

Preface

Eleven years ago the circular DNA of a novel single-stranded virus was cloned and partially characterized by Nishizawa, Okamoto and their colleagues. According to the initials of the patient from whom the isolate originated, the virus was named TT virus. This name has been subsequently changed by the International Committee on Taxonomy of Viruses (ICTV) into Torque teno virus, permitting the further use of the abbreviation TTV. Although initially suspected to play a role in non-A–E hepatitis, subsequent studies have failed to support this notion.

Within a remarkably short period of time it became clear that TT viruses are widely spread globally, infect a large proportion of all human populations studied thus far, and represent an extremely heterogeneous group of viruses, now labelled as Anelloviruses. TT virus-like infections have also been noted in various animal species. The classification of this virus group turns out to be difficult. Their DNA contains between 2,200 and 3,800 nucleotides, while related so-called TT mini-viruses and a substantial proportion of intragenomic recombinants further complicate attempts to combine these viruses into a unifying phylogenetic concept.

Although studied in many laboratories, the most interesting medical question concerning their possible pathogenic role in humans still remains unanswered today. We know of a substantial number of other infections that persist for life within infected individuals: members of the herpesvirus group, including the Epstein-Barr virus, and also polyomaviruses, such as BK and JC viruses, may serve as examples. In virtually all of these instances these viruses are able to induce human diseases, at least in some patients: e.g. Epstein-Barr virus may cause infectious mononucleosis and in immunosuppressed patients B cell lymphomas. BK and JC virus infections do not seem to cause acute conditions; immunosuppression, however, may result in BK virus-induced haemorrhagic cystitis or, in JC, virus-caused progressive multifocal leukoencephalopathy. Thus, it is not unreasonable to suspect that persistence of at least some specific TT virus genotypes may result in some infected individuals in a definable pathogenicity. We believe that this volume provides the first hints in support of this view.

When the editors were approached by Peter Vogt to compile a specific volume of *Current Topics in Microbiology and Immunology* on TT viruses, they were pleased and quickly agreed. For comparative purposes we also invited contributions on structurally related single-stranded DNA viruses, like chicken anaemia and plant

Gemini viruses. The response of invited contributors was exceedingly good and all of them delivered their contributions in time. We gratefully appreciate their help in compiling this volume, which seems to represent the first comprehensive documentation of this interesting virus group. We are also grateful to Springer, and specifically to Anne Clauss, for gently accompanying the editing and production process of this volume.

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TT Viruses

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