# Nestlé Institute of Health Sciences



# Nutrition 2.0 – Molecular Phenotyping in Humans

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# World Healthcare in 2020...











## ... 1 out of 5 will be over 65

- 70% of developed countries with more 50+ than 50-
- Over 200M people aged 65+ in China
- Requires healthcare systems better adapted to needs of the elderly

## ... 3 out of 5 will die from a chronic disease

- 50M Alzheimer's patients
- 7% of the world's adult population will live with Diabetes
- More emphasis on prevention and treatment of chronic diseases
- ... 1 out of 5 will be overweight or obese
- 120M people in the US
- 20% of people under 18 year in China
- > Need to treat increasing co-morbidities such as cardiovascular diseases and diabetes

### ... Malnutrition causes 35% of disease burden in children <5 years

- Maternal and child malnutrition is the underlying cause of 3-5 million deaths
- Associated to increased susceptibility to chronic disease later in life

## ... US\$ 5 to 10 Trillion will be spent on healthcare

- More than 16% of GDP spent on healthcare
- National health expenditures in USA per capita will reach US\$ ~14'000
- Requires radical ways to contain costs and / or increase available funding

# **Scientific Platforms...**



# ...to understand the interplay between...



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Kussmann, Hager, Morine, Sonderegger, Kaput. Frontiers 2013 Kussmann, Kaput. Appl. Transl. Genomics 2014

# **NIHS 2015**

- Employees: 150
  - $\rightarrow$  61% Ph.D., 19% Master
  - → 28 nationalities
  - → Average age : 39
- Scientific Development and Interaction:
  - 9 Adjunct Lecturers/Professors PhD & Master program with 20 mandates
  - > 100 publications
  - 4 grants
- Numerous collaborations with national and international partners





# What makes us special...

## 1. Integrated omics and systems biology

Genomics, Genetics, Epigenetics, Transcriptomics, Proteomics, Lipidomics, Metabonomics, Micronutrients Meta- and omics data. Translation into Diagnostics Data acquistion  $\leftarrow \rightarrow$  processing  $\leftarrow \rightarrow$  interpretation

## 2. Natural human cell models

ViaCyte partnership for human iPSC models Encapsulation and *in vivo* differentiation

## 3. Longitudinal human studies with safe challenges

Systems view of recovery from challenge and restoration of homeostasis rather than analysis of system « at rest » (fasting) Metabolic (e.g. high fat, high glucose), cognitive and physical (endurance / resistance exercise) challenges

4. Classical « top-down » phenotyping meets molecular « bottom-up » phenotyping

## 5. We study health !

Kussmann, Hager, Morine, Sonderegger, Kaput. Frontiers 2013Nestlē Institute of Health SciencesKussmann, Kaput. Appl. Transl. Genomics 2014





# **Molecular Biomarkers – Platforms and Staff**



# Molecular Biomarkers @ NIHS: Where Genes and Environment intersect...



# **Scope : Health Areas**



# Study Levels : Clinics $\rightarrow$ Analyses $\rightarrow$ Data



# **Proteomics:** Discovery and Targeted/Validation



Nestle Institute of Health Sciences http://www.nature.com/doifinder/10.1038/nmeth.2309

# **Human Plasma Proteomics**



- Concentration range: 10-12 logs
- Abundant proteins represent > 99% of the total bulk
- Abundant tryptic peptides dominate MS analysis
- Many variants and modifications of few abundant proteins

# "Sample preparation is key and has been neglected".

Bruno Domon, EuPA 2013 7<sup>th</sup> Annual Conf. Saint-Malo, France, Oct. 2013

## "We cannot do HT without sample preparation automation but nothing is available on the market".

Roman Zubarev, EuPA 2013, 7<sup>th</sup> Annual Conf. Saint-Malo, France, Oct. 2013

Nestlē Institute of Health Sciences Dayon, Nuñez Galindo, Corthésy, Cominetti...Kussmann. J. Proteome Res. 2014 & 2015

# **Human Plasma Proteomics**



Nader Rifai, Michael A. Gillette, Steven A. Carr, Nature Biotechnology 24, 971 - 983 (2006)

- Innovative biomarkers: discovery / verification / validation
- Small to higher number of samples for discovery

Nestlē Institute of Health Sciences Dayon, Nuñez Galindo, Corthésy, Cominetti...Kussmann. J. Proteome Res. 2014 & 2015

# **Human Plasma Proteomics Workflow**



Dayon, Nuñez Galindo, Corthésy, Cominetti...Kussmann. J. Proteome Res. 2014 & 2015

# **Human CSF Proteomics Workflow**

- Automation of proteomics of human CSF
- Application to CHUV AD cohort



# NMR–/MS–based Metabonomics



## NMR

## LC-NMR

## LC-NMR/MS

Rezzi/Collino/Martin/Kochhar/Nicholson et al. J. Proteome Res. 2007 + 2012. Anal. Chem. 2009, Trends Anal. Chem. 2013Nestlē Institute of Health SciencesKussmann, Raymond, Affolter; J. Biotechnol. 2006, Curr. Opin. Biotechnol. 2008

# **Metabonomics:** Clinical Screening and Discovery

Matrices: plasma, urine, saliva, synovial fluid, feces, cells, tissues...

