Introduction and Guest Background

Hello, everybody. I'm very excited about our next guest today. Dr. Vineet Datta from, well, from the guitar world. And so don't get those too confused.

He is separate of the company's namesake. But this man by no means is someone who sits back in the shadows quietly. I have been blown away by what I've learned from him over the last few years in this industry, and I'm excited to share all this with you.

I was a clinician who's been looking for tools to better lead a clinical decision making process for my patients, especially those who have come to the end of the line.

I've tried a lot of different, testing on the market over many, many years. and watched many of these companies come and go. And what I've been excited about with guitar is they're here.

They're not slowing down. What they're bringing to the world is changing. The world of especially the stage three and four oncology, outcomes. So, Dr. Datta thank you so much for being with us today.

Tell us a little bit about you and your company, and then we'll dive into some really, really interesting conversation. thank you Nasha Thank you for that very kind introduction.

so I'm a physician by training, an internist. I've trained across, two different continents, initially out of India, and then I trained formally in the United Kingdom.

did my membership with the Royal College of Physicians and Surgeons of Glasgow. I'm a fellow both for the Glasgow and the Edinburgh colleges. and I have a wide interest in terms of looking at, various subsets of innovation and data at the global level, predominantly with an interest, obviously, in oncology.

I've been with the group now close to nine years. So you're right, we are rapidly not straight down as a company. We're getting stronger and stronger.

We started off as a small group of 20 individuals. We're now over 250 people across the globe. We've got three global labs. We've got four global offices.

Currently we service well over 50 countries at a global level, providing our solutions, across the entire ecosystem of oncology. we are largely into smart genomics, and oncology is of focus.

It's our baby. it's there's enough to do in that space. And we focus on the entire ecosystem of cancer, looking at from early detection to standard of care therapies.

more importantly, the innovation looking at refractory difficult to treat those dirty cancers, as we call them, where survival benefits are very limited.

Patients come to the underlying very quickly, especially for patients who have been diagnosed late, failed multiple lines of therapy. And how can we then use, smart Multi-Omics genomics, something that we will talk about today?

And how can we look at that to individualize and personalized cancer care and hopefully lead to better clinical outcomes and what they're experiencing today?

and that is largely our focus. so the remit is very much oncology focused, but it is there's enough to do in that space. it's a quintessentially an extremely complex disease, as I always call it.

there are technologies that are evolving, quicker, better, faster, almost every day. So much so it's sometimes it's very hard to keep pace.

Why Some Cancers Are Harder to Treat

and we are clearly now in a position from a few years ago where we can quantify different layers of the biological elements that contribute to the development of cancer.

We understand it much better today. And that's always important because you want to make sure, as far as possible, you're looking at credible ethical, evidence based data that helps improve, patient outcomes.

And I think integrating this multi-omics, multimodal approach, is extremely an exciting space to be. And it's clearly gaining further momentum. We are getting far more insight into how the oncological phenomena is behaving.

and I think that's helping us move forward into this paradigm of changing, precision medicine using individualize and tailor made therapies for cancer patients.

Amazing. I mean, truly and you, you alluded to these sort of harder like these, these, these, these patients that stop responding to treatments or have exhausted all of the options out there.

Why are I mean, before we dive into the testing, we understand a little bit of the cancer biology. So why are some cancers harder to treat than others?

So I think it lays down to the fact that the cancers usually employ a myriad of different mechanisms and feedback loops, various levels of redundancies at various functional levels of these at various different courses, looking at not just primary coding and transcriptional regulation of protein synthesis.

It's well beyond just the DNA and the RNA and how the tumor cells are behaving, how we're looking at various levels of signaling pathways, how they cross talk to each other.

how do we get to various different levels of, of of modification post the translation? How is that heterogeneity of tumors? How are they different even within the same subset, both inter and intra tumor.

So even within the same site tumors may have behaved very differently. we all we are learning more and more this, this this evolution of the cancer. We're looking at more of resistant variations in various pathways.

