

Module 2: From "Healthy" Obese to NASH – What Happens?

Maternal Insulin Resistance and NAFLD Development



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STOPNASH: Symposium on The Origins and Pathways of Nonalcoholic Steatohepatitis
 NASPHGAN, October 7, 2015



World-Wide Childhood Obesity Epidemic

Critical Early Life Factors affect Health Across the Lifespan




Genes Gestational Exposure Post-natal Environment

The Childhood Obesity Pipeline is Full and getting worse

Health and Wellness Center


Maternal obesity increases offspring risk for obesity and metabolic disease

Obese Mother




- ↑ Cholesterol
- ↑ Triglycerides
- ↑ Leptin
- ↑ Glucose
- ↑ Insulin
- ↑ Inflammation
- ↑ Oxidative Stress

Offspring of Obese Mother




- ↑ Cholesterol
- ↑ Triglycerides
- ↑ Leptin
- ↑ Glucose
- ↑ Insulin
- ↑ Inflammation
- ↑ Oxidative Stress
- ↑ Fat Mass at Birth
- ↑ Risk of Obesity & Metabolic Disease

Placenta of Obese Mother



- ↑ Inflammation
- ↑ Oxidative Stress
- ↑ LPL Activity
- ↑ Lipids



University of Colorado Anschutz Medical Campus

What We Don't Know!

- What are the consequences of exposure to maternal obesity during pregnancy and lactation on fetal metabolic systems and neonatal adiposity? liver, WAT, bone marrow, appetite control.
- What are the potential mediators of these effects?
Maternal Lipids, inflammation, Breast milk? Microbiome?
- Is there a role for maternal nutrition in triggering epigenetic factors leading to NASH? DNA methylation/acetylation, in early infancy.
- What are the public health consequences of exposure to maternal obesity on the childhood obesity epidemic and the evolution of pediatric NASH?

Collaborative Research Oregon National Primate Research Center, University of Colorado

Long-Term Goal:



Kevin Grove, PhD
Oregon National Primate
Research Center

- To develop a Non-Human Primate Model to study the effects of Maternal Diet, Obesity and GDM on the development of metabolic systems (liver, muscle, fat, heart, brain) in utero and the effects on infant behavior and post-natal disease pathways.



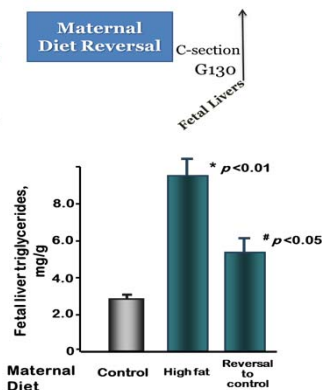
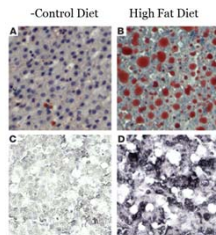
Maternal Obesity is Non-Alcoholic Fatt

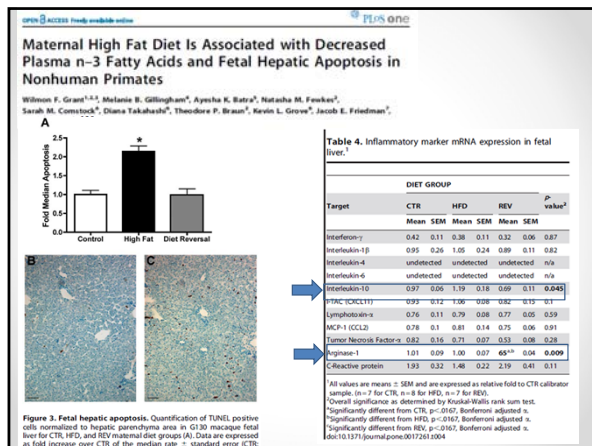
Maternal Diet Reversal

Research article
Maternal high-fat diet triggers lipotoxicity
in the fetal livers of nonhuman primates

Genette K. McCluskey¹, Jonathan M. Shalaby¹, Sarah M. Williams¹, Bernadette E. Grigoriou¹,
M. Susan Smith¹, James B. Pridemore¹, and Ronald L. Gaudel¹

