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8th vaccine renaissance: A creative nexus for vaccine developers

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The Institute for Immunology and Informatics (iCubed) at the University of Rhode Island held its 8th Annual Vaccine Renaissance on October 13-16, 2014. The conference serves as an annual nexus for conversations related to vaccine design, discovery, and vaccine acceptance. The annual event strives to provide a unique, interactive forum for the discussion of cutting-edge vaccine research, including the design and use of new tools and techniques for accelerating vaccine discovery. The conference also provides academic researchers, vaccine industry leaders and students of vaccinology with an opportunity to foster new professional relationships. Furthermore, the organizers of the 8th Annual Vaccine Renaissance are committed to extending attendance and presentation opportunities to young scientists and ‘scientific minorities,’ such as women, students from historically black colleges and universities (HBCUs), and individuals not native to the United States. The conference organizing committee invites such participants to present their research as a poster, and has organized “meet-the-expert” roundtable discussions as a way of conferring with experts.

Participants contributed to reports about developing vaccines against emerging infectious diseases and research updates on the effect of the human microbiome in responses to

vaccines. Field experts also described new cancer vaccine designs, provided overviews on the current state of animal vaccine research, and reported on HPV vaccine acceptance by at-risk populations. The four-day symposium included a one-day pre-conference, in which participants discussed their research involving the JanusMatrix tool developed by De Groot and colleagues [1]. The last day of the event provided opportunities for attendees gain hands-on experience in a variety of laboratory techniques as well as training on the iVAX suite of bioinformatics tools.

Nearly 100 individuals from industry, academia, and federal agencies such as the Walter Reed Army Institute of Research (WRAIR), the United States Army Medical Research Institute of Infectious Diseases (USAMRIID), the Department of Agriculture (USDA), and the National Institutes of Health (NIH) attended the conference. In addition to luminaries such as Bruno Guy (Sanofi Pasteur), Polly Matzinger (Laboratory of Immunogenetics, National Institute of Allergy and Infectious Disease), Thomas Nutman (Laboratory of Parasitic Diseases, NIH), Amy Rosenberg (Food and Drug Administration), Edward T. Ryan (Massachusetts General Hospital, Harvard Chan School of Public Health). Papers were presented by John Julias (United States Department of Homeland Security), Kimberly A. Kraynyak (Inovio Pharmaceuticals), Steve Meshnick (Department of Epidemiology, UNC Gillings School of Global Public Health) and Peter B. McGarvey (Innovation Center for Biomedical Informatics, Georgetown University Medical Center). Presenters represented a variety of affiliations as well as health-related interests, which stimulated participants to draw inferences and conceive connections between their colleagues' novel ideas and their individual research programs.

After the conference, presenters are invited to submit a manuscript related to their presentation, to the peer-review journal Human Vaccines & Immunotherapeutics (HV&I). Five speakers have accepted the invitation to submit, and their articles can be found within the current issue of HV&I. In this 8th compendium of papers, we are pleased to offer a selection of reports that focus on the means to rapidly develop safer, more effective vaccines. In sequential order of authors and their topics is as follows: Moise *et al.* [2] describes the iVAX suite of tools along with their applications for the design of vaccines for Tularemia, Smallpox, H. Pylori, Burkholderia, HCV, Lassa virus or H1N1 and H7N9. Eickhoff *et al.* describe the immunoinformatic strategy and *in vivo* validation of the identification of 30 epitopes that could be used in the design of Chagas disease vaccine [3]. Rose *et al.* discuss the choice of the adjuvant during vaccine design and demonstrate that while the adjuvants do increase the innate response in mice injected with *piggyBac* plasmids, no adjuvant increases the level of transfection of the antigen [4]. Carjaval-Yepes *et al.* developed a cellular model of IFNAR1-knocked-down avian cells that can produce H1N1 viruses and HA protein, and propose an alternative method of production of Influenza vaccines [5]. Lastly, Jamieson discusses the genetic and environmental factors that influence response to vaccination, with a special emphasis on the microbiome [6].

Two additional papers not included in this compendium have been accepted for publication and will be published out soon after the printing of this compendium. In those two manuscripts, Hoffmann *et al.* present their pre-clinical work on the development of a cancer vaccine targeting survivin expressing tumor cells. HIVax peptides expressed in Fowlpox vectors activate antigen-specific CD4⁺ and CD8⁺ T cells in healthy donors,

providing a rationale to move on to the clinical stage of the vaccine development [7]. Liu *et al.* present an immunoinformatics analysis of H7N9 T cell epitopes, providing a possible explanation for immune resistance to inactivated H7 HA vaccines. The results demonstrate that HA epitopes containing TCR facing residues identical to self-proteins can activate FoxP3⁺ Tregs, thus inducing immune tolerance and H7N9 “camouflage” from the immune response [8].

The variety of topics and expertise contained within the following reports is an accurate representation of the Vaccine Renaissance and its attendees. Qualitative exit surveys suggest that participants appreciate the interactive and interdisciplinary nature of the Vaccine Renaissance. The 9th Annual Vaccine Renaissance is scheduled to be held November 4-6, 2015 in Providence, Rhode Island, with informatics training held on Friday, November 6th. Please visit www.immunome.org for a list of speakers and to view the schedule of events.

Accepted Manuscript

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