So it it builds into something which, which which which it doesn't sound simple and it isn't simple at all. so it builds into the system where you've got these multiple functional layers, which are influencing processes, which are helping us then to understand better, what are both survival mechanistic, and how do they behave individually and collectively when they interface with each other?

obviously, that the disease burden is clearly is increasing. where I've train apps off in the UK, for example, every two minutes, some of these diagnosed with cancer and experts are now clearly telling us with the outcome of, of, of the pandemic, statistics globally are only going to get worse and we are going to see a tsunami of cancer cases.

There's been serious disruption to large scale screening, and that is obviously going to have a have have an effect on over the coming decade. We will see that.

I think we've clearly seen at a global level, the number of treated patients increasing by a single digit percentage over the last few years. and that number is only going to increase.

And obviously, couple of phenomena that are leading that process. We've got an aging population at a global level. We've got various different elements of, of of treatment.

that is now available, even in the less developed parts of the world. and care is getting far, far better. even within

low income straight at a global level, this widening access to some of those therapies, and that is leading to longer treatment duration, leading to higher number of patients receiving treatment every year.

and that is now leading to increasing complexity. And this is not just at the adult level. clearly at the pediatric level as well, is clearly starting to see much, much more interest gain in terms of research and data.

And I think that will only gain further momentum, in the coming few years. obviously with cost is critical to a number of these geographies, and that is obviously going to be important and critical to that process.

I think to the point that you asked, I think how do cancer cells survive? How do they grow? How do they, move into a distant environment? when it arrives at a location which is foreign to it, how do they colonize?

again, is is is key to the spread of disease and cancer and how they beat, various therapies that are provided within the ecosystem. And how do they in that space again, some of these cancers may come back, after initial treatment.

and they can may come back for a number of reasons, either the original treatment has not worked, has not got rid of all those cancer elements, and that space has left behind a few cancers that may come back and grow.

or the cancer cells may have spread to another part, and they are evolving into a new cancer in the new tumor. And we need to understand that. Not necessarily.

Even if you've got the same organ system, all the molecular patterns, the molecular behaviors similar we've seen far too often. even if this a metastases, unless there's variation within the molecular pathway, you've got different clones driving different molecular pathways.

And different targets. And if we don't attack them together, synchronously in that space, you may take care of one cancer, but you may not take care of another.

yeah. The other challenge that you've got is potentially may be related to, to to to, surgical outcomes where you may have certain cancer cells, certain bits of cancer cells that may have broken away from the primary cancer, but they're too small to see, to the naked eye.

And this is what we call as micro metastasis. and those may spread and come back with disease at a later stage. So the complexities, again, are also bearing to the fact that we understand from early stage, late stage, the survival benefits are completely, very, very different.

And if you've got indolent cancers, which are relatively hard to diagnose because then they're not in a compact and sealed space, they're not obviously visible.

they're not immediately palpable. then it makes it extremely difficult to diagnose them. And if you find them at a later stage, then obviously it's a little bit more firefight involved and looking at, curative intent of disease.

but that being said, I think there are a number of exciting technologies out there, which are evolving and looking at these different elements. and clearly one of them is looking at, small genomics involving not just tissue, but also, the liquid biopsy world that's evolving quite rapidly.

Now, we've seen huge strides and gains over the last 4 or 5 years in that space. Huge. And, you know, just to reiterate for the listener, because, you speak at a level that most clinicians would love most and patients we've got savvy patient consumers today.

But I want to re reframe some things here. What you're speaking to is the fact that what we've spent our time doing for the last 70 or so years in oncology is looking for a single target with a single treatment.

That's still unfortunately, the majority of where our research dollars go. What we have learned or been learning in the last decade or more is that, this you spoke to this concept of heterogeneity, which is that means that in one

single tumor, you could have multiple types, you know, multiple personalities within that tumor.

And when we go after the one target, one treatment approach, we leave those behind. And oftentimes leaving those behind those other cell forms, they are more aggressive and they become even more, you know, they come back with a greater vengeance.

