When Science Finds a Way

Season 2, Episode 7
Decoding cancer: how genomics is transforming treatment

Show notes

Episode description:

Genomics has revolutionised cancer research, offering new hope for cancer diagnosis and treatment. But there are challenges ahead. Alisha is joined by Dr Peter Campbell and researchers Dr Solomon Rotimi and Sara Gomez to discuss the breakthroughs and the issue of ensuring fair access to advancements for patients worldwide.

Mentioned in this episode:
Human Genome Project - an international scientific research project identifying, mapping and sequencing all of the genes of the human genome.

International Cancer Genome Consortium - a consortium of experts in genomics and informatics.

African Organization for Research and Training in Cancer (AORTIC) - an African based non-governmental organisation dedicated to cancer control and palliation in Africa.

Further resources:
Data and diversity in genomics: landscaping report - report commissioned by the Wellcome Trust and authored by IQVIA.

Transcript

(Music starts) 00:00

Peter Campbell CLIP 00:05
"It's a little bit like there came a revolution that, you know, having a microscope brought to looking at cells, right - you suddenly went from having no idea of what was going on at a sort of cellular level to suddenly seeing all this stuff. It was the same for the genome - we were able to see things in these genomes that had never been seen before."

Alisha Wainwright 00:26
Welcome to When Science Finds a Way - a podcast about the science changing the world. I'm Alicia Wainwright. And on this series, I'm talking to the global experts who are making a difference as well as the people who have inspired and contributed to their work.

We've talked about genomics on this show before and how understanding our genes can change our understanding of health. One example of this is the treatment of cancer.

Cancers are caused by mutations in our genes. So if we can just sequence the genomes of those cancers, we can find out useful information like what exactly caused a tumour or what treatment will be most effective.

Today I'm speaking with one of the researchers who took on this challenge, Dr Peter Campbell. Dr Campbell is currently the CSO & Academic Co-Founder at Quotient, but previously, he worked with the Wellcome Sanger Institute - a genomics research centre in Cambridge. Within the Institute he was the head of cancer, aging and somatic mutation and the senior group leader at the Cancer Genome Project. That project has been part of a years-long coordinated international effort to sequence the genomes of the most important and common cancers. And that research mission is mostly mission accomplished.

Dr. Campbell is here to discuss how this research has improved our understanding of cancer. We'll also look at how we can translate these wide ranging discoveries into action that delivers better outcomes for patients in an equitable way around the world.

Dr. Peter Campbell, welcome to the show.

(Music Ends)

Peter Campbell 02:03

Thank you very much and great to be joining you.

Alisha Wainwright 02:07

Fantastic. Okay. First of all, some context - can you tell us more about the genomic basis of cancers - what's happening at the genetic level when someone has cancer?

Peter Campbell 02:18
So, essentially, you're born with a genome that you inherit from your parents and every cell in your body has a copy of that original blueprint that you inherited. In order for every cell to have a copy of it, it has to copy - each cell has to make a copy of it when that cell divides. When it makes a copy of itself, it's a little bit like, you know, typing out a message on a computer - you can make typos when you do that and that will lead to a change in, in that genetic blueprint that will be inherited by one of the cells. We know that most of these genetic changes that happen as cells divide are pretty harmless. But if the wrong genetic change happens in the wrong gene, in the wrong cell, then that can, that can push the cell towards cancer. And if one cell accumulates enough of these changes, then that's what essentially provides the recipe for cancer.

Alisha Wainwright 03:21
And when you started working in the field of cancer genomics, what was the field like at the time? What was the most innovative thing when you started?

Peter Campbell 03:29
The Human Genome Project was ran mostly through the 1990s and was an attempt to map the original genetic code of a human, basically, what is the kind of, what is the, the sequence of the human genome? So I was very lucky. I started my PhD, um, just at the time that the human - the original Human Genome Project was completing its first draft so it was a great time to be starting because we had this - the kind of basic normal recipe of the genome. And there were a few kind of really amazing insights that came out of that initial kind of human genome project. The first is, that one - it was actually conceivable that you could sequence the entirety of a genome.

Alisha Wainwright 04:18
Which to me, currently in my brain, is still inconceivable.

Peter Campbell 04:20
Yeah, it's a pretty amazing…

Alisha Wainwright 04:21
But somehow they managed to do it.

Peter Campbell 04:23
It's a pretty amazing thing to be able to do. And then a lot of advances in science are prompted by a sudden kind of…

Alisha Wainwright 04:29
Innovation.

