Popular article

MULTI –OMICS APPROACHES

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Introduction

Our understanding that the gene function is very limited to 30%-40% open read frames without a common function is taught by the ability to sequence whole genomes (Dunn, 2008). Assured biomarkers can be useful for prediction of disease progression or reaction to therapy has also increased, of specific diagnostic markers for mRNA, proteins and metabolites. There has been a greater understanding of metabolism in many biological systems. An initial metabolomics, a cell or devices that have been described as a functional genomic tool that can be used to evaluate all metabolites (Fiehn, 2002). However, in the midst of big progresses we are still far from getting full coverage of all metabolites. Many data were created with metabolomic technologies in the last decade (Trivedi, et al. 2017). More than 20 years ago, "metabolomics" was introduced and since then computational platforms and pipelines for data processing have improved impressively. (Pinu, et al. 2018).

Metagenomics: It is a research technique and a field comprising many related approaches and methods. It is the study of variation of species in a complex microbial sample. Meta uses computational methods to maximize understanding of the genetic composition and activities among communities. The new science aims at a collective understanding of biology, transcending each human organism from one gene to the next and how genes affect one another's work to serve the functioning of one another. (Kasture, 2012). Metagenomics has grown as a powerful instrument to research microbial communities irrespective of the ability of member species to be cultivated by traditional insulation in the laboratory. It has provided the chance to describe microbial diversity in the ecosystem because many of them have not yet been cultivated. Using this it is possible to study microbial communities by sequencing the gene of choice or the whole genome or transcriptome without the need for culturing. Metagenomics are also defined as environmental and communal genomics that include genomic analyses of microorganisms by cloning DNA in the majority of environments microorganisms (Nazir, 2016). Metagenomics refers to genomic DNA extraction from the population to pool all genomes in the community. Genomes are typically extracted from the environment, broken and cloned into the organism by their replicable plasmid. Organisms are then cultivated to establish metagenomic libraries and then analysed by the sequencing of DNA.

Application of metagenome: For the large demand of new enzymes and biocatalysts, metagenomics has proven strong. Metagenomics is used to generate cellulases, lipases, xylanases, amylases, proteases and various other industrial enzymes.

1. Metagenomic plays important role in identification of novel antibiotics and compounds. One of the richest sources of new antibiotics may be the metagenomic. For example antibiotics Turbomycin A and B were isolated from a metagenomic Library of Soil Microbial DNA. In clinical or preclinical studies on the treatment of various types of cancers, over 30 compounds derived from marine microbes such as didemnin B (AplidineTM) and thiocoraline are available. The soil-metagenome gene used to manufacture indirubin displayed antibacterial activity. (National Research Council Report).
2. Subsequent to many industrial methods, biosurfactants are potentially substitutes for synthetic surfactants such as lubrication, watering, calming, dying, emulsion making, dispersion stabilisation, foaming, foaming prevention as well as food, biomedical and medicinal, bio-remedying and biomedical sites polluted by organic or inorganic contamination.
3. DNA libraries of petroleum-contaminated samples (silver, water, etc.) were made from Metagenomics and clones generated by biological factors were subsequently screened. Scientists have identified two bacteria (A-1 and B-1) that have been isolated on oil-L-agar plates with large emulsified halos around their colonies. The same biosurfactant, surfactin, was developed from these bacteria.
4. The metagenomic approach identifies and elucidates new genes and pathway lines in less well studied environments and leads to a wider perspective in petroleum reservoirs on hydrocarbon degradation processes. Using the feature guided metagenomic method, new functional metabolic pathways with aromatic compound biodegradation were obtained from a petroleum reservoir in a metagenomic library. In sludge samples from a petroleum refinement wastewater systems, researchers classify genes and metabolic pathways linked to degradation of phenol and other aromatic compounds with a metageomic approach (www.ncbi.nlm.nih.gov/books).

Metaproteomics: The metaproteomics of the different proteins present in the micrgrobe population include the recognition, function and expression. The principles of metaproteomics are supported by proteomics techniques like the 2D gel electrophoresis to classify proteins and peptides in a specific microbial culture. Mass spectrometry used to desorbid and ionise proteins by means of a gas on the liquid medium. For protein recognition and separation with TOF, MALDI (Matrix Assisted Laser Desorption/Ionization) is used to deliver best results. When HPLC and LC are used for peptides and proteins with computing instruments to sequent the peptides and proteins, the metaproteomics approaches are advanced (Raza and Ameen, 2017).

