BIOGRAPHICAL SKETCH

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NAME: Goodrum, Felicia D.

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POSITION TITLE: Professor of Microbiology and Immunology

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Virginia Tech, Blacksburg, VA	BS	01/1992	Biology
Wake Forest University School of Medicine, Winston-Salem, NC	PHD	01/1998	Molecular Genetics
Princeton University, Princeton, NJ	Postdoctoral Fellow	05/2006	Virology

A. Personal Statement

The major focus of my research program is to understand the virus-host interactions and mechanisms that regulate human cytomegalovirus (HCMV) infection and particularly those important to viral latency. We have identified viral genes important to latency and have worked to define the mechanisms by which they function through defining the host pathways they target. We have defined mechanisms by which viral factors mediate host endocytic trafficking and turnover of host receptors, growth factor singling, innate immune signaling and DNA damage responses. Our molecular virology approach is powerful in defining the complex cell biological pathways targeted or co-opted by HCMV for its infection. I have experience with mentoring young scientists at all levels. I have trained and mentored 9 postdoctoral fellows (5 currently in my laboratory), 9 PhD students (1 of these are currently in my laboratory) and 2 Masters of Science students. My laboratory and training environments are highly collaborative and multi-disciplinary. My dedication to my mentees, and particularly graduate training, is exemplified in my past leadership in directing the Graduate Program in Immunobiology and in Molecular Medicine and the development of professional development workshops and grant writing courses and workshops. I have been a co-Director of the T32 training program on Infection and Inflammation as Drivers of Aging (AG058503). I have served on over 20 dissertation committees and on 5 mentoring committees for junior faculty. I am excited to work with the trainers and trainees at Dartmouth College. I uphold the NIH standards of research reproducibility, responsible conduct of research while providing a safe training environment that strengthens trainees self-identifying as future scientists.

Ongoing and recently completed projects that I would like to highlight include:

R37 AI079059 (NIH/NIAID)
PI: Goodrum
07/30/2008-08/31/2029
Mechanisms of Human Cytomegalovirus Latency in Primary Human Hematopoietic Cells

R01 AI177392
Goodrum/Bosco (MPIs)
06/16/2023 – 05/31/2028
Host DNA Repair Pathways in Human Cytomegalovirus Replication

R01 AI169728
PI: Goodrum
02/07/2022-01/31/2026
Virus-host interactions regulating innate signaling for human cytomegalovirus latency

P01 AI127335 (Oregon Health & Science University [NIH/NIAID])
PI: Nelson | Role: Co-I
07/31/2017-07/31/2027

Human Cytomegalovirus Dysregulation of Host Hematopoietic Progenitor Cell Signaling Pathways to Modulate Latency, Reactivation and Hematopoiesis During Transplantation

1. Zeltzer, S., P. Longmire, M. Svoboda, G. Bosco, and **F. Goodrum**. 2022. Host translesion polymerases are required for viral genome integrity. *Proc Natl Acad Sci USA*, 119(33):e2203203119. PMID: 35947614
2. Longmire, P., S. Zeltzer, K. Zarrella, G. Bosco, **F. Goodrum**. 2025. Complex role for proliferating cell nuclear antigen in restricting human cytomegalovirus replication. *mBio,* Mar25:e0045025. PMID:40130902
3. Collins-McMillen, D.$^{\delta}$, D. De Oliviera-Pessoa, K. Zarrella, N.J. Moorman, J. P. Kamil, P. Caposio, M. Padi, **F.D. Goodrum**. 2025. Viral and host network analysis of the human cytomegalovirus transcriptome in latency. *Proc. Natl. Acad. Sci. USA*,122(22): e2416114122. PMID:40434638
4. **Goodrum, F.** 2022. The complex biology of human cytomegalovirus latency and reactivation. In *Adv.Virus Res.* v112. Aug 1. PMID: 35840181

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2025 -	Professor, Geisel School of Medicine, Dartmouth College, Microbiology and Immunology
2022 -	coEditor in Chief, *Journal of Virology,* American Society of Microbiology (ASM)
2020 - 2022	President-elect and President, American Society for Virology
2019 - 2025	Professor, University of Arizona, Department of Immunobiology, Tucson, AZ
2019 - 2022	Editor, Journal of Virology
2018 - 2022	Councilor of Animal Viruses, American Society for Virology
2017 - 2020	Editor, Virology
2015 - 2021	Standing member, National Institutes of Health, Virology A Study Section
2013 - 2019	Associate Professor, University of Arizona, Department of Immunobiology, Tucson, AZ
2006 - 2025	Research Scientist, BIO5 Institute, University of Arizona
2006 - 2013	Assistant Professor, University of Arizona, Department of Immunobiology, Tucson, AZ

