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The Eighth Annual Meeting of the Southeastern Association of Shared Resources (SEASR), Atlanta, GA, June 10–11, 2021

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INTRODUCTION

Despite the COVID-19 pandemic changing the lives of people throughout the world, including severely impacting science and research conducted at academic and government institutions and entities, the Southeastern Association of Shared Resources (SEASR; seasr.abrf.org), a chapter of Association of Biomolecular Resource Facilities (ABRF), continued to fulfill its mission. The SEASR annual meeting strives to provide a forum for core facility directors, managers, and technical staff. After canceling the 2020 annual meeting during the first phase of the pandemic, and in response to the prolonged subsequent waves of COVID-19 infections, for the 2021 annual meeting, SEASR quickly adjusted the mode of program delivery. Because shared resources faced new difficulties to provide services while addressing safety concerns and enduring economic upheaval, the decision was made to provide the 2021 meeting content entirely using virtual forums. Part of the 2021 meeting programming focused on timely issues, such as coping with the COVID-19 pandemic and ramping up work in shared resource facilities as laboratories reopened.

The SEASR 2021 meeting offered all virtual keynote and breakout concurrent sessions using the Zoom platform with licenses supported by the ABRF. In addition to sessions devoted to cutting-edge technologies, topics relevant to core facility operations were included that ranged from social-distancing practices to the reopening of cores, new core personnel responsibilities, and the well-being of personnel during the pandemic. By June of 2021, more than a year after the pandemic started, approximately 143 core facility resource directors, managers, administrators, and staff from 43 academic, government, or nonprofit institutions and 15 corporate partners registered to virtually attend the eighth Annual Meeting of SEASR held from June 10 to June 11, 2021 (Figure 1). Because of the overwhelming support from SEASR annual meeting academic and vendor sponsors, the registration to the virtual meeting was complimentary for all noncorporate attendees. The content of the one-and-a-half-day meeting included a combination of scientific topics, administrative and leadership sessions, and a virtual poster session as summarized herein.

FIGURE 1. Select members of the 2021 SEASR Organizing Committee along with Emory IT support personnel. Photograph credit: Thayumanasamy Somasundaram.

OPENING SESSIONS

Opening remarks

The SEASR virtual meeting began with the welcome remarks from Thayumana Somasundaram, PhD (SEASR President, Director, X-Ray Facility, Florida State University), and opening remarks by Ken Schoppmann (Executive Director, ABRF). Dr. Somasundaram thanked the meeting sponsors and spoke briefly about SEASR, its mission, and coping with the difficult year during the pandemic. He thanked the current SEASR Executive Committee for their continued support and then honored the work of Dr. Kimberly Dahlman (Vanderbilt University Medical Center), SEASR Executive Committee Member, and two-time SEASR President, as well as Ms. Susan Constable, SEASR Executive Committee Member and Treasurer. Ken Schoppmann then spoke about the ABRF and its chapters and the benefits of individual and institutional ABRF memberships.

Keynote lectures

How T-cells recognize tumor cells (Timothy Chan, MD, PhD, Director, Center for Immunotherapy and Precision Immuno-Oncology, Cleveland Clinic)

Dr. Chan discussed how genomics is being applied to immunotherapy for patients with cancer. Immunotherapy has transformed care for patients with cancer and has resulted in durable antitumor responses for many individuals. He shared how his research group uses cutting-edge genomic approaches to understand why some patients respond and some do not respond to immune checkpoint inhibitors.

Developing and deploying vaccines at pandemic speed (Carlos del Rio, MD, Executive Associate Dean and Professor of Medicine in the Division of Infectious Disease, Emory University)

Dr. del Rio shared his experience and expertise in the preparation of a vaccine during a pandemic. Given his previous involvement on the H1N1 influenza task force, Dr. del Rio quickly became a leader during the COVID-19 pandemic. Dr. del Rio shared information about the development of COVID-19 vaccines, including the targets for the COVID-19 vaccines. He shared information on efficacy of the vaccines, including how effective the vaccines have been against COVID-19 variants. Dr. del Rio also shared demographic information about groups of individuals choosing to be vaccinated, and he shared the importance of gaining the trust of average citizens in an effort to increase the number of individuals who are vaccinated.

