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ABSTRACTS

KARGER
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T1 – Myokines

T1:PO.034

Change of circulating irisin concentrations in morbidly obese patients after roux-en-y gastric bypass

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Background: Irisin, a humoral factor secreted from muscle (myokine), has been known to stimulate the program of brown fat development in adipose tissue ("browning"). Recent animal studies suggested that irisin has possibility to enhance energy expenditure in obese patients. However, we have limited clinical data to understand biology of irisin in human, especially in morbidly obese patients taken bariatric surgery.
Methods: This is a pilot, single center, longitudinal, observational study. We recruited twelve morbidly obese subjects (25–56 years, 29.6~45.9 kg/m^2 of BMI) who underwent Roux-en-Y gastric bypass surgery (RYGBP) and visited the obesity center postoperatively. Fasting serum samples for measuring irisin were collected preoperatively, and one and nine months after RYGBP. We analyzed the association between irisin concentrations and clinical characteristics.
Results: Serum irisin concentrations, 1.0115 ± 0.2282 μg/ml ranging from 0.7347 to 1.4928 pre-operatively, altered bidirectionally on one month after RYGBP. Five out of twelve subjects showed increased irisin levels from 0.9028 ± 0.7387 (range, 0.8393 – 0.9865) μg/ml to 1.6975 ± 0.6593 (range, 1.0439 – 2.5102) μg/ml, while seven of them had decreased irisin levels from 1.0891 ± 0.2738 (range, 0.7347 – 1.4928) μg/ml to 0.8304 ± 0.1855 (range, 0.5535 – 1.1560) μg/ml. Serum irisin concentrations on 9 months were 1.1108 ± 0.1515 μg/ml (range, 0.9158 – 1.3481), and eight had elevated irisin levels by 0.1827 ± 0.1400 μg/ml and four had non-elevated levels by - 0.0675 ± 0.0538 μg/ml compared with pre-operative values.
Conclusions: The alteration of serum irisin level was associated with weight loss effect of Bariatric surgery.

T1 – Gut microbiota

T1:PO.035

Influence of panax ginseng on obesity and gut microbiota in obese middle-aged korean women

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Gut microbiota is regarded as one of the major factors involved in control of body weight. The anti-obesity effects of ginseng and its main constituents have been demonstrated, however, the effects on gut microbiota are still unknown. To investigate the effect of ginseng on gut microbiota, 10 obese middle-aged Korean women took Panax ginseng extracts for eight weeks and assessment of body composition parameters, metabolic biomarkers, and gut microbiota composition was performed using 16S rRNA gene-based pyrosequencing at baseline and at wk 8. Significant changes were observed in body weight and BMI, however, slight changes were observed in gut microbiota. We divided the subjects into two groups, the effective weight loss group (EWG) and the ineffective weight loss group (IWG), depending on weight loss effect, in order to determine whether the anti-obesity effect was influenced by composition of gut microbiota, and the composition of gut microbiota was compared between the two groups. Before ginseng intake, significant differences of gut microbiota were observed between both at phyla and genera and the gut microbiota of the EWG and IWG was segregated on a principal coordinate analysis plot. Results of this study indicate that ginseng exerted a weight loss effect and slight effects on gut microbiota in all subjects. In addition, its anti-obesity effects differed depending on the composition of gut microbiota before ginseng intake.

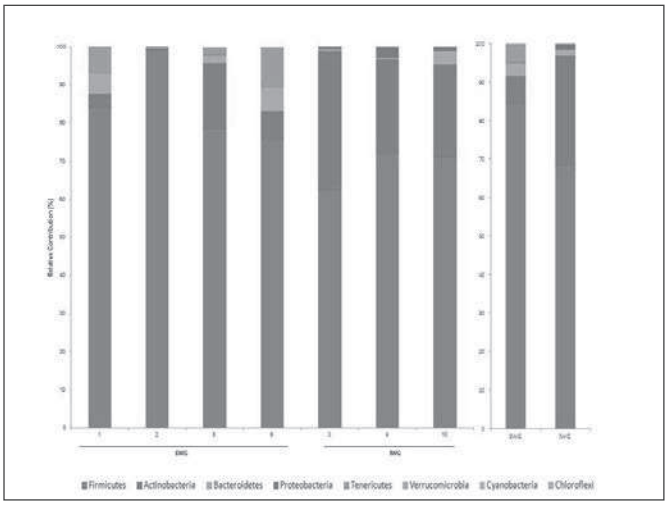

Fig. 1. The phylum compositions of fecal bacteria were compared before treatment in the EWG and IWG. The relative contribution abundance of dominant phyla identified from pyrosequencing data is shown. EWG, effective weight loss group; IWG, ineffective weight loss group.