Honors

2023 - 2024	Executive Leadership in Academic Medicine (ELAM), fellow
2008 - 2012	Pew Scholar in the Biomedical Sciences, Pew Charitable Trust
2005 - 2010	Howard Temin Career Development Award, National Cancer Institute
2003 - 2006	Special Fellow, Leukemia and Lymphoma Society
2000 - 2003	Fellow, Leukemia and Lymphoma Society
2023	Woman of Impact, University of Arizona
2022	Edith Sayer Auslander Emerging Visionary, University of Arizona's Commission on the Status of Women
2020	MERIT Award, National Institutes of Allergy and Infectious Disease
2019	Fellow, American Academy of Microbiology
2014	Jamie McNew Endowed Lecturer, University of Minnesota
2013	Distinguished Speaker for Graduate Hooding Ceremony, Wake Forest University
2012	Robert Honess Lecturer, American Society for Virology
2012	Top 25 Reviewers, Journal of Virology
2010	Priscilla Schaffer Lectureship, International Herpesvirus Workshop
2009	Kavli Fellow, National Academy of Sciences
2009	Top 20 reviewers, *Journal of Virology*
2008	Presidential Early Career Award for Scientists and Engineers, Office of President Obama

C. Contribution to Science

1. Human Cytomegalovirus (HCMV), like all herpesviruses, establishes a life long infection called latency. Latency is the maintenance of viral genomes in a non-replicative state, and is marked in the host by sporadic subclinical reactivation events. Latency is poorly understood for HCMV and my early work took a genetic approach using bacterial artificial chromosome clones of HCMV to identify viral genes important for suppressing virus replication. Clinical strains, but not laboratory strains, establish a latent infection. We identified and mapped genes encoded within the UL*b*' region of the genome that were replication-

suppressive. We identified a polycistronic locus spanning *UL133-UL138* using a library of recombinant viruses. None of these genes had been studied previously. Recombinant viruses containing disruptions in *UL138* exhibited a loss of latency phenotype and replicated productively in CD34+ HPCs. *UL138* is now broadly recognized as a key determinant of latency that has spurred a number of studies in other laboratories. Other genes within the *UL133-UL138* locus are important for overcoming *UL138*-mediated suppression or for virus replication in hematopoietic cells or endothelia cells. Identifying viral genes important for the establishment of or reactivation from latency provide a strong foundation on which to understand mechanisms of latency and provide targets for therapeutic intervention.

a. Bughio F, Umashankar M, Wilson J, Goodrum F. Human Cytomegalovirus UL135 and UL136 Genes Are Required for Postentry Tropism in Endothelial Cells. J Virol. 2015 Jul;89(13):6536-50. PubMed Central PMCID: PMC4468499.
b. Umashankar M, Petrucelli A, Cicchini L, Caposio P, Kreklywich CN, Rak M, Bughio F, Goldman DC, Hamlin KL, Nelson JA, Fleming WH, Streblow DN, Goodrum F. A novel human cytomegalovirus locus modulates cell type-specific outcomes of infection. PLoS Pathog. 2011 Dec;7(12):e1002444. PubMed Central PMCID: PMC3248471.
c. Grainger L, Cicchini L, Rak M, Petrucelli A, Fitzgerald KD, Semler BL, Goodrum F. Stress-inducible alternative translation initiation of human cytomegalovirus latency protein pUL138. J Virol. 2010 Sep;84(18):9472-86. PubMed Central PMCID: PMC2937619.
d. Petrucelli A, Rak M, Grainger L, Goodrum F. Characterization of a novel Golgi apparatus-localized latency determinant encoded by human cytomegalovirus. J Virol. 2009 Jun;83(11):5615-29. PubMed Central PMCID: PMC2681962.

