Viral Whole Genome Sequencing for Antiviral Resistance in a Child with DOCK8 Deficiency and Recurrent HSV-1

Sean Stout
*Children's Mercy Hospital*, sstout@cmh.edu

A. L. Greninger

Rangaraj Selvarangan
*Children's Mercy Hospital*, rselvarangan@cmh.edu

A. F. Freeman

Brandon D. Newell
*Children's Mercy Hospital*, bnewell@cmh.edu

See next page for additional authors

Follow this and additional works at: [https://scholarlyexchange.childrensmercy.org/posters](https://scholarlyexchange.childrensmercy.org/posters)

Part of the Infectious Disease Commons, Medical Genetics Commons, Pediatrics Commons, Skin and Connective Tissue Diseases Commons, and the Virus Diseases Commons

**Recommended Citation**
Stout, Sean; Greninger, A. L.; Selvarangan, Rangaraj; Freeman, A. F.; Newell, Brandon D.; Stahl, Erin; and Yin, Dwight, "Viral Whole Genome Sequencing for Antiviral Resistance in a Child with DOCK8 Deficiency and Recurrent HSV-1" (2019). *Posters*. 111.
[https://scholarlyexchange.childrensmercy.org/posters/111](https://scholarlyexchange.childrensmercy.org/posters/111)

This Poster is brought to you for free and open access by SHARE @ Children's Mercy. It has been accepted for inclusion in Posters by an authorized administrator of SHARE @ Children's Mercy. For more information, please contact library@cmh.edu.
Authors
Sean Stout, A. L. Greninger, Rangaraj Selvarangan, A. F. Freeman, Brandon D. Newell, Erin Stahl, and Dwight Yin

This poster is available at SHARE @ Children's Mercy: https://scholarlyexchange.childrensmercy.org/posters/111
Viral Whole Genome Sequencing for Antiviral Resistance in a Child with DOCK8 Deficiency and Recurrent HSV-1

Stout SC1; Greninger AL2; Selvarangan R1; Freeman AF3; Newell BD1; Stahl ED1; Yin DE1

1Children’s Mercy and Univ Missouri, Kansas City, MO; 2Univ Washington, Seattle, WA; 3National Institutes of Health, Bethesda, MD

Background

- Patients with dedicator of cytokinesis 8 (DOCK8) deficiency are prone to severe recurrent or chronic mucocutaneous herpes simplex virus (HSV) infections
- HSV strains may develop antiviral resistance over time
- We present the case of a child with DOCK8 deficiency and chronic, resistant HSV-1 mucocutaneous infections to illustrate clinical utility of viral whole genome sequencing to detect active and latent HSV resistance mutations

Methods

- Abstracted medical record data longitudinally
- Collected HSV-1 DNA from 7 stored viral culture specimens from 2015-2018
- HSV-1 DNA sequenced on an Illumina® MiSeq to >150X depth
  - Consensus genomes called using established HSV genome pipeline
  - Reads mapped to the HSV-1 strain reference genome (NC_001806)
- Sequence variants were checked against an online database of antiviral resistance mutations in:
  - UL23 (thymidine kinase)
  - UL30 (DNA polymerase)

Patient History

- 14 year-old boy with DOCK8, diagnosed at age 6
- Initial presentation:
  - Severe eczematous dermatitis
  - Eosinophilia, elevated IgE (initial 9660 kU/L)
  - Low CD4+ T cells (initial 248 cells/mm³)
- Complications:
  - Chronic obstructive and interstitial lung disease
  - Recurrent infections:
    - Staphylococcus aureus skin infections
    - Candida albicans thrush
    - JC virus causing possible PML
    - HSV-1
- Prophylaxis: subcutaneous IgG, trimethoprim-sulfamethoxazole, acyclovir
- Mucocutaneous HSV-1 infections, biopsy confirmed HSV vegetans (Figures 1 and 2)
- Clinical response to acyclovir IV decreased over time
  - Advanced therapies to high-dose acyclovir IV, foscarnet IV, cidofovir IV, topical cidofovir cream, and/or interferon-alpha with variable clinical response

Results: Resistance Assays

- Phenotypic testing:
  - Detected acyclovir resistance in HSV isolated from four samples while patient was on acyclovir
  - No resistance in a sample while not on acyclovir
  - Phenotypic foscarnet resistance was detected in one sample without prior patient exposure to foscarnet
- Viral whole genome sequencing:
  - Detected the UL23 variant R176Q (associated with acyclovir resistance) on all specimens, whether on acyclovir or not
  - Detected the UL30 variant T821M (associated with acyclovir and cidofovir resistance) only when on cidofovir
- When phenotypic testing and genome sequencing were discordant, clinical response appeared to be more consistent with genome sequencing results

Conclusions

- This patient with DOCK8 deficiency illustrates the potential severity of chronic, resistant mucocutaneous HSV-1 infection
- Viral genome sequencing for antiviral resistance mutations may provide additional information about the presence of clinically significant variants, which may result from detecting smaller or latent HSV-1 sub-populations