

**ABSTRACT**

Diabetes mellitus is a group of diseases marked by disordered insulin resulting in elevated blood glucose levels. This condition is considered to be a heterogeneous and multi factorial disease, influenced by both environmental and genetic factors. A link between Type 2 diabetes and gut microbiota has already been reported. The aim of this study was to assess the composition of the intestinal microbiota in humans with type 2 diabetes and to investigate the impact of human gut microbiota and high fat diet (HFD) in inducing Type 2 diabetes using mouse as a model animal. The study included 20 participants, among which 10 subjects were diagnosed with Type 2 diabetes. The fecal bacterial composition was investigated by biochemical and molecular characterization. Biochemically dominant bacterial isolates belong to genera *Bacteroides*, *Lactobacillus*, and *Prevotell* were selected for mice inoculation. *In vivo* experimentation was done to examine the effect of high fat diet and gut microbiota alone and in combination in inducing diabetes. 16 mice were treated with ampicillin for depletion of majority of existing gut microbiota and divided into four groups. Group 1 was fed chow diet. Group 2 was fed high fat diet. Mice from group 3 were fed high fat + gut microbiota. And group 4 was given chow diet + gut microbiota. After 12 weeks of experimental period body weight, blood glucose concentration and plasma insulin concentration were measured. It was observed that group 2 mice gained weight and developed higher blood glucose level and plasma insulin concentration ($P < 0.05$). Similarly, mice from group 3 also showed highly significant weight gain, higher plasma insulin and blood glucose concentration ($P < 0.05$) as compared to other 3 groups. Group 4 also showed significant variations in blood glucose and plasma insulin concentration ($P < 0.05$) but they didn't show weight gain ($P > 0.05$). Biochemical characterization of cecal bacteria isolated from sacrificed mice (all groups) showed abundance of *Lactobacillus*, *Bacteroides* and *Prevotella* sp. along with *Clostridia*, *Enterobacter* and *Serratia* sp. These findings suggest that high fat feeding and gut microbiota transfer modulates the gut microbiota composition and results in insulin resistance, as observed by high plasma insulin concentration in this study, which could lead to hyperglycemia and hence onset of Type 2 diabetes. So, specific strategies to modify the gut microbiota should be used because gut microbiota modulation reduce the incidence of metabolic diseases by lowering the effect of high fat diet.