Beyond genes: The exposome as the next frontier in precision medicine

Recent decades have seen remarkable progress in genomics and "-omics" technologies, bringing us closer to personalized medicine. Yet, genetics explain only ~10% of common disease risk – the rest lies in the environment.[1-4] Christopher Wild's 2005 exposome concept highlighted that life-course environmental exposures (chemical, physical, social) shape health just as genes do. We propose that the exposome must be embraced as the missing dimensions of precision medicine. By integrating the totality of exposures with clinical and molecular data, we can move from generic treatments to truly personalized prevention.

The idea of an exposome may seem vast, but recent advances make it tractable. High-resolution mass spectrometry can now detect hundreds of environmental chemicals and metabolites in a single blood sample.[5] GPS-linked sensors and satellite maps provide real-time air quality, noise, and light exposure profiles for individuals. Wearable devices continuously log activity, heart rate, and even lung function, enabling us to correlate these physiologic readouts with encountered pollutants. In parallel, breakthroughs in data science allow integration of these heterogeneous datasets. For example, artificial intelligence (AI)-driven exposome intelligence tools can systematically sift multi-omic and sensor data to identify hidden exposure patterns linked to disease.[6,7]

Several large cohorts are already showing the promise of this approach. The European HELIX study followed thousands of children with deep exposure profiling (pollutants, diet, stress) and multi-omic biomarkers, uncovering how prenatal air pollution and chemical mixtures negatively impact lung and neurodevelopment.[8] Newer initiatives like the EXPANSE project are building on this by linking environmental data with genomic and epigenomic profiles from adult population cohorts.[6,7] Even in routine healthcare, a patient's residence history and wearable health data can now be combined to estimate lifetime pollutant and lifestyle burdens. Such integrative analyses have revealed, for instance, that prenatal tobacco exposure accelerates blood epigenetic aging decades later. These insights go far beyond what genes alone could tell us.

Of course, the exposome's breadth poses challenges. Unlike the human genome (3 billion bases), our environments are infinitely variable. Exposomic studies must contend with thousands of chemicals, fluctuating exposures, and complex mixtures. Standardized methods and data sharing are still lacking. To address this, the exposome community is developing common protocols and databases. Efforts such as the Exposome-Explorer catalog validate exposure biomarkers; international networks (EHEN, HHEAR, NEXUS) are harmonizing analytics.[4,6] *Journal of Integrative Medicine and Research* (JIMR) can accelerate progress by requiring detailed exposure methodology in submissions and supporting FAIR data deposition. Reporting guidelines (analogs to STROBE or MIAME) should be formulated for exposome studies – defining how to report sensor calibration, sampling timing, and metadata – so that findings are reproducible and comparable.

Looking ahead, exposomics is poised to transform clinical research. We anticipate exposome-wide association studies where thousands of exposure factors are screened against disease phenotypes, paralleling genome-wide association studies but in the environmental domain.[6] Likewise, Exposome Risk Score – composite indices of toxicant loads – could be computed alongside polygenic scores to stratify patient risk profiles.[7] Longitudinal multi-omic cohorts, powered by wearables and home sensors, will allow quasi-experimental designs: for example, measuring how reducing household air pollution or dietary changes alters metabolic signatures and health metrics within individuals. Moreover, mobile health interventions could be tailored by exposome profile: imagine asthma patients receiving personalized air-filter recommendations or pregnancy supplements based on their unique exposure patterns.

For JIMR and the wider research community, this means actively promoting exposome science. We recommend soliciting interdisciplinary studies and reviews on environmental determinants of health, encouraging detailed exposomic data analysis, and organizing workshops to build capacity in this field. Policymakers too must recognize that addressing chronic diseases and health disparities requires environmental solutions: cleaner air, safer chemicals, and healthier urban design informed by exposomic evidence.

