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00:06 Sarah Crespi: Welcome to the Science Podcast for September 27th, 2019. I'm Sarah Crespi. On this week's show, Senior News Correspondent, Jeffrey Mervis, talks with me about big road blocks for Facebook's plan to release anonymous user data to social scientists that wanna study the site's role in the 2016 US election. And I talk with Jennifer Gruhn about counting chromosomes in human egg cells. It turns out errors in division that cause too many or two few chromosomes to remain in the egg cell may shape human fertility over our reproductive lives. Finally, in this month's book segment, Kiki Sanford talks with Daniel Navon about his book, Mobilizing Mutations: Human Genetics in the Age of Patient Advocacy. Now we have Jeffrey Mervis, he's a Senior News Correspondent for Science. Hi, Jeff.

00:58 Jeffrey Mervis: Hi Sarah.

01:00 SC: Okay, so today we're gonna talk about Facebook data and the US election, the 2016 election. Unfortunately we're not gonna be talking about conclusions that have been made from the data. We're gonna instead talk about how researchers have come really close to having it in their hands. Can you explain what's going on?

01:18 JM: Sure. It's an interesting story because social scientists thrive on data, and there's more data now in private hands than in public hands. And so quantitative social scientists, those that like to crunch large amounts of data, really need to go where the data are if they wanna do the best research. And this story is about Facebook and how a year-and-a-half ago it struck a deal with some prominent social scientists to make data available on the URLs that its users share so that the scientists could study Facebook's impact on elections, not just in the US, but around the world. How misinformation spreads, the kind of people who spread it, and other things that social scientists would love to know about, but in the past they've only been able to do that with very small controlled studies. This is a treasure trove of data that they've never had access to before.

02:23 SC: Just to clarify, shared URLs means when someone shares a link on Facebook, this data set will include that and information about who shared it, who clicked it, and also what the actual link leads to, what the page the link leads to has on it. Political news, fake news, anything.

02:43 JM: Right. All of those characteristics which are all gold mines for scientists to ask a whole bunch of questions.

02:50 SC: Let's talk about what spurred this. It wasn't just the US 2016 election, there was also what happened with Cambridge Analytica that made Facebook just sit up and say, "Maybe it's time to let social scientists look at what's going on." So, can you recap that for us?

03:06 JM: So this was, if you may remember, a scandal that broke in March 2018, in which a British consulting firm, Cambridge Analytica, had obtained data on millions of Facebook users, and

then they packaged it into voter profiles which they then offered to candidates. Facebook was very embarrassed by this. You may remember it led to congressional hearings, Mark Zuckerberg testified, there was lots of comment back and forth on whether senators actually understood what it was that they were investigating. In any case, that prompted Facebook to say, "We really need to do a better job making it clear what we are doing with this data and how we are protecting it." And coincidentally, a social scientist at Harvard named Gary King, had just gone to Facebook with a proposal to create this model partnership.

04:04 SC: This partnership would basically be anonymized data that goes from Facebook to researchers?

04:10 JM: Right. It would have a couple of parts to it. It would offer the data to scientists who could then study it and publish with no strings attached. This would be unprecedented because up until now, Facebook had allowed some of its data to be used by researchers but often in conjunction with a Facebook scientist, and often with pre-publication review, because after all it was proprietary information. So, what King proposed is that Facebook make it available without any restrictions, but in return the researchers would be vetted, and so a small group of scientists would make sure that the scientists didn't have an axe to grind and they weren't trying to get the information for nefarious purposes as it happened with Cambridge Analytica.

05:03 SC: So, researchers would have to apply to use the data set, be reviewed by a group of scientists, and then they'd be able to use these data to ask questions about politics and elections.

05:13 JM: Right. It actually had another safeguard which is that the data would be made available at a secure website that required two forms of log-in identification. Facebook would never actually ever release the data, scientists could never actually download it, but they could have access to it and they could ask whatever questions they wanted and get answers and then publish the results based on those analyses.

05:42 SC: But none of this has happened yet. What's been the hold up?

