

MiMeDB: The Human Microbial Metabolome Database

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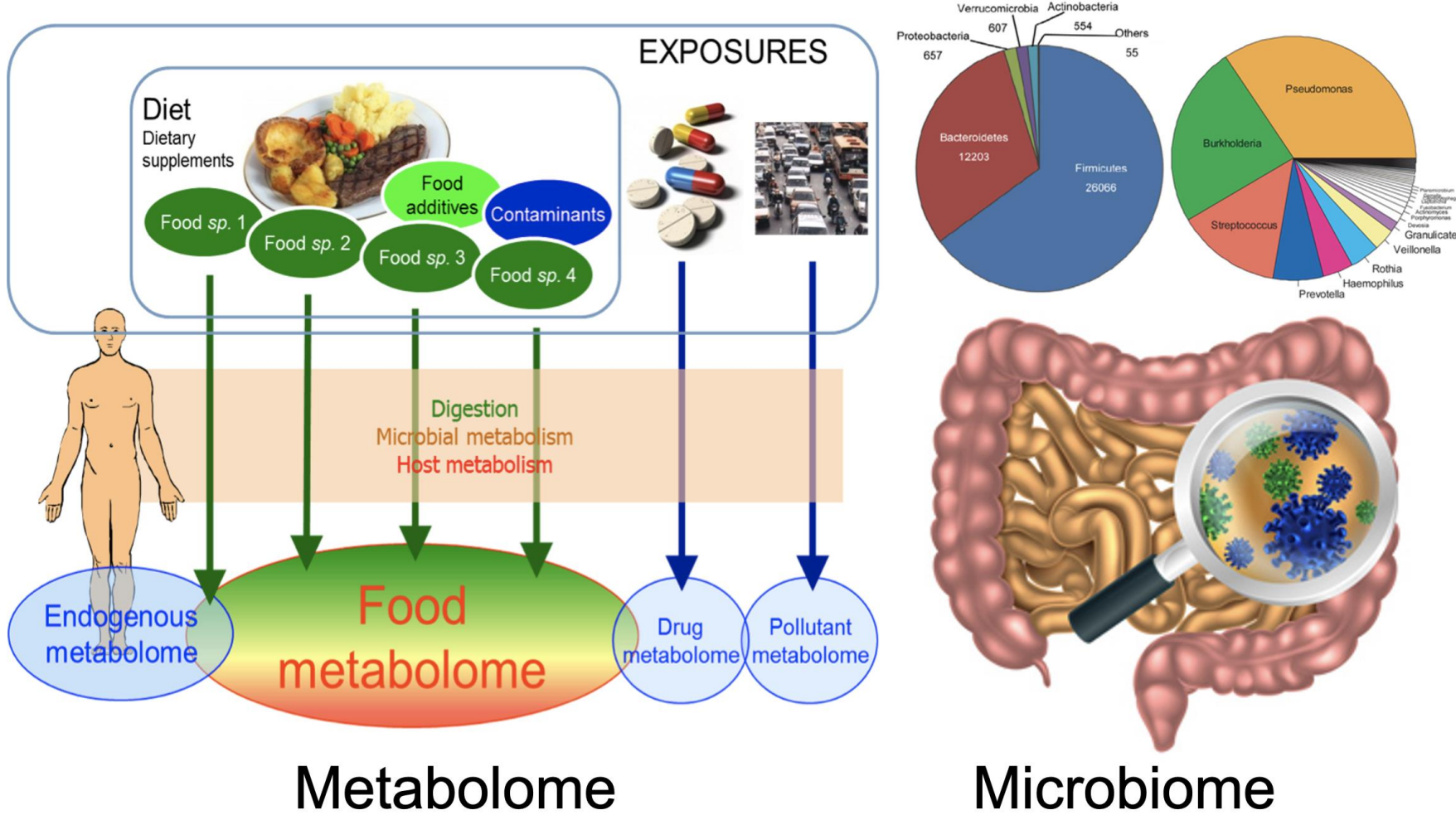
Abstract: The Human Microbial Metabolome DataBase or MiMeDB (<https://mimedb.org>) is a comprehensive, multi-omic, microbiome resource that connects: 1) microbes to microbial genomes; 2) microbial genomes to microbial metabolites; 3) microbial metabolites to the human exposome; and 4) all of these “omes” to human health. MiMeDB was established to consolidate the growing body of data connecting the human microbiome and the chemicals it produces to both health and disease. MiMeDB contains detailed taxonomic, microbiological and body-site location data on most known human microbes (bacteria and fungi). This microbial data is linked to extensive genomic and proteomic sequence data that is closely coupled to colourful interactive chromosomal maps. The database also houses detailed information about all the known metabolites generated by these microbes, their structural, chemical and spectral properties, the reactions and enzymes responsible for these metabolites and the primary exposome sources (food, drug, cosmetic, pollutant, etc.) that ultimately lead to the observed microbial metabolites in humans. Additional, extensively referenced data about the known or presumptive health effects, measured biosample concentrations and human protein targets for these compounds is provided. All of this information is housed in richly annotated, highly interactive, visually pleasing database that has been designed to be easy to search, easy to browse and easy to navigate. Currently MiMeDB contains data on 626 health effects or bioactivities, 1,904 microbes, 3,112 references, 22,054 reactions, 24,254 metabolites or exposure chemicals, 648,861 MS and NMR spectra, 6.4 million genes and 7.6 billion DNA bases. We believe that MiMeDB represents the kind of integrated, multi-omic or systems biology database that is needed to enable comprehensive multi-omic integration.

Why This Database?

