第５５７回 難研セミナー
第１３０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：２０１７年２月２７日（月） 15:00 ～ 17:00

場　所：難治疾患研究所 22 階セミナー室（MD タワー22F 北）

演　者：Prof. Narinder K. Mehra

(All India Institute of Medical Sciences)

演　題：Phylogenetic analysis of promoter regions of HLA class I genes: relevance in genetics of HIV infection

要　旨：

MHC is the most polymorphic region of the human genome and its components are associated with the genetic propensity to many diseases. We performed genomic and phylogenetic analysis for ~2kb upstream of the transcription start site of classical HLA class I genes. Our data indicate that promoter sequence divergence might directly impact promoter activity, leading to differential expression between lineages. In order to explore the genetic predisposition to HIV infection in the North Indian population, we performed candidate gene based studies. Particularly, we analyzed the genes that influence i) HIV cell entry, ii) viral replication as well as iii) pro and anti-inflammatory cytokines. These findings will also be discussed during the talk.

連絡先：分子病態分野・木村彰方（内線４９０５）
共催：ゲノム病理学分野・石川俊平

The 557th Medical Research Institute Seminar
The 130th Joint Usage/Research Program of Medical Research Institute Seminar

Date: Feb. 27 (Mon), 2017　15:00-17:00

Venue: MRI Seminar Room 22F　(M&D tower 22th Floor north)

Lecturer: Prof. Narinder K. Mehra (All India Institute of Medical Sciences)

Title: Phylogenetic analysis of promoter regions of HLA class I genes: relevance in genetics of HIV infection

Summary:
MHC is the most polymorphic region of the human genome and its components are associated with the genetic propensity to many diseases; however the mechanisms remain largely unknown. These may include allele specific expression of HLA which can partly be controlled by variants located within the untranslated regions of the HLA genes. We performed genomic and phylogenetic analysis for ~2kb upstream of the transcription start site of classical HLA class I genes.　A total of 68 alleles from 57 major lineages of classical HLA class I genes were analyzed by direct sequencing. The overall nucleotide diversity within this promoter segment roughly follows that seen within the coding regions (HLA-B>HLA-A>HLA-C). Our data indicate that promoter sequence divergence might directly impact promoter activity, leading to differential expression between lineages.
In order to explore the genetic predisposition to HIV infection in the North Indian population, we performed candidate gene based studies. Particularly, we analyzed the genes that influence i) HIV cell entry (chemokine coreceptors like CCR5, CCR2 and their ligands like CCL3L1), ii) viral replication (tripartite interaction motif 5 a (TRIM5α), apolipoprotein B mRNA-editing enzyme, catalytic polypeptide-like 3G (APOBEC), T cell/ transmembrane, immunoglobulin and mucin (TIM) family proteins, NFKB inhibitor like 1 (NFKBIL1) as well as iii) pro and anti-inflammatory cytokines. These findings will also be discussed during the talk.

Organizers: Molecular Pathogenesis/ Prof. Akinori Kimura/ ext. 4905

Co-organizer: Genomic Pathology (Prof. Shumpei Ishikawa)