Liquid Biopsy and Multi-Omics Testing

I also love the fact that there's sort of that component. But then you speak to this, I almost think of it as sort of a layer of an onion, that there's not just the DNA, the circulating tumor cell DNA, the regular DNA, the micro RNA.

Like all of these pieces, you go into the exosomes, you go into all of these components, these layers of of complexity here. And so what I think is really beautiful is that we have come to a time in the world today where we can both explore that heterogeneity from a kind of the big swimming pool, high bird's eye view, and we can go into the minutia through those layers of that onion to understand some of the key drivers and some of the key, key targets within that.

So this is where the technologies have come today, is we can look at an a much broader view of what's actually going on. And then what's what's what's what's interesting is this is now pushing it's putting pressure on a medical system to also get away from a single treatment for a single target, which what's happening is the data, in my opinion, is coming out.

But the clinical side is not quite catching up with the data. So I'm hopeful that in my world, in the clinician world, we are continuing to educate and empower clinicians to know how to use this information, you know, clinically instead of just have it be an intellectual experience, which is what a lot of them still see, a lot of clinicians I speak to today still think that testing like yours and others on the market aren't just an academic exercise.

And yet I have been able to use these tools in my own patient population that have taken patients that were given no hope, no options to having, frankly, multiple options.

And that's what's exciting to me of what's coming. So talk to us. You mentioned about the smart genomics to tackle these refractory cancers. But, I know you guys have been working with or developing or part of this concept of the encyclopedic tumor analysis, big word.

But tell us what what you mean by this and how what I just described in what you were just talking to release. Yeah. Thank you. So, I always go back to the analogy of, of Alan Breed, and not many mentioned him, but he was initial pioneer, in the automotive world.

And then in the late 60s, early 70s, eventually laid out technology which gave us, passenger airbags in a, in a car. and this is, you know, well over 50 years ago, the challenge exists at a global level today where not everywhere in the world is it mandatory to have airbags fitted in, as, as a device that can help save clearly hundreds of thousands of lives and potentially over a few years in that space?

and it's a very simple analogy, but it brings to us the fact that, you know, the reasonable man always adapts himself to the world, whereas the unreasonable one persists in trying to get the world to adapt himself.

And in that case, if, if, if the progress is linked to somebody who's unreasonable, I'm very happy to be able that reasonable. Thank you. And, and I think I think from, from your point of, of, of looking at genomics, I think I agree the world is moving into the concept now, looking at tissue and blood and tissue versus blood and the pros and cons and, and they are very important to discuss and debate with the clinical community, with the patients. Clearly, the examination of tissue from a genomic standpoint has, has, has credible value.

It's extremely important. liquid biopsy is a very recently emerged as, as potentially a reliable alternative. and they provide us with, with, with clearly some benefits, whether it's looking at precise molecular data for improving clinical, management, also looking at it clearly a much less invasive way of following up those individuals,

sometimes it's extremely impractical to keep on repeating physical biopsies.

clinical conditions of, of some of these vulnerable patients, may not allow us to have a physical biopsy every time in that space. And I think what we need to understand is whether it's, through a physical or tissue, but, largely these cancers are releasing, DNA fragments, tumor cells, well known as circulating tumor DNA or circulating tumor cells that are then responsible for either spread or for progression within various different elements, and as they originate from the cancer, which we are able to detect either through blood or tissue or blood fluid or even urine and sciatic fluid, it allows us to identify evidence of underlying cancer in that space.

these cells can again aggregate the various levels. they can for micro emboli. They can then look at a potential spread. But eventually when we look at evaluation of these, these, these various different biomarkers, it clearly applied to a host of information which probably wasn't available a decade ago.

And it helps us to look at a minimally invasive way of a simple blood test to look at with extremely high specificity, various different mechanistic that help us, as you alluded to, you know, the heterogeneity, different elements of how do we look at the cancer phenotype, how do we get more information with regards to different assays that help us look at identifying, specific targets, whether through mutations or fusions?

How do we look at copy number variations, which provide us a lot of information across different spectrums of data sets? How do we look at immuno immuno labeling?

