Establishment for big data base of Microbiota closely related to diseases - Showa U bank -

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The emergence of the next generation sequencer (NGS) and its technological progress have caused a major change in genetic analysis. Technological innovation by NGS had an enormous influence on the study of classification and analysis of intestinal bacteria inhabiting the intestine. It has been reported that in the intestines of humans, approximately 1,000 species, 100 trillion bacteria may coexist, and the intestinal bacteria could be about three times more than the number of cells constituting a human being. Following development of NGS, novel areas have been discovered in microbiota; however, in oncology, the relationships between microbiota and cancer have not been fully clarified. In recent literature, surprisingly, detection of gut microbiota in tumor issue itself has been reported. Microbiota might play a significant role in carcinogenesis. However, this phenomenon is not well understood, and research in this area has just begun. Gut microbiota and human beings are co-evolutionary, in a win-win symbiosis. Recently, there have been many studies and much research on the relationships between the gut microbiota and human disease. Gut microbiota seem to be strongly correlated with various kinds of disease, such as inflammatory bowel disease, diabetes mellitus, central nervous disorder, allergic diseases, and infectious diseases. On the other hand, the relationship between tumor and microbiota is not well clarified, and there has been yet clarified the relationship between Japanese patients and diseases. To clarify those, we have attempted to establish the big data base of Microbiota, we call, Showa U bank. We have sequenced V1 and V2 of 16s rRNA to determine the bacteria from specimen by NGS. In Showa University, we have 3,200 beds in the affiliated 8 hospitals. Our collaborations in Showa University makes possible accelerate the amounts of data of Microbiota related to clinical data from patients. From one of these data, microbiota from healthy subjects and cancer patients is much different. In this presentation, we will demonstrate the present data from Showa U bank.