Emily Ricotta, Ph.D., M.Sc.

Behind the Mask

May 3, 2021

Barr: Good afternoon. Today is May 3, 2021. My name is Gabrielle Barr. I'm the Archivist with the Office of NIH History and Stetten Museum. Today I have the pleasure of speaking to Dr. Emily Ricotta. Dr. Ricotta is a Research Fellow in the Laboratory of Clinical Immunology and Microbiology at the National Institute of Allergy and Infectious Diseases (NIAID). Today, she will be speaking about some of her COVID research and experiences. Thank you for being with me.

Ricotta: Thank you so much for having me.

Barr: I'm very excited. We're going to start off with some studies you contributed to. Please briefly describe the premise of the study that looked at whether an immune-based biomarker signature is associated with mortality in COVID-19 patients and discuss your role in this research.

Ricotta: Sure. This was a collaboration that started early on with a number of different researchers here at NIAID. It was a collaboration with some researchers and clinics in Italy. They had hospitalized patients from the outbreak that started really early. They collected some samples and clinical information, and they sent those to us here to do testing. We tested a large panel of biomarkers to see if we could detect some sort of correlates of more severe illness or mortality based on the biomarker signature that we saw. As an epidemiologist, I get brought in a lot to analyze data, but also to help place that data in context and help the researchers and clinicians interpret that data. We did a large analysis where we looked at all of the different biomarkers that they tested at various stages and over time, and we looked at how that correlated with mortality, and then worked a little bit with how it fits into the context and what it actually means. That was my role. It was a really large effort with a lot of different clinicians, Ph.D.'s, researchers, and fellows. It was a really interesting study and a complicated dataset to work with, because it's clinical data collected in the middle of a pandemic. It wasn't really set up for research, but we made it work.

Barr: How did you make it work? You've done a lot of data analysis. Was this one of the more complicated datasets you've ever worked with?

Ricotta: It was. It's hard when you're working with data that's not collected with any sort of regularity, or you don't necessarily have all the pieces that you want to have. We'd be missing some dates that we needed. The clinical team in Italy had to go back and dig through and find it when they still have patients to take care of and other work to do. It's a real big team effort to make sure that we have all the pieces that we need to make sure that we're analyzing the data appropriately—and also interpreting it appropriately based on what we have—so that we're not overstating anything, but we can be confident in the results we present.

Barr: Did you ever feel like you were missing huge chunks of things where you had to go back to the team in Italy and request data about a certain subject or at a certain time or for a specific patient population?

Ricotta: No, they were really great. They really got a lot of the data the first go around. It was a lot of piecing together. They would send us some clinical data, or we would get some data from the folks at Frederick, after they would update some of their biomarker tests. The only thing I really would have loved to have had is more regular samples from people. For some people, we only had one sample. For others, we had 13 or 14 samples, because they were in the hospital for a while. Sometimes they got a sample at admission, other times they didn't. As an epidemiologist, I want stuff at regular time points—but again, it's just not practical in a real-world situation sometimes. Everybody really did their very best to get as much data and to fill in as many holes as possible.

Barr: What was it like doing the analysis? How did you go about doing that? What kind of programs or models did you use?

Ricotta: I worked very closely with Jonathan Fintzi in the Biostatistics Research Branch. He helped us develop a Bayesian model to evaluate the biomarkers over time so we could say, “Okay, so here's what affects the level of the biomarker.” Then we were able to take that and build it into a second model that says how all of this relates to mortality. It was a large joint model system with some Bayesian properties that we use to assess not just one time point of biomarker, but the longitudinal expression of the biomarker in these participants. We’re R [statistical program] users. We also use some of the supercomputing resources here at the NIH. We have Locus at NIAID, which is our high-performance computing cluster. We also use Biowulf, which is NIH’s. Having those resources made it a lot easier to do this type of analysis.

Barr: How long did it going to take you to analyze all this data and clean it up? That must have been challenging.

