

Tracing the History of the Japanese Population Using Genetic Diversity

遺伝的多様性からたどる日本人の集団史

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The Japanese population comprises three genetically distinct groups: the Ainu, Ryukyuan, and mainland Japanese. Genetic evidence supports the dual structure model, which proposes that mainland Japanese are descendants of both the indigenous Jomon people and immigrants who arrived primarily from the Korean Peninsula during the Yayoi to Kofun periods. Approximately 13% of the mainland Japanese genome is estimated to have originated from the Jomon ancestry. Our research further suggests that most of these immigrants came to the Japanese archipelago during the same period (Kim et al., 2024).

To explore the regional patterns of genetic variation, we conducted principal component analysis (PCA) using allele frequencies at single nucleotide polymorphisms from individuals across all 47 prefectures (Watanabe et al., 2021). PCA revealed a clear geographic structure: neighboring prefectures clustered closely, suggesting limited long-distance gene flow and a history of local migration and intermarriages. The first component appeared to reflect genetic affinity for Jomon. Okinawa, known for its Ryukyuan population with high levels of Jomon ancestry, is positioned far from the Kinki and Shikoku regions, which exhibited the lowest Jomon affinity.

We further identified Jomon-derived alleles and calculated the Jomon Allele Score (JAS) for individuals from 46 prefectures (excluding Hokkaido) (Watanabe and Ohashi, 2023). Okinawa had the highest average JAS, followed by the prefectures in the Tohoku and Kyushu regions. In contrast, the Kinki and Shikoku regions exhibited lower JAS values, indicating a higher proportion of immigrant ancestry. Based on archaeological data, JAS was positively correlated with estimated population sizes during the Late Jomon period, suggesting that immigrants during the Yayoi period preferentially settled in regions where Jomon populations were smaller.

In addition, we estimated population-averaged polygenic scores for the Jomon and immigrant populations to assess the differences in complex traits between them. The results suggest that the Jomon were genetically predisposed to shorter stature and higher levels of triglycerides and glucose, whereas immigrants had genetic tendencies toward taller stature and elevated levels of C-reactive protein and eosinophils. These findings highlight the distinct genetic characteristics of ancestral populations, and illustrate how admixture has shaped the regional genetic diversity observed in modern Japanese populations.

Investigating the relationship between demand-supply related demographic variables and access to healthcare services

通所介護サービス施設の配置に影響するのは地域の労働人口か、高齢者人口か？

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Introduction

Currently, NPOs/NGOs (non-profit/non-governmental organizations) and companies are involved in the development of community-based integrated care systems. This change leads to a supply-demand balance consideration: a more labor-intensive area may be able to hire relatively inexpensive labor, reducing the operating costs of care facilities; however, such areas may lack sufficient demand from elderly people. In contrast, regions with many older people may be relatively remote, with a lack of labor that can be hired as a care service employee, making the salary much higher and difficult to operate continuously. Therefore, we aim to determine which factor plays a more important role: supply or demand.

Method

To understand the impact of changes in the supply and demand for care services on the elderly, accessibility is used to describe how easy it is for them to access care services. In this study, accessibility refers to the number of care employees that an elderly individual can seek within an average single-vehicle driving distance. The population data were described using the 500 m grid resolution Japan national census data in 2020, and the care facilities data were collected in June 2024 through the official portal site. A two-step floating catchment area (2SFCA) method was employed to calculate accessibility, and a machine learning-based Random Forest model was used to analyze the association between accessibility and supply-demand demographic variables for each grid.

Results

In Densely Inhabited District (DID) grids (commonly regarded as urban areas), accessibility is negatively associated with the proportion of males, whether working age or elderly. In non-DID grids (commonly regarded as rural areas), accessibility is negatively associated with the proportion and positively associated with any population size-related variable.

Conclusion

These findings suggest that in highly populated regions, sex differences may be an important factor associated with differences in the 2SFCA accessibility score for commuting care service facilities, whereas in less populated regions, the needs of the elderly are not undervalued, and the labor force (supply side effects) is relatively important.

