

Response to “Interaction between HIV gp41 fusion peptide and T cell receptor: putting the puzzle pieces back together”

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In his letter, Dr. Alexander Sigalov suggests an alternative interpretation to our results mapping the domain of FP₁₋₃₂ that mediates the interaction with the TCR to the FP₅₋₁₃ region (1). He suggests that, in addition to FP₅₋₁₃, the C-terminus domain of FP₁₋₃₂ contains a region capable of inserting itself into the membrane and interacting with the CD3 subunits of the TCR, thereby impairing TCR function. We consider this alternative explanation unlikely for several reasons. First, we have synthesized and investigated FP₁₇₋₃₂ and found it inactive in all assays (unpublished data). Second, a mutant FP₁₋₃₂ termed V2E shows a diminished ability to interfere with the activation of T cells both *in vivo* and *in vitro* (2), despite the fact that the mutation in V2E is located in the N-terminus and not in the C-terminus of FP₁₋₃₂. Thus, if any inhibitory activity resides on the C-terminus of FP₁₋₃₂, it must be secondary to the activity of the N-terminus. Thirdly, the current working model describing the mechanism of action of FP₁₋₃₂ during membrane fusion in HIV infection suggests that FP₁₋₁₆ inserts into the target T-cell membrane, while the FP₁₇₋₃₂ region does not insert, but remains positioned parallel to the cell membrane (ref 1, Fig. 1) (3, 4). This positioning of the different domains of FP₁₋₃₂ does not allow the FP₁₇₋₃₂ region to insert into the membrane and interact with the CD3 subunits of the TCR complex as suggested by Sigalov.

The alternative interpretation suggested by Sigalov is based on the different potency manifested by FP₁₋₃₂, FP₁₋₁₆ and FP₅₋₁₃ in Figs. 1 and 7 of our manuscript (1). However, a careful comparison of Figs. 1 and 7 reveals that FP₁₋₃₂ and FP₅₋₁₃ have similar inhibitory efficiencies; moreover FP₁₋₃₂ and FP₁₋₁₆ (Fig. 2) have similar activities *in vivo*. Thus, we attribute the differences in

the efficiency of FP₁₋₁₆ and FP₁₋₃₂ not as an indicator of the existence of another independent inhibitory region, but as the result of the different solubility and state of aggregation of the different peptides; this effect seems to be more important for *in vitro* assays (Fig. 1), but less important for *in vivo* assays (Fig. 2). Indeed, FP₁₋₃₂ is known to form oligomers (2, 4); this multimerization is facilitated by the C-terminus increasing fusogenic activity of FP₁₋₃₂ (3, 4). Whether multimerization plays a role in the immunomodulatory activities of FP and its peptides is still unknown. Nevertheless, we believe that the above-mentioned data rule out the alternative interpretation put forward by Sigalov, that the C terminus region of FP₁₋₃₂ plays a significant role in its immunomodulatory activity. FJ

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