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Reduced Levels of Mss1 in the ECP19 Cell Line May Influence HSV-1 Infection

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In addition to regulatory functions when associated with the 20S core proteasome, the ATPase proteins of the 19S cap have functions in transcription, translation, and DNA repair. During Herpes Simplex Virus Type-1 infection, we have shown that cellular chaperones and 20S proteasomes are recruited to specific sites in the nucleus called Virus-Induced Chaperone-Enriched domains. Mss1, one of the six ATPase subunits of the 19S regulatory cap, is also localized to VICE domains during HSV-1 infection, whereas the other five ATPases are not. The mouse cell line ECP19, has been shown to have reduced levels (3- to 7-fold) of Mss1 as compared to other cell lines. In another study, HSV-1 virus yield in ECP19 cells is reduced 100- to 1000- fold as compared to other cell lines. Real-Time PCR was used to determine the relative amounts Mss1 and the five other ATPase subunits in the ECP19 cell line as compared to two HSV-1-permissive mouse cell lines, L929 and A9. The L929 and A9 cell lines have a 7-fold higher level of Mss1 than is found in the ECP19 cell line. To investigate the impact of Rpt1 on HSV-1 infection a lentiviral expression system will be used to restore Rpt1 levels in the ECP19 cell line to levels similar to those found in the L929 and A9 cell lines. We predict that this will restore the permissivity of the ECP19 cell line for HSV-1 infection. The findings from this study will further understanding of the role of Mss1 on HSV-1 infection.