2. The *UL133-UL138* polycistronic gene locus encodes proteins that interact with one another, as well as host factors, and constitute system to sense and respond to host cues to modulate virus replication. Understanding these interactions and defining genetic or epistatic relationships has been a cornerstone of our work. *UL138* represses virus replication for latency, whereas *UL135* functions, in part, to overcome this repression for reactivation. Defects in reactivation associated with the loss of UL135 can be compensated by subsequent loss of *UL138* or by stabilizing a labile UL136 determinant of reactivation. This work suggested important interplay between genes encoded by the *UL133-UL138* locus in regulating latent and replicative states of infection.

a. Moy MA, Collins-McMillen D, Crawford L, Parkins C, Zeltzer S, Caviness K, Zaidi SSA, Caposio P, Goodrum F. Stabilization of the human cytomegalovirus UL136p33 reactivation determinant overcomes the requirement for UL135 for replication in hematopoietic cells. J Virol. 2023 Aug 31;97(8):e0014823. PubMed Central PMCID: PMC10506481.
b. Caviness K, Bughio F, Crawford LB, Streblow DN, Nelson JA, Caposio P, Goodrum F. Complex Interplay of the UL136 Isoforms Balances Cytomegalovirus Replication and Latency. mBio. 2016 Mar 1;7(2):e01986. PubMed Central PMCID: PMC4810493.
c. Caviness K, Cicchini L, Rak M, Umashankar M, Goodrum F. Complex expression of the UL136 gene of human cytomegalovirus results in multiple protein isoforms with unique roles in replication. J Virol. 2014 Dec;88(24):14412-25. PubMed Central PMCID: PMC4249117.
d. Umashankar M, Rak M, Bughio F, Zagallo P, Caviness K, Goodrum FD. Antagonistic determinants controlling replicative and latent states of human cytomegalovirus infection. J Virol. 2014 Jun;88(11):5987-6002. PubMed Central PMCID: PMC4093889.

3. To define mechanisms of latency, we have sought to understand how the UL133-UL138 proteins function using fibroblasts as a model for productive infection and in vitro (primary CD34+ hematopoietic progenitors and THP-1 cells) and in vivo model of latency. UL135 and UL138 antagonize the activity of one another by each targeting EGFR, a major receptor tyrosine kinase, but with opposing effects on the trafficking and signaling of EGFR. We have defined host protein co-opted by UL135 to regulate EGFR signaling and turnover. UL135 and UL138 together with EGFR comprise a molecular switch regulating HCMV latency and reactivation. We have shown that the EGFR stimulates Early Growth Response-1 (EGR-1) transcription factor and that this stimulates UL138 expression. EGR-1-stimulation of UL138 is importance to the establishment or maintenance of latency. The EGFR-EGR1-UL138 regulatory axis forms a positive

feedback that hardwires the virus into host biology to allow the virus to sense and respond to changes in the cell. Further demonstrating the importance of EGFR signaling in HCMV infection, our collaborative work with Drs. Jay Nelson, Dan Streblow, Patrizia Caposio (OHSU), and Andrew Yurochko, has identified a viral miRNAs targeting EGR-1 for reactivation.

a. Buehler J, Carpenter E, Zeltzer S, Igarashi S, Rak M, Mikell I, Nelson JA, Goodrum F. Host signaling and EGR1 transcriptional control of human cytomegalovirus replication and latency. PLoS Pathog. 2019 Nov;15(11):e1008037. PubMed Central PMCID: PMC6855412.
b. Mikell I, Crawford LB, Hancock MH, Mitchell J, Buehler J, Goodrum F, Nelson JA. HCMV miR-US22 down-regulation of EGR-1 regulates CD34+ hematopoietic progenitor cell proliferation and viral reactivation. PLoS Pathog. 2019 Nov;15(11):e1007854. PubMed Central PMCID: PMC6855405.
c. Rak MA, Buehler J, Zeltzer S, Reitsma J, Molina B, Terhune S, Goodrum F. Human Cytomegalovirus UL135 Interacts with Host Adaptor Proteins To Regulate Epidermal Growth Factor Receptor and Reactivation from Latency. J Virol. 2018 Oct 15;92(20) PubMed Central PMCID: PMC6158428.
d. Buehler J, Zeltzer S, Reitsma J, Petrucelli A, Umashankar M, Rak M, Zagallo P, Schroeder J, Terhune S, Goodrum F. Opposing Regulation of the EGF Receptor: A Molecular Switch Controlling Cytomegalovirus Latency and Replication. PLoS Pathog. 2016 May;12(5):e1005655. PubMed Central PMCID: PMC4878804.