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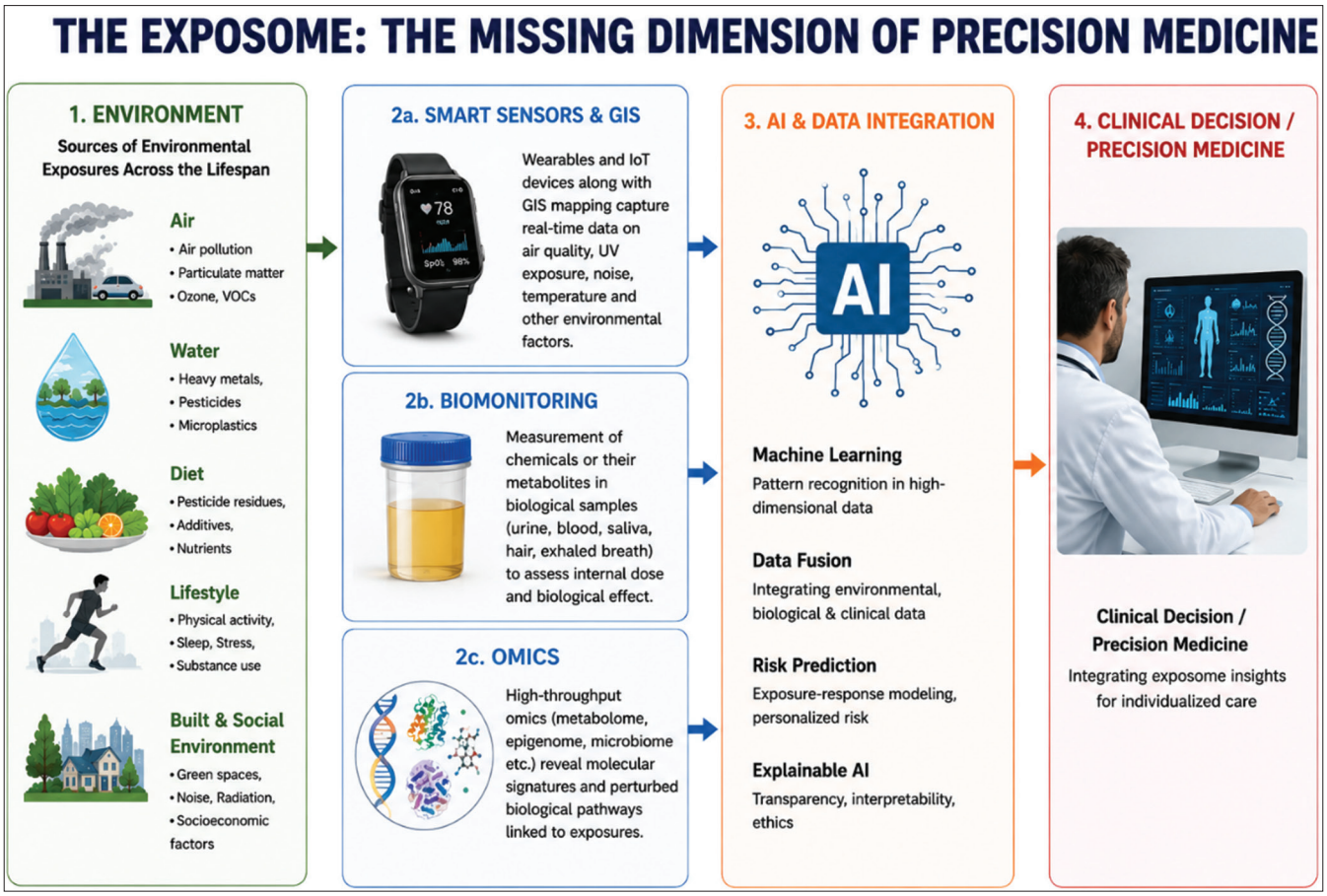

Figure 1: Conceptual framework of the exposome. This figure was generated using OpenAI tools

In conclusion, integrating the exposome is the logical next step in precision health [Figure 1]. By acknowledging that the environment is health's genome, we unlock new possibilities for understanding disease etiology and prevention. As the exposome community moves from descriptive studies to causal inference (using AI and causal models), JIMR can lead by example: championing research that looks not only at our genes, but at the air we breathe, the water we drink, and the lives we live. Embracing the exposome will ensure that in the future, our treatments and guidelines account for the full complexity of human health – not by chance, but by design.

Figure 1 was generated using OpenAI's ChatGPT. No copyrighted or third – party materials were used. The authors confirm that AI assistance was limited to figure generation and that all intellectual content is author–driven.

Nirmal Kumar Mohakud, Viyatprajna Acharya[1]

Departments of Pediatrics and [1]Biochemistry, Kalinga Institute of Medical Sciences, Kalinga Institute of Industrial Technology, Deemed to be University, Bhubaneswar, Odisha, India

Address for correspondence:
Dr. Nirmal Kumar Mohakud,
Department of Pediatrics, Kalinga Institute of Medical Sciences, Kalinga Institute of Industrial Technology, Deemed to be University, Bhubaneswar, Odisha, India.
E-mail: nirmal.mahakud@kims.ac.in

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