第553回 難研セミナー

第126回 難治疾患共同研究拠点セミナー

下記により難研セミナーを開催しますので、多数御来聴下さい。

記

- 日 時: H28 年 10 月 27 日 (木) 15:45~ 17:15
- 場 所: M&Dタワー23F 難研セミナー室
- 演者: Dr. Robert Gifford (MRC-University of Glasgow Centre for Virus Research)

演 題: Using endogenous retroviral (ERV) fossils data to explore the co-evolutionary relationships of retroviruses and vertebrates

要旨: Retroviruses (family Retroviridae) are reverse-transcribing RNA viruses that infect vertebrates. Uniquely among vertebrate viruses, retroviruses integrate a DNA copy of their genome into the genome of the infected cell as an obligate part of their life cycle. Consequently, retroviral infection of germ line cells can lead to integrated retrovirus sequences being inherited as host alleles, called endogenous retroviruses (ERVs). ERVs can proliferate within their host genomes via a range of mechanisms, including the production of infectious viruses that reinfect germ line cells, and intracellular retrotransposition in cis or trans. This talk will report the results of a long-term investigation into the co-evolutionary relationships of retroviruses can be reconstructed from ERV sequence data and analysed in vitro. Finally, I will examine how the distribution and diversity of ERVs has changed across the Cenozoic era, based on in silico analysis of over 200 vertebrate genomes, and discuss the molecular mechanisms and evolutionary selection pressures that have driven the proliferation of specific ERV lineages in particular mammalian species.

連絡先: エピジェネティクス分野 石野 (内線 4863)

共催:分子病態

The 553th Medical Research Institute Seminar The 126th Joint Usage/Research Program of Medical Research Institute Seminar

Date: Oct. 27, 2016 15:45-17:15

Venue: M&D Tower 23F Seminar room

Lecturer: Dr. Robert Gifford

Title: Using endogenous retroviral (ERV) fossils data to explore the co-evolutionary relationships of retroviruses and vertebrates

Summary:

Retroviruses (family Retroviridae) are reverse-transcribing RNA viruses that infect vertebrates. Uniquely among vertebrate viruses, retroviruses integrate a DNA copy of their genome into the genome of the infected cell as an obligate part of their life cycle. Consequently, retroviral infection of germ line cells can lead to integrated retrovirus sequences being inherited as host alleles, called endogenous retroviruses (ERVs). ERVs can proliferate within their host genomes via a range of mechanisms, including the production of infectious viruses that reinfect germ line cells, and intracellular retrotransposition in cis or trans. This talk will report the results of a long-term investigation into the co-evolutionary relationships of retroviruses and vertebrates. I will describe how functional versions of ancient, extinct retroviruses can be reconstructed from ERV sequence data and analysed in vitro. Finally, I will examine how the distribution and diversity of ERVs has changed across the Cenozoic era, based on in silico analysis of over 200 vertebrate genomes, and discuss the molecular mechanisms and evolutionary selection pressures that have driven the proliferation of specific ERV lineages in particular mammalian species.

Organizers: Department of Epigenetics

Co-organizer: Department of Molecular Pathogenesis