

Interaction Between Gut Microorganisms and Endocrine Disruptors - Effects on Hyperglycaemia

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Abstract : Background: Hyperglycaemia is the primary cause of metabolic illness. Recently, researchers focused on the possibility that chemical exposure could promote metabolic disease. Hyperglycaemia causes a variety of metabolic diseases dependent on its etiologic conditions. According to animal and population-based research, individual chemical exposure causes health problems through alteration of endocrine function with the influence of microbial influence. We were intrigued by the function of gut microbiota variation in high fat and chemically induced hyperglycaemia. Methodology: C57/B16 mice were subjected to two different treatments to generate the etiologic-based diabetes model: I - a high-fat diet with a 45 kcal diet, and II - endocrine disrupting chemicals (EDCs) cocktail. The mice were monitored periodically for changes in body weight and fasting glucose. After 120 days of the experiment, blood anthropometry, faecal metagenomics and metabolomics were performed and analyzed through statistical analysis using one-way ANOVA and student's t-test. Results: After 120 days of exposure, we found hyperglycaemic changes in both experimental models. The treatment groups also differed in terms of plasma lipid levels, creatinine, and hepatic markers. To determine the influence on glucose metabolism, microbial profiling and metabolite levels were significantly different between groups. The gene expression studies associated with glucose metabolism vary between hosts and their treatments. Conclusion: This research will result in the identification of biomarkers and molecular targets for better diabetes control and treatment.

Keywords : hyperglycaemia, endocrine-disrupting chemicals, gut microbiota, host metabolism

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