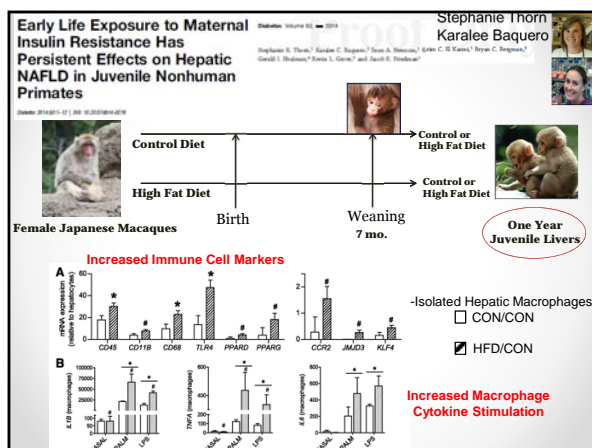
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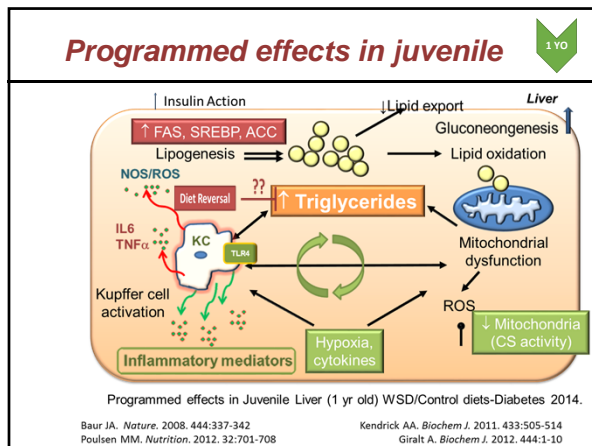


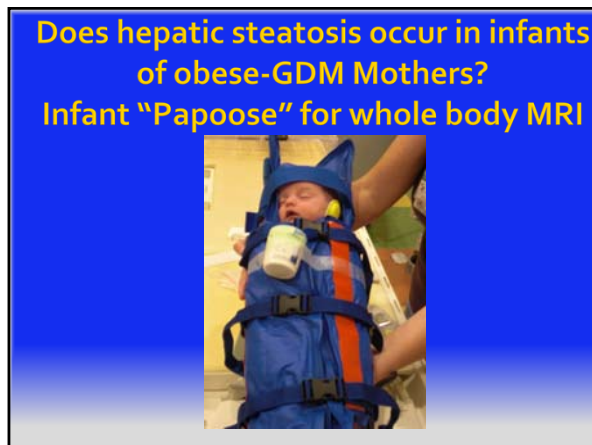


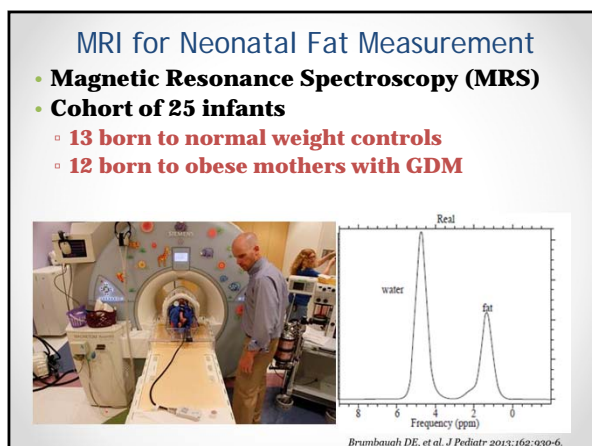
Juvenile Hypotheses

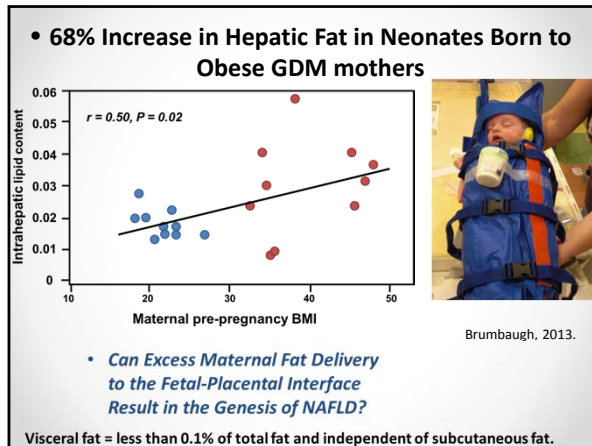
1. Maternal high fat diet exposure will result in hepatic steatosis, inflammation and insulin resistance in juvenile offspring at 1 yr of age.
2. These metabolic abnormalities will persist despite switching to a healthy diet up to 1 year of age.
3. Mechanism may involve persistent activation of inflammatory pathways in liver