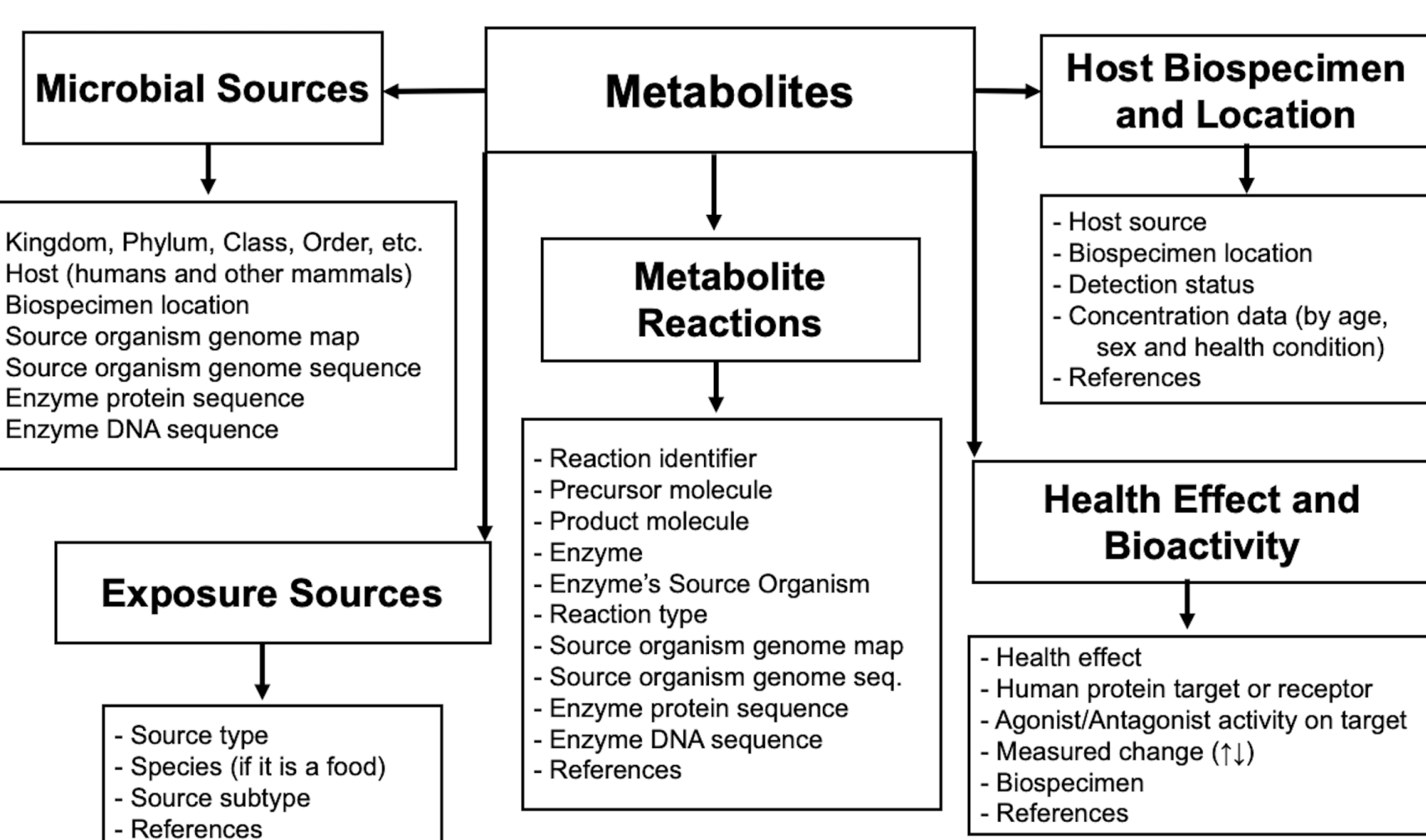
Over the past decade, many significant associations have been found between human gut microflora and gastrointestinal disorders, obesity, mood and immunity. While most human microbiome studies continue to focus on connecting health outcomes to measures of microbial taxonomy (such as microbe types or measures of microbial diversity), there is increasing awareness that it's not the microbes themselves that lead to specific health effects, it's the chemicals they produce. It was because of this fact that we decided to create MiMeDB – the Human Microbial Metabolome DataBase.

MiMeDB is designed to be a fully integrated multi-omic database that links the human microbial (meta)genome, proteome and metabolome to the human exposome – and human health. Our goal in creating MiMeDB was to create a resource that researchers with genomic, proteomic, metabolomic or exposomic data could use to query and interactively explore, visualize and interpret their data with other known multi-omic data on the human microbiome. In developing MiMeDB, we attempted to bring many of the best features of other databases such as VMH, HMDB, KEGG, GenBank, UniProt, BacMap, FooDB and HMDB, together into a single resource. These data have then been reformatted and integrated into a web-friendly database that allows users to perform sophisticated queries and interactive visualizations.

The Microbiome, Diet & The Metabolome Are Closely Linked



MiMeDB Design



MiMeDB – Home Page



<https://mimedb.org>

MiMeDB – Metabolite Page

MiMeDB – Reactions

MiMeDB – Pathways

MiMeDB – Food Sources

MiMeDB – Host Source

MiMeDB – Health Effects

Conclusion

MiMeDB represents one of the most comprehensive, interconnected, multi-omic databases ever constructed. Currently MiMeDB contains data on 626 health effects or bioactivities, 1,904 microbes, 3,112 references, 22,054 reactions, 24,254 metabolites or exposure chemicals, 648,861 MS and NMR spectra, 6.4 million genes and 7.6 billion DNA bases. Overall, we believe MiMeDB represents an important first step in the path to providing the integrated, multi-omic resources needed to advance their understanding of the human microbiome, the human microbial metabolome, the human exposome and their combined impacts on human health and disease.

Acknowledgements

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