

# Looking for the Integrome, When Metabolomics Talk about the Interactome

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## Abstract

Secondary metabolites are not produced in isolation; they are the result of the interaction of genes, metabolism and the environment. These interaction networks that are part of the biological systems are the most reliable expression of the functioning of living beings and is a great tool to obtain information that leads to promising applications in the diagnosis of diseases, drug development, as well as the conservation and restoration of ecosystems. In this way the multi-omics approach which constitutes the confluence of various high-throughput technologies that seeks to integrate all platforms in a multivariate model that provide comprehensive profiles of the same phenomenon, it confers the ability to be the link between different aspects of cellular populations relevant in biotechnology and ecosystems research. In this order of ideas, the aim of this editorial is to give an unifying canon under the concept of integrome, like that search result of the fusion of several omics disciplines that seek to solve problems by applying the discoveries.

**Keywords:** Integrome; Metabolomics; Interactome; Multi-omics approach

## Introduction

Integrome is defined as the connection networks that describe the interaction, the construction of this intercommunication system is the product of a multivariate analysis of the data obtained by the combination of several omics technologies (genomics, transcriptomics, metabolomic and proteomics) [1]. In this way, experimental omics approaches, share different characteristics as are: to be high-throughput and massive data-based; study the molecular phenomena, as an “integrated system” due to the incorporation of the interrelation between the information obtained; and to require a complex multivariate statistical analysis because to the large amount of data [2]. This multi-trans-inter-omics needs combine several methodologies with a previous hypothesis as are genome sequencing, RNA sequencing, chromatin immunoprecipitation sequencing (ChIP-seq), mass spectrometry (MS), expression proteomics, liquid chromatography, capillary electrophoresis and nuclear magnetic resonance (NMR) [3]. Following this order of ideas an integrated-omics conceptualization is necessary in microbiology looking for detect different properties of microbial cells in multiple functional states, with the objective of reduce the information disparity between gene expression and phenotypic variation [4]. Also, is very important analyze using bioinformatics tools of the entire omics dataset for determine the genetic associations (genome-wide association studies) and their interactions with metabolites as well as protein expression, with the end to elucidate the biochemical pathways and molecular targets the most used statistical instruments are BioGrid, JActiveModules, BioNet, DEGAS, GiGa, HotNet, NuChart and Key Pathway Miner Web [5-7]. In addition, epigenome association studies is other interesting factor for to take in account looking for to establish the effect of the environment on the cellular response [8]. In short, the correct elaboration of the working hypothesis is what defines the problem that requires the use of the integrome [9], because discoveries need questions before everything.

## Epigenetics the discovery of the unified field

In this way seeking for a multi-omics approach that can be included in a translational research concept, it will be very important perform environmental epigenetics studies that can provides explanations about

the molecular mechanisms that directly cause phenotypic changes [10], this neo-Lamarckian concept have to be unified for to perform a holistic approach that describes an autopoietic model in which is possible to establish the physical and chemical processes through which the system under study exists [11]. In addition, it is important to remember that this system as unity must comply with the rule of self-regenerating itself continuously as well as its network of processes [11]. So that, a real multi-omics research work must move towards a molecular autopoiesis thought describing the operation of unicellular and multicellular living beings [12].

## Multi-omics age

In fact multi-omics research is an integrative platform which can be used in combination with clinical data for the diagnosis of complex diseases [13], as well as being applied to determine the multi-target activity of drugs with which is possible to discover new treatments and predict drug interactions based on intercellular networks. In addition, it can determine what medications could be used in combination therapy for treatments resistant to conventional medication [14]. In this order of ideas, the functionality of cell populations will be a big step in this area, developing promising tools such as metatranscriptomic, metaproteomic or metametabolomic [15]. This new passion for integration will be able to evaluate our connection as living beings with our environment through our biological evolution from primal organisms to organized microbiomes [16]. This is how biological research accesses an ecosystem approach that will define us as symbiotic organisms beyond the isolated study of processes.

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