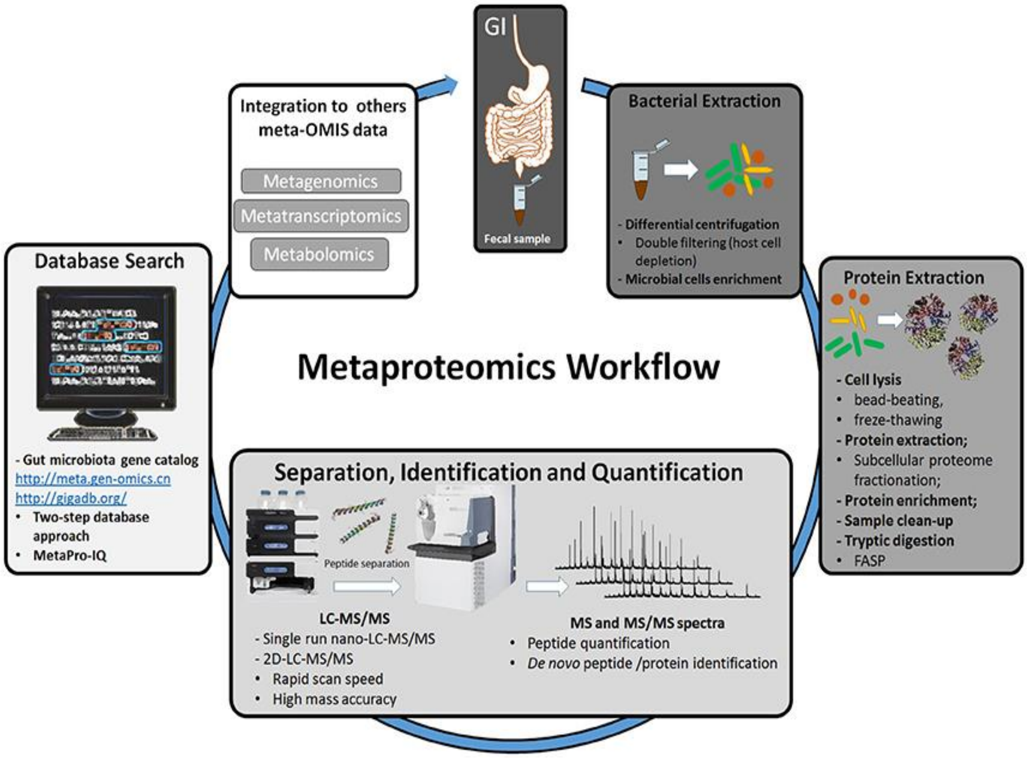

Fig. Metaproteomics Workflow

Metaproteomics workflow: Figure Representation of the faecal sample collected from the gut metaproteomically from a method of bacterial extraction accompanied by microbial protein extraction and enrichment, protein and peptide separation, identification and quantification, and genome database MS/MS scan. FASP; filtered-aided sample preparation **(**Bernardo, et al. 2017**).**

Metabolomics: Metabolomics refers to a systematic recognition and quantification of the biological system's (Cell, Tissue, Organ, biological Fluid or Organism's) small molecule metabolic products (metabolome) at a certain point in time. The most frequently used techniques for profiling metaboloma are mass spectrometry and NMR spectroscopy. A small molecule (or metabolite) is a low molecular weight organic compound, usually involved in a biological process as a substrate or product (Beale, et al. 2018). Metabolomics typically studies small molecules within the 50-1500 daltons mass range (Da). It needs research techniques like chromatography, molecular and mass spectrometry, along with multivariate analytical methods for data analysis. For the purpose study of the targeted compounds and the metabolic profiling, the main techniques include gas chromatography (GC) (NMR). These approaches are based on chromatographic separation, often linked to well-developed analysis calibrations.

As a broad application in the area of drug discovery and drug production, the emerging field of metabolomics has been extremely significant in recent years. Metabolomics is used to diagnose disease in a rapid medical diagnosis (Burton and Ma, 2019). The conventional biochemical tests are currently used to calculate individual metabolite levels to classify the state of disease (e.g. the blood-glucose level in the case of diabetes) (Savolainen, et al. 2017).

Metabolomics gives hundreds of metabolites the possibility of rapid detection, so that certain conditions can be detected far sooner. It has proven to be a crucial method for drug discovery and development with recent progress in the field of metabolomics (Cui, et al. 2018). Metabolomics can be used for developing herbicides and pesticides in the agricultural/chemical industry. Metabolomics may potentially be an effective tool that tracks and enhances food quality and food processing and quality control, or in plant breeding for improved crops and in the production of novel foods, since it is increasingly important for health and safety aspects of our foodstuffs. (Chong, et al. 2019).

Conclusion

There has been importance of functional analysis. These include studies on gene expression and protein (proteomics) and recently the network of metabolites (transcriptomics) (metabolomics). We believe that metabolomics can be used in large populations very effectively to treat biotic and abiotic stress in animals, plants or microbials, since this method usually offers less feedback and knowledge about what metabolic disruption externally affects in the field.

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