

# Chapter 11


## Multi-Omics

# Integration in Precision Pulmonology: Pathways to Personalized Care

**Hamza Iftikhar**

*National University of Science and Technology, Pakistan*

**Munir Ahmad**

 <https://orcid.org/0000-0003-4836-6151>

*Survey of Pakistan, Pakistan*

### **ABSTRACT**

*Integrative multi-omics approaches are redefining precision pulmonology by combining genomics, transcriptomics, proteomics, metabolomics, and epigenomics to provide a multi-layered understanding of complex respiratory diseases such as asthma, COPD, idiopathic pulmonary fibrosis, and lung cancer. These strategies enable robust biomarker identification, precise patient stratification, and predictive insights into therapeutic responses, surpassing the limitations of single-omics analyses. Successful clinical translation requires standardized data integration, advanced interpretative frameworks, ethical oversight, and scalable computational platforms, paving the way for personalized, patient-centered respiratory care.*

### **INTRODUCTION**

The industry of pulmonology is being transformed through precision medicine because the application of a universal approach to treating one type or another of

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respiratory disease is being approached in a more tailored manner (Guan et al., 2022; Hartl et al., 2021). Precision medicine provides individualized molecular, genetic information and has an environment to optimize diagnosis, prognosis, and therapy intervention of a patient (Biswas & Hasija, 2022; Sisodiya, 2021; Wang & Wang, 2023). In diseases like asthma, chronic obstructive pulmonary disease (COPD), idiopathic pulmonary fibrosis (IPF), and lung cancer, the inhomogeneous nature of the disease processes and inter-patient variability tends to constrain the benefits of traditional treatment. Precision pulmonology, therefore, is a hope of being able to individualize therapy to the molecular and clinical phenotyping of patients and increase efficacy and decrease adverse outcomes associated with the therapy.

Even though there has been great progress, single-omics, regardless of whether it is genomics, transcriptomics, proteomics, or metabolomics, have limitations when taken in isolation (Baysoy et al., 2023; Hayes et al., 2024). Susceptibility loci may be found genome, but not all dynamic processes of diseases and environmental factors can be discussed in this way. Profiling at a transcriptomic or proteomic level can capture functionality yet can be premature in its regulation or context within a range of metabolites. This, in turn, can lead to single-layer analyses that may give only partial information or lose the complexity of a multifactorial pulmonary disorder, being of reduced value in clinical decision making.

The limitations can be overcome with integrative multi-omics that integrate heterogeneous molecular levels into unified analyses. Currently, researchers can determine multifaceted associations between genes, proteins, metabolites, and regulatory networks, which influence disease pathogenesis by combining genomics, transcriptomics, proteomics, metabolomics, and epigenomics in a study. Such an integrated view can be used to identify clinically robust disease-specific biomarkers, molecular disease subtypes, and predictive markers of how patients respond to therapy. Moreover, multi-omics integration is beneficial when it comes to creating personalized treatment plans as it enables clinicians to tailor their responses to the distinct molecular profile of a patient. Consequently, multi-omics investigations imply a revolutionary innovation in accurate pulmonology, helping fill in the gap between molecular findings and clinical efficacy.

## **MULTI-OMICS LAYERS AND THEIR RELEVANCE TO PULMONARY DISEASES**

### **Genomics**

Precision pulmonology is anchored in genomics, which reveals the hereditary and nonhereditary genetic background that leads to the development and evolution

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