Peter Campbell 04:30
Change in technology and the change in technology that really transformed cancer genomics was the ability to sequence the whole of the cancer genome at a much lower cost. So when I came to the Sanger Institute - again, I was very lucky - that literally the first week that I arrived in the Institute my boss said to me, 'Well, we've got these new sequencing machines. We've not really tried them yet. Are you interested in, in playing with them?' - which obviously I was.

Alisha Wainwright 05:02
Yes!

Peter Campbell 05:03
And, uh, and so…and so we were, you know - I was very privileged to be able to kind of sequence - put the first cancer sample down one of these new machines. And the results were extraordinary. You know, you could see almost instantly that we could dream of sequencing the entirety of one person's cancer genome from the first base to the last base.

Alisha Wainwright 05:27
Just for our audience - and also myself - when you say sequencing an entire cancer genome, are you just like taking a piece of like a tumor or blood or what, um, what does it mean to sequence the genome?

Peter Campbell 05:44
So essentially what we do when I talk about sequencing a cancer genome is we - what we do is we take a piece of the tumour, which is probably 60, 70, 80 percent tumour cells, and then we take a blood sample and we sequence both of them. And what we're interested in, are what are the changes that are present in the tumour cells, that are absent from the blood cells. What that means is that you can look at the tumour cells and essentially subtract all the changes that the person was born with - the ones that they inherit from their parents - and you're left with the changes that that cancer has acquired as it's gone through life.

Alisha Wainwright 06:26
Is that the somatic mutation?

Peter Campbell 06:28
That's exactly - that's right. That's what a somatic mutation is - is a change that's happened in the tumor that's missing from the - that wasn't inherited, basically.

Alisha Wainwright 06:38
That must have been very fascinating for you as a young scientist being able to use this new technology to make these comparisons.

Peter Campbell 06:46

It was an amazing time because essentially we were able to see things in these genomes that had never been seen before. You know it's a little bit like the kind of revolution that, you know, having a microscope…

Alisha Wainwright 07:00
Right.

Peter Campbell 07:01
…brought to looking at cells - you suddenly went from having no idea of what was going on at a sort of cellular level to suddenly seeing all this stuff. It was the same for the genome. You know, we had, you know, from the very first genome that we sequenced, we could see just these wild patterns of genetic change. You know, entire chromosomes being shredded and then stuck back together in kind of random pieces. Kind of massive pieces of DNA that were present at 100 copies per cell where they should have been present at two copies per cell. And all sorts of other amazing changes that we just had almost no idea would exist.

Alisha Wainwright 07:43
The work you were a part of at the Wellcome Sanger Institute was part of the

International Cancer Genome Consortium. Can you tell me a bit more about what that is and, and how your work specifically contributed?

Peter Campbell 07:55
When we were sequencing the first two or three cancer genomes, we recognised that there was a, there was an opportunity to really scale this up and do it in thousands of patients and do it across all tumour types. But we also realised that we weren't going to fund or do that entirely by ourselves - that this was going to need a big international consortium. And at the time we were thinking there's other groups around the world were obviously thinking the same thing. So through a kind of network of people that we worked with who were interested in the same area, we built up a collaboration - a consortium - to essentially divide up the cancers amongst the different groups and make sure that the big tumour types were covered. So for example the National Cancer Institute in the U.S., the DKFZ - which is the big German cancer consortium - a number of other international kind of cancer groups decided to kind of join together and fund this project.

So yeah, this was a non trivial expense - basically, each tumor type we wound up spending something like 10 to 20 million pounds on sequencing by the time that kind of infrastructure was put in place and the personnel were trained and the sequencing was done. It was a... broad effort. And I think it needed that international collaboration because no one country could fund it themselves.

Alisha Wainwright 09:29
Can you tell us some of the ways the findings of the International Cancer Genome Consortium has expanded our understanding of cancer?

Peter Campbell 09:39
I would say that the major impact of the Cancer Genome Consortium has been to identify the genes that are responsible for driving cancer when they carry these mutations.

So, it turns out that every type of cancer has its own set of genes that are recurrently changed, and it's those genes that specifically drive that cancer to behave in the way it does. So, what the Cancer Genome Consortium - by systematically mapping all of the genes in the genome, we were able to identify which genes drove each particular type of cancer.

