Human Cytome Project Initiative

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Why do we need a human cytome project?

HCP-V

Resolution of Biocomplexity: bottom-up

- current vision
 - molecular biology/proteomics: elucidation of the organisation of genetic networks and protein pathways and of their contribution to cellular and organismal phenotype (Collins FS et al Nature (2002) 422:835)
 - systems biology: iterative & integrative study of biological systems in response to perturbation (C Auffray C.R.Biologics (2003) 326:879)
- problem: high complexity, long time frame with 30-40.000 genes
- examples:
 - 3D protein structure
 30 years of research do no permit to exactly predict 3D protein structures from amino acid sequences (20 amino acids)
 - pharmaceutical industry investment doubling during last 10 years provided only half as many new candidate substances than during preceeding 10 years

Resolution of Biocomplexity: top-down

- shortcut: human cytome project
 - evaluation of disease processes as nature induced differentials
 - differential screening of molecular single cell phenotypes like diseased versus healthy or differentiated versus undifferentiated
 - molecular hotspot identification by standardized relational classification
- advantage: immediate application potential
 - predictive medicine by cytomics for personalized medicine
 - identification of new drug targets using retrograde pathway modelling of molecular hotspots by systems biology
 - relevant information is collected at reduced complexity

Categories

genome genomics proteome proteomics cytome cytomics

- cytome: cellular network (cell system, organ, organism)
- cytomics: analysis of cytome heterogeneity by multiparametric single cell molecular phenotyping in combination with exhaustive bioinformatic knowledge extraction.



- top-down approach with
- cells as elementary units

single cell analysis

- differential screening of molecular cell phenotypes
-hypothesis free identification
of molecular hotspots
- predictive medicine by



cytomics

- molecular reverse engineering for pathway modelling by systems biology (3)
 - identification of new drug targets
 - multigene activation and regulation



genome proteome

as inventory of the biomolecular capacity of organism's



hypothesis driven parameter selection

Human Cytome Project

cells instead of biomolecules as elementary units

- identification of molecular hotspots by differential screening of molecular cell phenotypes e.g. diseased versus healthy single cells

medicine

predictive medicine
 by cytomics
 individualised therapy in stratified patient
 groups

drug discovery &
basic sciences
- molecular pathways by
systems biology
(reverse engineering)
- new drug targets for pharmaceutical industry

Human Cytome Project proposed milestones: medicine

- leukemia/lymphomas: stem cell transplantation versus chemo-

therapy

- rheumatoid diseases: early identification of high and low

therapy requiring patients

- allergies: detection of predisease sensitization for

asthma, neurodermitis, ekzema a.o. in

risk families for early preventive therapy

- infections: prediction of infection and disease course

in newborn, intensive care and elderly

patients to apply early preventive therapies

Human Cytome Project proposed milestones: cytome characterization

- stem cell differentiation relationally standarized description of

differentiation and cell cylce phases & cell cycle:

molecular topology of intracellular - cell proteomics:

proteins

- cell organelles: systematics of molecular organelle

function

- drug target identification: retrograde pathway modelling of molecular

hotspots

Conclusions

- 1. molecular cell phenotypes resulting from genotype and exposure can be *top-down* analyzed by single cell *flow* and *image* cytometry, using for example differential screening of diseased versus healthy cytomes.
- 2. discriminatory molecular hotspots are obtained in this way. *Reverse-engineering* of these hotspots by systems biology may be used to find *disease* inducing molecular pathways and new *drug targets*.
- 3. a human cytome project will favor the more detailed understanding of medically relevant *genome realization* mechanisms. Furthermore *patients* in everyday medicine will profit from individualized disease course *predictions* through individually tailored therapy schedules.

From Fascination to Finances

Indiana University

Dec 16, 2004

http://newsinfo.iu.edu/news/page/normal/1770.html

METACyt project:

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- metabolomics
- cytomics

Indiana University will use \$53 million Lilly Endowment grant to boost life sciences in Indiana

BLOOMINGTON, Ind. -- Indiana
University President Adam W. Herbert
announced today (Dec. 16) that the
Lilly Endowment Inc. is giving IU
Bloomington \$53 million to broaden
and intensify its life sciences research,
retain its distinguished scientists,
attract new world class scientists and
contribute to the state's economic
development by transferring
technology to new and existing life
science businesses. The grant is the
largest IUB has ever received.

These funds will be focused on metabolomics and cytomics, emerging fields that are bringing an explosion of genetic information to bear on scientists' understanding of metabolism and the inner workings of cells. The new Indiana Metabolomics and Cytomics (METACyt) Initiative will build on the foundation of genomic and proteomic research already taking place at IUB and complements the 2001 Indiana Genomics Initiative at

Human Cytome Project

further details at:

https://www.classimed.de/cytompr1.html https://www.classimed.de/concept1.html https://www.classimed.de/cellbio.html