BACKGROUND

• Pediatric obesity is growing at an alarming rate and 1 in 5 children have the metabolic syndrome (MetS).

• IDF Globalized Definition of MetS in Children is complicated

• Paucity of data in children that are obese and non-diabetic compared to healthy controls

AIMS

The goal of this study was to compare global metabolic profiles in plasma collected from pediatric/adolescent patients with metabolic syndrome versus healthy controls in order to define a signature of the Metabolic Syndrome.

RESULTS

SUBJECTS AND METHODS

• This study was approved by the IRB at Baylor and subjects were recruited using fliers and advertisements in the Campus and all subjects and or their guardians gave informed consent.

• Healthy controls had a age and gender specific BMI percentile of <85% and Obese had a age and gender specific BMI percentile > 95%

• The IDF table was used to define the obese subjects that had MetS that were included in the study as given in Table 1.

• Following an overnight fast, EDTA-anticoagulated blood was obtained. Samples were centrifuged and were immediately stored at -80°C.

• At the time of analysis samples were extracted and prepared for analysis by LC/MS/MS using a dataset of 427 compounds of known identity (named biochemicals) from Metabolon.

• Following log transformation, Welch’s two-sample t-test was used to identify biochemicals that differed significantly between experimental groups.

• Subject node size proportional to the measurement indicated below the figures

SUMMARY AND CONCLUSIONS

• In addition to the IDF defined criteria, standard biochemical variables may help identify these subjects at risk for diabetes and heart disease

• Metabolic pathways appear to uniquely determine obese subjects that have MetS and provide a causative link

Network Mapping of Metabolites from Controls vs Met S Subjects using Cytoscape

p<0.05

PCA Profile of Controls vs Met S

Network Associations-Mapping of the Different Biochemical Variables

Network Mapping of Metabolites from Controls vs Met S Subjects using Cytoscape

SUMMARY AND CONCLUSIONS

• Metabolon original data is now normalized (z-score) using the mean and STD of healthy control (lean) kids

• Red = Obese; Green = Lean; Light blue = Metabolites

• Circles = Metabolites; Rectangles = Subjects

• Subject node size proportional to the measurement indicated below the figures

 ballooning

• Increased expression of TLR2 and 4 in the kidneys in lean vs obese children

• Metabolomic pathways appear to uniquely determine obese subjects that have MetS and provide a causative link

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