Investigation of the Determinants of Inflammation on Ojika island, Nagasaki prefecture 長崎県小値賀島における炎症の環境要因の探索

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Introduction

Ojika island is an isolated island in Nagasaki prefecture, Japan with 51% of the population aged 65 years or older in 2020. In such aging populations with limited medical resources, maintaining the health of older adults is a crucial issue. Chronic inflammation has been proposed as one of the biochemical mechanisms underlying age-related health problems. Many possible determinants of inflammation have been identified, e.g., age, obesity, diet, and psychological stress. This study aimed to investigate the determinants of inflammation exhaustively to determine its main driver on Ojika island, Nagasaki prefecture.

Progress and future plans

This study was conducted in July and August 2022. Residents of three neighborhood community associations on Ojika island aged 40 years or older were recruited. The total number of participants was 162 people. Participants answered a questionnaire on basic lifestyle characteristics, a food frequency questionnaire (FFQ), and the 5-item World Health Organization Well-Being Index (WHO-5) questionnaire. The Dietary Inflammatory Index (DII) score will be calculated from the nutrient intake data obtained from the FFQ to estimate the inflammatory potential of diet. The WHO-5 score indicates mental wellbeing. An interview survey on social relationships was also conducted. Dried blood spot (DBS) samples were collected to assess the level of inflammation by high-sensitivity C-reactive protein (hs-CRP) concentration. hs-CRP concentration will be measured by an enzyme-linked immuno-sorbent assay (ELISA) method. For statistical analysis, the association between the possible determinants of inflammation and hs-CRP concentration will be examined by multiple regression analysis. The following possible determinants of inflammation are planned to be considered in the analysis: age, sex, body mass index (BMI), smoking, economic status, education, occupation, living alone, hometown, WHO-5 score, DII score, and social relationships.

Asymptomatic infections with enteric viruses and the association with gut microbiome in rural residents of Northern Laos

ラオス北部における腸管系ウイルス不顕性感染と腸内細菌叢との関連

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Introduction

Presence of asymptomatic infections of enteric viruses makes it difficult to prevent and control their spread. However, individual factors that are associated with asymptomatic infections of enteric viruses have not been systematically clarified. The objectives of the present study were: 1) to investigate the prevalence of asymptomatic infections of enteric viruses among rural residents in Northern Laos; and 2) to compare individual characteristics including gut microbiome diversity and composition between asymptomatic carriers of enteric viruses and non-carriers.

Methods

The present study was conducted in rural residents who inhabited three villages (Nam Nyon, Na Savang, and Na Lae) in Oudomxay province, Northern Laos. Stool samples were collected in August 2018, and March 2019 from participants without diarrhea and high fever. Enteric viruses (norovirus GI, norovirus GII, rotavirus, and human adenovirus) were detected by RT-PCR or PCR. Individual characteristics were compared between asymptomatic carriers of enteric viruses and their non-carriers.

Results

Overall, of 255 samples, 12 (4.7 %) were positive for norovirus GI, 8 (3.1%) for human adenovirus, and 1 (0.4%) for norovirus GII. Gut microbiome analysis showed higher microbial diversity (evaluated by the number of operational taxonomic unit) in asymptomatic carriers of norovirus GI or human adenovirus than their non-carriers. Gut microbiome composition was significantly different between asymptomatic carriers of norovirus GI or human adenovirus and their non-carriers.

Conclusion

Asymptomatic infections with enteric viruses might be associated with gut microbiome diversity and composition in Norther Laos.

Modernization, Trace Element Exposures, and Oxidative Stress among Indigenous Populations in Northern Laos

ラオス北部住民における近代化、微量元素曝露、および酸化ストレスの関連

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Introduction

Modernization-induced changes in lifestyles may impact oxidative stress in indigenous populations. Exposure to trace elements also may change due to modernization and be associated with oxidative stress; thus, the exposure can be a determinant of oxidative stress in subsistence society undergoing modernization. This study aimed to examine associations among modernization, trace element exposures, and oxidative stress among indigenous populations in Northern Laos.

Methods

This study included 341 adults of three villages with different modernization levels. We measured urinary concentrations of trace elements (arsenic, cadmium, and selenium) and oxidative stress markers (8-hydroxy-2'-deoxyguanosine [8-OHdG] and 8-isoprostane) with inductively coupled plasma mass spectrometry and liquid chromatography tandem mass spectrometry, respectively. We conducted multilevel analysis to examine differences in urinary concentrations of trace elements and oxidative stress markers among villages and associations between urinary trace element and oxidative stress marker concentrations.