What emerges from this is that - is several things. First of all, these genes make really interesting drug targets. So, you know, if because they fundamentally cause the biology of cancer - so they instruct the cell to proliferate out of control, they instruct the cell to spread around the body, et cetera, et cetera - if you can identify that fundamental biological cause and then turn it off with a drug, then that has, you know, can potentially stop a cancer in its tracks.

My favourite example is actually a gene that was identified at the Sanger Institute - before I joined - by my bosses at the time which is this - in malignant melanoma, so melanoma is the nastiest form of skin cancer and is one of the highest causes of

mortality in a number of countries around the world - and the specific mutation that was identified is in a gene called BRAF and it's, these mutations are found in about 50 percent of patients with melanoma, so it's really a very frequent genetic change in these cancers.

And essentially through a series of firstly the genetic testing and then biological studies, it was shown that the mutations activate the protein that the mutations are in and lead to uncontrolled proliferation of the skin cells. So that leads to a fairly obvious opportunity to develop drug therapies that, if you can block the effects of this protein, then maybe you can switch these cancer cells off.

And indeed a number of drug companies have now developed BRAF inhibitors as therapeutic options. And they really do melt away the melanoma - so patients will often get a really quite remarkable response to the drug. Unfortunately, in the initial studies the cancer came roaring back because the cells became resistant to the effects of the drugs. But with further work and further refinement and using combination therapies, actually now we're able to often achieve quite durable responses to these BRAF inhibitors and other drugs - in a similar vein - in malignant melanoma. And it's really a particularly nice example of how understanding the genetics can lead to rational therapeutic design.

The other thing that turns out to be really interesting from all of this, is that these mutations act as blueprints for the cancer and we can use them diagnostically. So, for example, it's surprisingly common that you will see a cancer and you won't actually know what cell type it comes from. And by looking at the kind of pattern of mutations - which genes are mutated - you can often make a pretty good educated guess at what type of cancer that is. And the third thing you can do is that it, again, it turns out that because these genetic changes fundamentally drive the biology of the cancer, they kind of - they tell you about how aggressive someone's cancer is. We can use them really to make a statement about how risky that person's cancer is. And by doing a risk profile of a given patient, we can, um, we can begin to work out how aggressive we need to be in our therapies for that person. So if they have a pretty low risk cancer, then we can be a little bit gentler with the treatment. If they have a very high risk cancer, then maybe we need to escalate the intensity of the therapy for that person. And so those are the sorts of ways that we're beginning to use the information that's come out of these studies for underpinning, you know, patient care.

Alisha Wainwright 14:11
So what stage is the International Cancer Genome Consortium at now and have we finished sequencing these cancer genomes?

Peter Campbell 14:19
This initial discovery phase that I was outlining - that is largely complete now. There's still lots more to be discovered, but the kind of most frequently mutated genes in the most common cancers have all been mapped now. So that phase of this is complete.

There are a lot of efforts internationally around how do we - how do we stitch this diagnostic approach into routine clinical care, and how do we use what we already know to make the best predictions about what is going to happen to those patients

that we're sequencing in the clinic? And then how can we use that information to continue improving the quality of the predictions for future patients. And that's the sort of phase that the consortium is moving towards now. So you can imagine if you've got, I don't know, 2000 patients with breast cancer where you've sequenced their tumors and you know what happened to those patients, then if you've got patient 2001 and you've sequenced her breast cancer, then you can make a prediction based on your 2000 about what might happen to her and what treatments might be best for her.

Alisha Wainwright 15:36
Speaking from personal experience, I've had a genetic test because I was potentially at risk of having a hereditary genetic mutation that, thankfully, I don't have. But can you explain the similarities and differences between the kind of genetic tests that I took and your work looking into cancer genomes.

Peter Campbell 15:58
Right. So the testing that you had is testing of the genome that you were born with - so essentially you inherit half of your genome from your mother and half of your genome from your father. And that genome - because we're all, you know, unique individuals - each person has their own unique genetic makeup that's present in all of their cells. And it so happens - as happened in your case - that occasionally you can inherit a variant that puts you at an increased risk of cancer. And that's what we would call familial predisposition to cancer would be the technical term for it - but basically it's an inherited form of cancer risk.

What we do when we sequence a cancer genome, when we sequence the tumour and the blood, we actually for free, if you like - not quite for free but as part of it - we do wind up getting the sequence of the genome that you're born with - that's essentially why we sequence the blood because that tells us the genome that you were born with - but in addition to that, we also find the somatic changes that are specific to the tumour. So when I talk about sequencing a cancer genome, we're looking at both the somatic mutations and the variants that are inherited - the germline variants.

