Profil Mikrobiota Usus Pada Subjek Obesitas Dengan dan Tanpa Diabetes Melitus Tipe 2 = Gut Microbiota Profile of Obese Subjects With and Without Type 2 Diabetes Mellitus

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Abstrak

Obesitas dan diabetes tipe 2 adalah masalah global dengan angka kejadian yang meningkat pesat. Hubungan antara obesitas dan diabetes melibatkan resistensi insulin dan mikrobiota usus. Namun, belum ada studi di Jakarta yang menganalisis profil mikrobiota usus pada obesitas dengan atau tanpa diabetes tipe 2. Penelitian ini bertujuan menganalisis profil mikrobiota usus dengan metode sekuensing 16S rRNA pada subjek dengan dan tanpa diabetes tipe 2. Hasil analisis menunjukkan perbedaan komposisi mikrobiota usus antara obesitas dengan dan tanpa diabetes tipe 2. Beberapa kelompok bakteri berkaitan dengan kondisi tersebut. Filum Firmicutes dan Bacteroidota, famili Oscillospiraceae, genus Faecalibacterium dan Clostridia UCG-014 berkaitan dengan non-obesitas dan berkorelasi negatif dengan kadar lemak tubuh. Sementara filum Proteobacteria dan Bacteroidota, famili Enterobacteriaceae dan Erysipelotrichaceae, genus Eschericia Sighella dan unspecified Lachnospiraceae berkaitan dengan obesitas dan berkorelasi positif dengan kadar lemak tubuh dan IMT. Beberapa kelompok bakteri juga berkaitan dengan diabetes tipe 2, seperti filum Bacteroidota, famili Oscillospiraceae, dan genus Oscillospiraceae UCG-002 yang berkorelasi negatif dengan kadar GDP, GDS, dan HOMA-IR, serta filum Actinobacteriota, famili Veillonellaceae, genus Dialister dan Bifidobacterium berkorelasi positif dengan kadar GDP, GDS, dan HOMA-IR. Perbedaan pola distribusi mikrobiota usus juga terlihat pada analisis alpha dan beta diversity. Hasil penelitian ini memberikan wawasan baru tentang peran mikrobiota usus dalam obesitas dan diabetes tipe 2.
......Obesity and type 2 diabetes are global health issues with rapidly increasing prevalence. The relationship between obesity and diabetes involves insulin resistance and gut microbiota. However, there has been no study in Jakarta analyzing the gut microbiota profile in obesity with or without type 2 diabetes. This research aims to analyze the gut microbiota profile using 16S rRNA sequencing on subjects with and without type 2 diabetes. The analysis results show differences in gut microbiota composition between obesity with and without type 2 diabetes. Several bacterial groups are associated with these conditions. Phylum Firmicutes and Bacteroidota, family Oscillospiraceae, genus Faecalibacterium, and Clostridia UCG-014 are associated with non-obesity and negatively correlated with body fat levels. On the other hand, phylum Proteobacteria and Bacteroidota, families Enterobacteriaceae and Erysipelotrichaceae, genus Eschericia Sighella, and unspecified Lachnospiraceae are associated with obesity and positively correlated with body fat levels and BMI. Some bacterial groups are also associated with type 2 diabetes, such as phylum Bacteroidota, family Oscillospiraceae, and genus Oscillospiraceae UCG-002, which are negatively correlated with GDP, GDS, and HOMA-IR levels, as well as phylum Actinobacteriota, family Veillonellaceae, genus Dialister, and Bifidobacterium, which are positively correlated with GDP, GDS, and HOMA-IR levels. Differences in gut microbiota distribution patterns are also evident in the alpha diversity analysis. The results of this study provide new insights into the role of gut microbiota in obesity and type 2 diabetes.