We are now looking at far beyond just just individual DNA targets. We're looking at immunotherapy that got Car-T that that's knocking on the doors. We've got various different elements of technologies that are moving through the ecosystem.

Or obviously we use circulating tumor cells within our own ecosystem in a variety of ways. Obviously, one is very hard core therapeutics. And, the encyclopedic tumor analysis that I will discuss, but also in the space of, of diagnostics as well, I think the reason why the biomarkers are appealing is because it's it's a blood sample.

It's a blood draw. it's easy to do. You can do it from the convenience of your home. You don't necessarily need to get hospitalized. and there are clearly, certain cancers, brain tumors, deep seated lung tumors, deep seated GI tumors.

They're not always easy to access in that society. Yeah. Right. Correct. And that that's really what creates this, this multi-level layer. And I was mentioning we've got so many different pathways that are integrated within the ecosystem, which look at the complexity of these multiple markers across multi-modal, actions across the interactome.

so that the, the vision of the encyclopedic tumor analysis, why it's why we call it encyclopedic is because we're bringing across a host of data from different elements that are contributing at various levels, to the cancer.

And they are looking at providing us this multi-layered bit of information that helps us with not just identification of data set for, treatment, but also to look at prognostication, to look at follow up, to look at monitoring and various different elements of that activity.

And that those biomarkers help us personalized cancer therapy that can be used, focusing just within the element of DNA. As you and I discussed before, it leads to clinical relevant outcomes for patients in less than less than a third of those patients.

how many of them clinically benefit from identifying a target as a completely different matter? So I think I think the interest at a clinical level for an organization like data is not so much of how many targets can be identified.

It is identifying various levels of targets, identifying successfully therapy options that can work on those individual patients and they can clinically benefit through a progression free survival.

And overall survival is is the ultimate name of that process. Otherwise it just is reduced to an academic process in that ecosystem. And when we look at the, combination of the the DNA, the RNA, the tumor cell, the pharmacogenetics, the germline, you know, simple things.

When you identify a tailor made of therapies, how can you look at using, smart genomics from the point of looking at drugs that you can combine safely, intelligently with high success rate but less side effects?

That's also important because because we know our patients are seriously immuno depleted by the state of multiple lines of therapy within that ecosystem.

So so increasingly, I think what we are now sensing is that molecular science is now giving us clearly, an ability to look at transforming current strategies that are undertaken to look at those therapies.

I think clearly over the last few years, we've seen a huge amount of data come in which has started to look at a number of solutions which are widely used in clinical practice.

I think this is only going to get going to get stronger and better, and I think we are going to see much, much more, benefit from the data that, that that is being driven from a science standpoint, I think with the benefits of, of genetic disease getting better established, I think it's also important that we make a serious effort to also look at access to those who can benefit and at what cost. Yes.

clearly, we've seen a lot of data around moving across, you know, next generation sequencing, looking at whole exome sequencing versus whole genome sequencing.

Again, the choice between looking at the whole exome and the whole genome is largely looks at, well, what information do you need? What's the application of the data.

Is it clinical versus research. Are we creating more loggerheads of data which is redundant, which will may not help the clinician and the patient immediately may be more important for data logging at a later stage.

I think that's really what we need to identify within the ecosystem. And there are multiple factors at play when we're looking at, very different mechanistic of cancer.

So you tend you have to deal with trying to match up specific and driver alterations, mutations that are taking place. How do we build in a lot of, a lot of the data set that is taking into account the entire tumor or heterogeneity?

And how are we looking at these specific alterations. And I'll be finding an overview that that encompasses a lot of the data that we need to create, information that can help identify combination of therapies in that structure.

So in my view, the acquisition of these hallmarks of data sets are not limited to DNA. we are now clearly looking at a wider spectrum of the genome, the epigenome, the transcriptome, eventually the metabolome that you clearly are, very excited about in terms of your own individual capacity.

And I think these, these multi-omics the different levels of genomics which are coming in, they vary within that complexity. And we need to understand that.

