Existing and advancing trends in -omics development for the study of complex biological interactions in different organisms

International Centre for Genetic Engineering and Biotechnology

Omics technologies and human health

In recent times, -omics technologies refer to the study of biological systems at the molecular level. The reason why they are called "-omics" is because they include different types of technologies, namely genomics, transcriptomics, proteomics, and, more recently, metabolomics. Taken together, these technologies have the potential to revolutionize human health by providing new insights into the underlying causes of diseases, facilitating the development of personalized medicine, and enabling the discovery of new drugs and therapies [1].

Briefly, *genomics* is the study of the complete set of DNA sequences in an organism, including genes, regulatory elements, and non-coding DNA. Advances in *genomics* have led to many advances in different fields both at the basic and the applied level. In basic science, for example, genomics has revolutionized our understanding of the evolution of life on earth and the relationship between different organisms. Most importantly, at the level of human health the ability to sequence individual genomes has allowed the identification of genetic variants associated with various diseases, such as cancer, cardiovascular disease, and neurodegenerative disorders. An offshoot of *transcriptomics* is represented by *epigenomics* that studies the modification to a cell's DNA that affect gene expression without altering the DNA sequence.

Following on *genomics*, the development of *transcriptomics* has allowed the study of all the RNA molecules produced by a biological system. In all organisms, including humans, the information stored in DNA before being transformed in proteins must be "mediated" by a messenger molecule known as RNA. Before RNA can be translated into proteins, it can undergo many modifications that can change this information to allow specific developmental and metabolic pathways that are essential to form complex organisms (such as the human body with its many different tissues and organs). By analysing the RNA produced in different cells, *transcriptomics* can provide insights into the expression of genes, their regulation, and the functions of different RNA molecules.

Once proteins are produced by RNA molecules, the introduction of *proteomics* involves the study of all the proteins in a biological system. This type of approach is made necessary because proteins can also be modified by many hundred post-translational modifications that include phosphorylation, glycosylation, etc. All these modifications can substantially affect the function, half-life, and localisation of proteins within a cell. By analysing many of these modifications, *proteomics* can provide insights into the functions of proteins, their interactions with other proteins, and how they are regulated. As with *genomics* and *transcriptomics*, proteomic approaches have the potential to lead to a better understanding of disease and the development of new therapies.

Finally, a more recent approach has been the development of sophisticated experimental approaches based on mass-spectrometry analyses that are dedicated to the identification of small metabolites in easily accessible bodily fluids (such as blood, urine, but also sweat and tears). This approach, known as *metabolomics* is the study of all the small molecules (metabolites) in a biological system. Metabolites play a critical role in many biological processes, and changes in metabolite levels can be indicative of disease states. Therefore, like all the three previous approaches, *metabolomics* has the potential to lead to the development of new diagnostic tools and therapies for diseases such as diabetes and cancer.

In conclusion, -omics technologies have the potential to transform the way we diagnose, treat, and prevent diseases, leading to improved human health outcomes. Of course, there are also significant ethical, legal, and social implications associated with the use of these technologies, and it is important to consider these factors as well. Nonetheless, a few recent actions/lessons have clearly shown their usefulness at the international level. For example, during the Covid emergency, -omics studies have been invaluable to better understand the response of the human immune system to the disease, the different response of individuals to vaccines, and to keep track and identify variants of the virus [2,3]. In addition to international emergencies like a global pandemic, omics studies have acquired great relevance at the regional/local level by helping to revolutionize the study of specific diseases, such as malaria. Historically, the sequence of the pathogen for malaria, *Plasmodium falciparum*, was first published in 2002. Since then, omics technologies have allowed to greatly expand on this first achievement by sequencing many strains of the parasite in many different locations in affected countries. As a result, we have now gained great insights in the evolution and biology of this parasite that will greatly helped in the search for a cure for this disease [4].

As can be ascertained from the above such technologies can impact on multiple levels of human health, ranging from disease prediction and prevention, diagnosis, and therapy. These cut to the heart of SDG3 of Good Health and Well Being. However, these technologies are 'state-of-the-art' and it is imperative that access to such technology, through appropriate capacity enhancement and education (SDG4) ensures no one is left behind (SDG10). Here ICGEB plays a fundamental role to transfer these innovative skills to scientists and researchers in its member countries, mainly located in the Global South. As should also be apparent these technologies are interdisciplinary – and that in turn involves networks and collaborations, not only between scientists but also between countries – thereby ensuring a critical role for SDG17.

