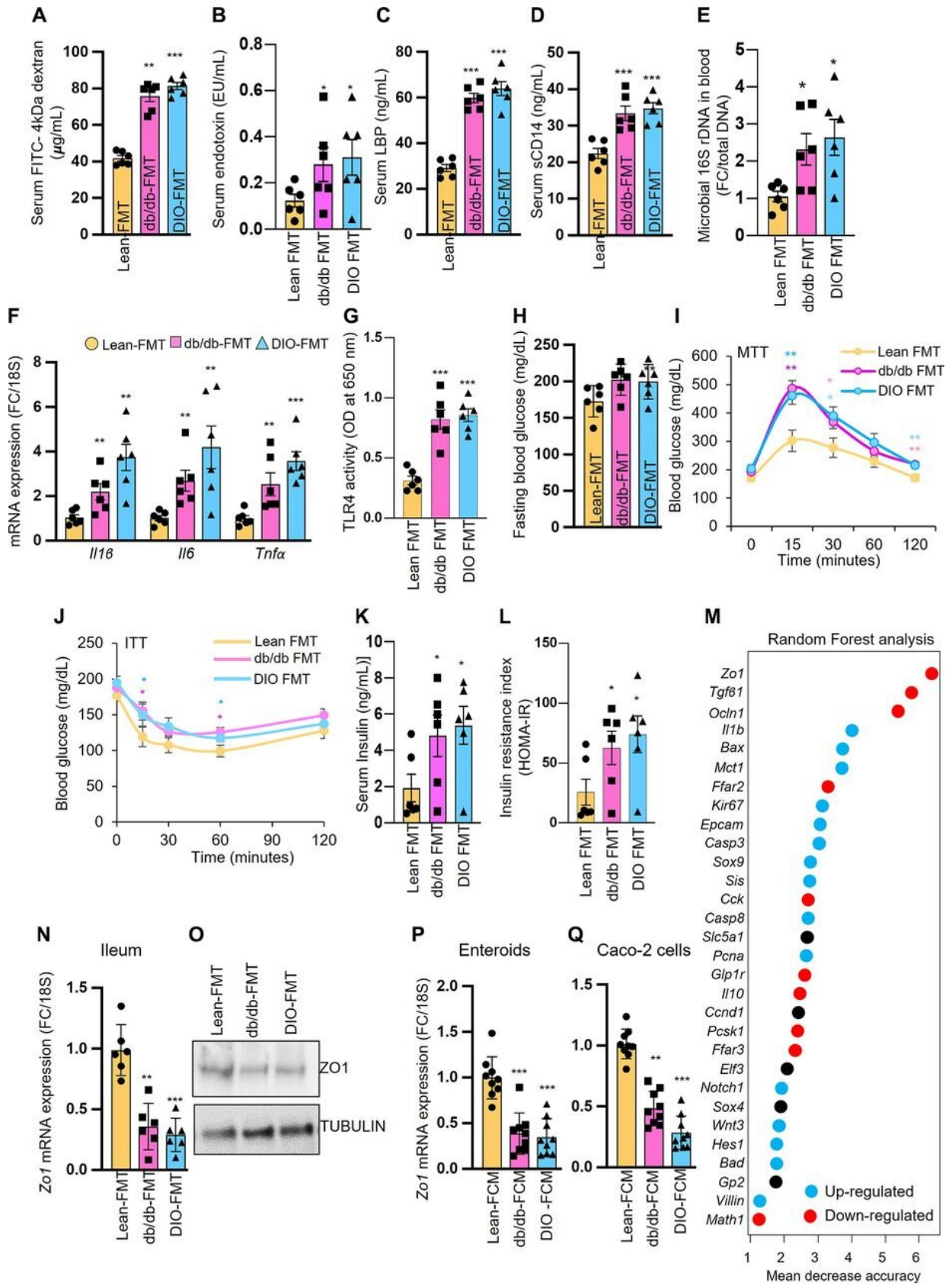


Study examines leaky gut syndrome

August 17 2023, by Ryan Randall



Obese microbiota is causal to instigate elevated gut permeability, inflammation and metabolic dysregulation. (A, B) Mice receiving FMT from both db/db and DIO mice showed significant increase in FITC 4kDa-dextran (A), endotoxin (LPS) (B) leakage from gut to blood compared with their lean control FMT recipient mice. (C–F) In addition, these mice also show significantly increased levels of systemic markers of elevated gut permeability (LBP (C) and sCD14 (D)), as well as microbial 16S rDNA (fold change (FC)) in serum (E) mRNA expression of inflammatory markers (Il1 β , Il6 and Tnf α) (F) compared with their controls. (G) The TLR4 activity (absorbance at 650 nm) was significantly increased in HEK-Blue mTLR4 cells treated with serum of db/db and DIO FMT recipient mice compared with the lean FMT controls. (H–L) Obese FMTs also increased fasting hyperglycemia (H) along with impaired meal tolerance test (MTT) (I), insulin tolerance test (ITT) (J), increased serum insulin (K) and insulin resistance index (HOMA-IR) (L, M) Random forest analysis of gene expression data revealed that obese FMTs and FCMs treatment dramatically reduced Zo1 expression in intestine and enteroids, respectively, compared with their lean FMTs/ FCMs treated controls. (N–Q) Further, the expression of Zo1 mRNA (N–P) and protein (O) in the ileum (N, O), enteroids (P) and Caco-2 cells (Q) of obese FMTs recipient mice and FCMs treated enteroids and Caco-2 cells, respectively, compared with their controls. Values presented are mean (n=5–8 mice per group) and error bars as the SEM. Enteroids and Caco-2 cell culture experiments were performed in triplicates and repeated 2–3 times. *p

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