



Review

Foodomics in microbial safety

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ARTICLE INFO

Keywords:

Biomarker
Cellular marker
Food analysis
Foodomics
Food pathogen
Food safety
Microbial contamination
Microbial proteomics
Microbial safety
Toxins

ABSTRACT

With traditional methods of food analysis, foodomics offers considerable opportunities to assess production, delivery and monitoring of the quality and the safety of food. Omics analyses of food pathogens, and of food that is contaminated with microbial agents and toxins provide reliable information about microbial activities during the infection, the outbreak of disease and the recovery period. Omics methods are effective tools for identifying cellular markers for the adaptive behavior of pathogenic microorganisms under different stress conditions and markers for microbial contamination of food.

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1. Introduction

Microorganisms are essential for the function of the digestive tract of humans and animals, and, for millennia, they have been used by human kind as necessary tools for fermentation processes in food technology and biotechnology [1]. There are also more than 250 microbial pathogens known to cause food-borne illnesses. New risks are being encountered because of changing characteristics of the relevant microorganisms and food-production methodologies, and changes in the environment and ecology, and the increase in the global trade of foodstuffs. In addition, demands on food safety increase steadily. Due to the nature of both food pathogens and our food chain, measures to ensure food safety have

to be implemented on a global scale, necessitating also a general approach to this important topic [2]. The number of outbreaks of illness caused by food pathogens was recently reported as rising in some industrialized countries. There is also a shift from the traditional problems with food from mostly animal origin (e.g., meat, eggs, and milk products) to food of plant origin, shellfish, and traditional fermented food products. In recent years, numerous incidents have occurred in contamination of fresh and processed food with foodborne pathogens [3].

Proteomics, peptidomics and metabolomics techniques offer considerable opportunities to assess animal and plant health and production, and to monitor the quality and the safety of food of animal and plant origin. Some of these methods and the strategies for their use are listed in Table 1.

Genome, proteome, lipidome and metabolome analyses of pathogens and their metabolites in contaminated food provide reliable information about their activities during infection, out-

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breaks of disease and healing periods. Importantly, functionally relevant proteins and products of metabolism are identified in order to trace microbial infection, so *in-vivo* proteome and metabolome data can help to guide further functional analysis efficiently [4–6].

Technical shortcomings in the past limited quantification, identification of post-translational modifications (PTMs), coverage of secreted and low-abundance proteins, and identification of low concentrations of microbial metabolites in foodstuffs. New omics methods introduced into food analysis, so called foodomics that includes proteomics, peptidomics, glycomics and metabolomics,

together with already established genomic methods, are emerging to overcome most of these limitations and challenges. This will further improve *in-vivo* investigations and enhance the value of these techniques as an important resource to investigate and to combat infectious diseases [4–6]. This perspective brings the opportunity to develop new targets in order to ensure food safety that is important for human health and for agriculture, food processing and food storage. Ensuring food safety in the future will require new methods for identification, monitoring and assessing food-borne hazards during production, storage, delivery and consumption.

Table 1

Some omics data on-line repositories. {Modified according to [53], with permission} *

Data types	Online resource	Description	URL
Genomics	Genomes OnLine Database (GOLD)	Repository of completed and ongoing genome projects	http://www.genomesonline.org
	Microbial Genome Database (MBGD)	MBGD is a database for comparative analysis of completely sequenced microbial genomes (ortholog identification, paralog clustering, motif analysis and gene order comparison)	http://mbgd.genome.ad.jp/
	National Microbial Pathogen Data Resource (NMPDR)	The NMPDR provided curated annotations in an environment for comparative analysis of genomes and biological subsystems, with an emphasis on the food-borne pathogens	http://www.nmpdr.org/FIG/wiki/view.cgi
Transcriptomics	Gene Expression Omnibus (GEO)	Microarray and SAGE-based genome-wide expression profiles	http://www.ncbi.nlm.nih.gov/geo
	Stanford Microarray Database (SMD)	Microarray-based genome-wide expression data	http://smd.princeton.edu/
	ArrayExpress -functional genomics data	Functional genomics experiments include gene expression data from microarray and high throughput sequencing studies	http://www.ebi.ac.uk/arrayexpress/
	ExpASY – Bioinformatics Resource Portal	Links to transcriptomics	http://www.expasy.org/transcriptomics
Proteomics	World-2DPAGE	Links to 2D-PAGE data	http://us.expasy.org/ch2d/2d-index.html
	ExpASY – Bioinformatics Resource Portal	Link to protein sequences and identification	http://www.expasy.org/proteomics/protein_sequences_and_identification
	ExpASY – Bioinformatics Resource Portal	Links to mass spectrometry and 2-DE data	http://www.expasy.org/proteomics/mass_spectrometry_and_2-DE_data
	BIOBASE	BKL PROTEOME™ is a database and data analysis platform containing manually curated details from the PubMed literature in a highly structured and easily searchable format	http://www.proteinscience.com/databases.htm
	PRIDE – Proteomics Identifications Database	The PRIDE Proteomics IDentifications database is a centralized, standards compliant, public data repository for proteomics data, including protein and peptide identifications, post-translational modifications and supporting spectral evidence	http://www.ebi.ac.uk/pride/
Metabolomics	MetaCyc	MetaCyc is a database of nonredundant, experimentally elucidated metabolic pathways	http://metacyc.org/
	The Molecular Ancestry Network (MANET)	MANET database traces evolution of protein architecture onto biomolecular networks	http://www.manet.uiuc.edu/
	Kyoto Encyclopedia of Genes and Genomes (KEGG)	KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially largescale molecular datasets generated by genome sequencing and other highthroughput experimental technologie	http://www.genome.jp/kegg/pathway.html
	Metabolite and Tandem MS database (METLIN)	The METLIN Metabolite Database is a repository of metabolite information as well as tandem mass spectrometry data	http://metlin.scripps.edu/index.php
Lipidomics	Lipid Metabolites and Pathways Strategy (LIPID MAPS)	Genome-scale lipids database	http://www.lipidmaps.org
	The official database of Japanese Conference on the Biochemistry of Lipids (JCBL)	Lipid class database	http://www.lipidbank.jp/
	Avanti,Polar Lipids,Inc.	Services in research and pharmaceutical scientists with the highest quality phospholipids, sphingolipids and sterols	http://avantilipids.com
	The AOCS Lipid Library	The AOCS Lipid Library	http://lipidlibrary.aocs.org/index.html
	Cyberlipid LipidHome	Lipid databases and encyclopedia “LipidHome” theoretically generate lipidc molecules and useful metadata	http://www.cyberlipid.org http://www.ebi.ac.uk/apweiler-srv/lipidhome

* This table presents some of the databases that store and distribute genome-scale omics data sets through publicly accessible Web sites. Some omics technologies do not yet have associated data-dissemination resources such as glycomics and fluxomics, and are therefore not included in this table. This table does not represent all publicly available omics data resources, but, rather, provides a reasonably broad sample of the data that are readily accessible to researchers today.

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