

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

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場所

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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.

申込みは不要です。皆様のご参加をお待ちしております。

■医学専攻および環境医科学専攻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