is how long. So if you start here with the patient being diagnosed. And overtime obviously some patients have problems related to their tumor. What you can see us by the different colors of these different groups there are very different outcomes. For example the blue line which is the with tax way -- WNTpathway. --Some of these other groups it's very different. Obviously these are patients where we need to think about different strategies, different treatments are clinical trials. This type of information can really help us provide information to our families and other oncologist.

>> And there's also obviously the dream is to design drugs to use for these. This is an example published about five years ago for the disease of Medulloblastoma , and adult with Medulloblastoma . The Medulloblastoma had spread outside of the brain and went throughout the body and it was treated with a specific pathway inhibitor targeting the hedgehog which was mentioned.

>> This is the before, each of the black bits are places where tumor has spread. It is really all through the skeleton and the spine and the shoulders the pelvis and it bones. --Hipbones. In this panel shows what happened after treatment with a single inhibitor. Basically all of these dots are gone. This is the hard in as the bladder. The tumor when entirely away temporarily. Our finding medicines that work, but using it in combination with other treatments just like for other cancers. This treatment alone, the tumors started coming back.

>> So that's what we are trying to discover I find drugs that will improve the outcome for patients and figure how to use them with other therapies.

>> That is the overall goal of using genomics for personalized cancer care. Taking these methods we are talking about whether they are exome sequencing or genome sequencing, to take care of patients and take care of their families. Instead of a patient having surgery and being diagnosed with a particular tumor type like Medulloblastoma, all getting the same treatment, hopefully by our knowledge of the gene biology we can decide which patients need what treatment and what treatment they might best have.

>> That is the dream in the personalized medicine.

>> The rest of the talk I will move to talking about ways we are trying to study this process and overcome these challenges and what type of information we can get in this approach.

>> This is a list of some of the challenges.

>> The challenges to be on the take genetic information and then use it. It is a long list. First of all we don't understand what many of the mutations in much of the biology we find these tumors. It is a very gray area. Our basic research we can find some gene that mutated into a brain tumor and study what that means for this model. The subcultures and that sort. In terms of direct, applicable in the -- applicability to patients there is some lag time.

>> And secondly there's a relative limited number of preclinical models. Various types of models we can test therapies.

>> The third is all of this information about specific genes and targets is relatively recent. So drug companies are rapidly developing agents and drugs to use for these purposes. There is an ever-increasing number of them. The fact of the matter is it still an area of growth. We are still acquiring a number of drugs even if we find a particular mutation in a gene often times there is not a drug available to target it.

>> And the fourth, we are not used to using these sorts of test in the clinical. The broad genomic testing, giving all sorts of information about tumors and how it developed. Much of what I'm going to talk about the rest of the talk is our experience here at Texas Children's Hospital at Baylor College of medicine, doing a study of this type of setting for our patients and what we will learn from it.

>> The last is there is a lot of challenges of clinical trial design. It is great to say that the Medulloblastoma for example is not one disease but a number of different diseases and we will treat them all in different ways. What that means is if we do clinical trials where we separate them out in the subtypes, trying to improve using our drugs in clinical trials so we can improve care for the patients.

>> Then we get into smaller numbers, very specific biologic tumors. The other part I would say is often times for patients of brain tumors coming back, biopsies, getting material to use for the treatment of what a patient might get can be a challenge. So it's a longer list.

>> So the rest of the study I will talk about a particular article study we are doing as an example of the ways in which researchers and cancer doctors are trying to learn more about how to do this process a study called BASIC3 . I share it with --at cancer geneticists here at Texas children. Sharon plan.

>> So the goal is to take medicine --certified in the clinical laboratory, sequencing in the care of the patients. Setting up a process to do this clinically, explaining it to the patients, and interpreting and figuring out how to use it that is the goal. And then evaluating the impact of the information for the families and our patients and physicians ear it isn't a study when studies are being dictated by the results of the genomics that one where we are doing genomic studies in the political arena and then finding where we can have useful information. I will walk you quickly through.

>> For a couple of years we were and rolling about 280 children with either brain tumors or other solids. Blood and tumor samples are acquired from the patients. They go to the CLIA to have the genome sequencing done . And like other clinical test, the blood Countess done in the hospital in there are certain quality criteria, standards for citing the results and interpreting them. It's all done in that same way in then you do a clinical test. To reports get generated, this anomic somatic --the somatic. The other is a germline list which has information about why the patient might have --in the blood and why the might of developing cancer or have risk. The question is how much information --.

