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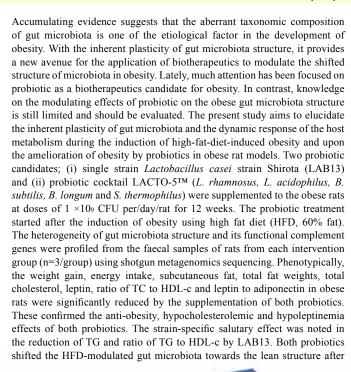
Title : MODULATION OF GUT MICROBIOME BY PROBIOTICS IN OBESITY AND

RELATED METABOLIC ABNORMALITIES

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the supplementation being given seven weeks after the induction of obesity. Comparative analysis revealed that the abundances of 68 bacterial genera were altered by HFD and probiotics. HFD uniquely modulated 21 genera, 17 of which were promoted and positively correlated with at least one of the obese phenotypes in obese control rats. Thus, these genera may be relevant to obesity. LAB13 modulated 32 genera, the enrichment of 16 genera of which were correlated positively with the ameliorated obese phenotypes. LACTO-5<sup>TM</sup> modulated five genera, of this, the enrichment of genus Coxiella was positively correlated with the ameliorated obese phenotypes. Out of this, three genera were also found reduced by LAB13. Theoccurrences of 13 out of 26 annotated functional categories were enriched in the HFD modulated gut microbiome; suggesting a relative higher metabolic capacity in the obese gut microbiome. Whereas both probioticmodulated and STD-modulated gut microbiome had lower occurrences of several protein-coding genes for metabolism of carbohydrate, lipids, and nutrient transport; suggesting a relative lower energy harvesting capacity in comparison to the HFD microbiome. Metabolomics analysis showed increment in bile acid synthesis and reduction in glycerophospholipid and fatty acids metabolism after probiotic treatment. These had increased the lipid clearance in body which improved the obese phenotypes. Results from this study suggest the salutary effects of probiotic, in part, are mediated by the changes in the gut microbiota structure and its metabolic capacities in host metabolism particularly bile acid biosynthesis. This study proved the possible mechanistic links between gut microbial-host interactions and its role in obesity.