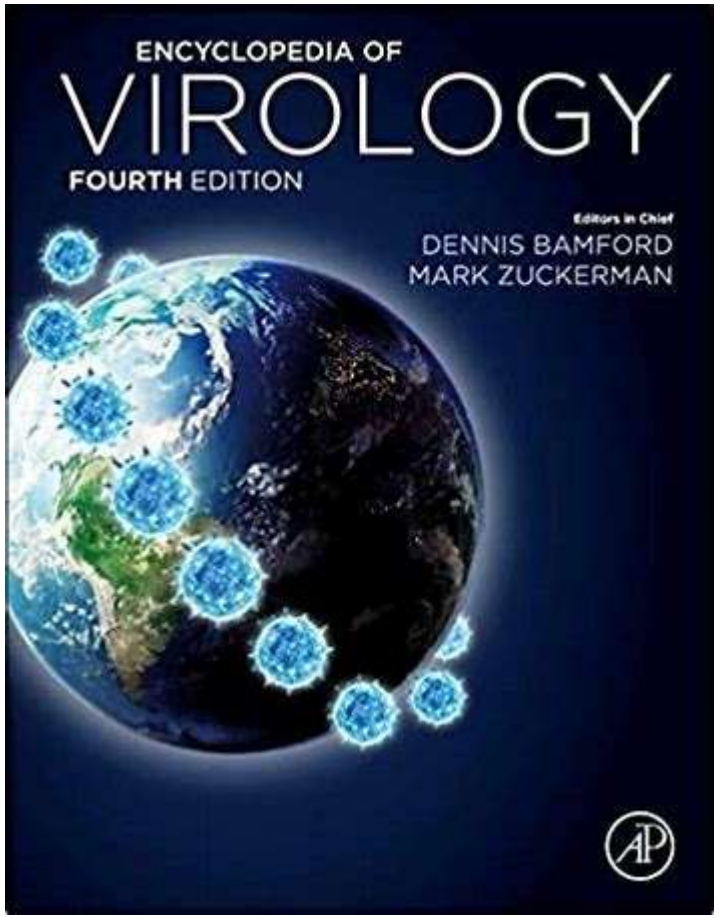
vitalant℠
Research Institute

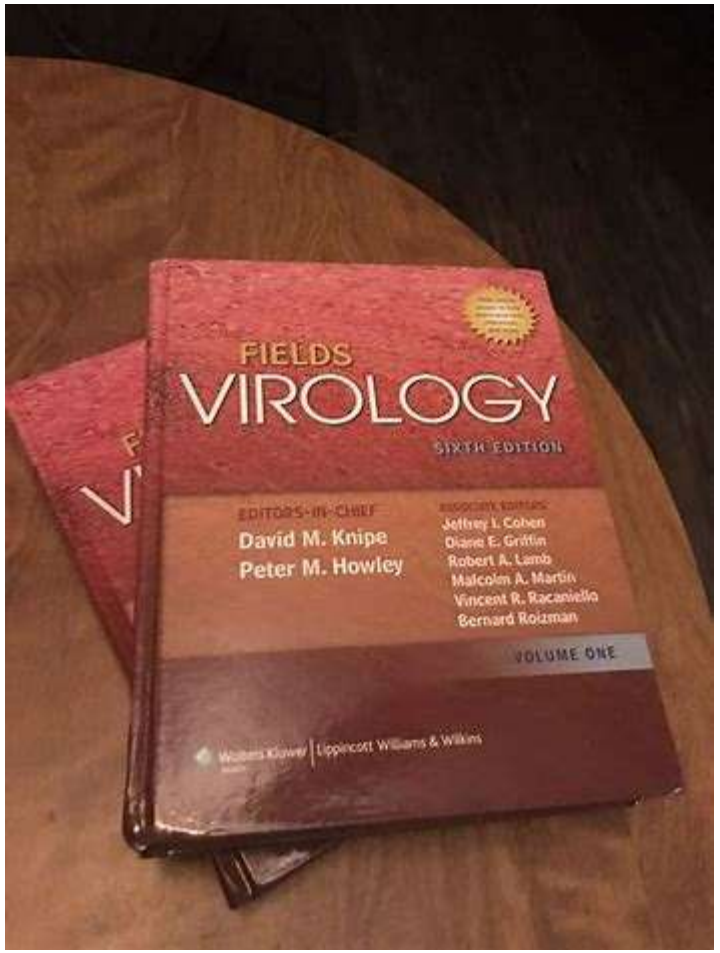
National Institutes of Health Human Virome Program (HVP)