Mass spectrometric innovations for translational and clinical research (Richard Yost, PhD, Professor, University of Florida)

Dr. Yost discussed recent advances in mass spectrometry relevant to translational and clinical research, especially in the area of metabolomics, tandem mass spectrometry, and mass spectrometry imaging. He also presented methods of direct tissue analysis using matrix-assisted laser desorption/ionization and microextraction and ion mobility mass spectrometry as well as high field asymmetric waveform ion mobility spectrometry that his research group has pioneered. His talk fit the SEASR mission, as he has not only developed new methodologies in the area of mass spectrometry but he has also supported the Southeast Center for Integrated Metabolomics, a core facility at the University of Florida.

Importance of culturally competent healthcare (Tristen Brenae Johnson, PhD, Diversity Education Specialist, Moffitt Cancer Center)

Dr. Johnson started her talk with reviewing ways to remove the power of our own biases and explained how to understand what implicit bias is and how it can negatively impact patient care, team diversity, and inclusion. She reminded the audience that we are constantly bombarded with much more information than our brain can properly process, leading to our unconscious decision-making processes influencing our actions >99.999% of the time. Dr. Johnson also warned about conjunction fallacy, wherein we make erroneous decisions about the possible outcomes when we are front loaded with information about the context. She then shared outcomes of a study in which caregivers presumed that African American patients have a higher threshold for pain than Caucasian counterparts and hence required less pain medication, leading to real-world health disparities. She concluded that self-awareness of implicit biases could lead to a reversal in otherwise biased outcomes.

Precision immunology through deeper single-cell profiling: new approaches and new insight (Pratip Chattopadhyay, PhD, New York University)

Dr. Chattopadhyay announced that he has recently left NYU Langone Health to become the founder and CEO of Talon Biomarkers for biomarker discovery and the Cofounder and Chief Operating Officer of TerraFlow software solutions. Overall, the mission of precision immunology is to reveal new biomarkers of disease or treatment outcomes and to better define mechanisms of disease using high-parameter single-cell technology. However, it is relatively inefficient to study in great depth a single cell or molecule of interest one at a time in every cell type each time an interesting marker is revealed. Therefore, the strategy his laboratory has employed is to use cutting-edge single-cell technology to gather as much information as possible about every cell in every sample, measuring as many interesting targets at once as technically possible with minimal sample input and at high definition. Dr. Chattopadhyay developed the BD FACSymphony, and his laboratory was the first to use a 28-color panel for flow cytometry. The major challenge of a high-parameter approach is data analysis using supervised clustering based on known markers, missing the context of those cells that do not match the predefined clustering profiles. TerraFlow is a new data analysis tool that mines combinations of six markers at a time and, in an unsupervised way, identifies the most important and simplest phenotypes that describe a difference between patient groups; these are then grouped into families of cell populations by understanding networks of populations that share relationships and features. This approach prevents the identification of populations of cells that do not exist in a

sample or are very rarely represented. Traditional gating can be subjective (e.g., where to draw the gate between positive and negative subpopulations), so a nongating analysis approach was also developed in TerraFlow. Cell events are weighted by the fluorescence intensity, such that as signal decreases, the weights decrease, creating "pseudo-gates." TerraFlow identifies core sets of markers ("families of phenotypes") that drive differences between patient groups through streamlined combinatorics, nongating combinatorics, and a recursive feature elimination protocol. This pipeline allows for the development of simpler cytometry panels focusing on the most important diagnostic markers for clinical assays and may suggest optimal combinatorial therapies for treatments based on the unbiased identification of the key family of phenotypes within a population.