>> The results go back into the medical record or the EMR. Along with the patient's primary oncologist and genetic counselor, those results are given back to the family and discussed with the family and then any appropriate follow-up or intervention, whether another clinic or treatment can be taken pick

>> Then we follow the patient for several years after that to see what decisions get made based on this information and what the outcome is. The mutations are.

>> This is a study of the practicality of doing genomic in the clinic. Learning about the process and how we can best do this for our patients. The rest I will be talking about is some of the preliminary results in the examples of what we can learn from this study which I hope will be interesting

>> So we are more than halfway through the study so far. This 150 patients enrolled and also parents of the patients because not they have the genome testing done but they are interviewed and surveyed and provide blood for the child testing.

>> All of our pediatric oncologist, a similar source study, in this case children at Texas children. This pie chart shows where not ticking specific diagnoses, were talking about all different types of tumors. Medulloblastoma is in blue , low grade: Noma is in red. In both adult and pediatric cancers, there's a pretty great diversity in the sorts of things. We are trying to study not just one type but all of them.

>> So the first observation I make is our families and patients are very excited about this approach. Both a blessing and an opportunity and a challenge. More than 80% of the families agreed to participate in the study. Of the ones that say not participate, the majority is because they are not interested in dissipating in a research study at all because they're so overwhelmed by the new diagnoses. Or they are just so busy with stress and etc., are not able to participate.

>> The number who have objections are about the privacy and the genetic testing, the blood draw is much lower. So the families mostly agreed to participate in the challenge is to make it clear to them that this is still an area of investigation and we cannot promise the person will see benefit to this. We were really trying to learn. That is one of the challenges.

>> So this slide just shows an example of some of the practicalities with using this type of approach. Everything has to be figured out. Talking to the families and patients and contain --obtain consent for example how the samples get handled. Newly diagnosed patients, they have surgery, study enrollment is offered. The tumor sample goes to the clinical diagnoses. And if there's any left there is some fresh frozen tumor and if the patient enrolled in the study that gets sent to the clinical lab and handled appropriately. --Are molecular pathologist here.

>> The simple fact of getting tumors where they need to go for high-quality samples is critical.

>> I member of research questions we try to answer in the study. The first is number one the clinical questions. For example the goals of providing the tumor results, what we can learn about the cancer, is response might be to the treatment.

>> And also about the blood and the results of the germline. What we will talk about mostly is the tumor genomic results and how that might be applicable to the patient. In particular those patients whose tumors come back and they need additional treatment.

>> We try to look at how important a mutation we find our in a number of ways. First of all we observed with the oncologist do for the patient. For example if we find a mutation based on this type of testing do we actually use it to make decisions about what drugs to give the patients. We also survey and interview the oncologist at various time points. The other thing we do is the list of mutations they get identified, they range from none in their to mature around 80. They categorize

based upon how clinically applicable they are. Ranging from category one radiation --category one mutations whether some establish clinical utility. There is information about prognosis or specific therapy. These are the things that get tested for anyway basically. Category 2 is a much more interesting category with potential clinical relevance. Cases where there might be experience with targeting a particular gene, for example met. Not commonly known to this particular tumor.

>> And they might say I think this drug potentially could be of use to this patient, but there is not a lot of data. That's where we try to learn about this.

>> And third, mutations and other genes associated with cancer but we don't have clinical --.

>> And then gray is all other mutations. We don't know almost anything about what they mean for the patient's cancer. There are all types of mutations.

>> One thing I show us the majority of this lightest gray. Most of the mutations that are found in patients tumors, we don't know what the relation is to the cancer.

>> This shows each row the different patient, the different tumor types, they are all just lined up. From the most mutations to the least ear and then the height of the bar is how many mutations were found. It ranges from about 80 going down to zero.

>> The vast majority of these as I said are gray, meeting additional research is necessary to figure out what it means for patients.

>> You can see there's a little bit of yellow, red and orange. Those are cases where there is something that's potentially --that's what we are focusing on.

>> This is another way of looking at that. From an individual patient level how often we find mutations at different levels with clinical levels. The color coding was on the previous slide. For example about half of the patients don't have mutations in any gene that we understand to be related to cancer. That's for future research.

