

On The Fringes of Life

THE VIRAL TREE OF "LIFE" Compiled by Jill Adams | April 12, 2004

In the late-19th century, scientists showed that certain infectious agents, such as those causing tobacco mosaic virus and yellow fever, were distinct from other microbes because they were so small. Still, it was presumed that they were living organisms until 1935 when tobacco mosaic virus was crystallized. The discovery of its acellular structure made viruses "seem more like nonliving chemical entities of disease," a view still held by many, writes Luis Villar-real of the University of California, Irvine, in an E-mail. Most definitions of life include the processes of metabolism, growth, and reproduction, which viruses cannot do on their own. But viruses can employ the machinery of the host cell to perform these functions. Further, viruses evolve over time, satisfying the long-term adaptation requirement of living things.

David Mindell of the University of Michigan suggests considering them as living, with recognition of their unique status. "Doing so provides better context for studies of the evolution of life," he writes in an E-mail. The study of viral origins and evolution has informed the mapping of their phylogenetic relationships. The International Committee on Taxonomy of Viruses <http://www.ncbi.nlm.nih.gov/ICTV> has considered descriptive criteria, including morphology, genome composition, pathogenicity, and mode of transmission to group viruses into orders, families, genera, and species.

TAKING ROOT IN OTHER TREES

Viruses may be on the fringe when it comes to the definition of life, but they are right in the heart of things when it comes to the phylogenetic tree of life.

1 "Viruses play a very fundamental role in the origin and evolution of all life," says Villarreal. "They are not merely pathogenic parasites. Genomic sequences now clearly indicate that viral footprints are everywhere."

Indeed, retroviral-like elements account for 8% of the human genome, including many human endogenous retroviruses (HERVs), the sometimes active remnants of ancient viral infections. The HERV database, a sequence collection on the Internet, contains information on hundreds of HERV families and subgroups.

2 HERVs have been grouped into three major classes.

Class I – related to gamma retroviruses and includes the subgroup HERV-W, which produces an envelope protein crucial in placental formation

Class II – related to beta retroviruses and includes proviruses in the HERV-K (HLM-2) subgroups, which appear only in humans

Class III – distantly related to spuma retro-viruses and includes HRV-L related to the murine endogenous retrovirus Fv-1, which confers resistance to a leukemia virus