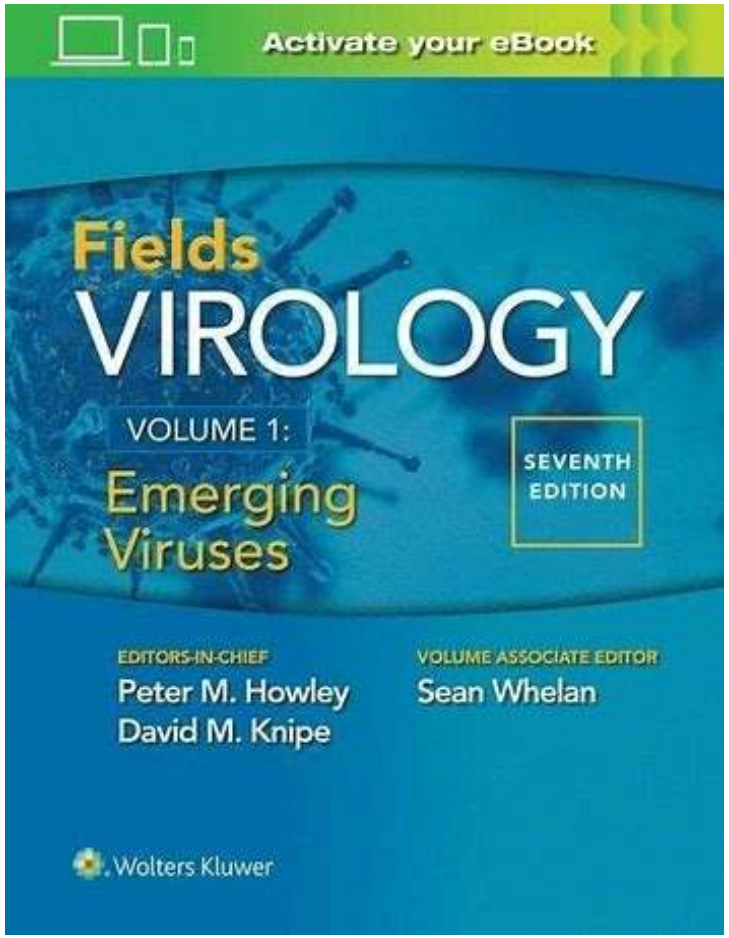
Michael Busch, MD, PhD

Vitalant Research Institute

Department of Laboratory Medicine, UCSF


ENCYCLOPEDIA OF
VIROLOGY
FOURTH EDITION
Editors in Chief
DENNIS BAMFORD
MARK ZUCKERMAN


FIELDS
VIROLOGY
SIXTH EDITION
EDITORS-IN-CHIEF
David M. Knipe
Peter M. Howley
Jeffrey I. Cohen
Diane E. Griffin
Robert A. Lamb
Malcolm A. Martin
Vincent R. Racaniello
Bernard Roizman
VOLUME ONE
Lippincott Williams & Wilkins


Activate your eBook
Fields
VIROLOGY
VOLUME 1:
Emerging
Viruses
SEVENTH
EDITION
EDITORS-IN-CHIEF
Peter M. Howley
David M. Knipe
VOLUME ASSOCIATE EDITOR
Sean Whelan
Wolters Kluwer

The NEW ENGLAND JOURNAL of MEDICINE
NEJM 369:22 2152-2158 2013

MEDICINE AND SOCIETY

Contagious Diseases in the United States from 1888 to the Present

Willem G. van Panhuis, M.D., Ph.D., John Grefenstette, Ph.D., Su Yon Jung, Ph.D., Nian Shong Chok, M.Sc., Anne Cross, M.L.I.S., Heather Eng, B.A., Bruce Y. Lee, M.D. Vladimir Zadorozhny, Ph.D., Shawn Brown, Ph.D., Derek Cummings, Ph.D., M.P.H., and Donald S. Burke, M.D.