05:45 JM: Right. So the problem was soon after they announced this agreement, Facebook realized, "Uh-oh, we don't have sufficient privacy protection. We've never done this before on a scale of two billion users sharing URLs, millions and millions of URLs, and lots of different characteristics." It turns out computer scientists have shown that even if you anonymize data, which is what this would have been, aggregated data, there's so much other information about all of us out there, and there's so much more computing power, that you can crack that barrier of anonymity and actually find out with three or four or five bits of information like date of birth and gender, who an individual is. And so, Facebook said, "We're not ready to release this data. We need to work on what's called differential privacy. We need to come up with a frame work before we can release any of the data."

06:46 SC: What is differential privacy?

06:48 JM: Well, it's a mathematical way of assuring that you can't identify someone. And the way

you do this traditionally is by adding what scientists call noise. In other words, you disturb the data. If it's a column of ages, instead of writing 32 which is the correct age, you might write 33 or 34 or 35. Now, obviously the bigger the range, the more protection there is for the individual. But the bigger the range, the noisier the data is, and if it gets too noisy then it's of no use to researchers. So you have to strike a balance, you have to come up with the right amount of noise without degrading the data. And that's what Facebook has been working on for the past year.

07:38 SC: It's taken so long that grant money that's been set aside for this project, it's going away?

07:45 JM: Well, so what's happened was, when Facebook agreed to do this they also realized that if they funded it people would suspect the results, they wouldn't trust them. And so King and Facebook went to some foundations, in particular the Hewlett Foundation, and said, "Do you think you could round up some other foundations to support this?" And they did. Eventually seven foundations agreed to contribute $11 million. So they put up this money, they held the competition, they vetted the proposals, they made the awards, but they said to the researchers, "The data aren't available yet." Well, now their funders have decided that they can't keep that money idle indefinitely. They love the idea, they love the fact that researchers are gonna be able to answer some very important questions, but they can't tie up the money indefinitely. So they've set a deadline of September 30th.

08:46 SC: This is the deadline for the release of these data?

08:50 JM: For the data to be released in a sufficiently full form, or the organization that's running the grants process is going to have to wind down.

09:02 SC: Are the funders asking for money back from the researchers?

09:07 JM: They're not gonna do that. And the organization, Social Science Research Corporation, that is running the grants process has said they're not gonna pull back any of the money. There's actually a second round of researchers that they selected but haven't funded. And I think they're gonna go ahead with those projects if the researchers feel they can do the project with the amount of data now available. Facebook has made some information available, they've made information on the characteristics of the websites for example. But they haven't made available the information on the demographics of the users themselves.

09:44 SC: Is the funding mechanism really key here? Will the researchers just move on or will they move forward even if the foundation money isn't available?

09:53 JM: Well, that's a good question. Of course, funding is always nice.

09:56 SC: Yeah.

09:57 JM: But researchers always have several balls in the air. And I've talked to several of them and they say, "Well, if we can't go ahead with this project at this time, we'll do something else. I was hoping to replicate what I had done with the Facebook data for example, but if that's not

available we'll do something else and hope eventually that the data are available and we can come back to that project." Scientists are resourceful, and so they're not sitting on their hands. But it is disappointing.

10:25 SC: Yeah. And Facebook will continue to work on this, to make the data private enough, anonymous enough?

10:31 JM: Right. Facebook says they're gonna continue to work on this project. And Gary King, who, along with a Stanford Law professor named Nate Persily, created an organization called Social Science One, which is the repository for whatever data are released. They say that they're gonna continue. And King puts it this way, he says, "This is the future. The data are in private hands, and if social scientists want to study the important questions for their discipline, including how democracies work, you have to go where the data is, and that means you have to make arrangements with private companies like Facebook." In fact, everyone gives Facebook credit for being willing to do this. Other companies like Google and Twitter were offered in and they declined at least for the moment. And so people are giving Facebook points for even trying, but so far they've been less than satisfied with the results.

11:36 SC: Okay, Jeff, thanks so much.

11:38 JM: Thank you, Sarah.