Julia Gillard 17:21
Hello! I'm Julia Gillard, chair of Wellcome. Thanks for listening to our podcast, When Science Finds a Way. Wellcome supports researchers around the world to make discoveries and help solve urgent health challenges. We believe in the power of science to build a healthier future, and the need for inclusive collaborative action to ensure that everyone can benefit. To get involved, visit wellcome.org, that's Wellcome with two l's. Now, back to the story.

Alisha Wainwright 17:54
One of the issues around all these kinds of tests, and cancer genomics research more generally, is equity - how can we ensure everyone has access to the benefits that come from projects like the International Cancer Genome Consortium?

Sara Gomez is a behavioral health researcher from Colombia who has worked in the U.S. - specifically, in communities of predominantly Black and Latina women, who were at risk of hereditary breast and ovarian cancers. In these communities her work

has focused on increasing engagement with genetic testing. Sara describes her role as being at the intersection of translational genomics and health equity.

She told us what that means and shared her thoughts on issues of equity and access.

(Music, into)

Sara Gomez 18:44
So translational genomics is a little bit of an emerging field. The way that I like to think about it is how can we translate what is happening inside a lab, which is basic science, into the real world and have an impact on real patients. If we had patients that were recently diagnosed and they were undergoing treatment, most of them - at least in the United States - they would immediately get that cancer genome sequence to inform their treatment and their surgeries moving forward.
For women, like the ones that I was working with, who were mostly immigrants and they had lower incomes and no insurance - which it was much harder to get the genetic tests covered. In Latin America the story is extremely different because typically only people who are already diagnosed with cancer will be offered a genetic test but it is very expensive and either it's covered by insurance, but you have to fight for it, or you have to pay for it out of pocket.

So there are different steps that we can take as an international community to make accessibility to genetic testing for hereditary cancers more equitable. I think the first one in terms of access is building capacities in countries or in our region - and that is both in terms of infrastructure, so the ability to have labs that can analyse the tests - and also in terms of the workforce.

The second one, which is not so much in terms of access, but in terms of making just cancer genomics more equitable, is about the sample - because on one side we want to be able to have information from the most diverse and representative sample as we possibly can. And on the other side, we want to be protective of people's privacy and their needs.

And this is their genetic information. So it is a little bit of a balance in making sure that if people are sharing their genetic information for a data repository - for research, for example - that they are truly informed about what is happening to that information and how it is being used. So one of the biggest challenges with genome sequencing and genetic testing has been specifically the ethical component of it and it is about the data collection as well.

(music, into)

Alisha Wainwright 20:59
I love that term Sara used - translational genomics - because that's what this is about - using all this open source, high level research data to improve outcomes at the patient level. So what are some of the challenges in applying the findings of high level research like the International Cancer Genome Consortium into clinical context?

Peter Campbell 21:22
I think one of the challenges that we see as a cancer genomics community is how to improve access and availability of these technologies - these genome sequencing technologies across the world - not just in high income countries, but also in low and middle income countries. There are, I think, a number of things to think about in improving that - the broadness of that access. One needs the sequencing machines and these - they're fairly greedy in terms of money and electricity and everything else. And then once one generates this massive data - I mean the data that these sequencing machines generate is enormous - you need a really large computer, basically, to analyse the data that comes off the end. And I think what a lot of health systems, starting in high income countries, are doing - but increasingly penetrating middle income countries and hopefully in the future low income countries - what's happening is that this infrastructure is being built within the health system. And I think that that makes a lot of sense. Obviously every country's health system is different so each country is kind of coming up with the solution that best fits in their health system. And there are, you know, there are kind of ways of taking some of the best practices that we've built up in our research world and trying to transition them into these health systems.

And that offers interesting opportunities for looking at differences between different countries and similarities between countries. Identifying things that might be rare in one country, but if you have the world's experience, would no longer be quite so rare and you could spot the signal. And so I think that one of the challenges that we're working towards as a cancer genomics community, is how do we…how do we work out how to share this experience while respecting the confidentiality and uniqueness of each individual patient and each country's jurisdiction.

