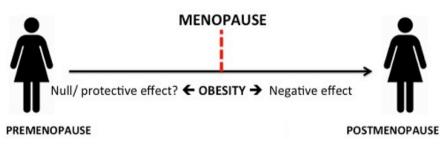


Exploiting transcriptomic data in genome scale metabolic networks: new insight into obesity

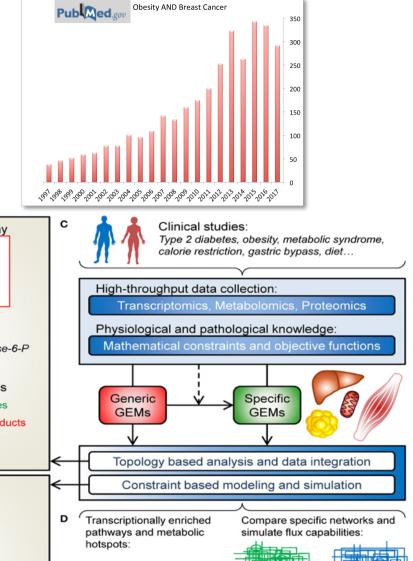
Flash poster presentation (Poster P5)

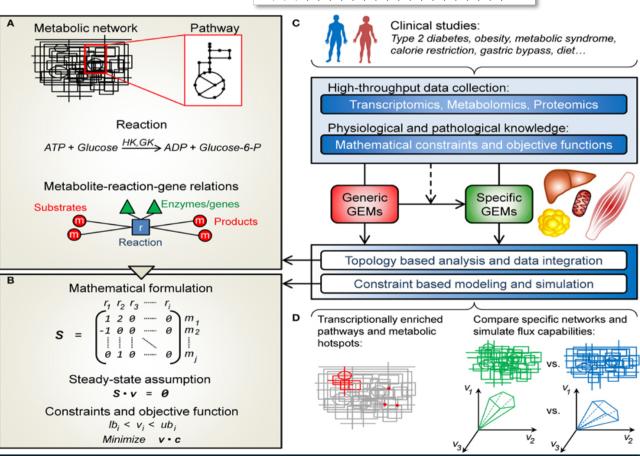


Obesity & Breast Cancer



Genome-scale Metabolic Network





Genome Scale Metabolic Model: iAdipocytes 1809 (Mardinoglu et al. 2013)

N = 90

Basal-

like

GSE78958 405 postmenopausal breast cancer samples

131 subjects BMI<25 142 subjects BMI>30

N=50

Her2

N=226

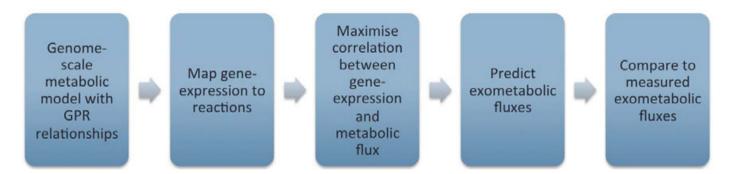
Luminal

■ Transcriptomic Dataset:

■ Integrative Method:

Improving metabolic flux predictions using absolute gene expression data

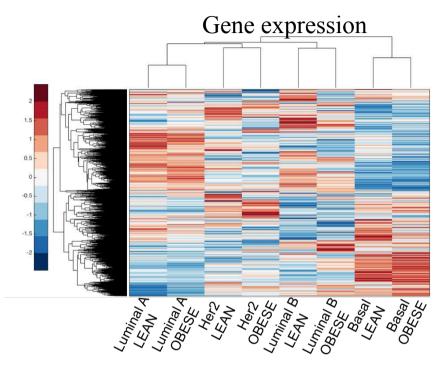
Dave Lee^{1†}, Kieran Smallbone^{1†}, Warwick B Dunn¹, Ettore Murabito¹, Catherine L Winder¹, Douglas B Kell^{1,2}, Pedro Mendes^{1,3} and Neil Swainston^{1*}



