The exposome: integrating the environment into multiomic research at NIH

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Christopher Wild coined the word exposome in 2005 as a way to provide an environmental complement to the genome. Often the word is used to summarize the totality of exposures throughout one's lifespan. The challenge is that achieving the goal of measuring the totality of exposures is impossible, which has created an intellectual barrier to the field. Rather than focusing on the totality the goal should be to capture the measurable in as comprehensive manner as possible. By combining the cumulative measure of environmental exposures even at a single point in time and coupling that with the corresponding biological responses, the impossible becomes plausible. The exposome should be viewed as a biological challenge--biochemical pathways, physiological systems, and mechanisms of toxic action must be at the core of exposome research. High-resolution mass spectrometry together with cheminformatics, bioinformatics, and data dimension reduction is a reasonable first step to assess the environmental influences, but it must be integrated with genomic, epigenomic, proteomic, metabolomic, and clinical datasets. The exposome must become part of the multiomic framework at NIH.

The pragmatic solution will be to provide sensitive and validated tools that allow investigators outside the field to systematically integrate the environment into their research. There are numerous cohorts supported by the NIH that have biobanked and geocoded samples, including the ongoing NIH All of Us program. We must advance our workflows so that conducting exposomic analysis on >100,000 participants is feasible, as it will yield important discoveries regarding the environmental basis of human disease. The exposome is big science. This is not the type of project that can be conducted in an isolated laboratory. A concerted effort to harmonize data collection and analysis across cohorts and laboratories will be crucial for success. For the exposome to become a scientific and public health reality it must also build upon the already existing multiomic framework that exists at NIH. Efforts should be focused on the technologies and approaches that can leverage these existing resources as they will be most likely to transform our understanding of the environment. Furthermore, by having a similar level of resolution and quality of data as the genome, the exposome can help reveal further insights into the genome itself by better understanding the gene by environment interactions. Only when the assessment of the environment is on par with that of genome can we truly understand the basis of health and disease.

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