Results

Higher arsenic, selenium, and 8-OHdG and lower cadmium concentrations in urine were observed in more modernized village(s), while there are no village differences in urinary 8-isoprostane concentration. Urinary arsenic and cadmium concentrations were positively associated with urinary 8-isoprostane concentration. The positive association between urinary cadmium and 8-isoprostane concentrations was stronger when urinary selenium concentration was lower.

Conclusions

Modernization may be associated with trace element exposures and oxidative stress among indigenous populations in Northern Laos, while the associations were more complex than expected. Additionally, this study suggested that their trace element exposure is associated with inter-individual variation in oxidative stress, especially oxidative lipid damage.

A Regional History in Oceania Viewed from the Genealogy of Banana Cultivars of Japan and Palau 日本およびパラオのバナナ品種に対する系統解析によるオセアニア地域史の考察

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Introduction

The purpose of this study is to reveal the historical interaction between various regions of Japan and Palau, by comparing banana cultivars mainly using DNA analysis. Distribution, dispersal processes and intercomparison of banana cultivars have been rarely examined in Oceania. Since domesticated banana cultivars reproduce only by vegetative reproduction, constructing a phylogenetic tree would indicate the history of human interaction. The analysis of banana cultivars is an effective method in clarifying the regional history and exploring the origins of agriculture in Oceania and Asia.

Subjects and Methods

Banana cultivars were sampled in Ogasawara Islands, Hachijo, Ryukyu Islands, and Palau, which are historically included/excluded in "Japan" and geographically considered as a part of Oceania. Morphological classification and interviews on local names, origins, and usage were conducted, with referring historical documents to interpret the phylogenetic tree. Genomic DNA was extracted from each sample of leaf piece using an extraction kit. A restriction site associated DNA (RAD) library for high-throughput DNA sequencing was constructed according to the Flexible ddRAD-seq method. Molecular phylogenetic analysis was run using maximum likelihood approach-based a software: IQ-TREE

Results and Discussion

Phylogenetic results of AAB genotype group were consistent with the description of the previous study that this group was brought from Oceania Islands. Results of ABB genotype group propose continuous intermigration of banana cultivars between Ogasawara, Hachijo, and "Nanyo," although not all cultivars were brought from "Nanyo." Considering productivity and nutritional value, the contribution and distribution of ABB cultivars to human adaptation to the environment in the Oceanian Islands should not be ignored. Results of AAA genotype group is consistent with interview data from the Ogasawara and Hachijo informants, who stated this cultivar was brought from Taiwan. Such as "Cavendish" and "Lakatan," which are named in the global market, were probably brought in from Asian plantations, the diversity of banana cultivars of subject regions keeps changing in the global market today. "Our study" in Bangladesh for 13 years バングラデシュでの 13 年間の「我々の研究」

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<u>Background</u>: Over 30 million people in Bangladesh have been exposed to arsenic via drinking groundwater. Many studies on the health effects of arsenic have focused on skin lesions and cancers. However, accumulating evidence has shown that arsenic exposure is also associated with the risk of common diseases, such as hypertension, diabetes, and respiratory diseases, although the underlying mechanisms remain unclear.

<u>Purpose and methods</u>: In collaboration with Prof. Hossain at Rajshahi University, we have attempted to clarify the dose-response relationship between arsenic exposure levels and hypertension, diabetes, and asthma, as well as the underlying mechanisms. For that purpose, we measured arsenic concentrations not only in drinking water but also hair and nails of individuals and various blood biomarkers.

<u>Hypertension</u>: The primary question is why non-obese rural residents in Bangladesh exposed to arsenic showed higher incidences of metabolic disorders, such as hypertension and diabetes. As the biomarker for hypertension, we measured serum levels of Big-endothelin-1 (a precursor of vasoconstrictor endothelin-1) and exhaled levels of nitric oxide (a vasodilator). We found a dose-dependent increase in Big endothelin-1 and a decrease in exhaled NO by arsenic exposure. We also found increases in oxidized LDL, vascular adhesion markers (VCAM-1 and ICAM-1), inflammation markers (CRP), and a decrease in HDL in the serum of arsenic-exposed residents. These results suggest that arsenic is a vascular toxicant inducing atherosclerosis and hypertension.

<u>Diabetes</u>: To clarify the cause of arsenic-induced diabetes, we conducted a glucose tolerance test and found that arsenic exposure enhances insulin resistance. Currently, we are exploring the possible involvement of arsenic-induced muscular loss as a cause of insulin resistance.

<u>Asthma</u>: To test whether arsenic exposure causes asthma, we conducted a respiratory function test using a portable spirometer (Hi-checker). We found that about 10% of the arsenic-exposed residents showed characteristics indicative of asthma accompanied by elevated serum levels of IgE and Th2 cytokines. These results suggest that arsenic exposure enhanced type 2 inflammation, leading to higher sensitivity to allergic asthma.

I will also refer to the word "our study."