N=43

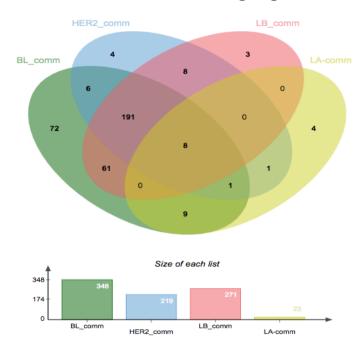
Luminal

RESULTS

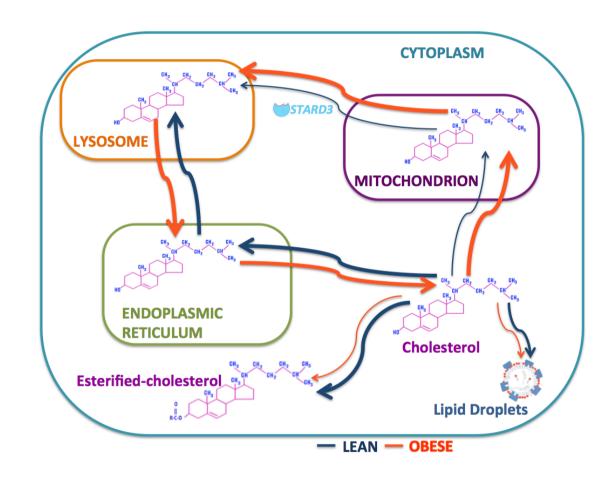


Subsystem annotation of subtype specific dysregulated reactions	
Basal-like	Her2
Transport, endoplasmic reticular	Fatty acid activation (cytosolic)
Transport, extracellular	Transport, extracellular
Pool reactions	Transport, peroxisomal
Glycerophospholipid metabolism	Transport, endoplasmic reticular
Transport, mitochondrial	LB
Terpenoid backbone biosynthesis	Glycerophospholipid metabolism
Carnitine shuttle (cytosolic)	Transport, extracellular
Carnitine shuttle (endoplasmic reticular)	Transport, mitochondrial
Beta oxidation of even-chain fatty acids (peroxisomal)	LA
Formation and hydrolysis of cholesterol esters	Transport, extracellular
Tryptophan metabolism	Transport, extracellular
Tricarboxylic acid cycle and glyoxylate/dicarboxylate metabolism	Transport, mitochondrial
Glycolysis / Gluconeogenesis	Transport, mitochondrial
Inositol phosphate metabolism	
Nucleotide metabolism	

Reactions with changing fluxes



RESULTS



In Luminal A subtype the reactions associated to cholesterol transport and esterification showed different rates between lean and obese subjects

RESULTS

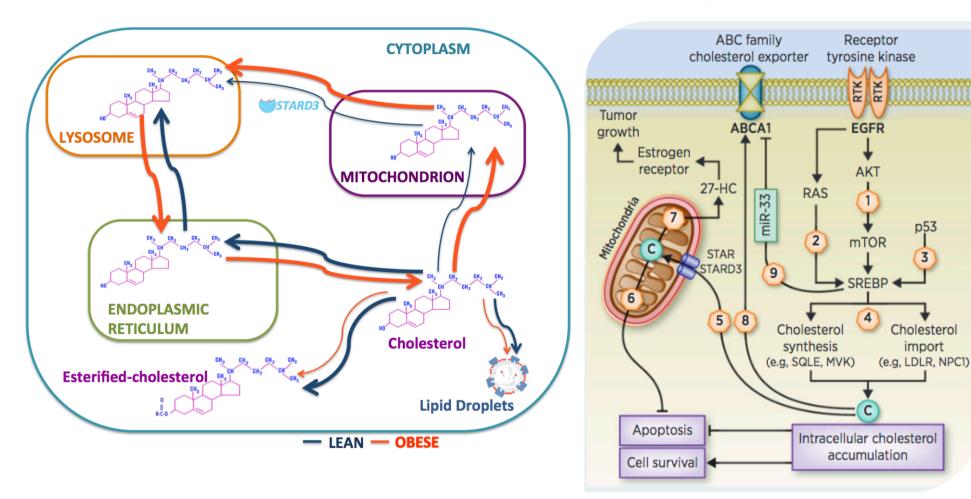
Published OnlineFirst April 5, 2016; DOI: 10.1158/0008-5472.CAN-15-2613

Canc

Cancer Research

The Role of Cholesterol in Cancer

Omer F. Kuzu¹, Mohammad A. Noory¹, and Gavin P. Robertson^{1,2,3,4,5,6,7,8}



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Mara Sangiovanni

Enrico Troiano



Conclusions

- The integration of gene expression data into the adipocyte GEM allowed the identification of reactions and associated genes dysregulated in obese cancer patients.
- The knowledge at metabolic level overcomes the limit of looking at the gene expression alone without investigating the effect on cellular mechanisms.
- Intracellular cholesterol accumulation, inferred by flux rates in LumA obese women, is suggested to play an important role in development and progression of breast cancer.
- Further investigations are needed to unravel the differences in terms of mechanisms and outcomes of the obesity-BC subtypes association.