BREAKOUT SESSIONS

Breakout session I

Network of connectivity to expand your opportunity space (Marti Head, PhD, Director Joint Institute for Biological Sciences, Oak Ridge National Laboratory)

At Dr. Head's previous position at GlaxoSmithKline, she led the Computational Chemistry team, which did not develop small molecules, or anything "tangible," but rather generated hypotheses and experimental designs to drive a drug discovery program forward. She realized that she had to focus on the question, how should the group purposefully build relationships and engage with people so that their work was translated into real action that would benefit patients? She was initially inspired after hearing a story about the Iraq War of how the US military used social network analysis to find insurgents responsible for roadside bombings. Social network analysis allows for an understanding of the key influencers who connect the greatest number of people in an organization. Dr. Head showed an example of social network mapping, in which points represent individuals and blue lines represent the connections between individuals in the team. Some people are not connected at all, whereas in other subgroups, there are tight connections, and there is typically a yellow dot representing the person who had the most connections. She then elaborated on how this approach benefited the National Virtual Biotechnology Laboratory initiative for COVID-19, spanning 17 Department of Energy laboratories across 5 programs, including molecular design and analysis to inform therapeutics related to COVID-19 through leveraging high-performance computing, chemical, biological, and analytical services and light and neutron sources. The Molecular Therapeutics Team alone included >150 people across 9 of the 17 national laboratories across 6 states spanning 4 time zones in

the United States; some team members had never worked together before. Physical resources and computational data had to flow seamlessly across the United States. The team identified multiple antibodies and active inhibitors of the viral proteases and 6 families of other inhibitors that target other viral proteins. The important leadership features were (1) a shared mission (easier during a worldwide pandemic); (2) at the beginning, taking the time to get to know all of the laboratory members and to receive feedback from everyone; (3) developing subgroups that worked on concrete tasks; (4) thanking team members who stopped their regular work to be a part of this team; and (5) providing frequent recognition to team members. Dr. Head advocated that we should all aspire to become our own "yellow dot" and to strive to be purposeful in building authentic relationships while expanding own our networks of connectivity.

Academic leadership: up, down, out, and in (Kimberly Kerstann, PhD, Senior Director for Research Administration, Emory University)

Dr. Kerstann began the talk noting that several members of the audience have a breadth of scientific knowledge but do not necessarily have any formal leadership background or training. However, she noted that in core facility settings, we frequently find ourselves in positions of leadership. Based on her varied governmental, industrial, and academic experiences, she noted that in academic leadership roles, we may find that we may not necessarily fit into a distinct hierarchy, but we are asked to lead projects, people, and practices. She also noted the difference between transactional and transformational leadership styles; the latter is often found in the academic setting, wherein leaders set directions and goals rather than direct the work. Dr. Kerstann also dispelled the common notion that scientists are not natural leaders, but in fact, scientific training is highly parallel to the lean leadership process of the "Plan–Do–Check–Adjust" paradigm. Finally, she spoke about intentional leadership skills, which we employ to identify and to solve the root cause of a problem.

Breakout session II

Exceptional responders: inferences from n of 1 experiments (David Wheeler, PhD, Director, Precision Genomics, St. Jude Children's Research Hospital)

The basis of Dr. Wheeler's presentation was that although an "n of 1" is an oxymoron in experimental science, the response of a patient with cancer patient during treatment is a highly useful $n = 1$ experiment. In advanced adult cancers in particular, the outcomes of most new drugs studied within large cohorts have been modest at best. The rationale for studying the rare individual patients who respond very well to therapy led to the development of the NCI Exceptional Responders study. All samples

in the study were formalin-fixed paraffin-embedded specimens, and normal tissue was frequently unavailable. Overall, there were 110 specimens that were subjected to whole-exome sequencing, amplicon sequencing, mRNA sequencing, and DNA methylation and immune cell profiling. Colorectal and breast cancers were the most frequently represented rare responders. Over the course of the study, investigators noted several examples of "*n* of 1" cases that revealed interesting genomic alterations that provided novel mechanisms of drug action; in essence, he proposed that tumors from exceptional responders may harbor their own Achilles' heel. Dr. Wheeler presented several examples of exceptional responders, suggesting that cancer researchers only need to sequence the exceptional responders (and not all patients) for a given tumor type. The take-home message was that exceptional responders will provide valuable information likely generalizable to a larger population of patients, even if a drug of interest "fails" in a large cohort and therefore does not lead to Food and Drug Administration approval. A variety of examples of the lessons learned from exceptional responders were reviewed.