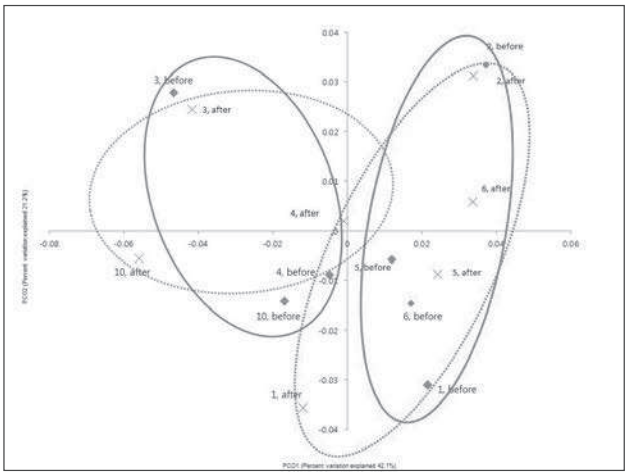

Fig. 2. Principal coordinate analysis (PCoA) plot. The plot showed the clustering pattern between the EWG and IWG based on weighted pairwise Fast UniFrac analysis.Full line circles indicate grouping of the communities in the before ginseng intake and dotted line circles indicate that in the after ginseng intake.

T1:PO.036

High-fat diet-induced obesity rat model: A comparison between wistar and sprague-dawley rat

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Introduction: In the past decades, obesity and associated metabolic complications have reached epidemic proportions. For the study of these pathologies, a number of animal models have been developed. However, a direct comparison between Wistar and SD Rat as models of high-fat (HF) diet-induced obesity has not been adequately evaluated so far.
Methods: Wistar and SD rats were both assigned for two experimental groups for 17 weeks: standard (St) and high-fat (HF) diet groups. To assess some of the features of the metabolic syndrome, oral glucose tolerance tests, systolic blood pressure measurements and blood biochemical analysis were performed throughout the study. The gut microbiota composition of the animals from each group was evaluated at the end of the study by real-time PCR.
Results: HF diet increased weight gain, body fat mass, mesenteric adipocyte's size, adiponectin and leptin plasma levels and decreased oral glucose tolerance in both Wistar and SD rats. However, the majority of these effects were more pronounced or earlier detected in Wistar rats. The gut microbiota of SD rats was less abundant in Bacteroides and Prevotella but richer in Bifidobacterium and Lactobacillus comparatively to the gut microbiota of Wistar rats. Nevertheless, the modulation of the gut microbiota by HF diet was similar in both strains, except for Clostridium leptum that was only reduced in Wistar rats fed with HF diet.
Conclusion: Both Wistar and SD Rat can be used as models of HF diet-induced obesity although the metabolic effects caused by HF diet seemed to be more pronounced in Wistar Rat. Differences in the gut microbial ecology together with other mechanisms, such as increased gut permeability, may account for the worsened metabolic scenario observed in Wistar Rat.

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T1 – Gut hormones/incretins

T1:PO.037

The relationship between serum amylase and fasting plasma ghrelin, peptide yy3–36 in healthy men