## **Key features**

High throughput:

5 min scan for urine, 15 min for plasma Both solid and liquid state Highly robust/reproducible: CV: 0.02% across QC samples 0.04% across instruments

## Provides information on:

- Central E metabolism
- Amino acids
- Lipids (lipoproteins)
- Glucose
- Microbial metabolites

## Provides guidance for

subsequent targeted analyses

## Metabolome coverage

(based on known metabolites):

- Urine: 209 (out of 605) compounds
- Plasma: 50 compounds
- CSF: 54 compounds Nestle Institute of Health Sciences







Da Silva, Godejohann, Martin, Collino...Franceschi, Hervonen, Spraul, Moco. Anal.Chem. 2013 Moco S, Colino S, Rezzi S, Martin FPJ. Ped. Res. 2013. Collino, Martin, Rezzi. J. Clin. Pharm. 2013 Rezzi, Collino, Goulet, Martin. Trends Anal. Chem. 2013

600 UltraSh eld

Jrine

Lipid extracts

# AGEING



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# What is ageing and how does it progress ?

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Prenatal Childhoo Infancy	d Maturi Puberty	ty Reproduction		Ageing	
Genes Epigenetics Maternal behaviours Environmental factors Family behaviour Learned behaviour Family environme E G G G G G G G G G G G G G G G G G G	s urs ent Biological factors Genes/epigenetics Fat mass / obesity Family behaviours earned behaviours	Environm Biological Poor new Previous I	ental pres ageing adaptatic maladapta	ssures Di Di ation	isease

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Collino, Martin... Moco, Franceschi, <u>Kussmann</u>, Offord Mech. Ageing Dev't 2013

# **Ageing and Nutrition**



- Role of nutritional deficiency in the development of frailty was suggested long ago. However, research in this area is only recent.
- 2%–16% of community-dwelling elderly are nutritionally deficient in protein and calories (Whitehead 1997). If mineral and vitamin deficiencies are included, malnutrition in persons older than 65 years may be 35% (Chandra 2002).
- Low energy and protein intake and low nutrients positively associate with frailty. Energy intake, serum Se, carotenoids and albumin levels are lower in frailty (Smit et al 2013). MMA: marker for available vitamin B12 (Mocchegiani 2010).
- Elderly become particularly vulnerable to compromised nutrient intakes.
   → Their diets should be nutrient-dense to ensure adequate intakes of e.g.
   n-3 fatty acids, protein, dietary fibre, B vitamins and other micronutrients such as iron, combined with low intakes of sodium.
- → Need better nutritional assessment tools for both successful diagnosis of malnutrition and development of appropriate and comprehensive treatment plans for frail (and others).



## Metabolic phenotyping reveals differences between biological and chronological age



The observed metabolic distributions suggest that chronological age differs from metabolic (biological) age

Nestlē Institute of Health Sciences Collino, Martin... Moco, Franceschi, Kussmann, Offord Mech. Ageing Dev't 2013

## Longevity (centenarians) as a model of healthy ageing

**Pvalue** 

a(\*\*\*), b(\*\*\*)

a<sup>(\*\*\*)</sup>. n/a

n/a

a (\*\*\*). b (\*\*\*)

a(\*), b(\*\*\*)

a(\*\*). b(\*\*)

a (\*\*), b (\*\*\*)

a (\*\*\*), b (\*\*\*)

a(\*\*\*). n/a

a, b<sup>(\*\*\*)</sup>

a .b(\*)

a,b(\*\*\*)

a.b(\*\*\*)

n/a

Young

22.1±2.0 (18.3.24.6)

n/a

n/a

162.3<sup>±</sup>28.4 (133-207)

71.7±32.1 (28-143)

51.8<sup>±</sup>8.7 (38-66)

89.8<sup>±</sup>51.5 (49-144)

 $0.72\pm0.4$  (0.28-2.08)

n/a

20.3±17.5 (2.70-28.2)

19.3±13.3 (4.4-46.6)

2.38±2.58 (0.80-3.80)

18.5±28.5(5.80-65.5)

n/a

Elderly

26.9±4.6 (16.7-54.7)

2.81±2.57 (0.20-28.9)

25

201.0±37.2 (5-335)

129.9±65.7 (44-530)

55.2+20.4 (20-147)