I think not every every component brings in a significant degree of value. And they may be different across a spatial or temporal dynamic when you're dealing with different cancer.

Encylopedic Tumor Analysis and Personalized Therapy

So I think that's very, very important when we look at those different dynamics and when we started our journey pre-COVID, at that stage there was very little data that existed that was looking at treatment strategies for these difficult cancers, for these refractory relapsing solid organ cancers.

So you know that the triple negative breast, the brain tumors, the pancreas, the late stage advanced lung and cancer, ovarian cancers, and what we wanted to look at was be look at a comprehensive multi analyte molecular analysis that will build in data from the DNA from the RNA transcriptome, which could be synchronous with looking at circulating tumor cell activity.

And can we that could be then look at a very label agnostic manner. So for us almost every patient then became a clinical trial to look at. Because even if you put two breast cancer patients together, you and I know they behave differently because of the inherent nature of their molecular pathways.

And that's what we built in when we did our first resilient data set, pre-COVID. that we published where we looked at label of organ agnostic treatment using the encyclopedic tumor analysis, again, leveraging our knowledge of looking at the multi-layer tumor interactome and finding data set that combined various elements of targeted and cytotoxic therapies that came together in that element.

And I think over the years, we've now started to really look at outcomes. When we followed up those individuals over a longer period. I'm sure we'll discuss that as part of the data set of the encyclopedic tumor analysis.

Amazing. Well, one thing that just blows my mind that you brought to the forefront here for listeners that may not be obvious to everybody, but for somebody, who who plays in more the integrative field, I am always, always intrigued by that.

We are still classifying and treating patients based on a huge subset like your breast cancer, your prostate cancer, your pancreatic cancer. And we go through this very sort of algorithmic approach of, okay, we're going to start with this, you know, guideline.

And if that fails then we go to this one. If that fails we go to this one. So we're literally just I'm it sounds terrible. It it feels like a guessing game.

But up until a few years ago, that was the only way we could do it. We had to classify it in that way. It was just too big, too much going on. But the testing that's become available, and in particular with data's work, you have been able to show exactly what you spoke to.

You take ten women with breast cancer and you put they might be of the same demographic, the same age. They might have the same like maybe they're triple negative, or maybe they're your positive or whatever, whatever their classification of, they're all the same.

When you look deeper in this multi analyte tumor interrogation method that you all use, you will see that they all have very different personalities, very unique, which then requires a unique approach to that individual.

And so I love that you spoke to like basically when you started this process, you were looking at each individual basically as their own trial. That's how I practice and have been practicing for almost three decades, and many of my colleagues that I train.

But this is not well, this is difficult to do in our standard of care models today. We are very much an algorithmic model based on sort of the time you can spend with the patient and the and the insurance coverage and that whole like there's a whole system behind why we aren't doing this naturally, which is what frankly, makes the most sense.

And I'm hopeful it's going to take a while because we have to unravel an entire ecosystem outside of the cancer testing realm to help implement, to help adopt this tool, and the knowledge this tool brings into clinical practice and into clinical trials, and into reinsurance, reimbursement and all of the things, because many of the things that you are also alluding to, we're finding are actually really powerful tools in the off label drug world when it comes to managing our patients.

And instead of just going, okay, well, this is the standard of care we typically give to this cancer type. We're starting to find. Wow, there's actually some some less toxic therapies or some therapies that are actually used for other

cancer types that have more efficacy here, or perhaps a certain combination of these that has never been done before, you know, not through a clinical trial environment would be more beneficial for this patient.

So you're pushing us into having to be more critical thinkers. You're pushing us truly into more of an end of one process, but you're giving us the ability to do so based on, you know, like being evidence informed.

We may not have the evidence based or the RCT studies to say, let's, you know, let's let's do this in a big, broad, broad study. It's difficult because each patient is is entirely unique.

And so this is the challenge, I think, that we face here with, with regards as taking this amazing data and applying it at the bedside. So what I want to understand is through what you've learned over these few years through this amazing multi omics ecosystem that you've been exploring.