TWiV 1113: Influenza virus H5N1 in cows' milk with Richard Webby

May 12, 2024

Richard Webby joins TWiV to review the history of avian H5N1 influenza virus, the recent change in epidemiological patterns, infection of dairy cattle in the US, and the risk of an outbreak in humans.

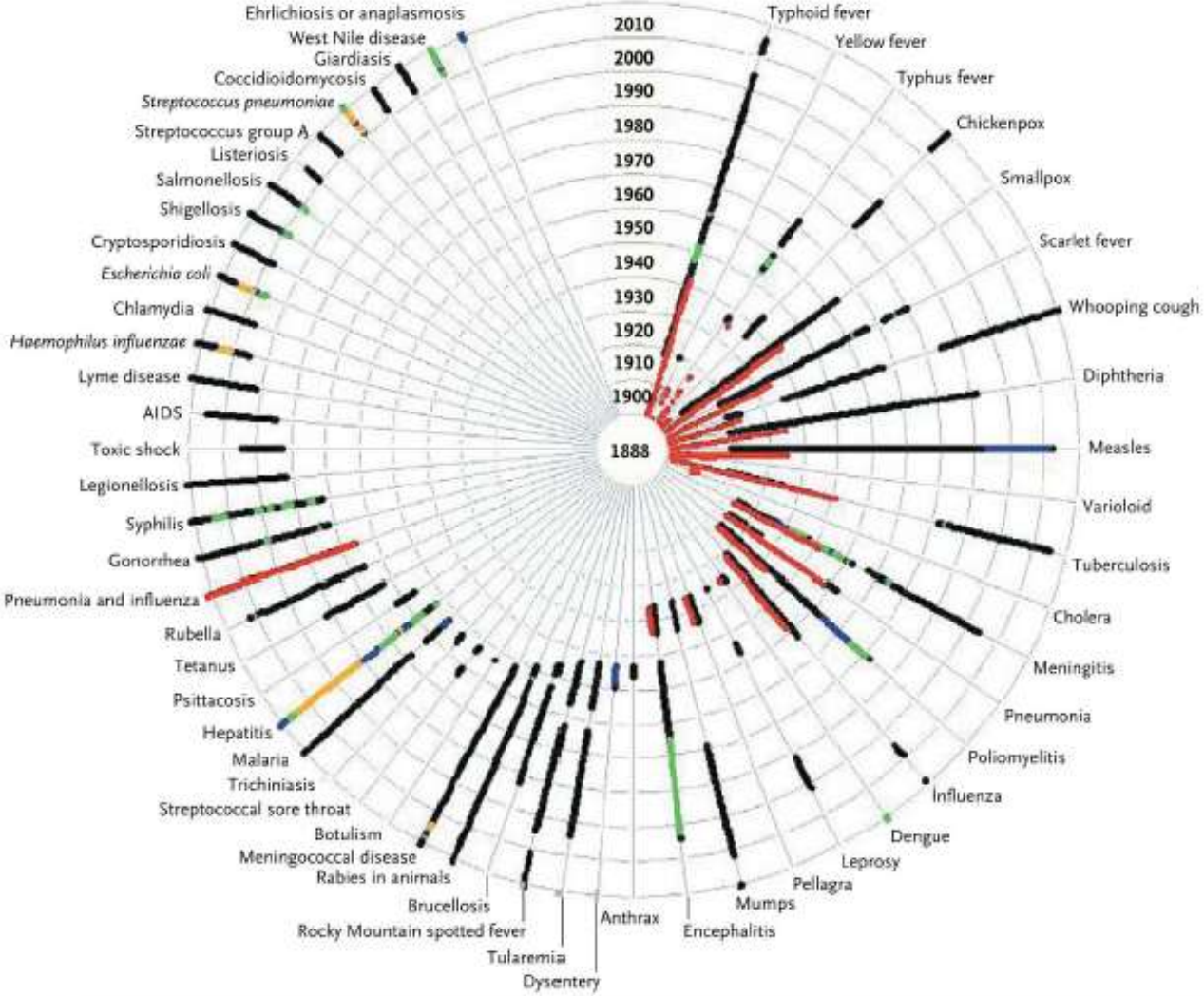
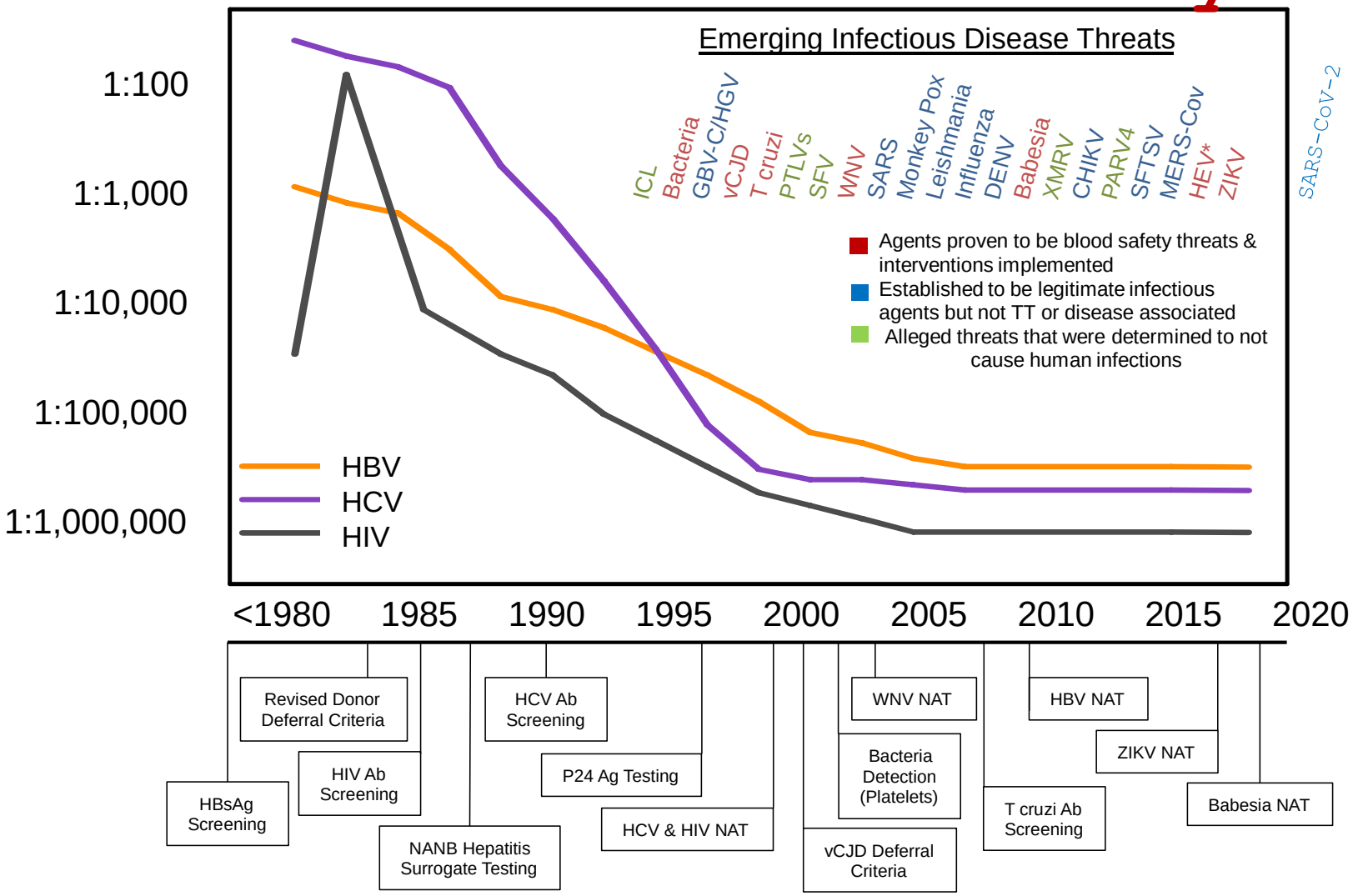