>> About half of them do have mutations that are either direct utility or other cancer genes that we are still trying to learn pics this is from one test.

>> So combining different types of test we make this red, orange and yellow, to provide better information for most patients.

>> This is just a list of some of the genes not specifically important. There are some genes we see that are frequently mutated. Those are obviously clinically interesting. Again this many important genes we only find mutated in 1/80. For example there is a okay --out --these different mutations. These are something that are interesting in the findings.

>> A specific example of one of those cases work a 14-year-old boy with a tumor in the cerebellum. Under the microscope it look like Medulloblastoma and that was the diagnosis. The pathologist, did unders --other stains to look and see what biologic subtype we think it is and that sort of thing. Those results in this patient were a little confusing.

>> So we did the tumor test. A number of different results that are potentially interesting. Each one of these blocks is an analysis of a different gene.

>> In each case the normal sequence in the present --patients blood is on the top. And this is a read of the DNA. You don't see any changes here. Where in the tumor you can see some cases where there's a different letter. Those are where there is a mutation. In this case there was one mutation in a gene --. And also another in this gene. So these define the patient tumors to a specific subtype of

Medulloblastoma , which pathway. Those patients have an improved prognosis and this is important information, especially how to talk with your families.

>> And then there's another me Tatian --also has some information for some patients about prognosis. There is various clinical trials to target pathways related. And there's also mutations in this and that gene. These are cases where the biologic pathway are ones that are kind of targets for investigational agents. By doing this testing we can see not just confirming more about the molecular diagnosis or subtype, but also potentially relevant information for future therapies.

>> That is the sort of things were trying to get. So we have now the WNT , the prognosis is good and then it include specific genes that might be relevant.

>> The other thing we try to do is the exome sequencing , but also all sorts of other test. To learn what is the, in the end the methods we can use as useful information. The are in a, not just the exome but a couple of things with genome sequencing. So the case family also gives us permission for other studies.

>> We are working to learn more about the tumors.

>> From this point I will talk about the tumor in which we find mutations. The other thing we are working actively on is trying to figure out more about with the mutation means that we have a list of mutations, ideas about what that means for treatment, but the question is is that useful. If you targeted one of those genes that is mutated into a tumor would it actually do anything. There are all sorts of methods we are using to develop model systems. And this is a researcher at Texas children's. You develop these models of brain tumors by using tumors and this is --injected into mice. They can take a human tumor which has all of the biology of the human tumor and put it in a mouse and then you can do the certain models to learn more about the biology and also test ways to test particular treatment approaches with drugs or immunotherapies that might just do this before it gets to the patient.

>> Even though we have a list of mutations we can learn about what we are doing.

>> So far I've been talking entirely about the tumor, the last couple of slides we will point out this other considerations they get a lot of attention pick

>> We are also by sequencing the blood of the patient we are trying to provide germline or inherited test results from families. We can see if there are risk that years there that explains or helps to explain why the patient developed cancer. If there's a mutation in the gene that predisposes patients to varying tumors and other cancers ear and that obviously can have potential impact for genetic testing of family members of that surveillance strategies for example, MRI scans or other screenings for patients we know that are at risk of developing those tumors. To hopefully diagnose early.

>> And were interesting in finding results that are critical to patients but not related to the cancer. Other diseases.

>> This is an example of one of those cases of inherited answer mutations. We had a patient of 14 years who had a brain tumor. The medical record showed no evidence of any family history of cancer. So the blue Mark is that there were cancer and then the other siblings and father and mother none, however when we talk more to the family there is cancer it's just not directly in the mother or father.

>> It was suspicious for concern about some familial risk. So when we sequence the patients blood we were able to find a mutation of a particular gene called MSH2. So identifying these results it has implications of both potentially in some cases up for the treatment but also for other family members

who might or might not have this sort of result. One of the things were trying to do is not just treat tumors but prevent them or diagnose them early if we can pick --. The results can also be related to inherited possibilities.

>> So these are other test like exhume --exome sequencing . For instance the tumor report, and the blood or germline report where you can get pathogenic information related to cancer or if they have another disease. We also get VUS which is significant. In a cancer gene for example but we don't know how. So the equivalent of some of the tumor mutation we are still figuring out. Those are there and we can also find mutations that are medically actionable in other ways. Said the patient is at risk for heart rhythm problems or heart attack, having seizures or something along those lines. An example of that is this --sodium channel mutation associated with the risk of heart rhythm problems.