Ricotta: I always joke that every data analyst spends 70% of their time cleaning the data and 30% analyzing it. There was a lot of help with the data cleaning. One of the fellows, Mike Abers, who was also one of the lead authors of the paper, did a lot of work cleaning the data. It takes weeks really to go through to learn what's missing and what needs to be cleaned and what can't be. It's an iterative process. Running the analysis would usually take a couple of hours just because of the processing power required to do the sheer number of biomarkers and the number of patients and what we were asking it. It takes a lot of time. There's a lot of time invested in making sure that the data is clean upfront. Otherwise, you get estimates that don't make sense and you have to figure out what happened to them. It's an involved process.

Barr: Can you speak a little bit about the study you participated in that looked at how an oral antiviral drug called Molupiravir, or MK-4482, inhibits SARS-CoV-2 in Syrian hamsters?

Ricotta: This was a study that was actually initiated by the Rocky Mountain Laboratory and the group out there. They were looking to evaluate whether this drug would inhibit the replication of SARS-CoV-2 in the lungs. This drug had actually been designed to treat hepatitis back in the early 2000s. A lot of groups were basically going

back through medications that had already been approved for other things—so we knew that they were safe in humans—to see if they have specific efficacy against this virus in particular. This happened to be one that they landed upon that looked like it had good anti-coronavirus activity. That's why they chose this one to test.

Barr: Can you speak a little bit about why you use Syrian hamsters as opposed to other kinds of hamsters? It seems very specific.

Ricotta: I don't actually know why they chose Syrian hamsters as opposed to other hamsters. I know why we chose Syrian hamsters as opposed to something like ferrets. Syrian hamsters specifically are very susceptible to SARS-CoV-2 and develop a very pronounced lung infection, and so it's a good model organism to evaluate SARS-CoV-2 infection in the lung because you can see a lot of pathology. It's really nice. You can see the viral replication. Kyle Rosenki at Rocky Mountain Labs was the lead where they actually showed that the Syrian hamster was a good model for COVID illness. There was another study looking at this drug in ferrets. But ferrets are actually a better model organism for transmission of SARS-CoV-2. They don't actually get the same lung pathology that the hamsters do. That's why you see these two different studies and they look like they've got similar results, but they've got slight differences. That's because of the model organism and how the virus infects the ferret versus the hamster. Animal models are a science unto themselves.

Barr: Are they testing this drug in humans yet?

Ricotta: Yep. This already had been tested to treat hepatitis. There have been some clinical trials that have been looking in humans to see efficacy of this drug against SARS-CoV-2 infection in humans. They're looking specifically to see whether it can help reduce viral replication in hospitalized patients. They are interested in this drug because it's orally delivered, which is why it's different than something like remdesivir. Remdesivir has to be provided intravenously. One of the reasons that it's good that it's delivered orally is that it can be used to help stop transmission events, or it can be given prophylactically. If somebody has a high-risk encounter, we could give them that drug, just like you would do after an HIV exposure or a rabies exposure. We have post-exposure prophylaxis. There's thought that potentially this drug could be used in that sort of scenario. Testing hasn't been done on that yet.

Barr: Have you been a collaborator on any other COVID studies or been part of any other campus-wide COVID initiatives?

Ricotta: I'm actually one of the few epidemiologists in the Division of Intramural Research at NIAID so we have the opportunity to work with a lot of different investigators. I have been working with Sameer Kadri and his team at the Clinical Center, doing a study looking at hospital surge and how that impacts mortality, and looking specifically at what the hospital surge looks like during COVID. We used a large electronic health record dataset, and we compared what admissions looked like last year [2019] during April through September and what they looked like in 2020 during that same time period, to see whether a there was a surge and whether that surge impacted mortality in a way that was different from other times we've seen hospital surges. We're working on revising that manuscript right now. It's under review and resubmission. I've also been working with Dan Chertow and his team. We're studying a cohort of patients who are on ECMO [Extracorporeal Membrane Oxygenation],

and who have been hospitalized with COVID. We're collaborating with the University of Maryland Medical Center. They collected an extensive amount of data on these patients. Basically, your lungs can't support themselves and your heart starts having problems pumping blood, and so they put you on ECMO to help. It's basically a type of life support to help your body give itself time to recover while your organs don't then have to overwork themselves. These are very sick patients—these are the sickest of the sick. They had a cohort of patients, and they took samples every day from them. They collected an extensive amount of clinical information, so we're going to be able to look at biomarkers in these patients and will be able to look at viral kinetics, drug dynamics, and things like that. We're still early in the study design of the analysis of the samples. But that's another project that I'm working on currently with Dan Chertow and his team. Also, I just joined the board of the NIH COVID Scientific Interest Group. I'm lucky to be involved with helping to select the speakers we're going to have next year and helping to arrange fellows' tea with the speaker. If fellows are interested in meeting with any of our speakers, they can usually come afterwards and talk with them and ask questions in a smaller setting. I've been very lucky to be involved with a lot of different things over the last year. I mean, who would have thought epidemiology would be having its time in the sun?

Barr: Now we're going to speak about a study that you are the principal investigator (PI) on and that just kicked off on April 20 [2021]. That's really exciting, so congratulations. Will you please introduce your study that is looking at how people with immune deficiencies and dysregulation respond to COVID-19 vaccination?

Ricotta: Sure. When we do vaccine studies, we typically just take healthy people. It's not that extensive, especially when we're testing the safety and the efficacy of vaccines. This leaves a lot of groups out. One of those groups usually are people who have immune deficiencies. This could be that they have some sort of genetic mutation that causes something in their immune system not to work. Sometimes these happen at birth, so they've lived their whole lives with these immune disorders. Other people could have acquired immune deficiencies, based on medications they take or chemotherapy—there are a number of different things that can cause immune suppression. All of these people are very understandably concerned, not just with COVID infection, but if they are protected from the vaccine. What is this vaccine doing? Can they go out and be among people? Everybody else can go out now. Our study is designed to study a number of different immune deficiencies—primary and secondary, like I just covered, to see what the antibody response is. What are the other immune cells that are maybe produced? How effective are these antibodies at neutralizing the virus? We're also looking at adverse events that were experienced in this population. We're looking at prior COVID infection. We're also going to be analyzing the rate of post-vaccination COVID infection, so we can see if these people are getting infected. Does that correlate with antibodies or other immune cells or variants of the virus? It's a large and complex study, but we're hoping to get those answers of what immunity people have, how long that is actually going to last, and how effective the immunity is that your body has produced.

Barr: How is your team defining immune deficiency and dysregulation for this study? There's so many different types of immune deficiencies and people have different levels of immune deficiencies.

Ricotta: We've deliberately kept it pretty open because there really aren't too many studies that are doing this type of analysis right now. There are some that focus on very specific groups. I'm sure most people are familiar with the Hopkins study. There's one looking at autoimmunity and there's one that was looking at solid organ

transplants. We'll include those people in our studies if they're on active immune suppressants. But we're also interested in looking at some of the rare immune deficiencies—some of these primary immunodeficiencies. That's actually how this study got started. Initially it had been pitched at looking specifically at NIAID's population of primary immune deficiency patients to see what their COVID experience looked like. It evolved into looking at the immune response too, and specifically the immune response to vaccines—because NIAID is well situated to do that, seeing that we have this large population, but we do have it deliberately open. We're taking different types of cancers; we're taking certain people who have different types of organ transplants, certain amount of autoimmunity, or are on different kinds of drugs. If people are interested, we're willing to consider and review their specific circumstance and see if they qualify.

Barr: It's very interesting that there's such little information about this topic, because the news kept talking about how this group was the most vulnerable for COVID-19. Has there been any analysis about any of the topics that you are looking at within patient records?

Ricotta: Not so much. Earlier in the pandemic, when we started really seeing these infections, we didn't really know what was going on, and so the data that was collected wasn't the most helpful or most reliable. As we go, this community is just very mindful of their health. I mean, they're very aware of what's going on. This is a very medically literate population of people, so they protect themselves. They know what they can and shouldn't be doing and things like that, and so, luckily, many of them mitigated their risk a lot and so then we didn't have data on them because they didn't go on to get COVID. Or if they did, the numbers are small. Again, these are rare diseases that we're talking about for a lot of them. Not necessarily the auto-immunities and the cancers, but a lot of these others are rare. There just isn't the data to be able to really assess with large enough numbers any sort of immunity or severity of disease in patients with immune deficiencies. There have been smaller studies that have cropped up here and there, but nothing at a large enough scale to really give us good answers.

Barr: When did you begin to conceive of this study? What was the process like for you to get this protocol up and running?

Ricotta: Originally, I had designed this cute little epidemiology study where I wanted to look at the symptoms and severity of COVID in our patient population here. Then Dr. Holland, the Director of the Division of Intramural Research at NIAID, came to me and said, "Well, what if we expanded on your study, and we looked at immune deficiencies?" From there, it really kind of snowballed. We got started with things in January, and it has been a race to the finish trying to basically get our protocol up before everybody got vaccinated. It was great for the community to be vaccinated—not so great for our study. Planning a protocol takes a lot of time. We had to get the science down first. The way that this happens at NIAID is that you go through scientific review, so your protocol is peer reviewed by experts and other scientists, and they check the science. Then it has to go to regulatory reviews and things like that, to make sure we're utilizing NIH resources appropriately. Then it has institutional review board review, which is making sure that we are ethically researching and making sure to take that into consideration as well. Then it's just the getting everything organized. Honestly, one of the hardest things was figuring out all these little nitty gritty details, like where to take FedEx things on campus to drop things off. Or how do I get boxes to ship things? I have really been leaning on the study coordinators and the nurses here, who are amazing. They know how to get everything done, and they've been very gracious in

helping me. This is, as you said, my first time being a PI here, so it's been a lot of learning very quickly—all of the different data systems and getting all of the trainings. In the week and a half since the study's been up, we've had over 400 people email us. We've had an overwhelming response, which is excellent. But there are [only] four of us working on this, so I spend my evenings and weekends going through volunteer emails. We're all just trying to keep things coordinated. It's crazy.

Barr: How are you keeping it coordinated? That's a lot of information to keep track of.

Ricotta: It is. We work with the CRIMSON team here at NIAID. They are our research data system. They've customized the database for us with basically everything we needed. They've been amazing. We use that system. I have a master Excel document even though as a data analyst, Excel makes me a little nervous. It's just a lot of communication. I communicate with my team all day, every day, basically—through email, [Microsoft] Teams, or the phone, or seeing them in person if we're on campus. It's just a lot of trying to be communicative, utilizing technology to the best of our ability. I'm sure we'll get better at it as we go. It's a little disorganized and kind of crazy right now, but we'll get the hang of it.

Barr: Can you please describe your methodology, including some of the criteria that you had for enrolling participants, the number of participants you're looking for, the kind of equipment and tools that you're using, and the metrics for evaluation?

Ricotta: We are going to be taking blood samples from participants over a number of time points. Hopefully we'll get a baseline before they get vaccinated, and then a month after their first dose, a month after their second dose, and at six, 12, and 24 months. If people have already been vaccinated, we're enrolling them—that's fine. We just plop them in where they're supposed to be and then we keep going. The nice thing about our study is that you don't actually have to come to the NIH to get sampled. You can if you're here, and we have already had a few people come and do their sampling, but we can provide remote sampling options. We can send participants a finger stick at-home sampling collection kit where they just prick their finger and put it on a sampler and send it in. We're working on getting a contract set up with a national commercial laboratory so that participants can go to their local clinic and have blood drawn and send that to us. Because I don't have my own lab as an epidemiologist, I am collaborating with a ton of amazing investigators here. We have Katelyn Sadler, who is a tenure track investigator at an NIBIB [National Institute of Biomedical Imaging and Bioengineering]. She has designed this great serology assay to look at the different spike nucleocapsid and receptor binding domain proteins and antibodies that are generated. She's going to be doing all of our serology for us and it's a lot of work. She's designed it and it's really excellent. She also was in charge of the NIH 10,000-person serosurvey that happened. We're gonna have the same assay as that study, so we'll be able to do a little comparison, which is cool. We're going to be working with NCI [National Cancer Institute]—they are helping us. They have a biobank repository there, so we're going to be sending our samples to NCI for storage and then later use by both my team and other investigators who might be interested, so that's going to be available. Luigi D. Notarangelo is looking at a lot of the T cell and B cell receptors that patients are doing. We've got John Tsang, who is going to be doing some transcriptional analysis for us. And Vincent Munster and his group out at Rocky Mountain Labs are going to help us. They're going to be doing some analysis. At the Department of Laboratory Medicine Sanchita Das is doing our PCR [polymerase chain reaction] testing for us. It's a very large study. We have a lot of