Investigating Physical and Biological Aging: A Focus on Telomere Length

身体的老化および生物学的老化についての研究:テロメア長に焦点を当てて

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Abstract

Introduction

Telomere length (TL) is increasingly being considered an indicator of biological aging, influenced by chronological age, yet distinct from it. TL is being associated with age-related diseases and disabilities. Understanding the determinants of TL and their relationship with physical aging parameters is crucial for promoting healthy aging strategies.

Methods

This study integrates a systematic review approach to understand which physical aging parameters reflect biological aging, and population-based analysis findings for the factors associated with successful biological aging in the Japanese community.

Results

The subjective measures of physical aging are sensitive indicators of biological aging. The composite measures of physical performance/ability demonstrated a strong and consistent parameter of physical aging linked with TL. This population-based study highlighted the influence of social determinants, lifestyle factors, and micronutrient levels on biological aging, as reflected by TL.

Conclusion

While physical aging, which is more observable, offers a tangible way for individuals to monitor their health, TL serves as a valuable biomarker for assessing age-related health risks at the cellular level. This population-based study identified that educational attainment, employment status, smoking habits, and serum micronutrient levels play significant roles in biological aging. TL shortening is linked to age-related diseases and mortality, highlighting the potential benefits of mitigating premature TL shortening to reduce significant health risks.

Introduction of the Komo-Ise Cohort Study

こもいせコホート研究の紹介

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Abstract

The Komo-Ise study was established and conducted by Prof. Shosuke Suzuki, former Associate Professor at the Department of Human Ecology, and his colleagues. Prof. Suzuki designed the study in collaboration with Prof. Robert E. Roberts and Prof. George A. Kaplan, who conducted the Alameda County study, so that a US-Japan comparison could be made on the psychosocial factors related to health of elderly people. The Komo-Ise study was a prospective cohort study involving 11,565 individuals at baseline in 1993, whose mortality and migration data were collected until December 2008. Participants were recruited among the residents of a rural area, Komochi Village, and an urban area, Isesaki City, Gunma Prefecture, Japan. Several studies were conducted using this dataset. One of the most cited is Iwasaki et al. (2002), who revealed for the first time in Japan that more active social networks are associated with a lower mortality risk among middle-aged and elderly men and women. I and my colleagues have published four papers using this dataset (Konishi et al. 2016; 2018; 2022; Stickley et al. 2018). Here, I will introduce the Komo-Ise cohort study and its findings. The dataset is well-structured with a small number of missing values, which can be utilized to publish high-quality papers.

References

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**Observations during the Field Visit in Southern Ethiopia: Exploration of Gut
Microbiomes that Suppress Alcohol-Induced Toxicity**
南エチオピア予備調査報告: アルコール毒性を抑制する腸内細菌の探索プロジェクト

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Abstract

Alcohol is toxic to humans. Regular consumption beyond a certain threshold damages various organs, and a clear dose-response relationship exists between daily alcohol intake and the risk of non-communicable diseases. The Derashe in Ethiopia have a staple diet containing an alcohol called *Parshota*. It is a fermented grain product with an alcohol content of 3%, and adult males consume approximately 5 L/day. This equates to an alcohol intake of approximately 150 g (Sunano, 2016), roughly equivalent to five large bottles of beer with 5% alcohol content. However, cases of alcoholism or alcohol-related organ damage have rarely been reported in the Derashe society.

The human gut contains 1–2 kg bacteria. These bacteria survive on undigested food remnants and substances excreted in the human gastrointestinal tract. Recent studies have shown that the gut microbiota significantly affects disease risk, nutrition, and immunity. Metabolites synthesized by the gut bacteria can act as toxins, nutrients, or medications. The area with the least research is the "medications" produced by gut bacteria. Given that the gut bacteria possess over 100 times more genes than humans, certain bacterial metabolites absorbed from the gut can plausibly reduce alcohol toxicity in Derashe individuals. A human ecological study to clarify the mechanisms of alcohol detoxification is currently in the preparation stages.

In this presentation, I will provide an overview of the project and report my observations during my field visit in February 2025.

[Reference]

Sunano Y. (2016) Procedure of brewing alcohol as a staple food: case study of the fermented cereal liquor "Parshot" as a staple food in Dirashe special woreda, southern Ethiopia. Food Science & Nutrition, 4: 544-554.