4. Infection of hematopoietic cells results in a burst of viral gene expression that is gradually silenced for the establishment of latency. It is not yet understood how this transient gene expression contributes to the outcome of infection. Understanding how the viral program of gene expression is contributes to and is controlled for the establishment of latency and reactivation from latency is a major focus. Through collaboration, we have identified novel sequences in the major immediate early locus that specifically reactivate immediate early viral gene expression in hematopoietic cells in response to reactivation stimuli. Through our collaborative work with Drs. Nat Moorman (UNC, Chapel Hill) and Jeremy Kamil (Louisiana State University Health), we have shown that these elements are controlled by AKT signaling and the FOXO3a host transcription factor. Our work has further defined the viral transcriptome associated with latency and has begun to understand how host transcription factors associated with cellular programs of differentiation regulate viral latency and reactivation.

a. Domma AJ, Henderson LA, Goodrum FD, Moorman NJ, Kamil JP. Human cytomegalovirus attenuates AKT activity by destabilizing insulin receptor substrate proteins. J Virol. 2023 Sep 27;97(10):e0056323. PubMed Central PMCID: PMC10617551.
b. Zhang H, Domma AJ, Goodrum FD, Moorman NJ, Kamil JP. The Akt Forkhead Box O Transcription Factor Axis Regulates Human Cytomegalovirus Replication. mBio. 2022 Aug 30;13(4):e0104222. PubMed Central PMCID: PMC9426471.
c. Hale AE, Collins-McMillen D, Lenarcic EM, Igarashi S, Kamil JP, Goodrum F, Moorman NJ. FOXO transcription factors activate alternative major immediate early promoters to induce human cytomegalovirus reactivation. Proc Natl Acad Sci U S A. 2020 Aug 4;117(31):18764-18770. PubMed Central PMCID: PMC7414233.
d. Collins-McMillen D, Rak M, Buehler JC, Igarashi-Hayes S, Kamil JP, Moorman NJ, Goodrum F. Alternative promoters drive human cytomegalovirus reactivation from latency. Proc Natl Acad Sci U S A. 2019 Aug 27;116(35):17492-17497. PubMed Central PMCID: PMC6717278.

5. Our current focus is on dissecting the intersections between host pathways and viral proteins targeting them to define how the virus senses changes is the cell and responds by modifying its gene expression and infection state. Beyond EGFR, UL138-host interactions regulate innate immune signaling and DNA damage responses through its interaction with the UAF1-USP1 ubiquitin protease complex. UL138 sustains STAT1 signaling while directing DNA damage and repair pathways by stimulating the removal of a monoubiquitination from PCNA, which regulates its recruitment of cellular factors for DNA repair. Following from this, we have shown that HCMV recruits specialize translesion synthesis (TLS) host polymerases and that this is important for viral genome stability. In addition, we determined that the UL136 p33 isoform, which is required for virus reactivation, is targeted for rapid lysosomal turnover by the liver X receptor (LXR)-inducible degrader of low-density lipoprotein receptor (IDOL). IDOL is highly expressed in

undifferentiated hematopoietic cells but is rapidly downregulated by differentiation- a stimulus for reactivation. IDOL targets several other proteins important for maintaining lipid homeostasis in addition to low-density lipoprotein receptor (LDLR). This finding indicates that HCMV has evolved to sense changes in LXR signaling to make decisions around latency and reactivation. Collectively this work begins to define a complex network of host pathways commandeered by HCMV to regulate its infection states in the host. A foundational observation that underlies much of HCMV's control of host signaling (e.g., EGFR) is the means by which it alters endocytic sorting. Ongoing and future work will define how HCMV modulates host pathways through its control of protein trafficking.

a. Mlera L, Collins-McMillen D, Zeltzer S, Buehler JC, Moy M, Zarrella K, Caviness K, Cicchini L, Tafoya DJ, Goodrum F. Liver X Receptor-Inducible Host E3 Ligase IDOL Targets a Human Cytomegalovirus Reactivation Determinant. J Virol. 2023 Jul 27;97(7):e0075823. PubMed Central PMCID: PMC10373547.
b. Zarrella K, Longmire P, Zeltzer S, Collins-McMillen D, Hancock M, Buehler J, Reitsma JM, Terhune SS, Nelson JA, Goodrum F. Human Cytomegalovirus UL138 Interaction with USP1 Activates STAT1 in infection. bioRxiv. 2023 Feb 7; PubMed Central PMCID: PMC9934528.
c. Zeltzer S, Longmire P, Svoboda M, Bosco G, Goodrum F. Host translesion polymerases are required for viral genome integrity. Proc Natl Acad Sci U S A. 2022 Aug 16;119(33):e2203203119. PubMed Central PMCID: PMC9388158.
d. Zeltzer S, Zeltzer CA, Igarashi S, Wilson J, Donaldson JG, Goodrum F. Virus Control of Trafficking from Sorting Endosomes. mBio. 2018 Jul 24;9(4) PubMed Central PMCID: PMC6058287.

Complete List of Published Work in My Bibliography:
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