>> In addition we can find mutations in genes PCG, pharmacokinetic. They can tell us how a patient might metabolize at higher or lower doses of drugs. We can also find information about talks about the risk of being a carrier for other genetic diseases and all sorts of other things. This is just an example showing we may do this testing we need to not just consider the tumor results not what we can see in terms of other diseases and findings as well.

>> --Having people available for this testing could be very important in the clinic.

>> So these are diversity of results. I set up 34 patients. The germline or blood result and the tumor results and the different categories of what types of clinical health information. You can see there are all different dots in these categories but a number of patients who have findings either in the tumor or the blood that is some potential relevance. So defining this further, figuring out had use better test to yield these things for patients is critical.

>> The other thing I would say I haven't talked about at all is in addition to doing this testing we have a whole team of emphasis and social sciences specializing in --who record some of these visits between oncologist in families where they explain the results and they can try and learn what we are not teaching or explaining well. What types of questions families asking how we can better address them with the testing.

>> Also about the preferences and attitudes of both the oncologist and the family members regarding these tests. How we can use this information. That the idea is to integrate this for care.

>> So were trying to use these in --trial. What I'm talking about here is all observational. Meaning we are doing this testing to provide the information to the oncologist, but we don't also necessarily dictate this. It's more interventional where we can depending on what the test shows patient gets different therapies, but more importantly we need a study that in clinical trials because of the approach we are taking. That is what we are trying to do it the challenge becomes as we mentioned on numerous practicalities. This slide when we surveyed some of our oncologist at Texas children's, talking about with different genetic pathways or the biologic pathways are important to target in the clinical trials. And the size of each of the is --these words is about how frequently they came with the response. A number of different things. The fact of the matter is although we have great ideas about these things, and some of them are in current clinical practice, many more are in investigational practice, still learning with the to --doses in toxicities. A complex process but it's very exciting

>> In conclusion I will tell you that hopefully this was an example of some ways in which genetic and genomic approaches are helping us learn about rain tumors and other Central nervous system cancers.

>> The second is the results of these studies as real clinical applications and a parcel bull lead to improvement in patient care.

>> We are still learning about the process. There is some testing that can be done but nothing like what will be in 5 to 10 years we can get a great deal more of information about why tumors have developed and the sensitivities what they might be. We can figure out better ways to implement that and use it for our patients.

>> This is a slide to show a small representation of the many people involved in the BASIC3 study I talked about . Starting with Schering-Plough and -- SHaron Plon. So doing the sort of things in the clinic requires I human approach.

>> The last thing I would say is the ABTA , basically which funded me in the laboratory studying in the lab several types of brain tumors, that is now involved into not just a study of those brain tumors but more clinical studies and trials to help patients. I'm very graded --grateful to the ABTA. And last but not least I should mention thank you to our patients who participate with us.

>> I will stop there. We can take Westerns.

>> Thank you very much, that was very educational Dr. persons. So Dr. persons will now take questions. If you have a question you would like to ask, please type and submit it using the question box in the webinar control panel. On the right-hand side of the screen.

>> We have a few that were sent ahead of time. Someone is asking about if they have a family history of melanoma and prostate, a strong suspicion that the genes predispose them to tumors. So what does someone do when they think that there is this trend in their family, how can they start the process to know if they are predisposed? Wherewith they reach out to?

>> That's when they need to take advantage of their oncologist. Although the an apologist are not -- oncologist are not trained specifically in genetics and genetic diseases. What they can do is help take an initial, careful family history. Often we are hurrying trying to figure out what treatments to give, asking really important questions from the family about other family members and which types of cancers or how old they were, getting that information as the oncologist with the patient they can decide whether they need to beef I --referred to a genetic oncologist.

>> Providing that information, having some good information on various family members, not just a vague sense there was some cancer back in my grandma's generation but actually having data you can provide so they can assist the risk is very helpful.

>> And you mentioned, two different parts that genetic counselors were important, and at the very end you talked about the applicable considerations. Can you talk about how those work together, because people are interested in the fallout that happens when you do find out the results that there may be these things in their genes. How do the counselors work together with the families to minimize the worry that's going to happen when they find out there might be possibilities that could happen to them.