Alisha Wainwright 23:30
Speaking about that knowledge bank, one of the limitations there is representation. So, for example, there weren't any countries in Africa represented in the International Cancer Genome Consortium. To talk about why that's significant, we spoke to researcher, Dr Solomon Rotimi. He's a professor at the Covenant University in Nigeria, and he works with groups to advance the state of cancer genomics research in Africa - groups like the Prostate Cancer Transatlantic Consortium, and AORTIC, which is the African Organization for Research and Training in Cancer. In his research Solomon uses the kind of open source data generated from projects like the one Peter was a part of. But he also acknowledges that the level of cancer genomics research taking place in Africa is low. He explained to us why these population level understandings can be so significant.

(music, into)

Solomon Rotimi 24:33
I'm interested in knowing why do Black men - and perhaps women now - develop some kind of cancers, particularly if you take for example, prostate cancer. And when they develop this disease, why is it so aggressive in Black people? The cancer genomic research that is done in Africa, the level is still very low - particularly if you look at the depth of genetic diversity that we have within the African population.

However, from the research and the genetic studies that we have done and we have published, we have identified that Black indigenous African population, are reached with mutations in a particular group of genes that actually regulate cell growth. These genes - for example, we're talking about BRCA1, BRCA2, APC, ATM gene - we have identified that Black indigenous African populations are enriched with this mutation. That increases their risk of developing this prostate cancer.

However, that is not the end of the story - individuals with mutation in this gene can benefit from a class of precision oncology drug. So this particular drug targets mutation in BRCA1, BRCA2, APCATM - generally whoever has this type of mutation in this gene will benefit more from this treatment. The implication of that is that African populations, based on the genomic findings that we are discovering, can benefit very well from this type of drugs that will make their cancer to probably be cured.

The reason why we have not really mobilised this type of drugs across Africa is because we didn't have evidence. And where the gaps are right now, is that we don't have enough information about cancer genomics within the indigenous African population. And so, concerted effort needs to be made to then focus on studying that.

For us to make cancer genomic research more equitable, we must understand that representation is important. You cannot just stay in one corner and study one population - it's a global village that we have now. Um, so that is where we are. So I can say the past few years, more researchers have been coming out. We're definitely not where we used to be, but we're not where we should be. And that is why, you know, collaboration is very, very important to move us forward.

(Music, into)

Alisha Wainwright 27:00
The point he brings up is interesting in that it's something we've heard before on the show - the importance of population level research. How significant are the genomic differences between populations in terms of prevalence or treatment of different cancers?

Peter Campbell 27:17
There are some cancer predisposing genetic changes that are more common in some populations than in other populations. And that leads to variation in cancer risk across the globe. That's actually probably dwarfed by the effects of different environments across the globe. And so, we know from, uh, epidemiological studies, for example, that there can be up to tenfold variation in the risk of a particular cancer in different countries. Um, some of that is explained by the kind of genetic differences between the populations, but most of it's explained by, often, unknown factors in the environment.

One of the projects that's led by my colleague Mike Stratton, together with the International Agency for Research in Cancer, have been trying to do is to kind of collect cancers from all around the world and then sequence the genomes in a pretty

unbiased way and compare the differences in signatures between high risk areas and low risk areas for a given tumour type. And that is yielding some fascinating insights - we are seeing, for example, in kidney cancers that, uh, there are…there are some country specific mutational signatures that you don't see in other countries.

Alisha Wainwright 28:43
Wow.

Peter Campbell 28:45
And this is a - these are kidney and liver cancers that seem to be caused by chemicals in a plant which is called Aristolochia, and the chemicals are called Aristolochic acid - a complete mouthful, I have to say. But what's really fascinating about this observation is that the chemicals in Aristolochia - in the Aristolochia plant - they directly damage DNA, and they lead to this very distinctive change - set of series of changes in the genome. And we can tell whether a kidney cancer or a liver cancer has been exposed to this chemical because the set of changes is so distinctive that we can - it stands out a mile.

So, in particular, in some of the Balkan areas around Romania - and to an extent Serbia - you can see that almost all of the kidney cancers in these regions have this very distinctive signature. In East Asia, you also see this signature in some patients with kidney and liver cancer.

And it seems like the exposures are different in the two places - so in East Asia, the Aristolochia plant is used as a traditional herbal medicine. And in fact, it's definitely not a medicine - it's a carcinogen. And the people who are taking it as a medicine are actually exposing themselves to something that is directly damaging their DNA, and in a fraction of those patients will lead on to kidney or liver cancer.

In Romania and that Balkan area - that region of the Balkans where these signatures are seen - it seems like the exposure is more endemic - that people are just somehow exposed to this plant.