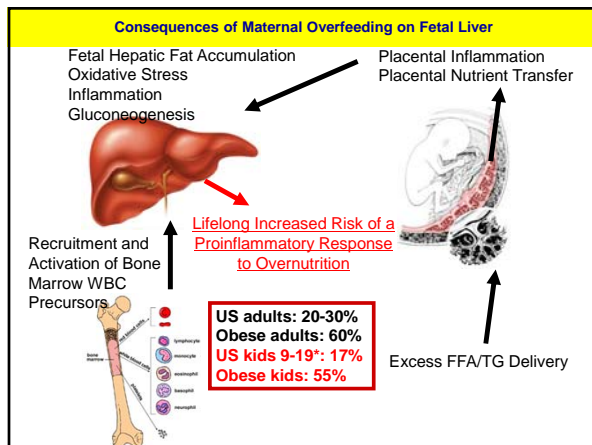


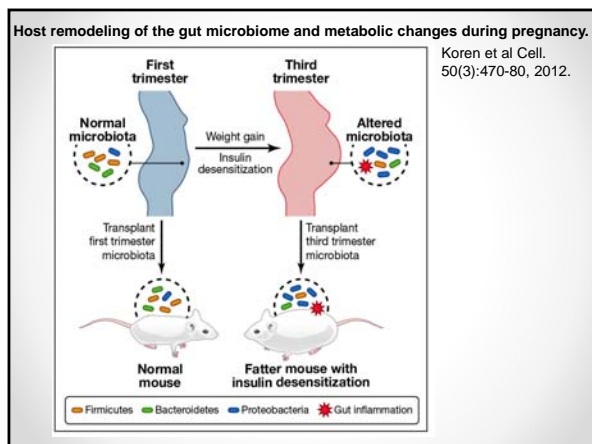


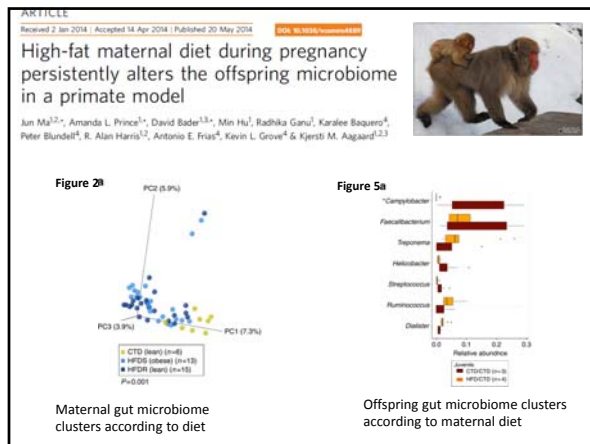










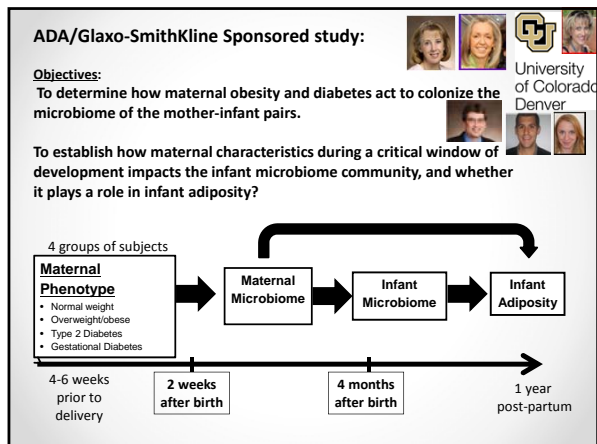


Microbiome

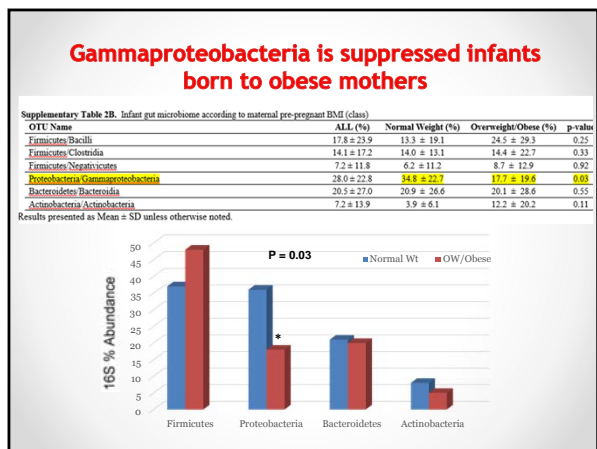
- Best studied is gut microbiome
 - 100 trillion microorganisms (10x more than the total of all other cells in the whole body)
 - Using 16S rRNA sequences, composition of microbiomes can be determined
 - >90% from 2 phyla: Firmicutes and Bacteroidetes
 - Human gut microbiome established by 1 year of age and depends on genetics, mode of delivery (vaginal vs C-section), and form of infant feeding
 - Later influenced by demographics, diet, and lifestyle
 - Evidence supports a role in inflammation, intestinal cell health and hormone production, efficiency of energy harvest from food, and appetite.

Gut microflora may stimulate hepatic fat deposition and promote NASH through several mechanisms:

1. It promotes obesity by improving energy yield from food.
2. It regulates gut permeability, low-grade inflammation and immune balance.
3. It modulates metabolism/genes directly in the liver.
4. It regulates bile acid metabolism.
5. It increases ethanol production by bacteria—ROS and mitochondrial function.



- ## Specimen Processing
- Bacterial DNA extraction
 - 16s rRNA (V1V2) amplification and sequence analysis (Illumina Miseq) of all samples
