P113

Cell Proliferation and Collagen Synthase Effect of *Ecklonia Cava* Extract *in* Osteoblastic MC3T3-E1 Cell Line.

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Bone formation occurs during embryonic development and postnatal growth and in adulthood during bone remodeling to support calcium homeostasis and in response to physical forces. This study evaluated the effects of *Ecklonia Cava*(EC) extract on growth of osteoblasts *in vitro*. Osteoblast cellular proliferation was elevated using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) and alkaline phosphatase activity assay in the osteoblastic MC3T3-E1 cell line. The effect of EC extract on cell viability was assessed using the 3-(4,5-dimethylthiazol-2-yl)-2,5- diphenyltetrazolium bromide (MTT). By the MTT assay, proliferation of MC3T3-E1 osteoblasts cell were elevated to 110 and 150% via control in the EC ethanol extract of 10 and 100 μg/mL, respectively. ALP is a representative enzyme for indication of osteoblast differentiation. In the presence of different concentration of EC, MC3T3-E1 cells produced increasing ALP activity at concentrations up to 100 μg/mL. Moreover, the collagen content increased in the supplemented EC extract group. These results suggest that EC extract was stimulates the MC3T3-E1 cell proliferation and collagen synthesis.

Key words: *Ecklonia Cava*, MC3T3-E1, ALP

P114

Analysis of Intestinal Microbiota in Anticancer Agents Administering Gastric Cancer Patients using PCR/DGGE

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We investigated the effects of anticancer agents on gastric cancer patients' intestinal microbial ecosystem by monitoring 16S ribosomal DNA of microbiota diversity in fecal samples by PCR, denaturing gradient gel electrophoresis (DGGE) and by analyzing the sequences. Intestinal microbiota is important factors in the development of immune defense mechanisms in the intestine. The treatment of anticancer agents significantly reduces temporal stability and changes diversity of microbiota. Chemotherapy often induce diarrhea and depress the immune system. An exploration of the diversity and temporal stability of the dominant bacteria and several bacterial subgroups was undertaken using the DGGE for the 16S rDNA gene. Re-amplification and sequencing of two bands present in all samples revealed *Escherichiacoli* and *Pseudomonas agarici*. Increased by the treatment of anticancer agents were *Serratia marsecens, Enterobactersp., Faecalibacterium prausnitzii, Stenotrophomonas maltophilia, Lactobacillus gasseri* and *Morganella morganii*. This study also focused on the survival of beneficial microorganisms, *Bifidobacterium* and *Lactobacillus*, in the intestine of cancer patients, which were identified by application of the species-specific PCR primers. The administration of anti-gastric cancerd drug led to a significant decrease in the *Lactobacillus* and *Bifidobacterium* population, while a moderate effect was shown up on the main bacterial groups in the intestine ecosystem. Taken together, these results showed the versatility of cultivation-independent PCR-DGGE analysis for visual monitoring of ecological diversity and anti cancer agents-induced changes in the complex intestinal microbial ecosystem.

Key words: PCR-DGGE, Anticancer agent, Intestinal microbiota