Omics and plant microbiomes

Like most living multicellular organisms, plants also host a very large variety of microbes in their natural environments, the totality of plant associated microbes is called the plant microbiome. Most of the microbial members of the microbiome have a direct or indirect effect on plants (positive or negative) hence the recruitment and maintenance of a healthy microbiome is crucial for plant growth. Plants create associations with microorganisms mainly at the root level in the rhizosphere which is the nearest soil area to the roots that is greatly affected by plant exudates. The rhizosphere microbiome provides a series of beneficial outcomes related to plant health and growth. This microbiome is recruited from bulk soil and a small proportion of the microbes in the rhizosphere enter the plant and establish themselves in the root endosphere and some then move to other plant compartments. The phyllosphere is the other major plant compartment located above the ground stem and leaf surfaces; its microbiome plays key roles in abiotic and biotic stress tolerance. Bulk soil possesses the most biodiverse microbiome hence plants have access to a large and richest variety of microorganisms and the plant microbiome is now considered as an external organ of plants. Unraveling plant-microbe interactions is a now recognized as a critical component in plant health as well as providing opportunities to harness this information to devise alternative applications/solutions for a more sustainable agriculture. Omics technologies allows to explore the associated mutually beneficial aspects of plant-microbe interactions such as plant growth promotion, nitrogen fixation, stress suppressions in crops as well as provides better insights on metabolic interactions between microbes and plants.

In this way, omics technologies provide a unique opportunity to study via a culture-independent molecular techniques for the deciphering the diversity of microbes in the various plant microenvironments and to gather more knowledge related to the molecular basis of the plant-microbe associations. Next-generation-sequencing (NGS) technologies (genomics and transcriptomics) is currently the most used omics in plant microbiome studies and allows the profiling of the microbial population giving an understanding of the structure of the community and phylogenetic variations as well as understanding the key biological and environmental conditions that shape its configuration. Entire plant microbiomes can be analysed via the extraction of DNA/RNA and either via the amplification of marker taxonomy genes (eg 16S rRNA gene profiling) or via metagenomic DNA or RNA sequencing, providing exhaustive information on the phylogenetic and functional aspects/identity of the microbiome. NGS technologies in plant microbiomes will allow the harnessing of the microbial members since this information can then be used via microbial-culturing-base studies in order to develop microbially-based products for a more sustainable agriculture.

Proteomics approaches involves liquid chromatography and tandem mass spectrometry techniques are can used to study plant-pathogen as well as plant-beneficial microbe interactions. They allow protein identification and their changes in plant-microbe lifestyles revealing a variety of microbial proteins in the environment using semi-quantitative methodologies. Metabolomics is also a novel technique for studying plant-microbe interactions which has some limitations mainly due to the lack of public metabolite reference databases however in the near future will likely also play a major role in deciphering plan-microbiome interactions and on how we can use this information to improve plant health and develop a more sustainable agriculture.

As can be ascertained from the **above such technologies can impact on multiple levels of agricultural industry, ranging from disease prediction and prevention, diagnosis, treatment through environmentally friendly biopesticides and bio-fertilisers**. These all have a tremendous impact on the attainment of SDG2- Zero Hunger, whilst at the same time meeting the challenges of SDG13 and SDG15. However, these technologies are 'state-of-the-art' and it is imperative that access to such technology, through appropriate capacity enhancement and education (SDG4) ensures no one is left behind (SDG10). As should also be apparent these technologies are interdisciplinary – and that in turn involves networks and collaborations, not only between scientists but also between countries – thereby ensuring a critical role for SDG17.

The ICGEB experience and lessons learnt/messages for policy makers

For many years, ICGEB (www.icgeb.org) has allowed member countries to access ways for integrating multi-omics research. The instrumentation and various groups in ICGEB have the capability of helping researchers/clinicians in member countries to generate, manage, and understand genomics data, through sequencing, bioinformatics analysis, proteomics, and high-throughput screening services. In addition, thanks to their in-house labs, ICGEB can provide interpretive collaborations and training of researchers. Of course, applying single- or multi-omics approaches to international, regional, or national level comes with many different challenges. First, it must be taken in consideration that all -omics approaches generate a huge quantity of data that needs to be correctly integrated. This requires special techniques based on machine learning and big data because even for a single omics approaches it is important for data to be correctly annotated, stored, and interpreted. These requirements for good data management become even more important when trying to integrate multi-omics approaches, raising the need of highly trained multidisciplinary teams where, in addition to correct data management, considerable experience is also required in information technology programming and artificial intelligence pipeline development for integrative database construction [5].

References

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