11:39 SC: Jeffrey Mervis is a Senior Correspondent for Science Magazine. You can find a link to his story at sciencemag.org/podcast. Stay tuned for an interview with Jennifer Gruhn about counting chromosomes in human eggs.

[music]

11:56 SC: This week's episode is sponsored by Simon & Schuster, publishers of The Tangled Tree: A Radical New History of Life by prize-winning Science and Nature writer David Quammen. The Tangled Tree chronicles the pioneering scientist whose discoveries in molecular biology, horizontal gene transfer, and immunology, have dramatically changed our understanding of evolution and life's history. Available now wherever books are sold.

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12:30 SC: This week's episode is also brought to you by MOVA Globes. MOVA Globes turn all on their own, with or without a base, in any setting with ambient lighting. No batteries needed, no sloppy cords to detract from your enjoyment. Instead hidden magnets provide the movement. With over 40 designs including world maps, outer space, and famous artworks, there's something for everyone. The outer space collection even features graphics provided by NASA and JPL complete with planets, moons, asteroids, and constellation designs. It's a great gift for the person who has everything, the science interested person, or a map lover. Or pair it with your own home decor as a conversation starter, I wanna especially call out the famous artwork globes. They have things like Van Gogh and Monet art work carefully recreated. They transform a flat painting into a three-

dimensional piece of art. And the Mars globe. This recreation presents a direct look at each crater along with multiple layers of red, brown, and tan colors to make up the surface. The graphics are satellite images taken by NASA, giving it a level of realism you won't find with other interpretations.

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13:58 SC: So back in grad school I had a part-time job working in a clinical cytogenetics lab, as one does. And in addition to polishing and archiving slides, I would set up samples that came in from hospitals and clinics. And these were blood or amniotic fluid, things like that. And the cells were allowed to grow for a few days and then we stopped them in metaphase. This is when it's really easy to see their chromosomes. They pair up and they line up. And the people, the actual cytogeneticists in the lab, would count them. They were looking for this magic number, 46. No more, no less. If there were 45 chromosomes or 47, that's Aneuploidy. And having the wrong number of chromosomes could be bad news. It's linked with Down syndrome, and also with miscarriage. And according to a new study by Jennifer Gruhn and colleagues, having the incorrect number of chromosomes in a certain type of cell may be key to how human fertility changes with age. Jennifer's here to take us through the study. Hi.

15:00 Jennifer Gruhn: Hello.

15:00 SC: Okay, so Jennifer, when I worked in the cytolab we worked with all kinds of cells, bone marrow, blood, amniotic cells. What kind of cells were you looking at in this study focused on human fertility?

15:12 JG: So we were actually looking directly in human oocytes, or eggs.

15:16 SC: Where did you get human eggs?

15:17 JG: Our samples actually come from two different sources. We have oocytes that were donated to us by women who were undergoing fertility treatment at IVF clinics, and then we also had a portion of oocytes that were collected directly from ovaries from women undergoing ovarian cortex cryopreservation.

15:38 SC: That means that they were having their ovaries preserved because they were concerned about their fertility over time?

15:45 JG: So these women have either cancer or blood disorders that require chemo-therapeutic treatments that damage the ovaries.

15:52 SC: Oh, okay.

15:52 JG: And so the ovary is removed and part of the tissue is frozen down to then implant later for fertility.

16:00 SC: How many egg cells were you able to include in your study?

16:04 JG: We probably looked at over 2000 oocytes. But for the aneuploidy analysis, probably closer to a little over 200.

16:11 SC: How old were the people included in the study?

16:14 JG: The ages were from nine to 43 years.

16:16 SC: You wanted to look at oocytes at young age and at older ages, and say, "What are different about these egg cells?"

16:24 JG: Exactly.

16:25 SC: Before we go further, I think we need to talk on this basic biology topic that probably most people have forgotten. And this is mitosis...

16:33 JG: Meiosis.

16:33 SC: Versus... Meiosis. [chuckle] Just to make sure everyone remembers their Intro Bio, Can you tell us... 'Cause this is what is special about egg cels in the human body. So can you remind us what the difference is between those things?