One of the really, kind of, interesting pieces of detective work that's going on at the moment is to try and find out exactly what is the source of exposure that's happening in Balkans. Because, it obviously sets up this really interesting public health opportunity to say, actually if we can figure out how people are getting exposed to this in these regions and we can correct that, then maybe we can decrease and prevent some of the - some people getting kidney cancer.

Alisha Wainwright 30:55
What’s the long term vision for how our improved understanding of cancer genomics could impact the way we treat and diagnose patients?

Peter Campbell 31:05
The vision is essentially to personalise the therapy for each patient. So essentially the idea would be that - that if you have a cancer, you would have its genome sequenced. That would yield the set of genes that fundamentally cause your cancer - so not the set of genes that cause all cancers, but your specific cancer is caused by

these four genes or these four genetic changes or whatever. We're quite a way from that at the moment, but we are making progress towards it. So there are some - there are definitely some genetic changes for which there's a very clear and obvious drug that particularly targets tumours with that genetic change. And the idea is that over time we kind of expand the repertoire of those genetic changes that have drugs available for them.

Alisha Wainwright 32:00
So when you first started in the field and you look back and to see where you are now, did you have any idea that this is how far we would come? What were your expectations? And…and I'd love to hear.

Peter Campbell 32:14

Yeah, when I - I can remember the the first cancer genome that we sequenced and, you know, I was pretty wet behind the ears junior scientist at the Sanger Institute, and I remember taking my first data to my boss and showing it to him and his eyes just widened at what we were seeing in that first cancer genome. And I didn't think too much more about it. But then a week later, he announced that we were switching off all of the types of sequencing that we'd been doing before, and that we were gonna pivot completely to this new technology.

Alisha Wainwright 32:54
Wow.

Peter Campbell 32:55
When he made that announcement - I, yeah - I was completely flabbergasted that he would be so bold to do this. But it shows that - it showed that it really was going to be possible to map the landscape of cancer biology in a way that I don't think any of us had dreamed would be possible in our lifetimes.

Alisha Wainwright 33:22
Can the approach in cancer genomics, over the last decade or two, be applied to other diseases?

Peter Campbell 33:28
That's something we're very excited about at the moment. So, um, I was talking about how we had begun to look at somatic mutations in normal tissues - we were seeing these patterns of genetic changes in normal tissues.

One tissue type that we were particularly interested in was liver cancer because liver cancer only - it really, almost always occurs in the setting of pre-existing liver disease. So this is liver disease, for example, that's caused by viral hepatitis, or by alcohol excess, or by obesity and fat buildup in the liver. And we had wanted to see if we could predict who was going to go on and get liver cancer when people had these various conditions. And it turned out when we went looking at the livers of people with these kind of background chronic liver diseases, that actually they had a whole series of genetic changes in their liver that were never going to go on and cause liver cancer, but were very informative about the particular liver disease that

they had, and were essentially genetic changes that protected the liver cells from the disease process.

And so suddenly that opened up this new way of thinking to us - well, maybe there are other diseases where the genetic changes that those cells experience as they go through life, can protect cells against the disease process. And maybe that opens up interesting possibilities like what we're doing in cancer for diseases outside of cancer, and that's an area of research, that really, we're just beginning to explore now.

Alisha Wainwright 35:09

I can't wait to make a future episode about that - that sounds truly fascinating, but on this subject of cancer genomics, I am so thrilled to have spoken to you about it.

I feel like I learned so much about it. I have a much more well rounded knowledge of the process and the benefits and the potential for the future. So I just want to thank you - Dr Peter Campbell - for joining us, so much. Thank you so much.

(Music starts)

Peter Campbell 35:34
Thank you.

Alisha Wainwright 35:40

Thanks for listening to When Science Finds a Way. And thanks also to Dr Peter Campbell, Dr Solomon Rotimi, and Sara Gomez.

I love hearing Peter’s memories of sequencing cancer genomes for the first time and that sense of wonder at all the discoveries they were making. We talk a lot about these kind of big, open-ended research projects on the show. But it’s important to keep in mind how all these discoveries can turn into real impacts that make the world a healthier place.

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Next time, we'll be talking about a newly published study, trialling an innovative digital intervention for people who hear distressing voices.

Vaughan Bell 37:17
People with psychosis have not always had a great experience of mental health services, and so having that long term relationship, working in partnership with people can really give people the experience of making an input, and working towards the common goal of making a therapy more effective.

Alisha 37:35
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(Music ends)