2022 AMA Research Challenge finalists compete to win top prize

Leelabati Biswas, an MD/PhD candidate at Rutgers Robert Wood Johnson Medical School, beat out four other finalists to win the 2022 AMA Research Challenge and the grand prize of $10,000, sponsored by Laurel Road.

The judges announced the winner on Dec. 7 at the conclusion of the virtual research presentations from the finalists.

Watch 5 finalists present research and compete to win

Host

Todd Unger, AMA chief experience officer

Finalists

Leelabati Biswas

- **Poster**: Decoding Pregnancy Loss: Validating a Novel Genetic Biomarker of Poor Egg Quality (PDF)
- **School**: Rutgers Robert Wood Johnson Medical School
- **Making the Rounds podcast**: Listen to the interview and read the transcript

Kanita Chaudhry

- **Poster**: The Aryl Hydrocarbon Receptor (AhR) as a Novel Therapeutic Target in Neuroblastoma (PDF)
School: Jacobs School of Medicine and Biomedical Sciences
Making the Rounds podcast: Listen to the interview and read the transcript

Arian Mansur

Poster: Stereotactic Body Radiation Therapy Versus Wedge Resection for Early-Stage Node-Negative Non-Small Cell Lung Cancer Tumors ≥8 mm: A National Analysis (PDF)
School: Harvard Medical School
Making the Rounds podcast: Listen to the interview and read the transcript

Benjamin Maxey

Poster: Audiovisual Feedback from a Handheld Monitoring Device Improves Manual Ventilation (PDF)
School: Louisiana State University Health Shreveport
Making the Rounds podcast: Listen to the interview and read the transcript

Garima Suman, MD

Poster: AI-Powered Fully automated Early Detection of Pancreatic Ductal Adenocarcinoma on Standard-of-care CT Scans (PDF)
Institution: Mayo Clinic
Making the Rounds podcast: Listen to the interview and read the transcript

Panel of judges

Kirsten Bibbins-Domingo, PhD, MD, MAS
Editor-in-chief, JAMA and the JAMA Network™.

Sanjay Desai, MD, MACP
AMA chief academic officer.

Clyde Yancy, MD, MSc, MACC, MACP
Vice dean of diversity and inclusion, professor of medicine and medical social sciences, and chief of the Division of Cardiology at Northwestern University’s Feinberg School of Medicine.
Transcript

Unger: On behalf of the American Medical Association, welcome to the 2022 AMA Research Challenge. I'm Todd Unger, the AMA's Chief Experience Officer. And I'll be your host as we showcase and judge the best of the best in research, from medical students, residents and fellows, and the international medical graduate communities.

But before we jump in, a little background on how we got here. Fun fact, this is the 20th anniversary of AMA's research event, and it's the largest event of its kind in the country. And for the second year in a row we've got a $10,000 grand prize on the line. So it's no wonder we got a record number of submissions. So a big thank you to everyone for your enthusiasm and interest in the AMA Research Challenge.

Just take a look at this year's incredible numbers. We started with nearly 1,200 submissions, with 800 selected for presentation in our virtual poster symposium. And of those, the top 50 scored posters competed in our semifinals and were scored by judges and AMA members. Which brings us to today's five finalists, a group whose work represents the innovative thinking needed to drive medicine forward.

Join me in wishing them all good luck as they compete for the challenge's $10,000 grand prize. And thank you, Laurel Road, for supporting research as the bedrock of science, medicine and improved patient care. And of course, for supporting our next generation of physicians.

So there you have it. That's how we got to today's final round of the AMA Research Challenge, where each finalist will have five minutes to present their idea to our fantastic panel of judges who will determine our winner.

Let's meet our judges. Dr. Kirsten Bibbins-Domingo, the editor-in-chief of JAMA and the JAMA Network™. Dr. Sanjay Desai, the AMA's chief academic officer. And Dr. Clyde Yancy, vice dean of diversity and inclusion, professor of medicine and medical social sciences, and chief of the Division of Cardiology at Northwestern University's Feinberg School of Medicine.

Welcome judges. Thanks for being with us here today. Now, let's meet our incredible finalists who are ready to compete for this year's 10,000 grand prize. Our first finalist is Leela Biswas, an MD/PhD candidate at Rutgers Robert Wood Johnson Medical School. Leela, what keeps you motivated?

Biswas: I'm motivated by a deep passionate love for understanding the cell and biology, as well as an unquenchable drive to improve patient care. It is the greatest gift to be able to do both at the same time in a way in which each meaningfully impacts the other. Where understanding the biology can translate to better patient care and real changes in a person's life. And where doing that kind of
science helps you understand the basic biology as well, which is impactful for the field. Knowing that I get to do that keeps me motivated every day. I'm so excited. In the difficult times of research that is the light that keeps me going. I'm very lucky.

**Unger:** Thank you, Leela. Our second finalist is Kanita Chaudhry, an MD/PhD candidate at Jacobs School of Medicine and Biomedical Sciences. Kanita, what are your plans after you graduate medical school?

**Chaudhry:** So after medical school, my ultimate goal is to become a physician scientist. So I'd like to see patients and care for patients in the hospital and in the clinic. But I'd also like to run my own lab and do basic science research and translational research. And in addition, I'd like to bring the findings from the bench into the bedside. And bring novel therapies to patients through clinical trials. And right now I'm very interested in pediatric oncology because I believe that there is a very critical and unmet need for novel therapies in this area. And that it's a very understudied area of research.

**Unger:** Thanks for being here, Kanita. Next, Arian Mansur. A second-year medical student at Harvard Medical School. Arian, what inspired you to go to medical school?

**Mansur:** Yeah, there are so many factors that inspired me to want to go to medical school. I was always passionate about the sciences as a kid, and the ways that we could treat individuals suffering who come to us at a vulnerable time. And as a child of refugees and the first in my family to go to higher education, I saw medicine as a way to give back to my family, to give back to my community, and give back to those suffering while doing what I love. My family has experienced a lot of hardships, both medical and financial. And to me medicine was a way to uplift my family. And even today there's still large disparities in medicine, and so I also entered medical school to challenge stereotypes, to become an excellent physician, and to be an inspiration for other first-generation low income Hispanic individuals.

**Unger:** It's great to have you here, Arian. Now let's welcome Ben Maxey, a third-year medical student at Louisiana State University Health Shreveport. Ben, what keeps you motivated?

**Maxey:** I think the biggest thing that keeps me motivated is just those small and big victories we see every day. So as far as research is concerned, getting reassuring data or finally putting together a device and it working correctly, just kind encourages you to keep pressing on. In the clinic or the hospital when you have a positive patient interaction or if you've been following for a while and starts improving, and you see the fruits of your work. That's really motivating, as far as me to keep pressing on.

**Unger:** Thanks, Ben. And our final contestant, Dr. Garima Suman. An MD and fellow at the Mayo Clinic. Dr. Suman, what are your plans after you complete your fellowship?
Dr. Suman: Well, right now I'm doing my fellowship in abdominal radiology. I have one more year of fellowship left. And then I'll be working as an attending radiologist. And I hope to be involved in pancreatic cancer research and AI going forward, as well. And our goal for early detection of pancreatic cancer is not accomplished yet. It's still ongoing. So I hope to continue to invest in it to help our patients.

Unger: Great. Thanks, Dr. Suman. And thank you to all of our finalists for being here today. Good luck, everyone. Let the research challenge begin. First up, Leela Biswas.

Biswas: Hello, my name is Leela Biswas. I am an MD/PhD candidate at Rutgers Robert Wood Johnson Medical School. Aneuploidy is the presence of an incorrect number of chromosomes in a cell.

Egg aneuploidy causes at least half of all pregnancy losses. Currently, the only biomarker for egg aneuploidy is maternal age. However, for some infertility patients egg aneuploidy occurs more often and earlier than is predicted by maternal age.

This graph illustrates the relationship between egg aneuploidy and maternal age. For most patients shown here in black, egg aneuploidy increases with maternal age, diminishing fertility. However, looking closely at the data, we find that some patients are statistical outliers to this trend. For these patients shown in red, age does not predict egg aneuploidy. For these patients another biomarker is needed. We hypothesized that certain genetic variants increase egg aneuploidy and could thus serve as predictive genetic biomarkers for this key fertility trait.

To test this hypothesis, we used a pipeline approach. Using whole exome sequencing data from 178 infertility patients, with statistically extreme rates of aneuploidy conception relative to maternal age, our team identified genetic variants enriched in patients with disproportionately high rates of aneuploidy. Based on preliminary data and bioinformatic analysis, we focused on patient variance in the gene KIF18A. KIF18A is an enzyme that regulates the length of the metaphase spindle. As a result, KIF18A impacts the number of chromosomes in a cell. So it's an exciting candidate gene for egg aneuploidy.

We screen the patient’s KIF18A variants in vitro. And for our most promising variant, generated a knock-in mouse and evaluated egg quality as I will describe next. For results, we identified two mutations in KIF18A enriched in patients with high rates of egg aneuploidy relative to maternal age. We call these KIF18A motor domain mutant and KIF18AC terminal domain mutant. Or KIF18AMDM and CDM for short.

First, we initially screened the patient's KIF18A variants in vitro, by first overexpressing each variant or wild type KIF18A in mouse eggs via micro injection. And then evaluating meiosis using high resolution confocal microscopy. Those confocal images are shown here. Here DNA is shown in blue and spindle microtubules in gray. We found that while overexpression of wild KIF18A or the KIF18ACDM variant
caused normal metaphase spindles, the variant KIF18AMDM caused the formation of abnormal metaphase spindles. Thus, KIF18AMDM emerged as a promising patient variant for affecting egg quality.

Next, we wanted to rigorously test the effect of this variant in vivo. So we developed a novel CRISPR knock-in mouse line, bearing the patient variant KIF18AMDM. The following experiments were conducted in this mouse line. First, I evaluated egg morphology. I super ovulated mice bearing the patient variant KIF18AMDM similar to the technique used in IVF clinics.

I examined egg morphology using high resolution confocal microscopy. Eggs from wild type mice have normal metaphase spindle shown here in green with DNA in gray. KIF18AMDM variant mice produced eggs with an increased trend of severe egg morphology abnormalities, including fragmentation, abnormal spindle morphology and DNA micronucleation.

This is the very first report of a KIF18A patient variant trending with abnormal egg morphology. Finally, I assessed the key phenotype of interest, egg aneuploidy. I harvested oocytes from KIF18AMDM mice and aged-matched meiotic controls. Cultured the oocytes so that they underwent one cell division. And assessed aneuploidy frequency using an in-situ chromosome counting assay.

I found that mice bearing KIF18AMDM patient variant have statistically significantly higher rates of aneuploidy egg formation than age-matched controls. Specifically, while wild type mice had 6.7% aneuploidy eggs, 49% were aneuploidy in KIF18AMDM variant mice with a p value of 0.0005 on a two-tailed t-test.

In conclusion, the genetic variant KIF18AMDM, which was identified in infertility patients with extreme rates of aneuploidy increases egg aneuploidy in female mice independent of maternal age. These findings lay the groundwork for future studies to evaluate KIF18AMDM as potentially the very first predictive genetic biomarker of increase egg aneuploidy relative to maternal age.

The identification of predictive genetic biomarkers for egg aneuploidy would bring a precision medicine lens to fertility care. Our vision for the future is that patients who want to become pregnant could undergo early genetic screening for key variants. And in the clinic, this information would be combined with maternal age to design a personalized care plan for optimized pregnancy outcomes. This work establishes KIF18AMDM as an exciting variant to be further evaluated as the first potential biomarker of egg aneuploidy in this new precision fertility care paradigm. Thank you for your attention.

Unger: Thank you very much, Leela. And now to our judges for their comments. Dr. Bibbins-Domingo, why don't you lead us off.

Dr. Bibbins-Domingo: Thank you very much. I really enjoyed this presentation. I thought that Leela did a really terrific job laying out the problem she was trying to solve. And then starting with the studies
in humans going into really helping us to understand the mechanisms first in vitro, and then in vivo.

And then really the icing on the cake is really showing that when you actually put these findings in mice again to reproduce and employ the phenotype. So I thought she did a very nice job of laying out the mechanisms. And then pointing us to the types of future studies that would have to be done in order for this to be something that we might think about in clinical practice.

**Unger:** Dr. Desai.

**Dr. Desai:** Yeah, I would agree. Miss Biswas, this was a very impressive set of portfolio assays, assessments, techniques that were brought together to answer an important question, or lead us in the direction of answering such an important question related to aneuploidy and miscarriage, ultimately clinically for our patients.

And I think to me what will be interesting is that the next phase of this, this is an example of precision medicine. And so how do we actually translate this now to humans and to integrate this into those complex decisions around family planning to actually inform and help advise our patients moving forward? So really very impressive job.

**Unger:** Dr. Yancy, anything to add?

**Dr. Yancy:** Yes, just a couple of things. I really applaud Leela for this incredible work, for three reasons. First it addresses an incredibly important everyday health problem. Infertility is an incredible burden for those that have to navigate through it and having any additional insight is helpful.

The second thing I applaud is this really appropriate intersectionality of observational science. Trying to understand who are the outliers that are not expressing the usual age-related changes in aneuploidy but are experiencing it earlier.

And then I love going to the translational space. In particular in the translational space, this is one of the few applications I’ve seen where we use gene editing as a knock-in technology to overexpress KIF18A in a way to identify the association of this particular genomic marker with aneuploidy. So I think this is brilliant across the board. And though these sorts of biomarkers don't always pan out in additional human experiment, what a terrific start.

**Unger:** Great feedback, judges. Thank you. Next up, Kanita Chaudhry.

**Chaudhry:** Hi, everyone. My name is Kanita Chaudhry, and I’m an MD/PhD candidate at the Jacobs School of Medicine. I’m working in the lab of Dr. Anna Bianchi-Smiraglia at Roswell Park Comprehensive Cancer Center.
Today I'm very excited to share with you my work, which focuses on the aryl hydrocarbon receptor, or AHR, as a novel therapeutic target in neuroblastoma. Neuroblastoma is a tumor of early childhood that arises from cells of the developing sympathetic nervous system. And it's the most common extracranial tumor in children.

Despite intensive multimodality treatments that are often highly toxic, approximately 50% of high-risk patients die from progressive disease. And this is mainly due to relapses that result from resistance to therapy such as retinoic acid. Among high-risk patients, approximately 50% harbor amplification of the MYCN oncogene, which is a major transcriptional driver of neuroblastoma disease progression.

MYCN amplification correlates with poor patient prognosis and poor response to retinoic acid treatments. However, MYCN remains undruggable, prompting efforts to indirectly impair its expression or function. Here we studied the aryl hydrocarbon receptor or AHR, which is a transcription factor that is known to modulate expression of MYCN and other cancer types. But its role in neuroblastoma remains almost entirely uncharacterized. Therefore, in the current study, we hypothesized that AHR acts as a novel tumor promoter that regulates MYCN and alters retinoic acid treatment effectiveness in neuroblastoma.

In order to test this hypothesis, we utilized two MYCN-amplified human neuroblastoma cells in which we genetically under expressed AHR by shRNA. We also utilized a pharmacologic approach in which cells were treated with clofazimine, a novel AHR antagonist that our group previously identified.

Using the system we asked three questions. The first is, is AHR a tumor promoter or tumor suppressor? And to ask this question we performed colony forming assays. And also interrogated tumor growth in vivo using a mouse model. Secondly, we used western blotting approaches to ask if AHR could regulate MYCN. And third, we used microscopy to ask if AHR could alter retinoic acid treatment effectiveness.

And what we found is that, when we performed our colony forming assay that cells depleted of AHR or treated with clofazimine had robust reduction in chronogenic growth of cells. And excitingly, when we performed an in vivo experiment in a mouse and we implanted mice with either control or AHR-depleted cells, there was a significant reduction in tumor volumes in the AHR-depleted tumors relative to control.

Collectively, these findings strongly suggest that AHR acts as a novel tumor promoter in neuroblastoma. Secondly, we found that when we deplete AHR by shRNA, this leads to a reduction in MYCN protein levels. And notably, treatment with clofazimine also results in a decrease in MYCN protein levels.

Finally, when we looked at the cells under the microscope, what we found is that clofazimine treatment and AHR depletion both induced the formation of neurites, as shown by the yellow arrows pointing to
membrane projections. These neurites are indicative of neuroblastoma differentiation. A shift towards a less cancerous phenotype.

When cells were treated with all-trans retinoic acid or ATRA, this also induced neurites formation, indicative of differentiation which is expected. But interestingly, when cells were treated with clofazimine or AHR depletion concurrently with retinoic acid treatment, this resulted in an increased percentage of cells with neurites relative to retinoic acid treatment alone. Indicating that AHR inhibition augments retinoic acid treatment efficacy.

In conclusion, our data shows that AHR is a previously unrecognized and novel tumor promoter in neuroblastoma. And that AHR inhibition with clofazimine decreases neuroblastoma growth, decreases MYCN protein levels and augments retinoic acid-induced differentiation. The overall significance of our work is that AHR is a novel therapeutic target in neuroblastoma. And importantly, our study utilizes clofazimine, which is currently FDA approved for the treatment of drug resistant tuberculosis and lepromatous leprosy. And clofazimine is orally bioavailable, safe with minimal toxicity and highly cost effective. Therefore, it could represent a potential and promising new neuroblastoma therapy that could be rapidly translated into the clinic. Thank you very much for your attention.

Unger: And thank you, Kanita. All right, judges time for your comments now. Dr. Desai, start us off.

Dr. Desai: Absolutely, I want to congratulate Kanita for this work. It is impressive on many fronts. I think first it's a devastating disease. And so to take on a problem that has such consequences is important.

And then I am very impressed with the way that she has presented her research and conducted the research. And specifically taking us with every step along the way logically following the step before, starting with the hypothesis, testing that hypothesis, going to an intervention, testing that intervention and then leading us to the next steps that would come of this.

The other, I think novel component of this work is the repurposing of a drug that has been used and has been tested and is deemed to be safe for another disease where the hypothesis, again as she demonstrated, held true. I'd be excited to see what will come of this next, particularly the translation to humans. And if the clinical effect in humans is as promising as has been demonstrated in her research.

Unger: Dr. Yancy?

Dr. Yancy: This is really quite extraordinary work. And I extend my congratulations as well. But uniquely, I'd like to congratulate the mentor. This is really extraordinary work that shows that Kanita was under some guidance, some direction that was very well informed. And it allowed her to bring together the hypothesis and execute brilliantly on this work.
I think this is the kind of work that needs to be done. We all understand that treating CNS tumors in particular is so challenging. Because we can't consider the usual approaches of extra patient in chemotherapy and targeting receptors and using novel immunological means to modify the natural history of CNS tumors really is the new target of the day in order to help so many people that have these devastating conditions. So I'm very impressed with this work. Again, lots of challenges ahead. But what a great way to start unraveling this neurobiology that impacts neuroblastoma. Really nice work.

Unger: Dr. Bibbins-Domingo.

Dr. Bibbins-Domingo: Yes, I'm echoing what my colleagues have said. And I think the things that I loved about this particular project was both the logic with which we understood the hypotheses that Kanita is exploring here, but also she's thinking about this tumor promoter and the ways to block it in two separate ways. So we learn things because it's consistent across multiple ways of approaching this problem.

And then additionally, I like that we're talking about repurposing an already approved drug potentially, and the mechanisms for understanding the clofazimine. And I think that's potentially a very important observation. And one that I think many are going to start exploring with repurposing existing drugs for novel purposes.

Unger: Well, thank you so much, judges. Time for our next contestant, our third one, Arian Mansur.

Mansur: Hello, my name is Arian Mansur. I'm a second-year medical student at Harvard Medical School. Thank you very much for the opportunity to present this work on stereotactic body radiation therapy versus wedge resection for early-stage node-negative non-small cell lung cancer tumors less than or equal to 8 mm, a national analysis.

Lung cancer is a leading cause of cancer deaths worldwide. Over the past decade an increasing number of small non-small-cell lung cancer tumors are being discovered either incidentally or through lung cancer screening.

The objective of this study was to evaluate the overall survival of patients with early stage N0 non-small-cell lung cancer tumors less than or equal to 8 mm, who undergo stereotactic body radiation therapy versus wide resection.

We queried the National Cancer Database, a prospective hospital-based tumor registry, from 2004 to 2017. The study cohort included 1,505 patients, 11% of whom underwent SBRT and 89% of them underwent wedge resection.
Table 1 presents the patient baseline characteristics of our cohorts. Patients undergoing SBRT were more likely to be older, white and have squamous cell carcinoma histology. Figure 1 shows the overall survival of patients stratified by SBRT versus wedge resection. Kaplan-Meier analysis demonstrated a five-year survival of 7.7% with a wedge resection group which was significantly greater than 44.4% with the SBRT group.

We next performed the sensitivity analysis limited to healthier patients with no major comorbidities and found similar results of the primary analysis. We next did a multivariable Cox proportional hazards model, adjusting for covariates, accounting for patient demographic, clinical and pathologic factors.

We found that wedge resection was also associated with increased survival when compared to SBRT in both the primary and sensitivity analysis. To further reduce the effects of confounding, we also performed propensity score match analyzes in the primary cohorts and in the cohort of patients with no comorbidities.

As seen in figures 3 and 4, wedge resection was associated with increased survival when compared to SBRT with propensity score match analysis. There are several limitations to the study. First, it is a retrospective study and there's always a chance for inherent confounding by unobserved variables. Second, the NCDB does not have data on post-operative complications.

Third, the NCDB does not have data on recurrence-free or disease-free survival. In conclusion, in this national analysis, patients with less than or equal to 8 millimeter non-small-cell lung cancer tumors undergoing wedge resection experience improved survival when compared to SBRT. Thank you very much.

Unger: And thank you, Arian. All right, time for the judges. Dr. Yancy, why don't you lead us off.

Dr. Yancy: Arian really should be commended. This is an important problem, non-small-cell lung cancer. And it's increasingly frequent. And not always associated with smoking, so we have to be careful about that. What I really like about Arian’s work is the incorporation of appropriate methods using observational data. So multiple regression analysis, propensity scoring, these are the kinds of research methods he needs to understand and all of us need to appreciate as we begin to look at more and more of the extant data sets as a way to generate hypotheses or answer questions that lead us towards more provocative research.

I’m also enthused that this is a second-year medical student who does this work with a national data set, and helps us understand the different approaches, whether it's stereotactic radiation, or wedge resection for a very compelling and increasingly important problem. So two thumbs up to Arian for doing this work. And I think he has a very bright future ahead.

Unger: Dr. Bibbins-Domingo.
Dr. Bibbins-Domingo: I also really appreciated this work. We're moving here to large data, large numbers of patients, and understanding two approaches to treating an important disease. I think this type of work requires a lot of time sitting on the computer and understanding what one is doing at each phase.

It's very different from doing bench science. But it is critically important, particularly for clinical medicine, and so I really applaud Arian’s approach to this important problem and to using these techniques to address and get to an important finding.

Unger: Thank you. Dr. Desai.

Dr. Desai: I would echo my colleague’s comments. I commend also this research. It really is again impressive. I think it demonstrates as has been suggested the power of large data sets. In this instance, it also is an opportunity for us to learn about the value and outcomes of a treatment that is less morbid in a condition that often has highly morbid interventions. And so again, the value I think in terms of quality for a patient is substantial in this.

And I look forward to the future of this work because it starts to make us think about prospective data and analysis related to these two interventions in patients that have lung cancer.

And specifically, looking at different types of non-small-cell lung cancer and whether those interventions have different outcomes related to them. So again, very impressive use of large data to answer an important clinical question.

Dr. Yancy: Dr. Desai, you make a great point. But I think the other very important point is that Arian is understanding the limitations of using these large data sets. And that's so incredibly valuable as he goes forward. His explicit commentary to say that there are confounding circumstances is the right way to begin this kind of observational data research. So another very important point that I think you'll endorse.

Unger: Great discussion. Next up, we’ll hear from Ben Maxey.

Maxey: Hi, my name is Ben Maxey, and I'm currently a third-year med student at LSU Health Shreveport. When patients are unable to breathe for themselves or aren't breathing adequately, short term emergency ventilation is most often accomplished through a bag valve mask or BVM, with which a provider squeezes a self-inflating bag with air into a patient's lungs.

Although simple in concept, effective ventilation with BVM systems still requires extensive training. And potential misuse can significantly diminish the BVM’s efficacy and safety. Hypoventilation and inadequate gas exchange are important concerns during manual ventilation. But hyperventilation is actually a more common and dangerous user error that can lead to serious injury. Delivering too great
a tidal volume increases the risk for potentially serious adverse effects, including direct volume trauma to the lungs leading to pneumothorax, gastric insolation, and aspiration, as well as ultra hemodynamics.

To improve the safety and efficacy of BVM ventilation, we developed the BVM Emergency Narration Guided Instrument, or the BENGI. The BENGI is a handheld device that provides simple and intuitive audio-visual feedback on the depth and quality of a user's ventilations. By giving accurate feedback on the delivery tidal volumes and respiratory rates, the BENGI could reduce adverse effects associated with incorrect BVM usage. The BENGI was constructed using freely available electronic components housed in a custom 3D-printed casing.

The core functionality of the device lies in a mass flow sensor, which measures flow rates of air or oxygen passing through it. By integrating these flow rates over time, the BENGI calculates the volume of air passing through it during a given ventilation. The device connects between the self-inflating bag and a mask in a BVM. And as the provider is delivering a breath, an LED pixel ring around the top of the device begins changing colors from green to yellow. And finally to red as the target tidal volume has been reached.

A speaker within the device instructs the user when to begin each respiration and tells the user if they're bagging too quickly or too slowly. To test the efficacy of the BENGI, we recruited 20 health care personnel, including physicians, med students and PA students from our medical school for a randomized crossover manikin study. Participants were randomly divided into two groups. Both groups ventilated a manikin with target tidal volumes and respiratory rates in mind. But one group used the BENGI while the other one did not. After a two-week washout period the groups switched. Participants were asked to ventilate the manikin in sets of five minutes with different tidal volume and respiratory rate targets for each 5-minute block.

While the participants were ventilating, their delivered tidal volumes and respiratory rates were measured and calculated via a flow sensor and a pressure sensor connected in line in the respiratory circuit. This enabled us to compare the true delivered volumes at rates with the target values.

The data shown on the poster represent the error and standard deviation in delivered tidal volumes and respiratory rates with a target of 500 milliliters per breath and 10 breaths per minute. But the trends in the data were very similar for all the scenarios we tested. The average absolute deviations from both the target tidal volume and from the target respiratory rate were significantly reduced with BENGI use, indicating that the BENGI improved participants' ability to manually ventilate more closely to a target tidal volume and to a target respiratory rate.

The BENGI did not alter the average values of other respiratory parameters, including inspiratory time, inspiratory pressure, as well as the working power delivered by the ventilations. Additionally, the standard deviation of the delivered tidal volumes and respiratory rates within each 5-minute block.
were reduced with BENGI use, indicating that BENJI improved the consistency of the ventilations.

Thus, we were able to conclude that use of the BENGI improved accuracy and consistency during manual ventilation with the BVM. The BENGI may have utility as a medical device for improving the quality of manual ventilation and reducing supply associated with manual hyper- and hypoventilation. Our plans for future work include testing the efficacy of the device as a training device and refining its electronic and mechanical design. Thank you.

**Unger:** Thanks so much, Ben. Now time for our judges. Dr. Bibbins-Domingo, please lead us off.

**Dr. Bibbins-Domingo:** I like that this presentation really focused on something we do so commonly in clinical medicine but clearly has consequences when we don't do it well. And thinking through a simple engineering solution that might help us. I thought that the statement of the problem and then the intervention to solve this problem was very well thought out. And the execution was quite nice.

The question I had after listening to this is whether we will think about this as a way to teach clinicians how to do mechanical ventilation better. Whether this is ultimately a teaching instrument or whether it will be used sort of consistently for each time we do bag ventilation, manual ventilation.

So I think that's what Benjamin has instructed us as to the future directions. And I'm looking forward to seeing what he does next.

**Unger:** Dr. Desai.

**Dr. Desai:** I think this is such a clever project. And I commend Benjamin on it. As a pulmonary and critical care physician, I am often around people who are being bag-masked ventilated, and have witnessed these complications regularly. So it's surprising to me somebody hasn't done this before.

And I think it's clever because it applies these engineering principles to a clinical application. And then uses the idea of real-time feedback to improve the rate of your ability to perform this skill adequately. So I think those are all really important things.

And I agree with Dr. Bibbins-Domingo. And I believe Benjamin said this. It seems that this is most likely useful in the training setting because as somebody does get better at this, then they would not need that regular feedback. But again the niche to me feels like it is likely in the training setting.

**Unger:** Dr. Yancy.

**Dr. Yancy:** Yeah, I really like this. In my usual way of thinking through these things, I see three things very quickly stated here. Very important. First I applaud the entrepreneurship. I think we need the next generation to think very provocatively about these problems that have been nagging us for which we haven't been able to achieve solutions.
Secondly, I think this really answers that question, how do you do meaningful research in critical care settings, specifically resuscitative medicine? Who would ever think about doing a randomized trial? How do you make this happen? And we’re seeing now a very effective strategy that Benjamin has created to test a meaningful way of improving outcomes with resuscitation.

Third, though, I want to echo Dr. Bibbins-Domingo. I would be concerned that this is only for training purposes. I think Dr. Desai would confirm that this would probably increase dead space ventilation through a use clinically, and that would be to very little avail. But the idea of training someone as we do with chest compressions, what’s the right depth, that was the right force for bag mass ventilation, that’s all for the good.

**Unger:** All right, judges. Thank you. Now it's time for our final presentation from Dr. Garima Suman.

**Dr. Suman:** Hello, everyone. My name is Garima Suman. I'm an abdominal imaging fellow at Mayo Clinic, Rochester. Today I'm presenting our study on AI-powered fully automated detection of pancreas cancer on standard-of-care CT scans.

Pancreas cancer is one of the most lethal gastrointestinal malignancies, with a five-year survival rate of approximately 10%. It is predicted to become the second leading cause of cancer-related deaths in the United States by the year 2030. Unfortunately, approximately 30% to 40% of pancreas cancer can be missed on CT scans because of their subtle imaging signatures and non-specific patient symptoms. Therefore, there's a huge need to leverage evolving technologies such as artificial intelligence to augment the expertise of the radiologists to enable timely and early detection of such cancers.

With that intent, we curated a CT abdomen data set obtained from more than 1,100 patients with pancreatic cancer, and more than 1,900 patients with normal appearing pancreas. We divided this data set into training and testing subsets with the ratio of 70 to 30. Of note, the majority of these CTs were acquired at other hospitals which highlights the diversity of this data set.

We then trained a 3D CNN deep learning model using algorithmically derived inputs, consisting of a bounding box containing pancreas and surrounding tissues, and a volumetric pancreatic segmentation mask. We then tested this model on multiple data sets including internal data set, publicly available multi-institutional open source data sets, and a unique cohort of pre-diagnostic CTs, which were acquired for unrelated indications between three months to three years prior to the eventual clinical diagnosis of pancreatic cancer.

It is important for me to highlight here that these free diagnostics CTs had normal appearing pancreas. And no underlying pancreatic mass had been identified on these CTs even by expert radiologists. On the internal test set consisting of more than 1,200 CTs, our model was able to differentiate between normal appearing and pancreatic cancer with an accuracy of 92%. It was able to identify correctly
pancreatic cancer in 88% of the CTs and was able to accurately rule out or exclude pancreatic cancer in 95% of the CTs. Similarly, the performance was generalizable on the public data sets with an accuracy of 86%, sensitivity of 88%, and specificity of 83%.

Interestingly, despite not being trained on pre-diagnostic CTs, the model was accurately able to predict pancreatic cancer in 84% of the cases, with an average lead time of one year prior to the clinical diagnosis.

Again, I want to highlight here that these prediagnostic CTs had normal appearing pancreas. So it is very likely that the prediction of the model was based on some subtle imaging features that are otherwise imperceptible to human eye. The performance of the model was also consistent across different T stages of the tumor, different patient demographics such as age groups or sex, and different CT acquisition parameters.

In conclusion, our study shows that AI-powered fully automated detection of pancreatic cancer is possible with high accuracy and generalizability. And AI can detect pancreatic cancer not only on diagnostic CT scans, but can also predict pancreatic cancer at a substantial lead time. Our model in combination with the new and emerging blood-based biomarkers can potentially be the way forward for early detection of such a lethal cancer. Models such as ours can also be deployed in some of the ongoing clinical trials, such as early detection initiative, which aims to assess the outcomes of screening strategies based on clinical risk prediction models and combination of CT scans to identify subjects who are at risk of developing pancreatic cancer. Thank you very much.

**Unger:** Well, thank you so much, Dr. Suman. All right, judges last round of comments here. Dr. Desai, please kick us off.

**Dr. Desai:** This is great. I commend Garima on such an important research study. This is an incredibly devastating disease. And so much need for us to improve our ability to identify these cancers earlier when they are treatable. And so Garima, on a few different areas, one is the problem that she’s addressing. But then secondly also, at the same time she’s teaching us about a new science. AI is being used more and more. And we need to learn about it more and more. And I think finding the appropriate applications of AI, as in helping and supporting physicians answering clinical questions is very important. And this is a step in that direction.

And I think it affirms for me that AI is a supportive tool for physicians. The conclusion of these findings was that there was an 88% sensitivity. We need even better. And so this will support physicians in using this plus other testing and other diagnostic technologies and strategies for us to be able to get that as high as possible.

But again, it affirms for me that this is a tool that we would use to support our clinical decision making. And I'm impressed with the use of this new science.
Unger: Dr. Yancy?

Dr. Yancy: I can only echo Dr. Desai’s comments. There is no malignancy that strikes more fear than the diagnosis of pancreatic cancer. And so having a way to get a lead time of at least a year or longer, for a first glance is exactly what needs to happen.

The questions we should have, have to do precisely with methodology. Typically when we're talking about training data sets for machine learning, the denominator is much larger than it is here. We have to be very careful that the baseline data inputs don’t carry forward biases just preferable to the patient population that constitutes the training algorithms.

And so really a terrific focus. An important use of a strong methodology. But like every other methodology, we have to allow ourselves to think carefully about how it’s deployed. I'd love to see this work continue, but with much larger data sets.

And I agree completely with Dr. Desai. We need better sensitivity than 88%. We do not want to miss these tumors. And we do want to find them earlier when they are curable. But I still applaud this work. It's great stuff.

Unger: And finally, Dr. Bibbins-Domingo.

Dr. Bibbins-Domingo: Yeah, I agree with my two colleagues. What I really appreciated about this presentation was its clarity, but also the recognition of what one needs when one is learning how to do new techniques like this. And the limitations of these techniques.

So I liked that there was a focus on the multiple types of data that were used, because there is bias with one data set. As Dr. Yancy said, we’d like to see more and larger data sets, so there's going to be a continuing need to do this as this work is repeated. And additionally, that the implications of these findings are not just for clinical practice but also for helping us to design better studies in the future.

And so I really appreciated Garima's awareness of the technique, but also what one has to consider when applying this technique.

Unger: Wow, those were five amazing presentations. Congratulations to all five finalists. Now the challenge shifts to our judges, and the tough decisions they need to make in deciding this year's winner. So let's check back in with our panel and get their final thoughts on crowning our 2022 AMA Research Challenge winner. All right, judges. Dr. Yancy, why don't you lead us off.

Dr. Yancy: Well first, the future of discovery science is secure. I think about 30 years ago when I was in the place where the finalists are right now. This was not the kind of research we were executing nor the kind of methods we were using. And so I am really emboldened by the direction these young
investigators took. And I'm excited that we saw innovation and entrepreneurship.

We saw the really expert use of observational data sets. We saw brilliant incorporation of translational science. And we even had a chance to vet new efforts using data science. This is really the new frontier. This is where we should be. And so I'm really happy about that.

The polish in the presentation style for each of the researchers was really laudable. It again indicates significant engagement with senior leadership, with mentorship. A very strong attribute as these young investigators go forward. So as we've deliberated once before, if I had five gold medals I'd pass out five gold medals. But I'll end where I started—the future of discovery science is sound. And I'm really pleased to make that statement.

Unger: That's terrific. Dr. Bibbins-Domino.

Dr. Bibbins-Domingo: Yeah, I couldn't agree more. I really appreciated that we saw a breadth of types of science across these five really extraordinary presentations. That we saw the mechanistic science, up through the population science, and then the adoption of new techniques.

I will say, as somebody who's now a journal editor, the thing that I appreciated is how clear the communication of the scientific findings were. I think it would be easy for somebody who was immersed in the science in these specific areas to understand the contributions of these new findings.

But it was also easy for somebody who might not know the details here to appreciate both the context as well as the specifics of the findings and where the future directions may lie. So communication is so key. And it's great to see it in people early on in their careers.

Unger: Thank you. And Dr. Desai, your final thoughts.

Dr. Desai: Yeah, I have to echo what my colleague said. It brings such joy to me and others as we listen to these young physician investigators. And their passion for science. Again, the breadth as was mentioned around foundational science, engineering, big data, artificial intelligence and analytics.

This is the future and I found it inspiring. I found it affirming for our future as a country and really as globally around the world for health with the excitement and passion that they have brought to their science. And also again as was mentioned, the clarity with which they approach this and the promise that this research holds for the future discoveries that I think will be built upon them. Such an incredible joy to listen to these presentations.

Unger: Well, thank you so much Dr. Desai. And judges, I do not envy you. These are five fantastic presentations. But we have to pick a winner. So we're going to give you a few minutes. And then we'll come back to you and get your final decision.
OK, it's time to check back in with our panel and get their final thoughts on crowning our 2022 AMA Research Challenge winner. Judges?

**Dr. Bibbins-Domingo:** Well, you've given us quite a difficult task. We had five extraordinary presentations representing really extraordinary science. We talked for a while about this. And we have decided that Leela Biswas is the winner of this year's AMA Research Challenge.

And I think the deciding factor for us was really the move on an important question from humans into mice in vitro, in vivo, and then back to really helping us to understand the phenotype of aneuploidy. And across that extraordinary breadth, really producing some very compelling science and presenting it in a very compelling way.

**Unger:** Dr. Desai.

**Dr. Desai:** Yeah, I would like to congratulate all of our finalists and especially Leela Biswas. The versatile and expert use of such sophisticated analytic tools and apply them to such an important clinical question was so impressive. Congratulations.

**Unger:** And Dr. Yancy.

**Dr. Yancy:** Everybody's a winner. It's so important to understand at this stage of your research career that the opportunity to have any success in discovery science is a kind of catalytic moment that keeps your career going. So everybody is a winner.

You've heard us use words like extraordinary, outstanding, excellent. That's not hyperbole. It identifies the potential work of these young scholars, these young investigators. I really do believe that the future's very bright. To see this kind of talent this deeply immersed in discovery science, really, really pleased to see this. And I'm grateful for the opportunity to be part of this AMA Research Challenge. Thank you.

**Unger:** Well, thanks again to our judges. That was really fun. And now comes the even more fun part where we get to tell our winner the big news. So we're going to bring Leela Biswas in now for that part.

Hi, Lela. This is Todd Unger at the AMA. How are you doing today?

**Biswas:** Good, Todd. How are you?

**Unger:** It looks like you're a little busy today. Thanks for taking a few minutes to join us.

**Biswas:** Of course, happy to join.
Unger: Well, we just talked thoroughly with our panel of judges. And there was one really important follow-up question. I'm sorry to kind of put you on the spot here. But the answer is pretty important. Are you ready?

Biswas: Sure.

Unger: How does it feel to be the winner of the 2022 AMA Research Challenge with a grand prize of $10,000?

Biswas: I'm shocked. Oh, my goodness my heart is beating. Wow, I'm very surprised. I was anticipating a lot of questions, and I was excited for a follow-up discussion on the research. But this is really great news. I'm very flattered because the research from my colleagues in both the semifinals and the finals was outstanding. I was in just an incomparable group of exciting clinicians and student researchers. So I feel very lucky to be selected as the winner. I'm very flattered. Thank you so much.

Unger: When you got into this, did you think that you might come out on top?

Biswas: My hope when I entered was really just to share my research with clinical colleagues, with a clinical audience. And especially a diverse one. The AMA Research Challenge is the largest multi-specialty competition. And that was really important to me that I could get perspectives and feedback and discussion from so many different specialties and so many clinicians.

Every specialty relies on interplay between other specialties. So it was really important for me to get those perspectives. So I was just looking to share my research with intelligent colleagues.

Unger: Well we know that research is a team effort. Is there anybody you'd like to give a special shout out to?

Biswas: Of course, yes. Number one, the individuals who contributed bio banking data to our studies. Those patients in the infertility clinic. First and foremost, we're extremely lucky to have those data which are very hard to come by. And of course my PI and our collaborators. So my PI, Dr. Karen Schindler at the Human Genetics Institute. And our collaborator in the computational end, Dr. Jinchuan Xing, as well as my MD/PhD program in my university. And my family. I'm incredibly lucky to have a very supportive mentorship system at Rutgers.

Unger: What do you think was the biggest contribution from your mentors?

Biswas: Sure. So there's of course the research end, and then there's professional development as well. So I've been able to get a lot of great feedback in terms of doing rigorous science. Doing the right statistical tests. Making sure we have the right power for our studies so that the results are valid.
But then I've also received a lot of really wonderful professional development from my mentors in terms of developing presentation and scientific communication skills, as well as things even like grant writing. I was very lucky to have received NIH funding as an F30 fellow. And none of that was possible without great feedback and great guidance from my mentors.

**Unger:** Well, it's clear that you got some fantastic guidance. And we are so lucky to have a $10,000 grand prize provided by Laurel Road. I'm not going to hold you to this, but do you have any thoughts about how you might use your $10,000?

**Biswas:** Yeah. Oh, my goodness. Well, I'm in an extremely long graduate education program. So it's twice as long as your traditional MD program. It's eight years. And so with that has come a lot of expenses. And so I think I'll invest in my education so that I can become a physician scientist and continue to give back to my community and to my patients long term. I'm very lucky to be able to do that.

**Unger:** Leela, we're so excited to have you. We're excited for your future in research. Keep going. You have such a promising start here. We can't wait to see what you do in the future.

**Biswas:** Thank you so much. I really appreciate it, Todd. Have a great day.

**Unger:** Take care.

**Biswas:** Goodbye.

**Unger:** Well, I think I've said wow too many times already. So I'm just going to say how fun was that. Congratulations to all our finalists and to our 2022 AMA Research Challenge winner, Leela Biswas. Impressive, thoughtful, relevant work, all the way around.

On behalf of the AMA, I want to thank again all the participants, co-authors and mentors for your contributions to research in this year's projects. And again, a huge thank you to Laurel Road. Research is what propels medicine and science forward. And judging from the enthusiasm and quality of the work that we're seeing at the AMA Research Challenge, we are in good hands.

I'll leave you with one last thought. In the coming new year, let's all do our part to recognize and support the vital role of research in medicine. Thank you and good night.

URL: https://www.ama-assn.org/about/research/2022-ama-research-challenge-finalists-compete-win-top-prize
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