Long road population genomics and forensics (Shawn Levy, PhD, Chief Scientific Officer, Genomics for Discovery Life Sciences, Hudson Alpha)

Dr. Levy presented on long-read sequencing technology and how resulting data can be applied in forensic science. The major project discussed was the "All of Us" research program subproject in progress at the Hudson Alpha Institute for Biotechnology to sequence a subset of these patients using the PacBio platform. Hudson Alpha's goals for this project are to improve resolution for large structural variants incompletely characterized by short-read data, to determine population frequencies for indel and structural variants to improve calling of structural variant events, and to improve resolution in challenging regions of the genome. Whereas the short-read genome sequencing coverage standard is 30× coverage, long-read sequencing with the PacBio circular consensus HiFi reagents is an emerging option at 10–15× coverage, which balances costs and performance along with higher accuracy than current versions of Oxford Nanopore technology. In the near future, the best of both worlds could be pairing Nanopore ultra-long reads with polishing using PacBio sequencing. At the end of the talk, Dr. Levy discussed how short-read sequencing typically optimized for oncology purposes could be used to assist with identifying unidentified and missing persons or to solve cold cases, even with highly degraded or limited quantities of DNA at 1× coverage. Therefore, the protocol optimizations developed in laboratories like Hudson Alpha have real-world implications outside of biomedical research.

Breakout session III

Mechanisms and applications of CRISPR-Cas Enzymes (Hong Li, PhD, Professor, Florida State University)

Dr. Li spoke about the molecular mechanism of a special CRISPR-Cas9 Type II-c system derived from *Acidothermus cellulolyticus*. She talked about how determining three-dimensional structures using X-ray diffraction and cryo electron microscopy methods helped their laboratory to learn about the system's potential for epigenetic editing and detection of edited genomes. She also spoke about a COVID-19 assay that her laboratory is developing, which is more sensitive than the traditional polymerase chain reaction tests that are currently available.

How to create a highly efficient genome editing shared resource (Shondra Pruett-Miller, PhD, Director, Center for Advanced Genome Editing, St. Jude Children's Research Hospital)

Dr. Pruett-Miller shared information about how CRISPR genome editing works and introduced the genome editing services that her core at St. Jude is offering. She shared methods and workflows to consider when performing genome editing, including the best methods for Cas9 and guide RNA delivery and for the validation of edited cells using next-generation sequencing strategies. Dr. Pruett-Miller shared some tips about developing genome editing services for cores as well as helpful instrumentation that can make these services feasible. She also discussed how her core changed operations to adapt to the COVID-19 pandemic.

CORPORATE PARTNER SESSIONS

Select SEASR corporate partners presented their newest technologies to the meeting attendees throughout the meeting:

- Enhance Your Core's Business (Illumina)
- What's New in Spatial Biology (NanoString)
- Helping Your Lab Implement Social Distancing Through Instrument Scheduling (Agilent)
- Innovative and Versatile Imaging Solutions (MetaSystems)
- Innovative Immunoassay Platforms from MilliporeSigma (MilliporeSigma)
- Optical Genome Mapping: The Key to Structural Variation Detection (BioNano)
- Using Covaris AFA Technology to Automate Your Genomic and Proteomics Workflows (Covaris)

- High Performance Digital PCR and NGS Solutions for SARS-CoV-2 Detection and Genomic Surveillance (Qiagen)
- Innovating for High Throughput NGS (PerkinElmer)
- Leading the Way in Target Enrichment: Exceptional Performance, Improved Efficiency and Rapid Customization of Targeted Methylation Sequencing (Twist)
- Cytometry at True Resolution: Resolving Complex Biology with Single Cell Multiomics (10XGenomics)

All of these sessions offered a Q&A period after the presentation. In addition, all sessions were recorded, and the links of the session recordings were shared with the registered participants after conclusion of the program.

POSTER SESSION

The virtual poster session opening coincided with the first day of the virtual meeting and continued through both days of the meeting. Several corporate and academic attendees displayed their products and research work during the session. Because the session was provided through links to a static website, no live discussions could be facilitated.

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