118.7±45.7 (23.8-199)

 $2.7\pm3.6(0.11-25.7)$ 

149.1±204.6 (0.01-186)

35.4±54.9 (0.28-28.2)

22.72<sup>±</sup>27 (2.3-100)

6.07±15.4 (1.5-20)

49.1<sup>±</sup>153.1 (0.1-80)

27.3<sup>±</sup>1.3 (1.3-31.0)

Our centenarians are lean, youthful-looking, energetic, independent, and have low rates of heart disease and diabetes



Centenarians appear to be capable of neutralizing/diminishing the deleterious effects of low-grade, chronic inflammation, characteristic of the aging process

Franceschi et al. 2007

# Healthy ageing involves the interaction between genes, the environment, and lifestyle factors, particularly diet

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Factor

BMI,  $kg/m^2$ 

HOMA, µU/mL

Diabetes<sup>1</sup>, n

Cholesterol, mg/dl

Triglycerides, mg/dl

HDL, mg/dl

LDL, mg/dl

CRP, mg/L

A-SAA, µg/ml

IL-6, pg/ml

IL-8, *pg/ml* 

IL-10, pg/ml

TNF-alpha, pg/ml

MMSE<sup>2</sup>

Centenarians

24.2+3.8 (13.3-31.2)

1.77±1.1 (0.20-23)

185.0±32.7 (112-264)

114.4±46.1 (60-283)

48.2<sup>±</sup>13.1 (25-99)

105.6±35.1 (75-165)

5.0±5.3 (0.28-28.2)

46.9±41.6 (7.5-225)

20.9±20.8 (6-71)

3.93±4.3 (0.6-19.9)

23.5<sup>±</sup>4.3 (0.40-113)

20.4±7.04 (1.3-30.3)

437.6±483.7 (15.5-851)

Rampelli S. et al, Aging 2013, Montoliu et al, Aging 2014, Collino et al. MAD 2014 Santoro et al. MAD 2014, Garagnani et al. Biomed research 2014, Cominetti et. al. 2014, AgroFoodTech

## **Human Longevity**

Most comprehensive genotype, microbiome, and phenotype database

	Milano **	Bologna *	Calabria ***	TOTAL	Mean Age (± std)	Male (N)	Female (N)
105+	29	33	20	82	105.51 ± 1.72	18	64
Offspring	28	22	13	63	69.83 ± 7.24	22	25
Controls	17	16	14	47	71.56 ± 8.02	26	37
TOTAL	74	71	47	192			

## NGS-based gut microbiota fingerprint



Unweighted unifrac, PCoA

Diversity analysis of gut microbiota composition resulted in significant segregation of 105+ from other groups

## Whole Genome Sequencing

	Mean	Standard deviation
Number of sequenced fragments	1,783,333,790.43	57,589,952.91
% mapped reads	92.65	0.85
Percent coverage (%) > 1 X-fold	98.16	0.76
Percent coverage (%) > 10 X-fold	97.64	0.74
Average coverage depth	110.03	2.87
# SNPs	3,605,779	31,319.02

- Developed and applied novel statistical genetic, bioinformatic, and data mining algorithms
- $\checkmark$  Genetic variants for pathogenesis, risk and protection
- $\checkmark\,$  Distribution of variants for single genes





## Sebastiano Collino, Laetitia Da Silva

# METABOLIC HEALTH

90

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# **DiOGenes**

- DiOGenes stands for Diet, Obesity, and Genes
- EU program incl. weight loss/maintenance in obese
- NIHS questions:

Can we predict success in weight loss/maintenance at baseline ? Who needs which diet to succeed ?



≈ 1'000 subjects
> 4'000 samples
> 7'000 variables
(clinical, food
diaries, behavior,
molecular)

Quantitative Multivariate Analysis





# **Proteomics and clinical center effect**





# **Proteomics and clinical variables**



# **Validation: C-Reactive Protein**

- Measured in clinics
- Measured by MS-proteomics

• Comparison of:  $log_2\left(\frac{CRP@CID3}{CRP@CID1}\right)$ 

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 Good correlation between techniques



# Variability of the proteins

- Protein variability is consistent across the time points.
- Technical variability is smaller than biological variability.
- Low-variability proteins can be used for normalization
- Complement C1r shows potential to be used as an internal protein standard in human plasma

## Protein variability in CID3 and CID1



## **Differential expression and fat mass increment relation**

- 46/183 proteins were significantly differentially expressed between timepoints
- Welch t-test on the fold change
- Multiple testing correction

Fold Change =  $\log_2 \left( \frac{\text{protein expression CID3}}{\text{protein expression CID1}} \right)$ 

- Fat mass change relation to proteins
  - Multiple proteins \_ involved
  - Large biological variability



# PAEDIATRIC METABOLIC HEALTH

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# **Juvenile Diabetes**

## Background



- How do diet, lifestyle and environment interact with genes and metabolism during childhood and adolescence ?
- How does that determine health in child- and adulthood ?

