Reviewer's report

Title: Stability of glycoprotein gene sequences of herpes simplex virus type 2 from primary to recurrent human infection, and diversity of the sequences among patients attending an STD clinic.

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Reviewer: Sigvard Olofsson

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This is new information of relevance for our understanding of HSV recurrent infections. Genome sequence had been ideal to reveal all possible sequence differences that may occur during the course of HSV infection from primary infection and onwards. Owing to the size of the HSV genome and the relatively great number of specimens I sympathize with the authors choice of a few viral genes to be compared. Moreover, the choice of the glycoprotein genes is advantageous since these could be expected to be the most variable ones, and, hence, excellent probes for variation.

Major compulsory revisions: None

Minor essential revisions: It is true that the data do not reveal any recombination but it is to go to far to formally exclude the recombination possibility, not least since three of the four indicator genes map closely together in the unique short fragment of the HSV genome. I agree with the authors that their conclusion as to no recombination is quite likely, but the difficulties to completely exclude recombination should be commented.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests