But if you have additional questions, so let's now turn to our second Speaker. Doctor Ellen Foxman is assistant professor of Laboratory Medicine and Immunobiology and Extensive work now really understanding the immune responses and natural responses to respiratory viruses. Which is certainly a very timely topic of research.
Uh, in 2020?
So we were really pleased that Alan could take the time to share her research with us.
Thank you. I'm happy to be here. And now I'm going to hopefully share the screen and it will. All will go well. Um?
So can you see the slides? Yes, OK, great. OK, well everyone,
I'm very happy to be here even though it's by zoom an be able to participate in my first Yale Cancer Center Grand rounds.
This actually is not going to be a talk about cancer. It's going to be a talk about COVID-19, which is also a topic on everyone's mind these days, so I'll tell you about some of the work our lab has been doing.

Looking at host response based detection of respiratory virus and specifically applications to COVID-19. This is just a disclosure that I'm going to inventor on to patent applications. So today I'll be talking about why are we interested in studying the early host responses against respiratory viruses,
or in this case in particular.

SARS coronavirus two,

I’ll give a brief overview on the basics of Cobra 19

then a project that we’ve been doing since March on screening using host biomarkers for this disease and then future directions of the project.

So as I was preparing this talk, I looked back at some of my previous talks and this is actually an intro slide I had from a talk I gave at the end of November to the virology faculty group,
and I thought it was kind of. It looks so different in the lens of our current environment that I thought I would show it. So I used to start my talk by convincing everyone of the importance of respiratory virus infections, which is a much easier sell now, but actually, even before this pandemic, these infections cause. Over 500 million infections per year in the US, so that’s more than one per person and granted a lot of those are common colds, but some of those are
serious illnesses such as. Influenza with hospitalization or hospitalization for asthma attack or CEO PD Exacerbation which are very often caused by viruses and also there has been this emerging this lingering concern about emerging infections with good reason. As we know now and I usually put up this photo to describe that that's actually a picture of the SARS coronavirus from 2003. But now when we see these pictures it definitely conjures up something else in all of our minds,
which is the 2nd SARS Coronavirus SARS Co V2. Uh, which causes the disease cobra, and I just checked on the Johns Hopkins Portal an at the moment there’s over 7 million cases and over 400,000 deaths described globally from Cobra 19, so this is definitely having a high impact. It’s impacting our seminar that were having if I zoom today, it’s impacting our work. It’s impacting our economy and of course our health and there’s still a lot of unanswered challenges trying to figure out how to deal with it.
Um, and even when this acute phase is over, there will be long-term impacts, both on the health of the respiratory system in the patients who are recovering, or have recovered and we also have to think what lessons can we learn from this that are going to help us with the next pandemic. So this is sort of a just a screenshot of my labs homepage to remind me to tell you a little bit about what we really focus on the lining of the respiratory tract, the airway mucosa as you see in this picture.
This is actually what the epithelial layer in the upper airway looks like, and these are these cells. The epithelial cells are the target cells of viral infection and viruses replicate in these cells. These cells also are the first line of defense that recognizes the infection and sends out signals to the immune system to come to the area and also sends out turns on affecter mechanisms to try to stop the virus from replicating. So there are very.

It’s a very highly active tissue.
The airway mucosa.

Our lab is focused on these early steps of host defense, and we’re also interested in repair. Actually, because after the way isn’t like the skin. It doesn’t constantly regenerate, but rather only when damage does it then regenerate, but it has the potential for these stem cells that you see here at the base of the epithelium to proliferate and recreate that issue. And one thing we’re interested in is how come that sometimes goes.
right and sometimes goes wrong,
NOTE Confidence: 0.90692675113678
and sometimes when it goes wrong
NOTE Confidence: 0.90692675113678
that leads to cancer and that I
NOTE Confidence: 0.90692675113678
hopefully I'll be able to come back
NOTE Confidence: 0.90692675113678
for a different grounds and talk
NOTE Confidence: 0.90692675113678
about that project at some point.
NOTE Confidence: 0.90692675113678
But for today I'm going to focus
NOTE Confidence: 0.90692675113678
on the upper respiratory tract.
NOTE Confidence: 0.90692675113678
As the gatekeeper against infection,
NOTE Confidence: 0.90692675113678
so most of the pathogens that
NOTE Confidence: 0.90692675113678
come into our airway come in
NOTE Confidence: 0.90692675113678
through the nose and mouth throat,
NOTE Confidence: 0.90692675113678
and this includes viruses and bacteria.
NOTE Confidence: 0.90692675113678
And often if that infection can
NOTE Confidence: 0.90692675113678
be nipped in the Bud in the upper
NOTE Confidence: 0.90692675113678
respiratory tract that protects
NOTE Confidence: 0.90692675113678
00:06:02.862 --> 00:06:04.888 the rest of the respiratory
NOTE Confidence: 0.90692675113678
00:06:04.888 --> 00:06:06.943 system from that that infectious
NOTE Confidence: 0.90692675113678
00:06:06.943 --> 00:06:09.066 agent getting down to the lungs.
NOTE Confidence: 0.90692675113678
00:06:09.066 --> 00:06:11.010 So when these offense defenses are
NOTE Confidence: 0.90692675113678
00:06:11.073 --> 00:06:13.575 effective in the upper respiratory tract,
NOTE Confidence: 0.90692675113678
00:06:13.580 --> 00:06:15.692 it can really be the difference
NOTE Confidence: 0.90692675113678
00:06:15.692 --> 00:06:17.620 between miles or asymptomatic illness.
NOTE Confidence: 0.90692675113678
00:06:17.620 --> 00:06:18.944 Versus a serious illness.
NOTE Confidence: 0.90692675113678
00:06:18.944 --> 00:06:20.930 And we know that that’s happening
NOTE Confidence: 0.90692675113678
00:06:20.990 --> 00:06:22.980 all the time, not just with SARS,
NOTE Confidence: 0.90692675113678
00:06:22.980 --> 00:06:23.610 Co V2,
NOTE Confidence: 0.90692675113678
00:06:23.610 --> 00:06:25.662 but other viruses that often there
NOTE Confidence: 0.90692675113678
00:06:25.662 --> 00:06:27.368 cleared from the become their
NOTE Confidence: 0.90692675113678
00:06:27.368 --> 00:06:29.279 detectable in a way for a time.
NOTE Confidence: 0.90692675113678
00:06:29.280 --> 00:06:30.144 A short time.
NOTE Confidence: 0.90692675113678
They and they are cleared without the patient knowing that they were there. That can happen, or you can have the opposite, where the patients in the ICU. So we’re interested in factors that modulate those defenses, and we like to think of it as like a marble sitting on a mountain where this is the very beginning and we like to think of it as like a marble sitting on a mountain where this is the very beginning of the immune response. That’s going to recruit certain immune cells in the respiratory system and sort of nudging that marble in One Direction. It will roll down the Hill one way,
and you’ll get one type of response, whereas if you nudge it in the other direction, it can have a very different outcome. So we’re very interested in understanding the molecular basis of that. This is a another picture of this as an upper respiratory tract from a child, and so what’s something that’s kind of interesting about this anatomy is I actually just myself today. Had a swab for this surveillance and we all notice swab goes Kobe 2 and
right in here in the nasopharynx,

and that swab also collect some of the

patients own cells and some of the

proteins made by the patient's own cells.

And in a study with Marie Landry

of the director of the clinical

virology lab back in 2018,

we showed that you can actually

detect the patterns of jeans and

proteins being made in the respiratory

tract and the huge changes that

occur in the rapid response to

viral infection. And if you think

about the progression of SARS,

there's you probably have all

seen a figure something like this.
And of course this will be refined over time, but the basic idea seems to be that at this early stage of infection we have upper respiratory tract replication and those kinds of symptoms. Then it moves to the long and then in severe cases there’s a host inflammatory response. It causes a lot of damage. At this early stage, what we can find out using these respiratory swabs is what can we think about alternatives and additional things we can do for the best diagnosis and even.
can we understand the difference

is an inflammatory response is the very beginning that dictate the way

So today I’m not.

I’m not gonna talk about bullet .2,

I’m gonna talk about bullet .1 today.

The diagnosis end.

So I’ll just start with giving a brief overview on diagnostics for a SARS Co V2.

I know we have a diverse audience here an I gave a full length,

uh,

detailed description of this stuff for one of the Deans workshops that’s available online.

That this is everything in a nutshell,
so I’m going to describe the test that we are currently doing at Yale.

The first test answers a question. Does the patient have the infection right now? And basically what you do for that?

Is you do the swab isolate are an RNA. Can you detect viral jeans from the viral genome in this patient sample an if the answer is yes, it means a patient has the virus or the viral RNA and their nasopharynx right now and that test is
very specific because we’re just looking at the genome of this virus and very specific regions.

Sensitivity depends on when your sampling and sample collection, and a few things like that, but it’s a highly specific test.

The other question, of course, is did the patient had the infection? Is there evidence of past infection and that’s serology?

So that’s asking has the patient formed antibodies against the virus because they’ve already had the infection? Usually for a minimum of two weeks.
00:10:12.888 --> 00:10:15.299 to have an adaptive immune response.

And kudos to our clinical lab for having both of these up and running for awhile now. Marie Landry in the virology lab, and, uh, Rick Tourism.

The clinical immunology lab have set these up and they’re available to order on the patients, and this is this is our go to test to know.

But there are still challenges. Are there still a lot of challenges that we’re facing right now? One is how to expand testing capacity,
and there's many different avenues this can go down.

There is a group with Nate groove on an Wiley doing great stuff with saliva.

Testing is one way, but there are other ways we can be screening or expanding testing capacity to help make sure we're not spreading this virus.

Further, as we restart the economy, another challenge is that some people who test positive by the PCR tests don't actually seem to be infectious based on a study from South Korea and a few other observations elsewhere of people who recovered and still test positive.
positive for a long time but don’t seem to spread the virus to their Contacts. So how can we tell the difference and then finally also very important is how do we find new viruses that are going to be the next pandemic that are going around and causing Ellis in our patient under our radar? These kind of questions are why we got into looking at the host response. In addition to understanding pathogenesis. But sort of on the practical side of how can it help us an once is to die for diagnosis.
We’re all familiar with them. I mean the basic one for infection is fever. Fever is a host response to infection and fever. Is fever elevated? Leukocyte count? Those are signs that the patient has an infection. They’re not terribly specific, but they are a host response has been used for, you know, long time, hundreds of years, even the the fever. But now we can get more granular better techniques to look at.
Patterns of gene expression, patterns of protein expression using Multi Plex Technologies like transcriptomics and.
The idea is if a patient comes in and is coughing, you don’t know what’s causing that, but if the if that’s being caused by a respiratory virus that’s replicating.
That’s activated, the immune system turned on antiviral defense is, which are different then defenses against an irritant or a bacteria or other things that cause coughing.
And if you look at the patterns of Gene
and proteins that the body is making, you can sort of interrogate the body's own diagnosis and know what's going on. And so, again, this is based on the study from 2018. A very simple question was, are there common patterns to all respiratory viruses that we can look at to say? Is this patient experiencing a respiratory virus infection right now or not? Because you may not know this, but in the winter seasons I'm not talking about this year but in past years between December, March redo thousands of panels.
00:13:24.600 --> 00:13:26.336 of symptomatic patients testing
00:13:26.336 --> 00:13:28.267 them for 15 viruses to see.
00:13:28.270 --> 00:13:28.636 Uh,
00:13:28.636 --> 00:13:30.832 which virus might be causing their
00:13:30.832 --> 00:13:32.949 respiratory symptoms and only about 1/3
00:13:32.949 --> 00:13:35.182 of them actually have a viral infection,
00:13:35.190 --> 00:13:37.647 so 2/3 of them may have some
00:13:37.647 --> 00:13:39.000 other process going on.
00:13:39.000 --> 00:13:41.254 So we asked whether we can look
00:13:41.254 --> 00:13:43.154 at Biomarkers of the antiviral
00:13:43.154 --> 00:13:45.304 response to identify who those
00:13:45.304 --> 00:13:47.469 patients with viral infection R.
00:13:47.470 --> 00:13:49.690 And this is to this is
00:13:49.690 --> 00:13:51.170 published something to sum
00:13:51.253 --> 00:13:52.689 it up very quickly,
but the idea is that we found that jeans and proteins that are highly induced during the antiviral interferon response. If you detect those in the nasopharynx, it’s a very good good indicator that there’s a viral infection there, and this colored graph just shows kcil 10. This is actually one of these interference stimulated jeans. It’s a cytokine. And it goes up many orders of magnitude during viral infection and the level of it highly correlated to the presence of the virus. So this is like the level on a log scale, and then these bars indicate
that there's a virus present. And we did two different studies at two different times of year with two different viruses circulating and in both of those are represented on these pie charts, which viruses were amongst the virus positives and it's basically any virus that we test for. We could pick up in this way and So what are the potential applications for Koba 19? The first one is we want to know do these pan viral biomarkers pickup COVID-19. It's possible it could be different, and if so,
how can this help us fight the pandemic,
so there's a lot of more ideas
this is a relatively new project,
but I'll just share some of our early
data and this project so far has
been spearheaded by ready chi Marla,
a postdoc in my lab who's been like
every day since this pandemic hit.
every day since this pandemic hit.
Trying to do the studies I'm going to.
Tell you about and get them down the
road and I also wanted knowledge.
The lab working group.
I'll talk about them again at the end.
Organized by Albert Cohen,
the School of public health who helped us at the beginning all get organised together to get the PCR testing going for research. You sent a support clinical use too. And so this is a graph of Cobra 19 Indiana, the country in our region. Green is the country. The first case was in January. But in our region of Connecticut, in New York, the first case was shown in the blue on March 2nd, Connecticut first case it was in Fairfield County on March 6th.
And our testing began on March 13th, which is actually very fast. You may recall there is some snafus with the CDC test and they allowed high complexity in clinical labs like ours to do their own test starting on February 29th. Anna Marie Landry and the folks in the clinical virology lab had it up and running by March 13th. So very fast, but nonetheless, did we miss any cases in those weeks before our testing started? So we performed a screen of the
about the two weeks before testing started as shown on this Gray bar.

And, uh, first,

so during this time period a lot of people have been tested on that complete panel for 15 viruses and 376 patients who are symptomatic and had suspected viral infection.

were negative for other viruses.

So we thought, well,

maybe some of those might have had SARS,

Kobe 2 and we screened with the button marker.

I mentioned CL 10 and out of all those negative patients,
only about a tenth of them were positive for the biomarker. So it seems a good setup like these are people who tested negative for other viruses, but there’s symptomatic. It may have a biomarker that a viral infection, their bodies fighting a viral infection. So then we tested all these people for with the PCR test, and it turns out that among these biomarker positive people were four patients who had actually did have SARS, including some surprises like an infant that was seen as an outpatient, that was a bit of
00:17:36.489 --> 00:17:38.580 a surprise to find that.

NOTE Confidence: 0.895463764667511

00:17:38.580 --> 00:17:39.300 And unfortunately,

NOTE Confidence: 0.895463764667511

00:17:39.300 --> 00:17:40.740 being here at Yale,

NOTE Confidence: 0.895463764667511

00:17:40.740 --> 00:17:42.900 we have so many great collaborators

NOTE Confidence: 0.895463764667511

00:17:42.900 --> 00:17:43.980 with different expertise,

NOTE Confidence: 0.895463764667511

00:17:43.980 --> 00:17:46.108 we were able to ask Nate Grubaugh

NOTE Confidence: 0.895463764667511

00:17:46.108 --> 00:17:48.747 slab in the school of public health

NOTE Confidence: 0.895463764667511

00:17:48.747 --> 00:17:50.812 to sequence those for isolates.

NOTE Confidence: 0.895463764667511

00:17:50.820 --> 00:17:53.095 This was a paper earlier published by

NOTE Confidence: 0.895463764667511

00:17:53.095 --> 00:17:55.118 the group lab showing using sequencing

NOTE Confidence: 0.895463764667511

00:17:55.118 --> 00:17:58.296 of the virus that a lot of the early

NOTE Confidence: 0.895463764667511

00:17:58.296 --> 00:18:00.371 cases coming to Connecticut were

NOTE Confidence: 0.895463764667511

00:18:00.371 --> 00:18:02.340 from transmission that were domestic

NOTE Confidence: 0.895463764667511

00:18:02.340 --> 00:18:04.860 rather than international an the four cases.

NOTE Confidence: 0.895463764667511

00:18:04.860 --> 00:18:07.020 I hope you can see this,

NOTE Confidence: 0.895463764667511
but the four cases that.

 Uh,

 Kind of fit this pattern.

 Three of the case is shown

 They do a track most closely with North American other isolates from North America as opposed to other countries.

 And then there was one that tracked most closest to strains from Western Europe.

 So this kind of fit the pattern will also is really interesting to me.

 Is that all these for patients that came within a couple of days the hospital none of their viruses were directly
00:18:41.106 --> 00:18:43.584 related were the same as the other,

00:18:43.590 --> 00:18:44.958 so this is independent

00:18:44.958 --> 00:18:45.984 introductions coming in,

00:18:45.990 --> 00:18:48.454 which was also probably says something about

00:18:48.454 --> 00:18:51.159 travel back and forth and things like that.

00:18:51.160 --> 00:18:52.972 So that was quite an interesting

00:18:52.972 --> 00:18:54.987 bonus of being a in collaboration

00:18:54.987 --> 00:18:56.837 with other folks at Yale.

00:18:56.840 --> 00:18:58.600 To find more information

00:18:58.600 --> 00:18:59.920 about those patients.

00:18:59.920 --> 00:19:00.256 Uhm,

00:19:00.256 --> 00:19:03.740 but we also had an idea just looking at this.

00:19:03.740 --> 00:19:05.124 Well this is interesting.

00:19:05.124 --> 00:19:06.854 Like here we used up,

00:19:06.860 --> 00:19:08.942 you know 376 PCR test to

NOTE Confidence: 0.895463764667511
00:19:08.942 --> 00:19:10.330 test all these patients.
NOTE Confidence: 0.895463764667511
00:19:10.330 --> 00:19:13.003 But really if we had only tested the 33
NOTE Confidence: 0.895463764667511
00:19:13.003 --> 00:19:15.540 that were positive for the biomarker,
NOTE Confidence: 0.895463764667511
00:19:15.540 --> 00:19:18.308 we still would have found all the cases.
NOTE Confidence: 0.895463764667511
00:19:18.310 --> 00:19:20.122 And so it suggested maybe this
NOTE Confidence: 0.895463764667511
00:19:20.122 --> 00:19:22.130 is a way of expanding,
NOTE Confidence: 0.895463764667511
00:19:22.130 --> 00:19:22.958 like conserving,
NOTE Confidence: 0.895463764667511
00:19:22.958 --> 00:19:24.614 testing capacity or directing
NOTE Confidence: 0.895463764667511
00:19:24.614 --> 00:19:26.946 it towards people who really are
NOTE Confidence: 0.895463764667511
00:19:26.946 --> 00:19:28.466 high suspicion to be positive
NOTE Confidence: 0.895463764667511
00:19:28.466 --> 00:19:30.847 and so we tried that so far just.
NOTE Confidence: 0.895463764667511
00:19:30.850 --> 00:19:31.831 Piloted one day.
NOTE Confidence: 0.895463764667511
00:19:31.831 --> 00:19:33.793 We picked one day in March
NOTE Confidence: 0.895463764667511
00:19:33.793 --> 00:19:36.143 where we were able to get all
NOTE Confidence: 0.895463764667511
00:19:36.143 --> 00:19:37.447 the residual samples from
NOTE Confidence: 0.881870329380035
00:19:37.523 --> 00:19:39.388 testing went 144 patients were
00:19:39.388 --> 00:19:41.954 tested that day for SARS, Co V2.
00:19:41.954 --> 00:19:44.730 And did the biomarker test an what you
00:19:44.811 --> 00:19:47.899 can see is again as a smaller proportion
00:19:47.899 --> 00:19:50.908 of people were positive than negative.
00:19:50.910 --> 00:19:53.339 And then we compared this to the
00:19:53.339 --> 00:19:55.852 results from the PCR testing and it
00:19:55.852 --> 00:20:00.779 turned out that 17 people were PCR
00:20:00.780 --> 00:20:02.760 positive for SARS Kobe to that day.
00:20:02.760 --> 00:20:03.750 And 16 of them were among
00:20:03.750 --> 00:20:05.822 the biomarker positive,
00:20:05.822 --> 00:20:07.380 but one wasn’t one was did not
00:20:07.380 --> 00:20:08.970 have the biomarker expressed,
00:20:08.970 --> 00:20:11.340 and that patient also happened
00:20:11.340 --> 00:20:12.990 to have a very low viral load,
00:20:12.990 --> 00:20:14.900 which is kind of something
00:20:14.900 --> 00:20:15.343
we’re following up on.

So if we had had all 17 up here, we could have said are negative predictive value. If you’re negative on this biomarker, you don’t have the virus is 100%, but we can’t say that we have to say 99% because of. This this one patient out of out of 144 that were screened and tested. Um, so we that got us interested in biological variables and how they impact this biomarker that’s induces approaching that’s induced by viral replication within the epithelial cells and possibly infiltrating cells.
And we looked at all the positive patients in our initial study, which was 59 patients. If you look at their age distribution there mostly in the older age groups, and if you look at the symptoms by age group, the people in the older age groups had more serious illness. As you might expect much more likely to be hospitalised and have things like pneumonia and hypoxemia. So what about the correlation with the biomarker? Well, if you look at, uh,
if you look at viral load versus the biomarker, there’s a positive correlation. As you might expect. Because, as I mentioned, the trigger for production of this biomarker is viral replication. Um, interesting if you look at age versus the biomarker, where this biomarker is lower and the people with the older age is. But there doesn’t seem to be a clear correlation between agent viral load in this same group,
so we’re still investigating this.

So we actually struck up a collaboration

including Tom Murray and Danielle

to delve into this further

and see if we can figure out what’s

going on with this age correlation.

I so finally I just want to mention um,

what’s ahead for this project?

I mentioned from these headlines

some of the challenges and we would

like to know Kenneth biomarker

help us to the question of who has

live infectious virus versus is a

persistent PCR positive but not infectious.

NOTE Confidence: 0.881870329380035
Anna question everyone always asked me. I'm just going to preempt it. It would be great to know what this type of biomarker an in general, what the host response to infection, how it's changing overtime during the course of what can be a long illness. And so we're actively looking at that right now. And I just want to finish. Briefly got pause. Dan is getting restarted now of trying to find the next pandemic virus before it hits using this strategy.
And this was spearheaded by Amelia Hammer in a Yale School of Public Health Masters student who is in my lab but graduated in 2019. And our idea there was the same idea of let’s look at people who their doctors suspected viral infection sent the test. They tested negative for all the viruses on our panel and see if we can find people who looks like their body was fighting a viral infection and maybe they have a viral infection that we don’t know.
viruses are causing disease in our patient population that were not catching with our panel. And so Amelia just took one week of January 2017 and screens 250. One negative samples with our biomarker that we talked about here CL. 10 and she had 60 of them that were had high levels of the biomarker at that time. We were not doing testing for the seasonal coronaviruses or parrot influenza virus. so she did that testing an interesting Lee. Half of these patients had seasonal coronaviruses and
00:23:55.928 --> 00:23:57.800 that actually tipped our hat.

00:23:57.800 --> 00:23:59.468 Let us know that seasonal Corona

00:23:59.468 --> 00:24:01.216 viruses are circulating in our patient

00:24:01.216 --> 00:24:04.876 has now added that to the clinical panel.

00:24:02.676 --> 00:24:04.880 So now that is those four

00:24:04.880 --> 00:24:07.990 viruses are on our panel,

00:24:07.990 --> 00:24:10.014 but this also as a proof of concept

00:24:10.014 --> 00:24:12.308 that our strategy works of picking up

00:24:12.308 --> 00:24:14.790 viral infections that we’re not testing for.

00:24:15.340 --> 00:24:16.990 we also have half the samples

00:24:16.990 --> 00:24:17.930 where we didn’t.

00:24:17.930 --> 00:24:19.415 We still don’t know exact

00:24:19.415 --> 00:24:21.350 well for some of them we do,
but many of them we don’t know what what infectious agents are in the sample, and we’re working that up and finding some interesting things, and we hope this will be a good strategy. Going forward to get an even more comprehensive view of the viruses that are circulating so we can be prepared for ones that we aren’t necessarily testing for right now. So, just to summarize, um, we’re interested in studying the host response to fight coronavirus today. I talked about diagnostic applications I was also really interested in getting.
insights into early stage pathogenesis.

And how this differs among people who have different outcomes.

Uhm, I talked about a host response based screening test that we’ve been working on, which allowed us to identify undiagnosed cases from early March and we’re looking at other utilities to sort of fill in some of our testing strategies, and hopefully I’ll be able to update you in a future talk on our undiagnosed viruses project as well. I saw with that before.
I conclude I'd like to thank all the many, many people in this Yale environment have contributed to projects on COVID-19. Definitely could have been done in a silo. It was very great to have lots of collaborators an it still is. I want to acknowledge my lab members including ready tomorrow. I mentioned who spearheaded the project. I talked about as well as Marie Landry on the clinical virology lab, especially Marino in and Robin Garner, who really helped us alot. Dezhen Zou, who's been helping with our bioinformatics,
I didn’t really talk about that today,
but he’s been a great help the whole group,
all lab and Nate grew bath for their
constant participation and help
As well as lab working group depicted here
from March 2nd which includes Albert Konate,
grew Bhasa Domer Akiko Isaki Marie Landreau. That’s me actually.
When there’s only 45,000 global cases on March 2nd. Uh, so with that?
Uhm, I think I made up some time.
Uh, in in speaking a little quickly,
but hopefully you’re able to follow.
And if there's any questions I would be happy to answer them now.

Thank you, Ellen. Thank you and congratulations to you and your entire research group on that impressive body of work in a relatively short time to address the pandemic.

and I know we’re just about the top of the hour or so, but let me just offer up a couple.

One is specifically. One is specifically.

I mean, I think the work you’re doing is really interesting in terms of testing strategy, and you mentioned that you’re
00:27:08.125 --> 00:27:09.750 anticipating one of my questions,
00:27:09.750 --> 00:27:11.634 which was, how does it change
00:27:11.634 --> 00:27:13.749 over the course of the illness?
00:27:14.647 --> 00:27:17.153 But I'm curious,
00:27:17.153 --> 00:27:19.241 do we have a sense of biomarkers that
00:27:19.241 --> 00:27:21.375 might predict the severity of illness
00:27:21.375 --> 00:27:23.427 that is almost to predict who's
00:27:23.427 --> 00:27:25.440 more likely to need more intensive
00:27:25.440 --> 00:27:27.323 care at the time of diagnosis?
00:27:26.140 --> 00:27:28.336 Yeah, that that's very interesting people.
00:27:28.340 --> 00:27:30.804 There's been a some work already published
00:27:33.360 --> 00:27:33.360 about blood like cytokines in the blood
00:27:33.360 --> 00:27:35.150 that could be indicated indicative
00:27:35.150 --> 00:27:37.486 of that we're looking even earlier.
00:27:37.490 --> 00:27:40.289 I mean it at the at the early stage
of infection, the nasopharynx.

And that's one reason why we're really interested in this potential difference between adults and kids. Because, you know, kids are seem relatively protected from pulmonary disease compared to adults, older adults.

So that's one reason why we struck up this collaboration with Pediatrics to try to understand.

Is there some difference in the robustness of that initial response that could you know that could possibly explain this? There's many explanations,
so that’s the kind of thing we’re looking into, but I don’t have the answer yet. This is it’s very rare to give a talk on a project that started like two months ago, but so that’s why there’s a more questions than answers at this point, but we hope to find that out. We’re looking at the whole. The entire pattern of gene expression. Um and not just this one biomarker to try to get it that in some specific groups of patients with different outcomes. So do we think that, uh, I mean,
likely the airway response. It is before the subsequent sort of larger immune response. The airway response is likely very different across ages. And you think that could be one of the major explanations why age is such a strong predictor for outcome in this illness. Possibly possibly, I'd like to have the data to answer you definitively, so hopefully will have that soon. Yeah, well, it sounds like more to follow. Well, channel and for two really superb talks and the work that they do.
Thank you all for joining us today.

I know a lot of folks also watch online as we as the labs reopened but.

Enjoy the rest of your day and thank you all for your work.

Thank you very much.