

Department seminar



日時 : 11 月 21 日 (月) 、 16:00-17:00

場所 : 工学部 3 号館 8B04

オンライン : <https://u-tokyo-ac->

[jp.zoom.us/j/83828422916?pwd=SkJ2cTdDU0NpRjcyOVdyWmxxaWxFdz09](https://u-tokyo-ac-jp.zoom.us/j/83828422916?pwd=SkJ2cTdDU0NpRjcyOVdyWmxxaWxFdz09)

ミーティング ID: 838 2842 2916 パスコード: 126363

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Functional analysis and interference of viral RNA interactions in dengue infection

The four serotypes of dengue virus (DENV) represent the most prevalent mosquito-borne viral pathogen that is endemic in >100 countries, with an estimated 390 million infections yearly. The infection occasionally develops into a potentially lethal complication called severe dengue (SD). Currently, no effective prevention and the therapeutic drug is available, and risk factors associated with developing SD are not identified. In this study, we profiled the global DENV RNA interactions with virus and host factors and pinpointed two specific, robust interactions onto the viral most conserved RNA elements in the 3' untranslated region (UTR) of the DENV genome. These included the unknown flaviviral promoter and the RNA aptamer against a human DEAD-box RNA helicase, DDX6. Interruption of the viral polymerase access to the promoter inhibited viral replication in infected cells. Moreover, a deletion in the DDX6 aptamer induced a live-attenuated virus strain. Our results suggested that viral RNA molecules have functional roles of the long non-coding RNA to specifically interact with viral and host factors to support the virus life cycle and pathogenesis.

このセミナーに関する連絡先

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協賛 JST-ERATO 鈴木 RNA 修飾生命機能プロジェクト