#### Earlybird Cohort:

- Longitudinal cohort study
- 300 children and their parents
- Measurement every 6 months/12 months from 5-19 years



2014

#### Describe:

2000

- Normal childhood and puberty
- Origins of childhood weight gain and IR
- Impact on long-term risks of diabetes and cardiovascular disease.

Unique longitudinal database across childhood:

- Body composition
- Dietary intake
- Clinical and metabolic status
- Energy expenditure

## Deliverables



- Establish relationships between genes, metabolism and childhood glucose metabolism
- Findings in mothers of IFG children suggest that β cell defect may be transmissible (gestational and/or genetics)
- Metabolic, anthropometric and nutritional characterization across childhood

### François-Pierre Martin

Nestle Institute of Health Sciences

Neg



## Forecasting metabolic trajectories, disease risk and childhood physiology

#### Growth curve reference





#### 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 ... days

INFANT NUTRITION

ORNELLA COMINETIT<sup>®</sup>, SEBASTIANO COLLINO, FRANCOIS-PIERRE MARTIN<sup>®</sup> "Corresponding outhoos Nestlé institute of Health Sciences SA, Melecutar Biomatiens, PPI, Innovation Park, Building H, 1015 Lausanne, Switzerland



Cominetti, Martin. Agro FOOD Industry 2014

💴 Nestlē Institute of Health Sciences Sperisen, Cominetti, Martin. Frontiers Mol. Biosci. 2015

Monitoring metabolism across childhood: biomarkers for nutritional health and disease risk management

## **KEYSTONE SYMPOSIA**

on Molecular and Cellular Biology

## Human Nutrition, Environment and Health (T1)

October 14-18, 2015 China World Hotel Beijing, China

Scientific Organizers: Martin Kussmann, Hannelore Daniel and Jacqueline Pontes Monteiro

Supported by the Bill & Melinda Gates Foundation

Global Health Travel Award Deadline: May 12, 2015 / Abstract & Scholarship Deadline: June 16, 2015 / Abstract Deadline: July 14, 2015 / Discounted Registration Deadline: August 13, 2015

	Hannon and the eat Branning		
Vijayalakshmi Varma, National Center for Toxicological Research, FDA, USA Adipogenesis and Adipocyte Response to Fructose: A Characterization Using Systems Biology Approach Aldons J. Lusis, University of California, Los Angeles, USA Animal Models for Complex Human Traits Patrick J. Stover, Cornell University, USA One-Carbon Metabolism	Juan B. Ochoa <sup>†</sup> , Nestlé HealthCare Nutrition USA, USA Personalized Clinical Nutrition for the Critically III Peter Gluckman <sup>†</sup> , University of Auckland, New Zealand Perinatal Nutrition and Maternal Health Short Talk Chosen from Abstracts Poster Session 3		
Short Talk Chosen from Abstracts	SUNDAY, OCTOBER 18		
Poster Session 1	Global Nutrition and Sustainability		
FRIDAY, OCTOBER 16	Jim Kaput, Nestlé Institute of Health Sciences, Switzerland Genetic, Cultural and Environmental Variability and Nutrient Needs		
Human Nutritional and Lifestyle Interventions Hannelore Daniel, Technische Universität München, Germany Characterizing Normal Human Metabolism Ben van Ommen, TNO, Netherlands Diet, Systems Flexibility and My Optimal Health Jacqueline Pontes Monteiro, Universidade de São Paulo, Brazil The Genomics of Micronutrient Requirements Arne Vernon Astrup, University of Copenhagen, Denmark	Zulfiqar A. Bhutta, Hospital for Sick Children, Canada Maternal and Child Nutrition: Global Challenges and Solutions Ted Bianco <sup>†</sup> , Wellcome Trust, UK Sustainable Nutrition Shawn Baker <sup>†</sup> , Bill & Melinda Gates Foundation, USA Global Nutrition Short Talk Chosen from Abstracts Meeting Wrap-Up: Outcomes and Future Directions (Organizers)		
Human Dietary Interventions to Probe Metabolic Health Short Talk(s) Chosen from Abstracts	Joint Session with Grand Challenges and Keystone Symposia		
Capturing and Monitoring Human Individuality	MONDAY, OCTOBER 19		
Speaker to be Announced Michael Snyder <sup>†</sup> , Stanford University School of Medicine, USA Longitudinal Omics in Humans Richard Weiss, Viocare, Inc, USA Self-Monitoring of Diet and Lifestyle	Departure <b>华大基天</b> BILL MELINDA GATES foundation		