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Abstract

Association of Inflammatory Biomarkers with the Gut Microbiota and Short-Chain Fatty Acids in Prediabetic Subjects †

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Abstract: Background and objectives: The gut microbiota performs many functions in the host organism, and metabolites derived from its activity, such as short-chain fatty acids (SCFA), are involved in immunometabolism. Alterations in gut microbial composition play an essential role in diseases such as heart failure, kidney disease, obesity, and diabetes mellitus. The current work aimed to analyze the associations of serum and fecal inflammatory biomarkers with the microbiota and SCFA in prediabetic subjects. Methods: 65 prediabetic patients, diagnosed according to the American Diabetes Association criteria, who participated in a randomized controlled intervention study with Moringa oleifera Lam. (2.4 g/day), were included. Inflammatory markers (Serum C reactive protein [CRP] and fecal calprotectin and sIgA), gut microbiota (qPCR), and short-chain fatty acids (SCFA; GC-FID) were studied before (V0) and after a 12-week intervention (V12). Relationships were explored using principal component analysis (PCA). Lineal regression models were performed to determine the predictive variables of inflammatory markers by including SCFA and gut microbiota groups as one block of independent variables. Fat mass percentage (BIA) and treatment group were used to adjust the models. Analyses were performed for V0 and V12 separately. Results: Only for calprotectin were significant models found at V0 ($p = 0.044$) and V12 ($p = 0.010$). *Lactobacillus* (standardized beta, β= 0.292; $p = 0.047$) and *Bacteroides* (β = 0.430; $p = 0.009$) groups were significant predictors at V0 and *Lactobacillus* (β = 0.339; $p = 0.015$) and the SCFA valeric acid (β = −0.533; $p = 0.014$) were predictors of calprotectin in V12. For CRP, a trend was found at V12 regression ($p = 0.079$), with significant contributions for the *Blautia coccoides–Eubacterium rectale* group (β = 0.585; $p = 0.016$) and the categorical binomial variable "Above normal fat mass percentage" ("yes", "no") (β = 0.478; $p < 0.001$). No significant influence of the treatment group was observed. Discussion: Calprotectin levels seem to be dependent on microbiota and SCFA levels. Calprotectin showed a positive and consistent relationship with *Lactobacillus* spp.; however, its relationships with the *Bacteroides* group and valeric acid were not consistent and deserve further exploration. CRP and sIgA do not seem to be explained to a significant level by the microbiota and SCFA concentrations in this prediabetic population.

Keywords: gut microbiota; inflammatory markers; short-chain fatty acids; prediabetes; body fat mass

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