**The Effect Of Herbal Extracts On Gut Microbiota’s Diversity By Flow Cytometric Fingerprinting**

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**Background and aims.** Nowadays, traditional medicines are used widely for the prevention and treatment of many diseases. However, the effects of these herbal extracts on the gut microbiota have not been extensively studied due to the difficulty in analyzing changes in population and composition of the microbiota. Flow cytometry (FCM) is a potential technique that can be applied in microbial composition analysis thanks to its ability to analyze diverse microbial populations in terms of quantity, reducing the time and cost of implementation. Therefore, this research aimed to apply the FCM technique to investigate the effect of herbal extracts on gut microbiota’s diversity.

**Methods.** *Orthosiphon aristatus*, *Perilla frutescens*, and *Camellia sinensis* leaf extracts were tested in *Swiss albino* mice for ten days. After administering each herbal extracts to the groups of mice, the changes in the gut microbiota’s composition of each group were investigated by analyzing mouse fecal samples with a FCM instrument. The resulting alpha diversity and beta diversity indices were calculated using the Phenoflow algorithm performed in RStudio software.

**Results.** In 10 days, the species richness and evenness (by alpha diversity index) of the gut microbiota in the control group and the testing group (n = 3) using *O. aristatus*, *P. frutescens*, and *C. sinensis* leaf extracts (1 mg/30 g weight) were 3491,267 ± 155,306, 3373,867 ± 243,268, 3160,435 ± 295,739 and 3643,257 ± 351,898 respectively. The mouse group using *O. aristatus* leaf extract tended to change the structure of gut microbiota similarly (by beta diverisity index).

**Conclusion.** This study successfully applied the FCM technique to analyze gut microbiota composition under the influence of *O. aristatus*, *P. frutescens*, and *C. sinensis* leaf extracts with notable datas regarding daily variations in gut microbiota richness and diversity as well as effectively evaluated compositional differences in gut microbial communities.

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