Washington University in St. Louis Washington University Open Scholarship

Volume 13

Washington University Undergraduate Research Digest

Spring 2018

Using the CRISPR/Cas9 System on Murine Cytomegalovirus

Trenton Dawson Washington University in St. Louis

Follow this and additional works at: https://openscholarship.wustl.edu/wuurd_vol13

Recommended Citation

Dawson, Trenton, "Using the CRISPR/Cas9 System on Murine Cytomegalovirus" (2018). *Volume 13*. 49. https://openscholarship.wustl.edu/wuurd_vol13/49

This Abstracts A-I is brought to you for free and open access by the Washington University Undergraduate Research Digest at Washington University Open Scholarship. It has been accepted for inclusion in Volume 13 by an authorized administrator of Washington University Open Scholarship. For more information, please contact digital@wumail.wustl.edu. TOWARD A BETTER UNDERSTANDING OF ...

USING THE CRISPR/CAS9 SYSTEM ON MURINE CYTOMEGALOVIRUS Trenton Dawson

Mentor: Wayne Yokoyama

The CRISPR/Cas9 system is a recently developed tool to quickly edit genomes. While most CRISPR research examines eukaryotic genomes due to their DNA repair processes, this project examines the use of CRISPR on murine cytomegalovirus (MCMV). The goal of this work was to familiarize ourselves with using the system on a virus. Since the CRISPR/Cas9 system cuts the DNA in a precise location but NHEJ is an imprecise method, the method of inactivation is largely unknown. Genes can be inactivated but their exact inactivating mutation can be quite unpredictable. We hope to use our findings to better characterize the molecular events that are occurring. Gene inactivation using the CRISPR/Cas9 system has extensive applications in the field of health and genetic research. Studies such as those described above examining the method of gene inactivation will help us to determine exactly how this complex functions.

Since the herpes viral family is non-zoonotic, trial and manipulation of the human herpes virus is difficult. Murine cytomegalovirus falls in the herpes cluster and provides a convenient and accessible analogue due to its remarkable similarity to human herpes virus and mouse host. After optimizing MCMV knockout methods, we explored the virus's immunoevasion capabilities through its ability to downregulate MHC-I receptors and elude NK cells. Using the CRISPR system on non-eukaryotic genomes, specifically those that evade the immune system with unknown molecular pathways, provides insight into viral-host interactions and using the CRISPR tool in novel ways.