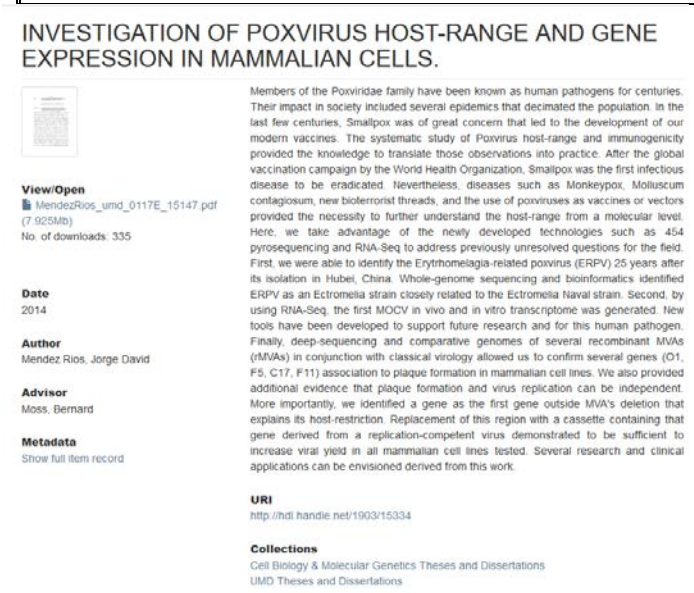
Año	Título de la Publicación	Nombre de la Revista / Libro	Vínculo o DOI	Indexador	Autoría
2014	[Investigación de genes relacionados al hospedero, y expresión génica de Poxviruses en células mamarias]	DRUMS	http://drum.lib.umd.edu/handle/1903/15334	DRUMS	PA,AC
Importancia: La tesis resume a precisión 3 proyectos relacionados a viruses Pox. Estos proyectos fueron llevado en su totalidad por mi persona, encontrando respuesta a preguntas de décadas en el campo de Poxvirus. 1) Identificación de un virus de Wuhan, China, aislado y secuenciado por NGS. 2) Primera descripción de la cascada de expresión génica del Molusco contagioso por NGS, 3) Identificación de múltiples genes asociadas al hospedero de los Poxvirus.					



INVESTIGATION OF POXVIRUS HOST-RANGE AND GENE EXPRESSION IN MAMMALIAN CELLS.

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Members of the Poxviridae family have been known as human pathogens for centuries. Their impact in society included several epidemics that decimated the population. In the last few centuries, Smallpox was of great concern that led to the development of our modern vaccines. The systematic study of Poxvirus host-range and immunogenicity provided the knowledge to translate those observations into practice. After the global vaccination campaign by the World Health Organization, Smallpox was the first infectious disease to be eradicated. Nevertheless, diseases such as Monkeypox, Molluscum contagiosum, new bioterrorist threads, and the use of poxviruses as vaccines or vectors provided the necessity to further understand the host-range from a molecular level. Here, we take advantage of the newly developed technologies such as 454 pyrosequencing and RNA-Seq to address previously unresolved questions for the field. First, we were able to identify the Erytrhomelagia-related poxvirus (ERPV) 25 years after its isolation in Hubei, China. Whole-genome sequencing and bioinformatics identified ERPV as an Ectromelia strain closely related to the Ectromelia Naval strain. Second, by using RNA-Seq, the first MOCV in vivo and in vitro transcriptome was generated. New tools have been developed to support future research and for this human pathogen. Finally, deep-sequencing and comparative genomes of several recombinant MVAs (rMVAs) in conjunction with classical virology allowed us to confirm several genes (O1, F5, C17, F11) association to plaque formation in mammalian cell lines. We also provided additional evidence that plaque formation and virus replication can be independent. More importantly, we identified a gene as the first gene outside MVA's deletion that explains its host-restriction. Replacement of this region with a cassette containing that gene derived from a replication-competent virus demonstrated to be sufficient to increase viral yield in all mammalian cell lines tested. Several research and clinical applications can be envisioned derived from this work.

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