 - Sequence sorting by OTU (phyla, etc) and relative abundance calculated (Explicit)
 - 2 week infant stool: Shotgun sequencing with sequence classification/analysis using MG-RAST.
 - SCFA analysis (Acetate, Butyrate, Propionate by MS-MS.



Importance of γ -Proteobacteria

- “Pioneering Bacteria”, marker of transition to mature MB. Low abundance found in infant stool in Premature neonates. Increases on HFD.
- May have disproportionate impact on intestinal microenvironment (LPS, oxygen tension, intestinal mucous production).
- Microenvironment changes may create conditions for critical establishing TLR4 based immunity, that persists into childhood?

Question:

Are these changes
meaningful biologically?

From Bedside (or toilet) to Bench: Germ Free Mice

Hypothesis: the reduction in the early pioneering γ -proteobacteria in obese offspring may allow a more pro-inflammatory gut to develop and SCFA may influence body fat in GF mice



Kristine Kuhn, MD, PhD



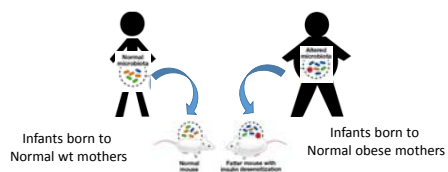
Lyndsey Babcock



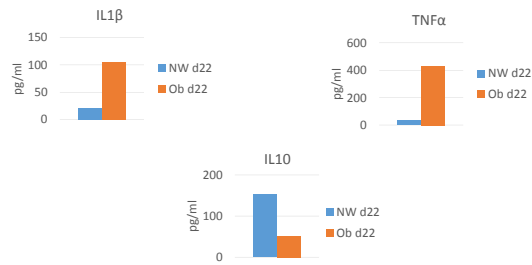
Taylor Soderborg,
T.D./PhD. Candidate



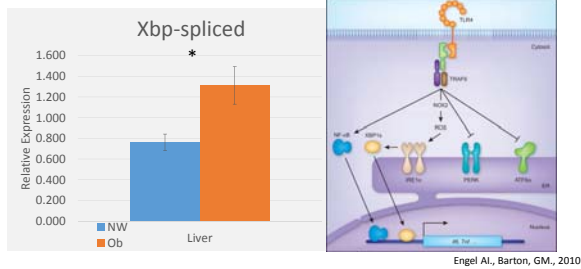
Erin Severs, BA, BS, CVT, RLATg



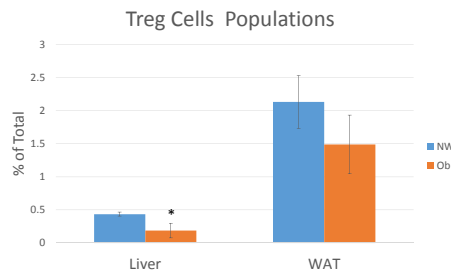
Increased Pro-inflammatory shift in plasma cytokines –hepatic portal vein.