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Objective: Both appetite and carbohydrate metabolism are important in development of obesity. Recently serum amylase has been shown to be associated with obesity as well as metabolic disorder. Here, we investigated the relationship between total amylase, ghrelin and peptide YY (PYY) in healthy men.
Materials and Methods: In this cross-sectional study, twenty-one men were enrolled and all subjects had no symptoms and no any medical history or diseases. Serum total amylase, fasting serum levels of ghrelin and PYY3-36, anthropometry and caloric intake per day were measured. Partial correlation coefficients adjusting for age and linear regression analysis were computed to examine association between serum amylase and ghrelin, PYY3-36.
Results: The mean age, body mass index and waist circumference (WC) of subjects were 51.5 ± 10.9 years, 24.2 ± 1.7 kg/m^2 and 87.0 ± 4.4 cm, respectively. The subjects had no significant difference in serum amylase, ghrelin and PYY3-36 according to presence of obesity. Serum amylase showed significant correlation with WC (r = -0.438, P = 0.054), ghrelin (r = 0.533, P = 0.015) and PYY3-36 (r = -0.511, P = 0.021) after adjusting for age. PYY3-36 showed statistically negatively associated with serum amylase in multivariate linear regression model including age, WC (β = -0.428, P = 0.045). In contrast, positive association between ghrelin and serum amylase became non-significant in multivariate linear regression model including age, WC (β = 0.260, P = 0.146).
Conclusion: Serum amylase levels were related with ghrelin and PYY3-36 in men. Amylase, ghrelin and PYY3-36 together may relate to obesity, although further research is required to find the mechanism behind these associations.

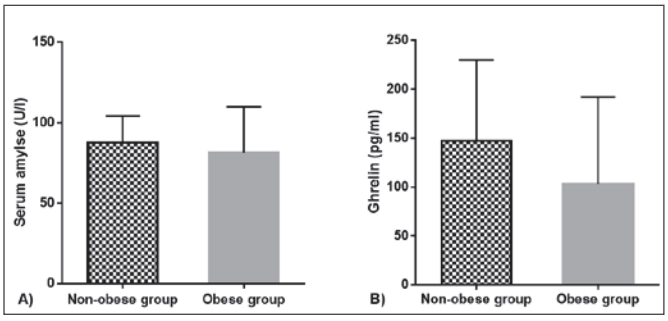

Fig. 1. Serum amylase (A) and Ghrelin levels (B) between obese and non-obese group. Statistical significance test between groups was done by Mann-Whitney U-test

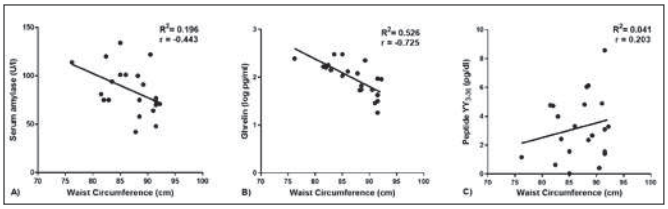

Fig. 2. Correlation between waist circumference and serum amylase (A), ghrelin (B), peptide YY3-36 (C)

T1:PO.038

Differentially nibbling endogenous cannabinoid cb1 and cb2 receptor subtypes in spontaneous and splice variants of ghrelin-induced feeding in rats

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Objective: Dysregulation of endocannabinoid system has been reported leading to the development of obesity and metabolic disorders. Endogenous endocannabinoids act on two cannabinoid receptor subtypes, type 1 (CB1) and type 2 (CB2), to exert their biological actions. However, comprehensive information regarding CB1 and CB2 receptors in modulating feeding behavior is important, but remains less understood.
Methods: We investigated the differential roles of CB1 and CB2 receptors in spontaneous and centrally-administered splice variants of ghrelin, O-n-octanoylated ghrelin and des-Gln14-ghrelin, stimulation of food intake in conscious rats.
Results: Intraperitoneal (IP) injection of different doses of selective CB2 receptor antagonist, AM-630 (0.3, 1.0, and 3.0 mg/kg), enhanced cumulative food intake during the first 12 hours with a dome-shaped dose-response relationship in freely-fed rats, with the most effective dose of 1.0 mg/kg. In contrast, the selective CB1 receptor antagonist, AM-251 (0.3, 1.0, and 3.0 mg/kg, IP) dose-dependently suppressed the cumulative food intake in 16-h food-deprived rats. Centrally-administered O-n-octanoylated ghrelin and des-Gln14-ghrelin-induced hyperphagic effects were counteracted dose-dependently by IP AM-251, but not AM-630.
Conclusions: We showed that endogenous CB2 receptor plays a role in inhibiting food intake in satiated state, whereas CB1 receptor promotes food intake in fasted condition. Central acyl ghrelin induces feeding is