Figure 1. Availability of Weekly Counts of Reported Diseases from Any U.S. Location, 1888–2011.
Each concentric circle represents a decade, starting with 1888 in the center. No single disease was reported weekly throughout the entire period, and for many diseases, the type of reports changed over time, as represented by different colors: red represents reports of death, and other colors represent reports of cases in different numbers of disease categories (e.g., hepatitis A and B) as follows: black, 1 category; green, 2; blue, 3; and orange, more than 3.

Risks of major transfusion-transmitted viral infections and emerging infectious agents of concern to blood safety



Busch MP, Bloch EA, Kleinman S. Prevention of Transfusion Transmitted Infections. Blood 2019

Program Overview

Objective: To characterize the human virome and define its role in health and disease

The Human Virome program consists of four initiatives that will work synergistically as a consortium of multidisciplinary and innovative teams who will collaborate to achieve the goals of the program.

Initiatives:

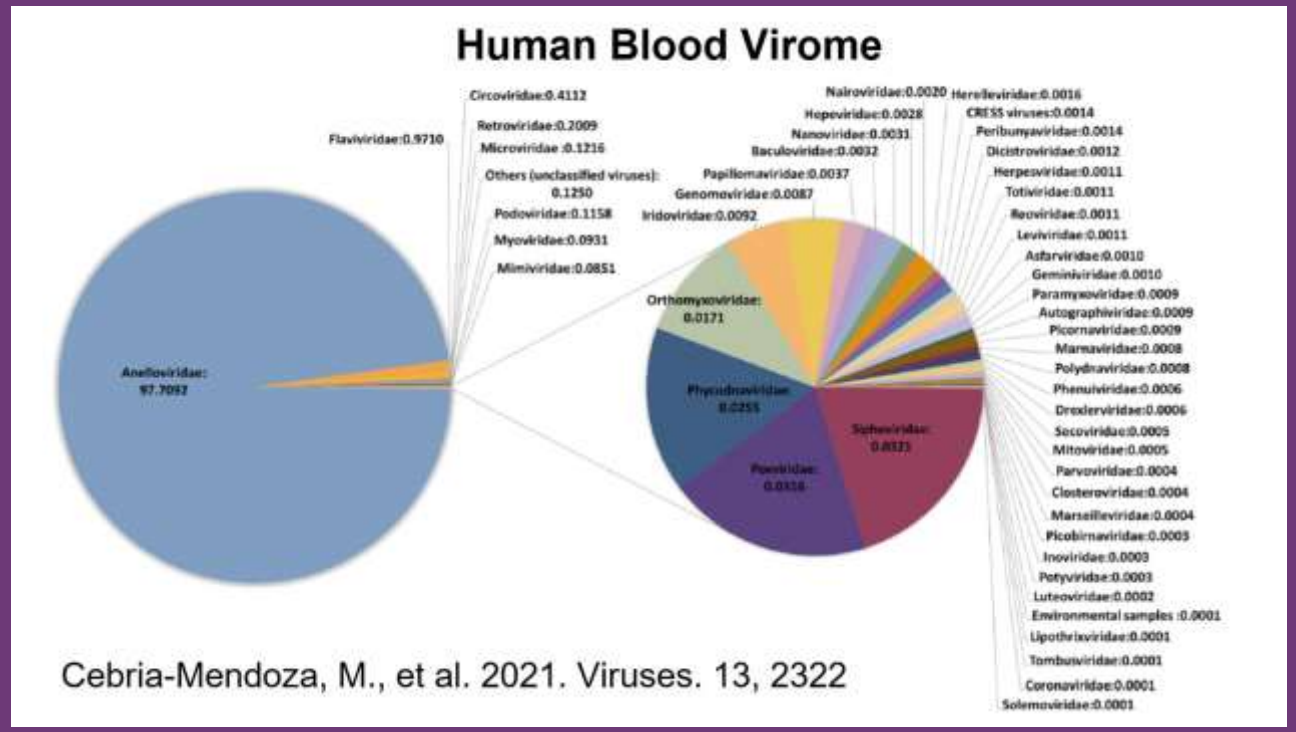
1. Characterize the human virome in longitudinal, diverse cohorts across the lifespan (RFA-RM-23-019)
2. Develop tools, models, and methods to interrogate and annotate the human virome (RFA-RM-23-018)
3. Functional studies to reveal the interactions between the human host and the virome (RFA-RM-23-017)
4. Consortium Organization and Data Collaboration Center (RFA-RM-23-016)