16:45 JG: Well, So in mitosis it's simply a replication of the original cell where you have one round of DNA replication and one cell division. In meiosis it's unique because you have one round of DNA replication followed by two subsequent divisions, and that leaves you with the haploid gamut. So either the sperm or the egg.

17:08 SC: Haploid means you have your half your compliment...

17:10 JG: Yes.

17:10 SC: Of chromosomes. Instead of 46, you have 23. And so that means that that egg cell can combine with a sperm cell and you get back to your 46, your goal. And so when you looked at the egg cells in your study you saw some unusual kinds of chromosome counts. What were the trends in those chromosome counts in the egg cells?

17:30 JG: We actually saw a variety of different types of errors. In human fertility, if you have one incorrect, one extra or missing chromosome, that's enough to lead to potentially a miscarriage. So even those single chromosome abnormalities are a problem. But we did see some more complex abnormalities where within one oocyte you saw multiple incorrect chromosome counts.

17:56 SC: Those were more common with younger and older people.

18:00 JG: So yes, in both the young population, so the under 20, and also in our advanced maternal age group, over 33.

18:08 SC: When I look at this graph that you draw for the rate of aneuploidy, it looks... It's a very familiar shape. Can you describe what the graph looks like?

18:16 JG: The rates of aneuploidy that we're seeing across the age spectrum form a very, very distinct U-curve. You see a increase in chromosomal abnormalities in both the young girls, as well as in women of advanced maternal age, above 33.

18:34 SC: It wasn't the same thing happening to young eggs and to old eggs, there were different mechanisms at work that were causing these abnormal chromosome numbers. Can you talk about those differences?

18:45 JG: When we were identifying the rates of these abnormalities, we identified that the type of segregation error was like you said different in the different age groups that, in the young group, you're more likely to have meiosis 1 non-disjunction. So that's when you have of your 4 chromatids for say chromosome two, all four of them will go into the egg, and none of them will go into the polar body at the first meiotic division.

19:13 SC: So they drag their sisters along so they have way too many of one kind of chromosomes.

19:17 JG: Yes.

19:17 SC: Okay.

19:18 JG: So that's what we consider our four zero split.

19:21 SC: Mm-hmm.

19:21 JG: And then in the older group, women of advanced maternal age, you're more likely to see what we call premature separation of sister chromatids or reverse segregation. So premature separation of sister chromatids would be a three one split. So you have one homolog and then a single sister from the second homolog in the egg, and only one sister chromatid in the polar body.

19:46 SC: So you still have too many, that sounds...

19:48 JG: Too many. Yes, you still have too many.

[laughter]

19:51 SC: But it's a different kind of error. It's a different part of the mechanism for separation of

the chromosomes is disrupted.

19:57 JG: Exactly. So in the paper, we discuss that the premature separation of sister chromatids and reverse segregation, those error types are more likely to be associated with essentially the degradation of the glue that's holding the chromosomes together.

20:13 SC: This is really cool and this is the one that happens in women at an advanced maternal age?

20:18 JG: Correct. So in women whose oocytes have been sitting in a dormant stage for up to multiple decades, that chromosomal glue will have potentially started to degrade and therefore are more likely to fall apart.

20:34 SC: So this is when you can make this link between time. How old the person is and why these chromosomal errors might be occurring. What about the younger side? Do you have any ideas about why it might be happening? And why these chromosomal abnormalities might be occurring in younger women?

20:51 JG: So we currently don't really have a mechanism for what's happening in the younger girls, but we have several speculations that we can make. It's possible that there are extra oocytes of genetic exchange that are still not quite repaired and therefore they're linking the homologs together, and so they can't segregate properly, they just, they're stuck together and entangled. Or it's possible that this chromosomal glue that's laid down, that has to hold these chromosomes together for, like I said, multiple decades, maybe the body knows this, and so it slathers on a bunch of glue at the beginning.

21:29 SC: Yeah.

21:29 S33: And so they're just stuck together. We don't really know.

21:34 SC: How does this relate to menstruation? Another limiting factor on human fertility that we know about.

