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Ebola virus infection, human Hsa-miR-1246, hsa-miR-320a and hsa-miR-196b-5p and predicted targets

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To the editor,

Sir, the present problematic Ebola virus (EBOV) infection in Africa is the global concern. The pathogenesis and host response to the EBOV infection is the interesting topic. Sheng et al. recently published an interesting article on the observation of "human Hsa-miR-1246, hsa-miR-320a and hsa-miR-196b-5p in human umbilical vein endothelial cells following expression of EBOV glycoprotein[1]." Sheng et al. mentioned that inhibiting those miRNA can result in protection against EBOV[1]. Sheng et al. also mentioned for observation of some target pathways relating to those miRNAs. Here, the authors use standard bioinformatics technique, Target Scan Human ("searching for the presence of conserved 8mer and 7mer sites that match the seed region of each miRNA[2]."), to assess the predicted targets of those miRNAs. The predicted results are present in Table 1. Of interest, the predicted target here is discordant with the report by Sheng et al[1]. (the adhesion-related molecules tissue factor pathway inhibitor, dystroglycan 1 and the caspase 8 and Fas-associated with death domain protein-like apoptosis regulator). The exact pathways and involved proteins in the inhibition of the three quote miRNAs should be further studied.

Table 1
Predicted target of Hsa-miR-1246, hsa-miR-320a and hsa-miR-196b-5p.

miRNA	Predict targets (the three best matched gene targets)
hsa-miR-1246	Family with sequence similarity 53, member C
	cAMP responsive element binding protein-like 2
	Anthrax toxin receptor 2
hsa-miR-320a	Lipid phosphate phosphatase-related protein type 1
	KIT ligand
	delta/notch-like EGF repeat containing
hsa-miR-196b-5p	No predicted target

Conflict of interest statement

We declare that we have no conflict of interest.

References

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