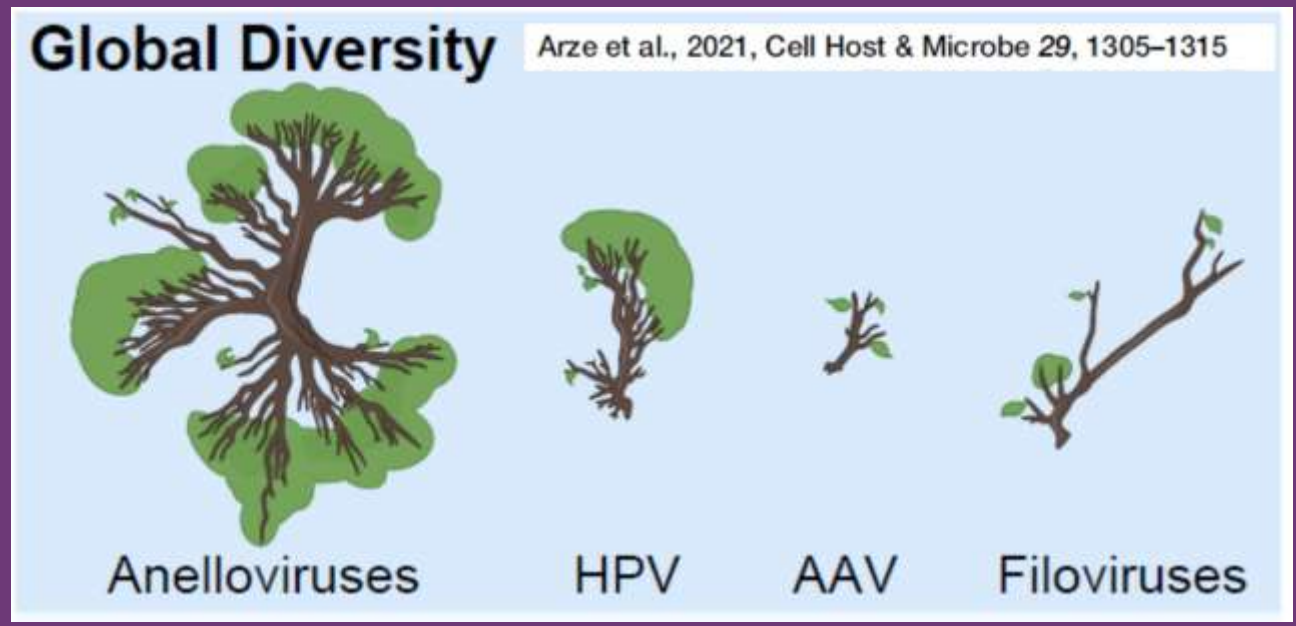
Program Duration: 5 years, FY2024-FY2028