21:40 JG: When a young girl first begins to cycle, that means that her body hormonally is ready for pregnancy. However, there are many other factors that are still developing. There's associations with hip development, there's associations with all sorts of different things that potentially the body isn't quite ready to be pregnant. These chromosomal abnormalities might be a way to potentially suppress fertility right at the very beginning of these early ages to kind of ease the body into it until it's really ready.

22:14 SC: How does this suppress pregnancy?

22:17 JG: So when I say suppress pregnancy, really what I mean by that is that the body is introducing oocytes or eggs that are not viable. So it's almost like a pregnancy spacing type thing. The body ovulates an egg that has no way of being viable for pregnancy. So it kind of prolongs

things a little bit.

22:38 SC: And similarly at the other end of things when the human body might not be able to support a pregnancy, because of age-related factors, this is a backup mechanism as well.

22:49 JG: Exactly. When the energy required for a pregnancy would be much better off helping the next generation, so the grandmother effect.

22:58 SC: Oh yeah, I was gonna ask you about that. The grandmother effect doesn't actually occur in a lot of animals, right? So would you expect to see this curve in chromosomal abnormalities in other species like chimps?

23:11 JG: Oh that is such a great question and I wish I had an answer for you.

[chuckle]

23:15 JG: Oh man. So absolutely, it would make a lot of sense to see similar types of curves in... Potentially in chimps or in other long-lived animals. In whales, they have menopause. But the problem is that because they're long-lived organisms, no one has done it. And I would be so, so excited to see an aneuploidy study in chimps, but I don't know of one.

23:42 SC: Okay, could you also use your understanding of what is happening here at the very ends of the fertility curve to help people who are having difficulty conceiving? Anywhere along that curve.

23:55 JG: It is distinctly possible. Aneuploidy is the leading cause of miscarriage in humans and it affects the whole age spectrum. So, helping us to understand the mechanisms of how this is occurring at any age, really is important for the whole... For all age groups.

24:13 SC: Alright, thank you so much, Jennifer.

24:15 JG: It's been an absolute pressure. Thank you for having me.

24:18 JM: Jennifer Gruhn is a post-doctoral research fellow at the University of Copenhagen, Center for Chromosome Stability. You can find a link to her paper at sciencemag.org/podcast. Don't forget to stick around for our book segment. This month, Kiki Sanford talks with Daniel Navon about his book, Mobilizing Mutations, Human Genetics in the Age of Patient Advocacy.

24:44 Kiki Sanford: Welcome to the book segment of the Science Podcast. I'm Dr. Kiki Sanford, and this month, I had the pleasure of speaking with Daniel Navon, assistant professor of sociology at UC San Diego. His book Mobilizing Mutations, Human Genetics in the Age of Patient Advocacy describes his academic exploration of how genetic mutations influence people's lives and shape what it means to be human. Thank you so much for joining me today.

25:09 Daniel Navon: Thanks so much for having me on, I really appreciate it.

25:11 KS: I'm really interested in how you came up with the title of your book. Can you explain the title phrase "mobilizing mutations"?

25:18 DN: When we find a mutation, there are many different things that shape how it comes to matter to people, or even whether it comes to matter to people. And for a long time, geneticists were discovering these mutations but they kind of just languished in human genetics externals. It's pretty easy to find mutations now, and we've been finding them for 60 years, but certain things have to happen in order for them to really shape people's lives and that takes what sociologists often call mobilization. Mobilization basically just means that a group of people take something up as a cause, and when you take a mutation up as a cause you can create new categories of human disease and difference that can really transform almost every aspect of a person's life. One of the things that really helps to mobilize a mutation is when a group of people interested in a common disorder or trait get interested in mutation because people see them as a pathway to understanding something much more common.

26:15 DN: I think that's something that's really important for us to understand as we move forward, this dynamic between biomedical researchers interested in big common issues and the way that they work with these communities who are dedicated to rare genetic disorders. Mobilizing mutations is always hard, but it's become much easier to find mutations to identify a bunch of people who share the same mutation to create a community and then to mobilize them. But it always... It's an empirical question. Does a mutation get taken up as an object of mobilization or doesn't it? And the book shows how radically different the outcomes can be depending on the kinds of networks that people develop and the kinds of movements people build up around a genetic mutation.