collaborators who are actually doing the research assays for us, but then we also have people throughout NIH who are referring their patients to us. We've got people from NIDDK [National Institute of Diabetes and Digestive and Kidney Diseases]. We've got people all through NIAID who are sending their patients to us to participate in the study. It's really a huge group effort. It's a ton of people and a ton of collaboration. It's very interesting and very exciting. We're going to get a lot of different data, I think, which is going to provide a really nice look at the immune response in this population.

Barr: Are there any types of immunodeficiencies that are considered so dangerous that they can't participate in this study?

Ricotta: We're not including individuals who have HIV at this moment in time. The logistics of shipping those samples is a little tricky. Because of the rest of the study being tricky, we decided to exclude those individuals at this time—although others at NIH, I believe, are setting up studies to evaluate that group. The only other group—and we did talk about this when we were designing the protocol—are some groups of patients for whom getting a vaccine, specifically the mRNA [messenger ribonucleic acid] vaccines, may not be the best idea just because they are at higher risk of having a severe adverse reaction to one of the vaccines. These are individuals who have things like interferonopathies or things. They already have immune systems that can get a little crazy overactive, and so the recommendation is that they don't get vaccinated. However, we are not vaccinating people on our protocol. At this time, people are getting vaccinated in the community, and we are working around their timelines. If somebody were to get vaccinated and have one of these illnesses, we can still enroll them. But we are not recommending that anybody of a particular group get vaccinated, that's a decision for them and their primary care physician or their team of clinicians. But if they do, we will potentially still enroll them.

Barr: That makes sense. Can you speak a little bit about the questionnaires that your group is distributing to those who may have had COVID? Do they have to have tested positive using a certain type of test in order to confirm that? So many people claim they had COVID, but it's unclear whether they actually did.

Ricotta: We are working with the REDCap [Research Electronic Data Capture] team to do our survey. All of our surveys will be offered electronically. It's great. You just email the participant, they click a link, and they can answer the questionnaires—and we have a number that they'll be filling out over the course of the study. We're collecting a lot of baseline medical history on folks so that we know what their medications are, whether they've had certain procedures, whether they have other illnesses, and things that could impact our results. We will also at that time be asking about COVID illness or COVID-like illness in the last year and a half now since January 2020. And we'll ask whether they had a positive test for SARS-CoV-2—but no, it's not mandatory that they have any sort of positive testing. One of the things that Dr. Sadler's assay actually can do is test for infection antibodies, essentially, because we're going to be looking at nucleocapsid, which is not a sequence contained in the mRNA vaccines. There's a little bit of internal checking that we can do that way. But otherwise, we'll have the people who report that they did have a positive and we'll be able to look that way. We can also look during the analysis to confirm COVID and here's what that looks like, and COVID-like illness and what that looks like. Then we can compare the two and ask how different they look. Does it matter that they had COVID, or just that they were having these symptoms, which was indicative of an immune response? That's the type of stuff that

we'll be able to look at and think about once we have the data and can start breaking our analyses down different ways based on what the data is telling us.

Barr: Are you concerned that one type of vaccine will be more represented than another amongst your study population?

Ricotta: Right now, it's actually pretty evenly split between Pfizer and Moderna. We have a few Johnson and Johnson snuck in—just because of the timing of that and then the stoppage due to the concern about blood clots, so we haven't had too many Johnson and Johnson. Otherwise, it's been pretty evenly Pfizer and Moderna—maybe slightly more Pfizer. But we're recording all of that information, so we'll have the specific vaccine that people receive. Also, then we can look at mRNA vaccines in general, and then break down the specific vaccines if we need to. Hopefully, we'll pick up some more Johnson and Johnson as we go. But it'll be interesting to see what that does pick up. We're also prepared if AstraZeneca gets an authorization. We're prepared to include that as well.

Barr: Can you speak a little bit about your role as PI for this project and can you introduce some of those working alongside you on this endeavor—you've talked about some of your collaborators at NIH, but the four other people who are your core team?