What have been your biggest takeaways and what what do you think is is hopeful on the horizon for both clinicians and patients? Yeah, so so so just just just to reiterate, I think there's clearly a value of looking at, an evidence based ecosystem that defines some level of decision making at a treatment level, which obviously has to be credible, ethical evidence based, within the system.

I think, the challenge we had ten years ago was that we didn't have the data that we have today. and I think we've got to be very open and receptive to understanding the data.

We'll have ten years from now will be significantly different and hopefully much more advanced and will help us identify and define how we were practicing ten, 15, 20 years ago.

and we may come back and say, look, 15 years, I know when we look back and say, well, is that what we were doing at that stage? and I think we're getting to just scratching the surface of the I think will clearly get much, much more information, data.

I think we clearly now starting to see both that are not static predictive, prognostic biomarkers being available, for us to personalized cancer therapies.

I think we clearly also know that only a small fraction of individuals benefit. When we look at a DNA alteration in isolation. I think we need to understand that you can't push the garb of personalized individual care if we don't benefit majority of patients that we see, or we evaluate through genomic profiling.

I think that's been one of the intense how do we look at better progression free survival when we bring in a methodology that looks at, you know, complex, comprehensive genomics, looking at expression profiling, immunohistochemistry, economic genomics, chemo sensitivity, bringing all those elements because they do contribute at various levels.

I mean, when you look at the small ecosystem combining genomic transcriptional data, it can be useful to improve personalized therapy outcomes. And we've just published a lot of data over the last year.

We presented some data last year, which again looked at various cohorts of patients where in a quarter of these patients heavily pretreated using the multi multi-omics approach, had a doubling of progression free survival and almost a quarter of those patients.

And that's, that's that's pretty much unheard of in a, in a middle stage activity that we're driving almost in 80% of the patients. using that approach we improve progression free survival compared to the previous standard of care modeling.

So again the data needs to be built, needs to be expanded across various spectrums. But I think clearly what we are starting to see is that from our findings over the last few years, when you co administer, target therapy with other anticancer agents that are well tolerated, which is, which is based not on just, you know, the hairs on the back of my neck, but really looking at evidence of genomics that you can use across various spectrums, then you

can achieve a significant response, even in heavily pretreated cohorts with advanced cancers, as you were mentioning in our practice, we've now seen so many patients who were completely written off, asked to go back home and put their affairs in order.

They are now doing well. They're leading an independent life. And that, for us, is the most gratifying in terms of the ecosystem of how it helps us to and motivates us to do more in that space.

clearly, the burden of noncommunicable disease is far beyond cancer. We know that you know, there's this advent and implications of of other elements of cardiovascular disease and stroke and diabetes and across the ecosystem, I think when we look at global oncology, I think it's clearly witnessing a change.

and a shift in terms of both, research, both in terms of innovation and looking at not just new therapies, that are coming in, but also how do we use science to break down the cancer in terms of our understanding?

And our understanding is just not based upon the fact that, how do cancers behave across a treatment system, but how do they behave when we're trying to outsmart them and with them?

And how are they then changing their profile to outdo the therapies that we are providing? And how is it that using a therapy as a one outcome cannot be a long term benefit for the patient?

Because over a course of time, mutations will change, the behavior will change, and we've got to be adaptable in terms of looking at that.

Future of Oncology and Ongoing Re-Testing

And obviously now the classical example is what we're seeing now in minimal residual disease, as we understand where we're able to see clearly benefit of virtual patients when we identify, minimal residual disease at a early, early stage within that ecosystem of patients.

that being said, I think I think clearly we are we are now looking at in various geographies, almost systemic population health management ecosystems.

and how can they adopt, some level of smart genomics within the system of managing of cancer? I think by next year, we can have almost over 60 million patients estimated to have had some element of their genome or exome sequenced, as part of their routine health care.

That was 20 years ago. The potential cost of that would have been would have been astronomical. I think, it's really exciting data. I read, I think two weeks ago, and this was, this was a paper from a couple of years ago that, I think a couple of years back, we had almost about 80,000 plus researchers from over 140 countries who had downloaded about over almost seven petabytes of data.

