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Strain FV-21 of simian foamy virus type 1 was cloned and sequenced after isolation from the Taiwan monkey *Macaca cyclopsis*

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With the recent findings of rare human infections of animal handlers with simian foamy viruses (SFV) [1], of possible foamy virus infection of peripheral fibrocytes of a patient with chronic fatigue syndrome [2], and of the presence of human foamy virus (HFV) *gag* and *bel*-2 sequences in the thymus of patients in Taiwan with myasthenia gravis [3], it has become even more important to carefully document the exact strains of foamy virus used in research. Surprisingly, the original paper of Kupiec *et al* in 1991 [4] did not indicate the specific strain of SFV type-1 (SFV1) used for their cloning and complete nucleotide sequencing. However, in their other papers [4-6], they mentioned that the NIH strain was used. The NIH repository strain of SFV1 is FV-21, isolated in Taipei, from the Taiwan monkey *Macaca cyclopsis* [7]. It was used to prepare many vials of virus and horse anti-foamy virus antibody deemed at that time to be needed for the NIH repository [8]. That particular FV-21 strain of SFV1 was used because it had several desirable features, and because the earlier rhesus MK-D strain did not grow well in 1960, perhaps due to its inadvertent contamination with *Mycoplasma orale*.

Recently, while discussing experimental latent foamy virus infections of rabbits [9], I asked Dr. Saib to inquire of the coauthor, Dr. Jorge Peries as to the SFV1 strain sequenced, and he replied that the NIH strain was supplied by his collaborator Dr. George Todaro. Dr. Todaro did not respond to my inquiries; thus one must assume that there was no alternate rhesus strain sequenced, and that the NIH strain actually sequenced was the widely used FV-21 since it was accepted by the NIH as the NIH repository strain, and was used to immunologically characterize new isolates [7,8,10-12]. Further evidence of this appeared last month when Dr. Matthias Schweizer [13] listed the SFV1 as arising from *M. cyclopsis* and published the Genbank accession number X54482, as deposited by Dr. Kupiec including only his 1991 reference [4]. The X54482 sequence contains a sequence of additional recent interest [14], being identical to the 154-nt constitutive transport element (CTE) found in the Mason-Pfizer monkey virus (MPMV), a type D retrovirus. They also found this sequence in mouse intracisternal type A particles (MIAP), and provided evidence for the nucleus to cytoplasm RNA export role of the CTE as thus being a conserved region in these distantly related retroviruses, or in retrovirus-like elements, and therefore emphasized the universality of the CTE function of MPMV.

Strain designation is also crucial because instances occurred in which seemingly normal replication occurred even in the absence of the bet gene; other data [15] describe a persistent infection with SFV3 even in the absence of an intact orf-2 accessory gene. In addition [16], there is evidence that evolution of SFVs shows divergence with respect to the natural host, so that the *M. cyclopsis* strain of SFV1 might differ from the rhesus strains despite their identity seen by neutralization tests [7]. Since most retrovirus studies on variability have focused on the SU domain, Schweizer *et al* [13] reported a comparison of SU of all four primate FVs which had been completely sequenced (SFV1, 3, CPZ and HFV). They found very little difference in SU length or sequence, concluding that there is a high degree of stability within a given cluster of African green monkey (AGM) strains. This differs markedly from the variability of other retroviruses such as HIV which evolves as immune escape mutants, for example [17]. Within a single colony of AGM animals, there was also considerable stability of sequence of SU within each of the five clusters appearing since 1982. SU length among these clusters occurred as only two groups.

Earlier partial sequencing of SFV1 [18] also mistakenly referred to the NIH repository strain as a rhesus isolate, but Dr. Richard Heberling of San Antonio, Texas, USA, later documented the *Macaca cyclopsis* origin of the seed virus he had sent to Dr. Mergia [19]. SFV2 is the other simian foamy virus widely occurring in Taiwan monkeys [7] and the FV-

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34 Taiwan strain was recently studied in great detail [20] with regard to development of sensitive assays including molecular probes. These were compared and contrasted to properties of the FV-21 Taiwan isolate of SFV1.

Given the importance of viral strains in studying viral sequence variations, it is imperative that great care should be taken in annotating and documenting these strains and their simian origins.

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