Ricotta: My team is composed of Maureen DeGrange, a nurse practitioner who works with the Primary Immune Deficiency Clinic here at NIAID. She's excellent. She's helping me do the informed consent process and some of the clinic notes and to place the orders. She's a credentialed medical provider. As a Ph.D. scientist, I don't have those credentials, so I can't give medical care. She is really crucial to this protocol because we need somebody to be able to do those things. She's been great. She has just jumped on board and has been super enthusiastic. We also have two postbaccalaureate fellows who are working with us. Milann Cox is a fellow—she has been working with one of our collaborators, Rachel Sparks, on one of Rachel's projects looking at the immune response to the flu vaccine. She was very familiar with how this process goes. I've been asking her all kinds of questions about how to do things and what I need to put in. We also have another fellow, Michael Stack, who has been working with Luigi D. Notarangelo and the COVID consortium dataset, so he's very familiar with data. Together all of us are managing all of the moving pieces of enrolling and screening patients and tracking them and consenting. Milan is going to be responsible for shipping out the kits and making sure that the samples get to where they need to go and things like that. My job as the PI is to oversee all of that—I see the forest and everybody else deals with the trees, although right now I'm also helping with the trees because there are [only] four of us, so I have – I wear a bunch of hats. I wear the PI hat, the study coordinator hat, the phone screener hat—all sorts of things. Everyone's been picking up whatever needs to be done and making sure that the study moves along and gets what it needs.

Barr: Did you get to meet some of your first participants at NIH?

Ricotta: Yes, I did—actually the very first person that we enrolled we did get to meet in person. I had to give them their signed consent form, and then actually showed them to where phlebotomy was because they had not been there yet. That was neat. They were super patient, because we were using iMedConsent for the

consenting and for the electronic signatures, which is a first for us and is new to NIH. This participant was very patient with us as we fumbled our way through figuring out the signature system and sending emails. I mean, all of the volunteers so far have been so excellent—so enthusiastic and very engaged. It's made the process a lot less scary as a new person doing this. No one has yelled at me or gotten angry if we've made a mistake, or if we've had to email them four times and ask them for things. It's been a really great process, just getting to talk to people, hear their stories, and talk to them about their excitement for contributing.

Barr: That's really wonderful. Now, to transition to you as a person during the pandemic. What have been some personal challenges and opportunities that COVID has presented for you?

Ricotta: I've been really lucky—as an epidemiologist and a data analyst, my work kind of travels with me. I was able to transition to working from home very easily, basically without missing a step. That part was nice. I'm lucky in that I have space in my home set up. I have a home office that I can work in. It wasn't a problem for me to do that. You miss working with people and seeing people. I missed those interactions with my colleagues where I could lean over and go, "Hey, I have a question about methods" or whatever. That's something that I've missed. But otherwise, I've been very lucky with the pandemic. It hasn't really impacted me as much as the majority of the rest of the world. It's been kind of good in a way. As an epidemiologist, again, this is what I've been trained for, and this is my expertise, so it's really given me an opportunity to get to work with a lot of people and interact with people that I wouldn't have normally, because here are these opportunities. It's also been a challenge. People don't necessarily understand what epidemiologists do, especially at the NIH. We've got amazing researchers and amazing clinicians. How do epidemiologists fit in? What do we bring? That's been a challenge—just all of us, I think, trying to figure out the best ways to collaborate. But it's been really good. Everyone's been really excellent to work with. It's been a good opportunity in that sense.

Barr: What do you feel epidemiologists bring?

Ricotta: Like I said earlier, epidemiologists help put things in context. We help put data in context. We study populations and how a disease transmits and how it works in a population. What clinical epidemiologists such as myself can do is to really help design studies. That's why I think I was brought in to help lead this study in particular. We have these large populations, so how do we design a study that answers the questions that we want to have answered and that makes sure that we get the data and the time points that we need from the beginning, rather than scrambling at the end trying to find things? How do we make sure that the data is collected well and that we are thinking through all of the different components that we need? How do we bring all these pieces together? And then interpreting the data and contextualizing it. As an epidemiologist, that's where I come in. We can help do this with basically anything. I mean, I had somebody ask me, "Well, you're not an immunologist. Why are you doing an immunology project?" Well, the type of data I collect doesn't matter. It's how the data is collected. It's how the study is designed. I could come in tomorrow and design a study looking at invasive fungal infections, and I can come in next week and I can design a study looking at antibiotic resistant bacteria.