I didn't even know what a beta might was. I could look it up. Oh, many. Obviously huge. but it was it was data that was downloaded from one of the European molecular biology labs and from their bioinformatics center, and it just tells me this, the interest that's equating now to look at data to, to, to to dissect the data, to look at the bioinformatics and that data.

It just that one year what was downloaded to try and evaluate, understand, read, learn, educate and was data of almost over 200 billion whole genomes that would have been sequenced and all of the data that was distributed.

This is just a small spectrum of of what's happening within the ecosystem of, I think, where we are. I think clearly we've got so much more happening with regards to, machine learning and AI and how do we build those digital platforms that helps us within that structure?

I firmly believe that that, you know, Multi-Omics is going to be an integral part of, of an everyday routine of an oncologist in the years to come. it will only happen when there's right training is education in place.

And I'm hopeful that believe that, you know, we will need to bring in various different elements of data, so that we can look at those different structures in different cohorts.

I also think, eventually the process will become seamless, where we have now the ability to look at the bigger picture and not just getting lost in small details of an isolated coding of an open genome set.

And we got that under the pretense of looking at using personalized medicine in that care, in that ecosystem. So for me, the future is clearly of cancer.

Genomics will look at this interdisciplinary approach of of both education information. upstream upscaling genomics, trying to understand clearly how can we use that data smartly?

How can we minimize the friction between the genomic ecosystem and the researchers at the lab level, the data scientists and the clinician to help the patient in terms of evolving ourselves, in terms of learning more, we do need to understand, within the ecosystem.

it's just not about a one off test that, that that prescribes to the entire ecosystem of therapy for a cancer patient. and, and as my, as my sign off note.

I think we are clearly heading into this, this scientific stratosphere, as I call this. You know, the data is going to be big. It's going to be exciting. It's going to be tough.

It's going to be complicated. It will give us a lot of hard nights, try and understand where we're heading to. But if we want to get there, clearly the data needs to be predictive.

It needs to be personalized, it needs to be preventative, but more importantly, it needs to be proactive. we just can't rely on data from a four year old tissue to to do a sequencing now and say, well, that's good enough to do.

you know, I climbed a couple of stairs, a flight of stairs, our blood pressure changes up, dynamics change in terms of body making, mechanistic cancer changes as well.

And we've got to make sure that we are using smart technologies not just genomics. This there's so much more out there that we use that smartly to try and understand, educate the clinical community first and then translate that to the patient.

Ultimately, the onus is on all of us to help using therapies, which can benefit the patient, and avoiding trips which which are likely not to do any benefit and potential harm.

Amazing, doc. My gosh. First of all, I want to speak to you the education PSU. and the, you know, the company data are really, really wanting to empower clinicians in this.

So we are looking at creating a year long program for clinicians to learn more about this topic. In general. It's it's an agnostic training that you're doing because like you said, this is the future of oncology.

It's not a single company pushing this forward. But you are one of the passion, passion project people pushing it forward. Number two, I really appreciate that you reiterated the fact that this is an iterative process, both the learning curve of the data, but also the learning curve of the cancer and the patient.

So this means that you really don't want to go back and use old tissue because of what you just described. In fact, in my world, I train clinicians to anything older than six months old that's been heavily treated.

We need to look again. It changes. So this isn't even a one and done testing. It's a things change as your body changes. So the patient is doing really well, but they've kind of hit a plateau.

We're starting to see the numbers start to encroach again after initial testing. Then it might be time to look under

the hood again. Because these little, these little cells find a workaround.

And so this is another with a noninvasive blood biopsy. We can do that more realistically to go and take another sample and see what information we're learning from the body.

This is a hugely exciting time to be part of of oncology and general integrative oncology in particular. And you give me and other clinicians and researchers and patients and your caregivers much hope.

Dr. Datta thank you so much for your amazing your amazing knowledge and your precious time with us. Thank you so much. It was an absolute pleasure Nasha. Thank you very much.