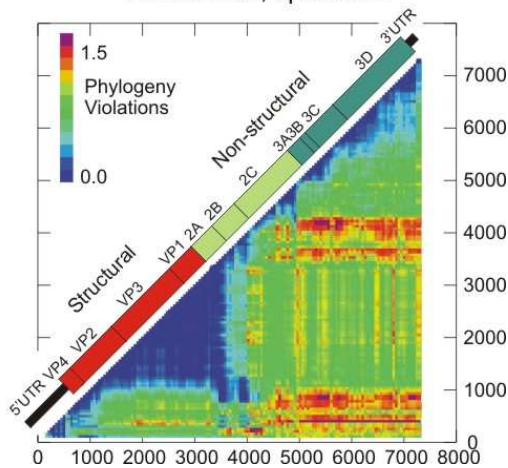


Enterovirus, species B



HIV PATHOGENESIS.

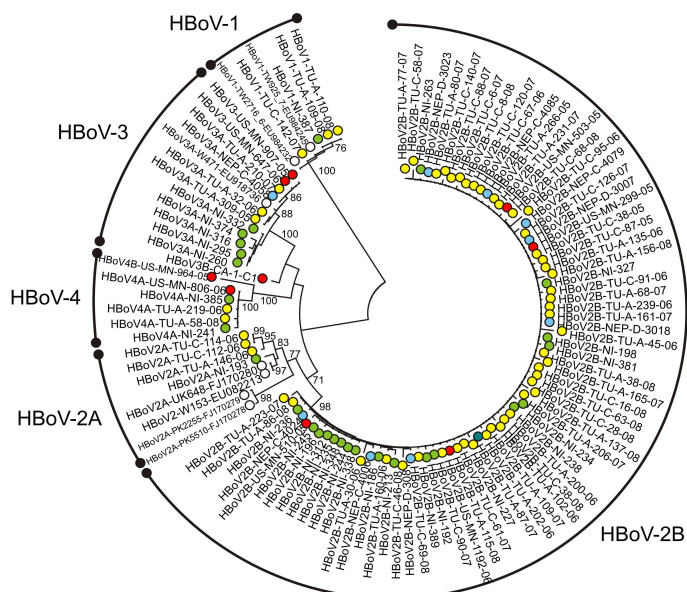
In the pathogenesis field, ongoing work follows our discovery of widespread infection of CD8 lymphocytes by HIV, and investigations of its potential contribution to the pathogenesis of AIDS. Recent findings that infected CD8 lymphocytes are a major virus reservoir that is productively infected and contribute substantially to the pool of replicating virus in late stage infection. These findings will fundamentally change current models of the pathogenesis of AIDS and the nature and aetiology of the immune collapse that underlies disease progression. Several studies in collaboration with Jeanne Bell from the Department of Neuropathology have documented the spread and micro-evolution of among HIV variants

recovered from different tissues of infected individuals. These have helped to illuminate the dynamics and mechanisms of HIV dissemination, the diversity of cellular targets in different tissues, and the potential adaptive changes that occur on infection of new cell types.

CLINICAL VIROLOGY.

I am involved in the development of molecular diagnostic assays with the Specialist Virology Laboratory, Royal Infirmary of Edinburgh. This work integrates assay development and clinically orientated virology research towards service development, molecular epidemiology investigations and evaluation of new or emerging viruses in human disease.

I have also initiated new studies on the prevalence and persistence of small DNA viruses, such as TT virus and relatives, human parvovirus B19, human bocavirus and PARV4, newly discovered human polyomaviruses and picornaviruses. The phylogenetic tree on the right shows the unexpected diversity and prevalence of human bocavirus type 1 (associated with paediatric respiratory disease) and the enteric types 2, 3 and 4 associated clinically with gastroenteritis among survey samples collected in Western countries and sub-Saharan Africa and the Indian sub-continent.



Recently we have developed new laboratory methods for investigation of the efficacy and resistance development arising from treatment of different genotypes of hepatitis C virus to protease inhibitors in development or current clinical trial. The project will determine the frequency and types of mutations associated with antiviral resistance observed among different genotypes of HCV, and develop rapid methods for phenotypic characterization of mutants amplified from clinical specimens.

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