



Editorial

Here come the omics!



A long-term goal of clinical care has always been to fit the specific treatment to the individual patient—what we would now call personalized medicine. However, the ability to predict which patient will best respond to which treatment has historically been nearly impossible. Accordingly, personalized medicine has typically involved significant trial and error with different therapies until desired clinical results are achieved. Fortunately for both patients and physicians, this paradigm has begun to change. It has been nearly 20 years since the first human genome was deciphered, allowing us to begin more precisely defining potential mechanisms of, and risk factors for, disease as well as responses to therapies. We now have the ability to determine in days (rather than months to years) an individual's genetic make-up, how their specific genes are being turned on and off, factors that modify expression of these genes, the RNA message coming from these genes, and the proteins being made from the RNA. In addition, we have found that the microbial communities living on and in us, as well as the varied environmental exposures to which we are constantly exposed, can individually or collectively directly affect our health. To effectively provide true personalized medicine, we have come to realize that understanding all these components and how they interact is an absolute necessity. However, cataloging the genes, how their expressions are controlled, RNA transcripts, proteins, microbial colonizers, and environmental exposures for even a single human remains a herculean task given the great amount of data generated by such an approach. Until recently, it has been very difficult to study and analyze these large data sets, but statistical tools available in the nascent field of bioinformatics have now come of age to allow for better analysis and, with this, the potential for use of these data in the clinic.

This issue of the *Annals* is dedicated to the study of these large data sets and their potential for developing truly personalized medicine. Indeed, the “omics”—genomics (study of genetics), epigenomics (study of factors that influence gene expression), transcriptomics (study of RNA transcribed from the expressed genes), proteomics (study of proteins), metabolomics (study of metabolites), microbiomics (study of microorganisms that live in and on us), and exposomics (study of environmental exposures, the so-called *envirome*)—will allow for the unprecedented ability to categorize more precisely individuals and communities. This categorization will ultimately provide us with a blueprint for better understanding the mechanisms of disease, treatment assignment, and outcome predictions—what can truly be called a precise and personalized form of medicine!

The collection of articles in this issue span the gamut on the “omics” revolution. We include a perspective from the National

Heart, Lung, and Blood Institute of the National Institutes of Health that discusses their approach to supporting “omics” research—all with the goal of developing effective precision medicine approaches for lung diseases.¹ The review by Virkud et al² is a primer on how these big data sets are generated and what the practicing clinician needs to know when confronted by “omics” studies. The review by Peden³ provides an overview of the multitude of environmental exposures that make up the *envirome* and how these affect allergic diseases, such as asthma, among other diseases. Donovan et al⁴ discuss current large data set studies in atopic disease and what the current impact of these studies is for our patients. Looking into their crystal ball, Long et al⁵ predict how these “omics” data sets will influence our clinical practices in the (relatively near) future and how we may use them to provide personalized care.

Together the articles in this issue provide an up-to-date overview of where the “omics” revolution is (at least in terms of asthma and atopic disease) and where it is likely going. The practice of medicine is always changing, but, as can be seen from this issue of the *Annals*, we are getting much closer to being able to provide truly personalized (and precise) medicine to our individual patients. We look forward to seeing greater integration of “omics” into daily clinical practice for the benefit of all the patients we serve!

Mitchell H. Grayson, MD*

Gailen D. Marshall, Jr., MD PhD†

*Division of Allergy and Immunology

Department of Pediatrics

Nationwide Children's Hospital

The Ohio State University College of Medicine

Columbus, Ohio

†Division of Allergy, Asthma, and Clinical Immunology

Department of Medicine

The University of Mississippi Medical Center

Jackson, Mississippi

Mitchell.Grayson@Nationwidechildrens.org

References

1. Croxton T, Gan W, Noel P, Kiley J. Precision medicine for lung diseases: a National Heart, Lung, and Blood Institute perspective. *Ann Allergy Asthma Immunol*. 2019;123:537–538.
2. Virkud YV, Kelly RS, Wood C, Lasky-Su JA. The nuts and bolts of omics for the clinical allergist. *Ann Allergy Asthma Immunol*. 2019;123:558–563.
3. Peden DB. The “*envirome*” and what the practitioner needs to know about it. *Ann Allergy Asthma Immunol*. 2019;123:542–549.
4. Donovan BM, Bastarache L, Turi KN, Zutter MM, Hartert TV. The current state of omics technologies in the clinical management of asthma and allergic diseases. *Ann Allergy Asthma Immunol*. 2019;123:550–557.
5. Long A, Bunning B, Borro M, Sampath V, Nadeau KC. The future of omics for clinical practice. *Ann Allergy Asthma Immunol*. 2019;123:535–536.

Disclosures: The authors have no conflicts of interest to report.

<https://doi.org/10.1016/j.anai.2019.10.011>

1081-1206/© 2019 American College of Allergy, Asthma & Immunology. Published by Elsevier Inc. All rights reserved.