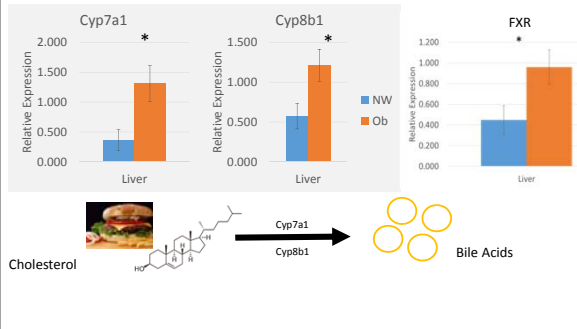
ER stress and heightened susceptibility for inflammatory processes

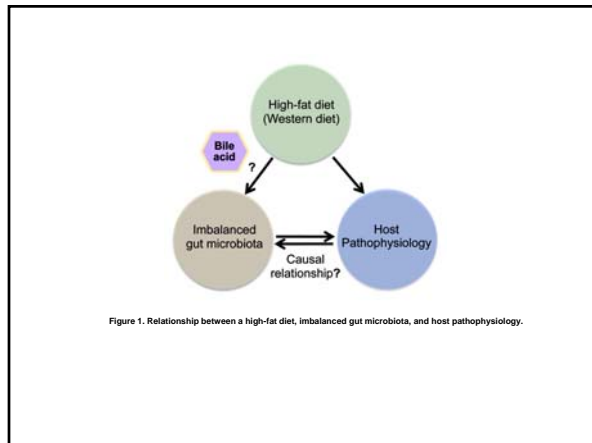


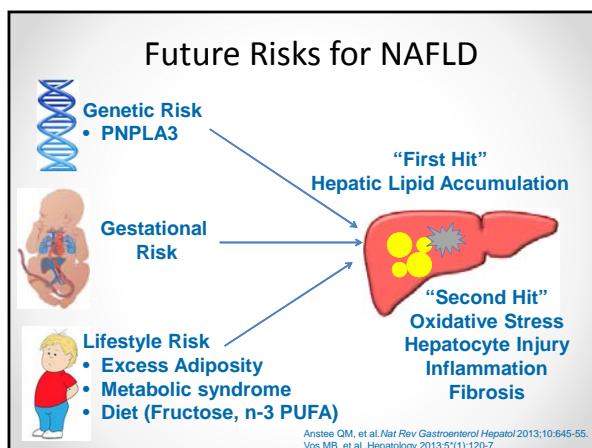
Treg cells reduced in Liver in mice with Ob infant microbiome

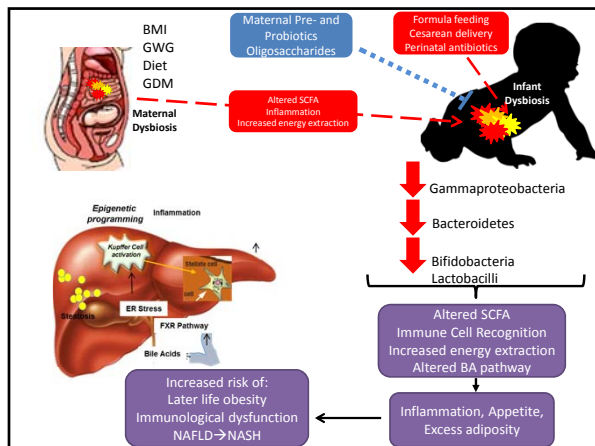


Surprise: Bile acid enzymes and BA receptor FXR are induced in mice with MB from Ob Infants











Thank-You !



Oregon Health Sci Ctr & Novo-Nordisk
Kevin Grove, PhD., Dan Marks, M.D. PhD.
Kjersti Aagaard, M.D. PhD – Baylor Coll of Medicine

NIH-R01 DK060685, R01 DK074643,
R24 DK090964, P30 DK048520, ADA
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Maternal-Child Clinical Translational Research
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