江大

益生菌

第一届益生菌、肠道微生物与人体健康国际研讨会

The 1st Symposium on Probiotics, Gut Microbiome & Health.

Organizers:

International Joint Center on Probiotics & Gut Health

UK-China Joint Center onProbiotic Bacteria

October 27, 2017.

Wuxi, China.

Symposium Agenda

Time	Content
12:30	Lunch break
13:30	*Selection of probiotic strains for human and animal applications* Michael Gänzle, University of Alberta, Canada
14:05	*Lactobacillus plantarum ZS2058 produces conjugated linoleic acid to ameliorate colitis* Wei Chen, Jiangnan University, China
14:40	*Modulation of Gut Microbiota by Probiotic Weissella confusa F213* I Nengah Sujaya, Udayana University, Indonesia
16:00	Inauguration Ceremony of UK-China Joint Center on Probiotic Bacteria 1.Speech of Bronte Zhang, Senior Science and Innovation Officer, British Consulate-General 2.Speech of Arjan Narbad, Director of UK-China Joint Center on Probiotic Bacteria, Quadram Institute Bioscience, UK 3.Speech of Wei Chen, Deputy Director of UK-China Joint Center on Probiotic Bacteria, Jiangnan University, China

I Nengah Sujaya works at School of Public Health, Faculty of Medicine, Udayana University, Bali, Indonesia. He completed his Ph.D. in 2002 at the Laboratoty of Applied Microbiology, Graduate School of Agriculture, Hokkaido University. He got his position as Postdoctoral Fellow at Nothern Advancement Center for Science and Technology, Hokkaido, Japan from 2002-2003 and since then he was appointed as an Assistant Proffessor at the Laboratory of Microbial Function and Ecology, Grad. School of Agriculture Hokkaido University. He resigned from Hokkaido University and back to Udayana University in 2004. He was a research fellow of International Foundation for Science in 2006 and the Australian Leadership Award fellow in 2008. His researches mainly on microbiology of traditional fermented foods espescilly the role of lactic acid bacteria in Indonesian traditional fermented foods and application of indigenous microorganisme as starter culture. Currently his researches also foccused on the development of prebiotic, gut microbiota and selection of lactic acid bacteria as probiotic for human.

Abstract

Human gut microbiota is a diverse consortium and is considered to contribute significantly to human health. Administration of lactic acid bacteria, endogenously present in traditional fermented foods or a designed-strain, is an interesting approach, which intented to improve human health through modulation of gut microbiota. Recently, a probiotic strain *Weissella confusa* F213 (WCF213), has been studied both *in-vitro* and *in-vivo* (animal studies). The strain has been found to be resistant to environment of rat intestine, and it exhibited good capability in lowering blood cholesterol. In current studies, the WCF213 was administered to healthy human subjects, either using capsule containing 7.5×10^7 cfu of WCF213 or formulated-milk supplemented with 10^8 cfu of WCF213. The WCF213 was detected in fecal samples, which demonstrated the resistant of WCF213 in human gastrointestinal tract. The WCF213 promoted the population of intestinal lactic acid bacteria, which consequently play roles in lowering the fecal pH and improved stool color and form. Decreasing trends were found in cholesterol, triglycerides (TG), low density lipoprotein (LDL) levels that were by 6.29, 7.76 and 8.54%, respectively, after 28 days administration of WCF213 as compared to before administration. On the other hand, high density lipoprotein (HDL) level was slightly increasing, about 0.19%, after 28 days administration. These data suggest that WCF213 might be a potential probiotic for lowering blood cholesterol level. The other results also revealed that administration of WCF213 improved diversity of human gut microbiota. However, the diversity reduced and tended to be fewer than those before and during WCF213 administration. Although this phenomenon is still unclear, however this might be due to the changes of gut micro-environment. Administration of WCF213 increased Bacteroides, while Firmicutes tended to be stable. The other finding showed that the population of lactobacilli was increasing during the administration WCF213. Nevertherless, WCF213 was not detected in the fecal microbiomic DNA verified using NGS analysis. This data is contrary with our previous finding where the WCF213 was detected in fecal microbiomic DNA derived using DGGE analysis. This discrepancy was likely due to different sequences in the 16S rDNA targeted in metagenomic analysis. This data suggested that WCF213 might be harbour unique sequences, therefore it should be carefully considered in selection of appropriate detection methods.

Conclusion: Administration of WCF213 have modified human gut microbiota, hence promoted the growth of several species of bacteria, especially from the group of Bacteroides and lactobacilli, which may contribute to the overall healthy outcomes.