Barr: Yes, I was going to ask you about that. I saw on your resume you've worked with so many different kinds of pathogens from tuberculosis and fungus to all kinds of bacteria and different viruses. How has COVID compared to some of the other disease pathogens you have studied and worked with?

Ricotta: Interesting question. The most interesting thing about working with COVID is that I don't think anybody anticipated the level of how much human behavior would weigh into the equation. Don't get me wrong. I mean, my Ph.D. was looking at human behavior and malaria transmission, so I'm familiar with how human behavior impacts, but I don't think any of us realized or anticipated people not wanting to wear masks to such a degree or not social distancing. That's been the weirdest thing. With all the other diseases, you can kind of focus on the disease, or on the treatment, but with COVID, you have to rely so much on the individual to play along, basically, in order to stop transmission. Whereas with other things, we give you a flu shot, and we don't really worry about it, or you take antibiotics and you're treated, or you take a malaria prophylactic pill before you go. We don't have any of that for COVID right now. We're getting the vaccines, but even those aren't perfectly effective. That's been the interesting thing. When it comes to doing the analysis and using the methods, that's all the same. It's the same over and over again, but it's the context of doing this analysis. You can do a logistic regression anywhere across the board. But what do you have to put in that equation in order to get the correct estimates? Again, that's where epidemiology comes in. That's been the weird thing with COVID, because it's what we would normally include, but we need these other things, too—things that we're not used to working at and we don't have the data for necessarily, because who collects that and where do we get it? That's been the interesting challenge of COVID.

Barr: That’s fascinating, and so true. What is one way you've tried to stay grounded in this very turbulent and uncertain time?

Ricotta: I've just really tried to keep in touch with my friends and my colleagues. I make sure to touch base with my staff weekly, if not more frequently than that. With my study team, it's all day. But with the rest of my trainees, I try to touch base at least weekly, if not more. I have calls with my friends and collaborators and co-workers, just to hop on and catch up and see what's going on. That's how I kind of kept things normalized. Working at home, you can get very isolated and just be in your bubble. But reaching out and making sure to keep up that little bit of normalcy, even though it's looking at somebody through Zoom, is still having that conversation and making that connection and having those collaborations. That's really been how I've kept things together through the pandemic.

Barr: That’s great. Was there anything else that you would like to add as an NIH scientist, but also as a person who's living through this pandemic, like everybody else on earth right now?

Ricotta: It's been really great to be working at the NIH during the pandemic. NIH is a great place. I've worked at a lot of different organizations and institutions, and this place is really unique. It's been amazing to see all of the scientists and fellows and the support staff at NIH—everybody—really come together to keep the research here moving and to really try to contribute to public health. That's been really amazing to see. It's been really inspiring. It's really given me purpose—my work has always had purpose, but this has really driven that home. I think all of us get it, everybody from the directors on down—even the scientists. We're all in the same boat and

we’re all experiencing things. There's been this disconnect between science and the community through a lot of this. I wish there wasn't, because, as scientists and as researchers, we’re people too, and we're experiencing this too.

Barr: A lot of demonization of science.

Ricotta: Yeah. What I hope for us as a community is that we get better as scientists at communicating, and the community gets better at being open-minded and asking questions and understanding how the scientific process works. And that we're able to really start working together, because this is not going to be the last pandemic that we're going to see. This is potentially just the beginning. We’re going to really need to continue working together and continue living together. Let's hopefully learn from this experience as an institution, as a community, and as a country. And let's hope that we can do better next time.

Barr: Thank you very much for your time and for your service. I wish you and your team all the best in your different studies and especially in the one that you're leading. I hope that you all continue to stay safe even though there's a vaccine. I guess we should all continue to stay safe.

Ricotta: Absolutely. Well, thank you so much. I appreciate being able to share my story and that of my team. It's been very nice talking to you.

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