

『Applicability of ancient genomics to decoding the legacy of human past in insular East Asia』

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日時

2023年 7月 25日(火) 16:30～17:30

場所

医学図書館 2階 十全記念スタジオ

要旨

Our chance of developing a particular disease is often dependent on our own genetic ancestry. Populations across the globe are distinct in their genomes due to demographic history and selective pressures, such as infectious diseases. Ancient genomes provide a powerful means to untangle episodes of growth, collapse, isolation and migration, as well as interactions with pathogens in the past. Our research specifically focuses on Japan, where the most significant cultural transformations have occurred in the last 3,000 years. These changes include the rapid shift from foraging to widespread rice farming, followed by the development of a technologically advanced imperial state. In this talk, I will explore the formation of Japanese populations, its regional variation, and pathogen loads imposed on these insular communities.

日本列島人の古代ゲノム解析からの最新の研究成果などについてご講演いただく予定です。申込みは不要です。皆様のご参加をお待ちしております。

■医学専攻Up-to-dateセミナーとして認定します。

■後援: 金沢大学十全医学会

■共催: 医薬保健研究域附属サピエンス進化医学研究センター

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