26:58 KS: A big focus of your book is to introduce the idea of genomic designation. Can you define or summarize this for me?

27:06 DN: The way we tend to think about genetics, when it comes to medicine, or traits is that we're gonna find a gene for this or that and we'll find something in the genome that can account for why we're different. And that gene 4 model really drove the Human Genome Project, and it really drives the way we think about genetics today. But in reality, it almost never happens. There's always a kind of discordance between the things we find in the genomes, the mutations and the categories we already know and care about. What I mean by genomic designation is the way that finding mutations leads us to completely reclassify medicine, development, psychiatry, and so on. And so you don't find one gene for autism, you find a bunch of genes that are associated with autism. But that's not the end of the story 'cause you find those genes and you say, "Well, actually this person has fragile X syndrome," which is a better way of understanding them than just autism, and this person has 22q13 deletion syndrome and that's a better way of understanding them than just autism. And so, genomic designation is just meant to capture the way that genetics reshaped medical classification rather than just explaining the old categories.

28:13 KS: You bring up the 22q11.2 microdeletion in, right off the bat in the first chapter. Why did you choose this mutation?

28:23 DN: One, it's a group, the 22q movement, we might call it headlined by the International 22q11.2 Foundation, that is really coming into its own. I could see them going from being a pretty obscure disorder that wasn't very well recognized and really making enormous strides. Another reason that I think it's useful is that it's actually quite common. So some recent studies suggest that it might be found in as many as one in 1,000 people, although the standard estimates more like one in 2,000 to 4,000, and that means that it's not actually that rare. It affects millions of people around the world, even though most of them don't know they have it. And then another reason is that, it's really highly variable.

29:02 DN: So a person with 22q11 can have infant malformations, developmental delays, they can go on to develop schizophrenia, they can have hypocalcemia, they can have all kinds of very serious medical and psychiatric developmental issues or they can have almost nothing that would be considered clinically significant. Nevertheless, when you know someone has a 22q11.2 microdeletion, it changes the way we look at them. So suddenly an IQ of 85, which is well within the normal range can be recast as a symptom of their disorder, if say both their parents IQs are in the 120s. It's a great case because it shows how genetics can not only remake patient identity and not only can remake medical classification, but actually can remake the kind of boundary between the normal and the pathological.

29:50 KS: I'd love to know more about this boundary between what is normal and what is considered pathological and how moving that boundary or reshaping it might affect populations or even identities.

30:03 DN: When we know someone has a mutation, it means that we might look at things that make them different in a different way. So one thing that social scientists of medicine have been interested in for a long time is the way that it's not just given by nature what is an issue for medicine and what is not. We know that some things weren't considered medical issues, and now are. What genetics does though is when you know someone has a mutation, something that seemed normal or at least didn't seem like a medical issue, can suddenly become a medical issue.

30:36 KS: You do bring up eugenics in the book and the history of eugenics predating modern genetics and genomics. Why was it important for you to include that history in your discussion?

30:48 DN: I think it's always important when we're thinking about the relationship between genetics and society to remember the history of eugenics and to remember that our first attempt to apply the science of genetics to human difference was a disaster. And it shapes the way the field works today, right? The field is very aware of that history and tries to avoid it. One thing that comes up with genetic testing for the kinds of conditions I talk about in the book for genomically designated conditions is that now that we're doing non-invasive prenatal testing, combined with selective termination, we are gonna see changes in the population distribution of these mutations. And for the communities that have been mobilized around these mutations, that has profound consequences.

