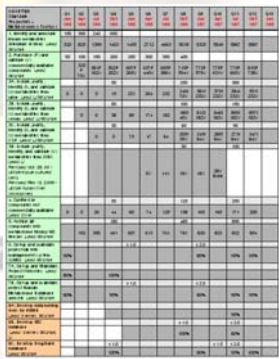


Introduction

The primary objective of the Human Metabolome Project (HMP) is to identify and quantify all major (>1 μM) endogenous and exogenous metabolites found in the human body. As secondary objectives, the HMP also maintains a number of internationally important databases and chemical libraries including the Human Metabolome Database (HMDB), DrugBank, the Food Component Database (FooDB), and the Human Metabolome Library (HML), a set of over 850 authentic metabolite standards. Just as GenBank has served as a foundation to modern genomic research, the intent of the HMDB and HML is to serve as a foundation to future research in metabolomics, systems biology, and clinical chemistry. The determination of the human metabolome and the assembly of the HMDB involve both "backfilling" via computer-aided text mining and experimental measurements of appropriate clinical samples (blood, CSF, urine, and liver microsomes) using NMR, GC-MS, FT-MS, MS-MS, and HPLC techniques. With the completion of this project, further developments and funding are being considered with the application of this new knowledgebase to healthcare, agriculture, nutrition, and food production.

Progress to Date

The HMP is approaching the end of its mandate and is set to finish by March 31, 2008. The project is ahead in nearly all of its milestones and is now wrapping up its efforts in metabolite isolation and identification.



HMP Metrics to Date

- ✦ 2916 endogenous human metabolites in the HMDB (312 exogenous)
- ✦ >4700 drug entries in DrugBank
- ✦ 1932 food additives in FooDB (eventually ~3500)
- ✦ 810 compounds acquired
- ✦ 738 compounds validated (91%)
- ✦ 200 compounds synthesized
- ✦ 232 compounds identified in urine
- ✦ 182 compounds identified in serum
- ✦ 84 compounds identified in CSF and 28 in microsomes
- ✦ 43 metabolomics SOPs
- ✦ Fully functional MetaboLIMS (Laboratory Information Management System)

HMP Key Deliverables

- ✦ Core infrastructure (NMR, FT-MS, QqQ-MS, GC-MS, UPLC, HPLC) for metabolomic analysis
- ✦ Clinical sample acquisition pipeline (>3600 clinical samples to date)
- ✦ Extensive network (>20) of international collaborators
- ✦ Infrastructure for sample acquisition, isolation, and synthesis (dedicated organic synthetic lab)
- ✦ Web-accessible metabolite databases (HMDB, DrugBank, FooDB, and NMR/MS Identification)
- ✦ Analytical software (MSfind, NMRfind, BioSpider, and PolySearch)
- ✦ Compound repository (HML)
- ✦ SOPs, Laboratory Information Management System (MetaboLIMS)

Future Plans

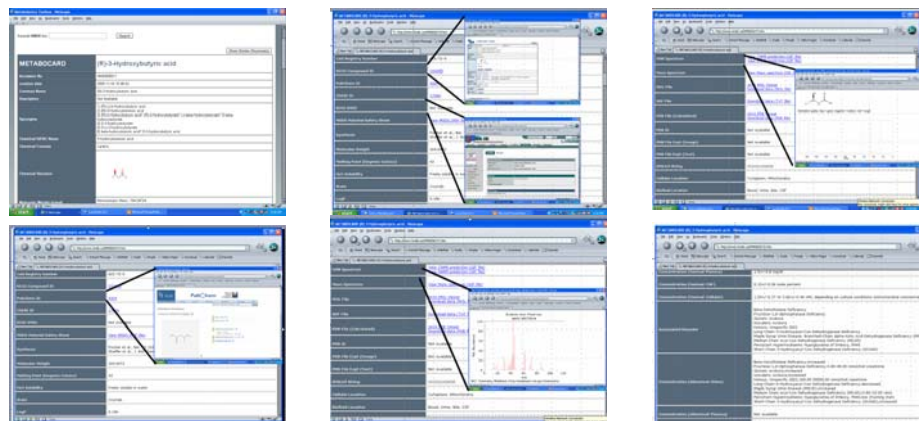
During the remaining weeks of the project, we would like to complete the annotation of close to 3000 metabolites in the HMDB. We also need to experimentally validate a number of compounds from the various biofluids (CSF, blood, and urine). It is also expected that almost 900 compounds will be fully validated and made publicly available through the HML. The HMDB, FooDB, and DrugBank are freely accessible web resources that are designed to assist clinicians, clinical chemists, nutritionists, pharmacists, pharmaceutical researchers, biochemists and students in all aspects of their training and research. If funding permits these databases will move from controlled, "curated" resources to archival database resources (like GenBank or the PDB) allowing public data deposition. **We need your feedback to make these resources better.**

The HMP is open to exploring opportunities for sustainability and continued collaboration. Please contact us through our Project Manager, Ian Forsythe (iforsythe@genomealberta.ca).

Human Metabolome Database

www.hmdb.ca

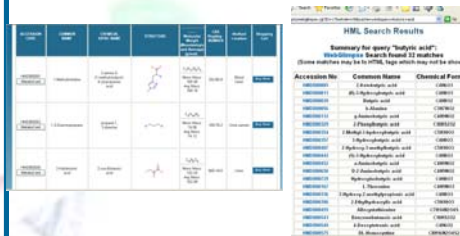
Over 2900 metabolites are annotated in "MetaboCards" consisting of over 100 fields including information on names, synonyms, descriptions, chemical formulas, SMILES strings, InChI identifiers, MW, solubility, pKa, synthesis, NMR spectra, MS spectra, biofluid location, concentrations (normal and disease), associated diseases, and all related data pertaining to the enzymes required to metabolize or catabolize the metabolite.



Human Metabolome Library

www.metabolibrary.com

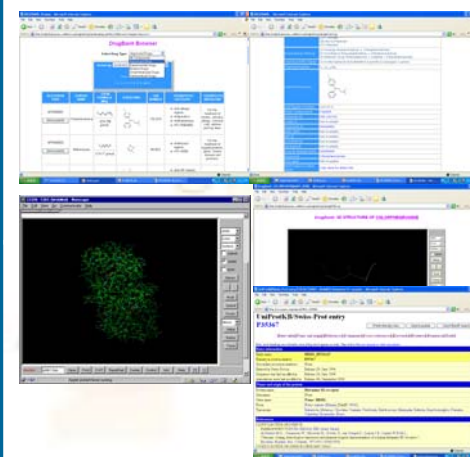
The HML is a one stop chemical resource to acquire compounds to confirm, validate or quantify suspected metabolites in tissues or biofluids. The preparation of the HML involves the purchase, synthesis, isolation/purification, and subsequent archiving of samples of known or identifiable metabolites. To date, more than 850 metabolites are available.



DrugBank

www.drugbank.ca

DrugBank is unique in that it combines detailed drug (i.e. chemical, pharmacological, and pharmaceutical) data with comprehensive drug target (i.e. sequence, structure, and pathway) information. The database contains over 4700 drug entries including 4635 small molecule drugs, 128 biotech (protein/peptide) drugs, 71 nutraceuticals, and >3200 experimental drugs. Additionally, more than 4500 protein (i.e. drug target) sequences are linked to these drug entries.



Partners