>> A couple of points. One is we have a pretty hard bar for considering things actual. Meaning were not reporting for the studies that someone might have an increased risk of diabetes as an adult, it's more cases where if I was the Dr. for this patient and I knew this particular result from the testing, there would be something I would be supposed to do for the patient whether referring them to another specialist are doing testing. Giving them the treatment.

>> In this case, the best case scenario is where this one academic group, we have two fantastic genetic sellers who work with us, the primary oncologist are involved in the study. The most important point as we have this team approach for genetic counselors, the questions that the oncologist is not comfortable asking or doesn't have time to answer, they can help. The most

important part I think is were not just in the business here of providing information, but providing information in helping the patient do what needs to be done next. Not just telling them you have a risk, but saying here is that finding and here's what we think the risk is and here is the other specialist or Dr. or test we should do to help take care of this. I think that is pretty effective hopefully in streamlining and reducing in our experience.

>> That sounds wonderful. Someone is asking a question is sequencing could help find this Pacific site where a drug could attest to a during --gene to shrink the tumor.

>> That is a great question. That is the sort of thing we are trying to do. For example there are specific mutations in certain genes that we know what it does to that gene. So it alters the structure of the proteins somehow and makes it so it does not find properly to some other protein. There are cases where we have a good idea of the mutation. Those cases, we are using we loosely, trying to design drugs that can target that structure or shape. In that way you're talking about. In some cases that has been shown to be effective. Some inhibitors of a gene called --some cases where that has been an effective oh approach.

>> That is our goal.

>> It's exciting to think that could happen soon. Where can patients expect to go. Is it happening only at teaching institutions, is it happening at a half a dozen places?

>> It is something that is happening more and more. Using some of these test, not necessarily as part of the big trial or using the exome sequencing , but some of these test to look at genes are doing more in both oncology and everywhere. What were trying to do and the advantage to doing it in a larger group, or a place where we have all the different specialist involved to do more to study like a process of how effective that can be. In terms of this type of testing, it is something becoming more frequent. The challenges that most often results are very difficult to interpret. Although there might be something that's biologically interesting in the results, it most often is not something directly relevant to taking medicines.

>> Do you worry that if the results are difficult to interpret, that someone is not reading them that should be reading them?

>> A good question. I do worry that the results, what we worry most about is the results can be interpreted. That is the challenge. The labs are trying to do these and explain what they see in the tumor. But then it is the oncologist, or the team taking care of the patient, who then has to interpret it and decide, like a result within an hour I --MRI, deciding what to do about it. That is the part that is still a gray area. That is the part that is both a challenge and exciting.

>> Absolutely. Definitely more to come. It's exciting for the future. It looks like that is all of the questions. And all of the time we have pick up want to thank you again for the presentation as well as answering all the questions Dr. Parsons . For more information on brain tumors and other topics, we want to refer you back to the website which is abtacares@abta.org . Also encourage you if you have any questions we didn't answer today to call our 800-number, 800-886-2282 . You can talk to the health care professionals here. If we can pause for just a moment, we will stop the recording. And then we invite you all back to the webinar series to the next to webinars, the first one is Thursday, June 5, from 2:58 PM. Radiotherapy for pediatric brain tumors. Radiotherapy is an effective treatment for many types of brain tumors. There are a number of special considerations. When it is used to treat these tumors. Join Dr. John Brenneman, as he presents a webinar discussing radiotherapy, pediatric brain tumors, --therapy and late effects of radiation and children. And on Wednesday, June 18, from 2 PM to 3 PM, --treatment and care update. --Are not tumors in

the classic sense but they can be similar to certain types of brain tumors. While they are often considered the nine, these --benign, they can cause symptoms similar to brain tumors and can be very serious.

>> Richard Pearson MDF regions Hospital Cancer Center will help us understand the different types of --the treatment options we hear about and how we cope with the diagnosis. We also want you to invite you to the family conference on July 25 and 26 at the Renaissance Chicago --. To register or more information please visit brain tumor conference.org. Or call us at 800-886-2282 .

>> This completes the webinar. Thank you for joining us and please, please, do the feedback survey you will receive tomorrow. You may now all disconnect. Thank you.

>>[Event concluded]