31:34 DN: So if you take a group like 22q, one of the great riddles for a group like 22q, and especially for even milder conditions like XYY syndrome or triple X syndrome is that most people

who have these mutations aren't diagnosed. Non-invasive prenatal genetic testing could change that. There could end up simultaneously being more people out there who know that they have these mutations, but fewer people out there with these mutations overall. And I think we need to be honest with ourselves that that is eugenics. We're remaking the population through genetic science. Now, it's not centralized coercive eugenics, I'm not arguing that it's wrong necessarily, but I do think it's something that as a society, as a community of scientists, as patient advocacy groups or people who support patient advocacy groups, it's something we need to reckon with. The last half of the last chapter really just argues we need to be looking at this.

32:28 KS: Throughout the book, you also bring up the idea of new kinds of people, and I'd love to hear your thoughts on what that means not only for these populations of individuals, who are mobilizing around a particular disease mutation but also for the general public.

32:47 DN: So I think what the term kinds of people can help us do is understand why classification matters so much. And that's a lesson for any kind of category, whether it's male versus female, sick versus healthy or for something like autism or whatever kind of category of human difference you care to think of. The point is that classifying people matters. The term comes from this philosopher Ian Hacking. And as he would put it, if you call some wet dirt mud, it doesn't change the wet dirt. But when you label a person, it changes them because labels come with expectations. They come with ideas of commonality with other people who share the label. And so the idea here is that when you label someone as having fragile X or 22q or any of the dozens and dozens of genomically designated conditions that are out there now, is it does something new. Saying they have this or that mutation matters 'cause it creates new expectations. It creates the potential to form bonds with people who share that mutation, and it changes what they're like and their experience of difference.

33:55 KS: But what about people who don't show any symptoms like people with 22q mutations, who don't seem to fit the phenotype?

34:04 DN: Hacking talks about what he calls looping. And that's how when you label someone as being a particular kind of person, they won't just conform to the label. They won't just create a self-fulfilling prophecy. It can actually loop back, as he puts it, to change the category because people behave differently or they reject the label or who knows what. And in the case of these mutations, as you test more people, you find people with the mutations, who don't fit the phenotype. They don't match what we thought the mutation did to people. And so that means you have to broaden the kind of person. You have to broaden what it means to have 22q11 Deletion syndrome or Fragile X syndrome or whatever it is. Just because we're classifying people using genetics, doesn't mean that classification becomes stable. It doesn't solve the problem that there's never a single fixed ultimate way of classifying what makes us really different. It's constantly in flux. Doing it with genetics changes the dynamics. It changes how it works, but it doesn't change that underlying fundamental fact that classification is messy, and it's dynamic.

35:12 KS: What are your hopes for this book?

35:14 DN: I hope that this book brings attention in the social sciences, but also more broadly to the fact that genetics is not just about explaining existing categories. Genetics is about creating new categories of people. And that has profound implications for the people who are told that they have

this or that mutation and their families. When people undergo genetic testing nowadays, they might do it because they're looking for an answer, but the answer they might get might not be to the question they were asking. And that can be very empowering. It can mean that they have a new community. It means they might have access to all kinds of testing and forms of early intervention that they wouldn't know just based on their phenotype or the way they present to doctors, but it also could have a downside, in that it could create biased expectations for their development. It could lead to worry about all of these things that may or may not happen as a result of the mutation. And so I hope that the book will help us begin to think about this as a new way of classifying people and all of the implications for the people who are undergoing genetic testing, which of course nowadays is a lot of people.

36:20 KS: Thank you so much.

36:22 DN: Thanks.

36:22 KS: And thank you for joining me for this interview with Daniel Navon about his book "Mobilizing Mutations: Human Genetics in the Age of Patient Advocacy." I'm Dr. Kiki Sanford, and I hope that you'll join us again next month for a peek between the pages of another science book.

[music]

36:39 SC: And that concludes this edition of the Science Podcast. If you have any comments or suggestions for the show, write to us at sciencepodcast@aaas.org. You can subscribe to the show on iTunes, Stitcher, and many other places, or you can listen on the Science website. That's sciencemag.org/podcasts. There you will also find links to the research and news discussed in the episode. The show was produced by Sarah Crespi and edited by Prodigy. Geoffrey Cook composed the music. On behalf of Science Magazine and its publisher, AAAS, thanks for joining us.