Potent Inhibition of Human Immunodeficiency Virus Type 1 in Primary T Cells and Alveolar Macrophages by a Combination Anti-Rev Strategy Delivered in an Adeno-Associated Virus Vector

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The following correction pertains to all of the above articles.

The heavy chain of the D8 anti-Rev single-chain variable fragment (SFv) has been reanalyzed and demonstrated to be an aberrant heavy chain sequence. This heavy chain sequence is very close to the aberrant heavy chain sequence published by P. Thammana (Molecular Immunology **31:**77–78, 1994), who derived it via RT-PCR directly from the RNA of the NS1 cell line which is commonly used as a fusion partner to construct mouse hybridomas. Therefore, it is likely that the aberrant D8SFv heavy chain was derived from a gene originating from the fusion partner cell line used to make the original D8 hybridoma and not from the heavy chain gene expressed by the B-cell precursor to this hybridoma. This aberrant heavy chain has a deletion in the framework region 3 (FR3) leading to a frameshift in CDR3 and downstream regions of the heavy chain gene. In addition, there were some individual nucleotide changes, on reanalysis, that brought the heavy chain sequence even closer to that described by Thammana. It should also be noted that the function of the aberrant heavy chain in the D8SFv is not known. As well, the initial 12 amino acids in the D8SFv represent a portion of the Vκ leader sequence. The possible effects, if any, of this segment on subcellular localization and/or secretion have not been investigated.

There was noted to be rather minimal binding data for the D8SFv available to be reevaluated at this time, including only a single ELISA for the D8SFv to recombinant Rev and a single binding study of the activation domain peptide of Rev. Comparisons to the original D8 monoclonal antibody are not obtainable since the characteristics of the original monoclonal antibody are not fully demonstrated at the present time. As well, complete original data dealing with anti-Rev D10SFv binding to peptides of Rev are not available at the present time.

On reanalysis, inaccuracies in the D10SFv sequence were noted. D10SFv on resequencing showed the following differences compared to the published sequence: T58 to A (ACA to GCA), T106 to S (ACG to TCG), and G115 to A (GGT to GCT). Nucleotide changes which did not alter the amino acid sequence were: 81C to T, 315G to C, 354T to A, and 357T to A (numbering started at initial ATG codon). A nucleotide was demonstrated to be missing at position 771 (G) (L257), compared to the original sequence, altering the remaining amino acids (DYWGQGTSVTVSSAKTTPPPVYPLAPGS). On reevaluation, the originally reported D10 sequence would connote a frameshift in the CDR3 of V_h, but now, as resequencing revealed the missing nucleotide, the frameshift is shown not to be present. Thus, D10SFv is, in fact, an appropriate antibody sequence.

Although further studies are planned, these additional findings do not alter the previous conclusions that intracellular D8 and D10 SFvs inhibit HIV-1. We regret any difficulties these inaccuracies in the original publications may have caused.