Total Available Program Funds : $222.78M

Program Scope

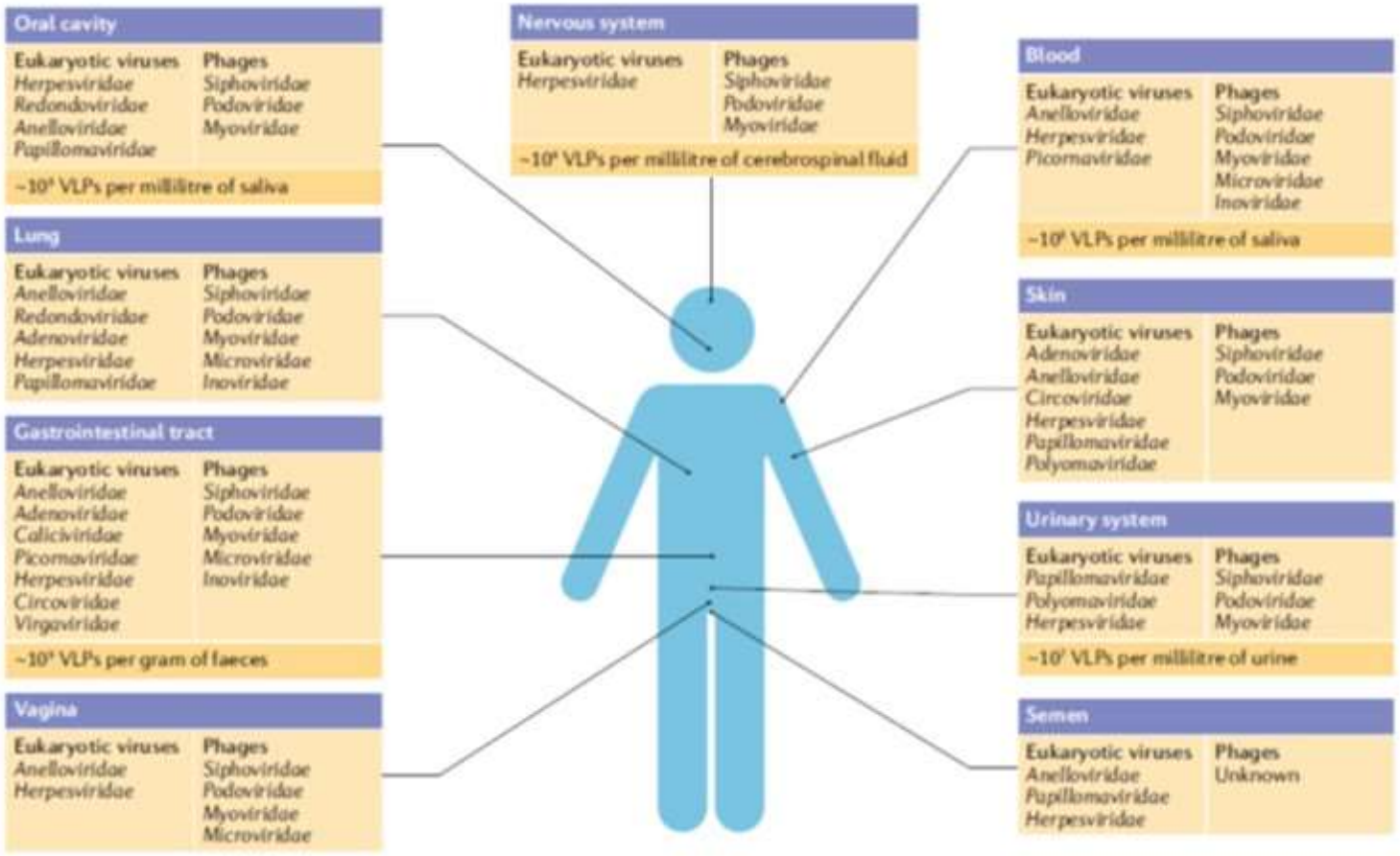
- The primary focus is on the commensal human virome
- Example: Anelloviruses
  - Humans across the globe are infected for their lifetimes
    - What is the source of initial infection?
    - Are they beneficial or do they cause disease?
    - What host cells support Anellovirus replication?

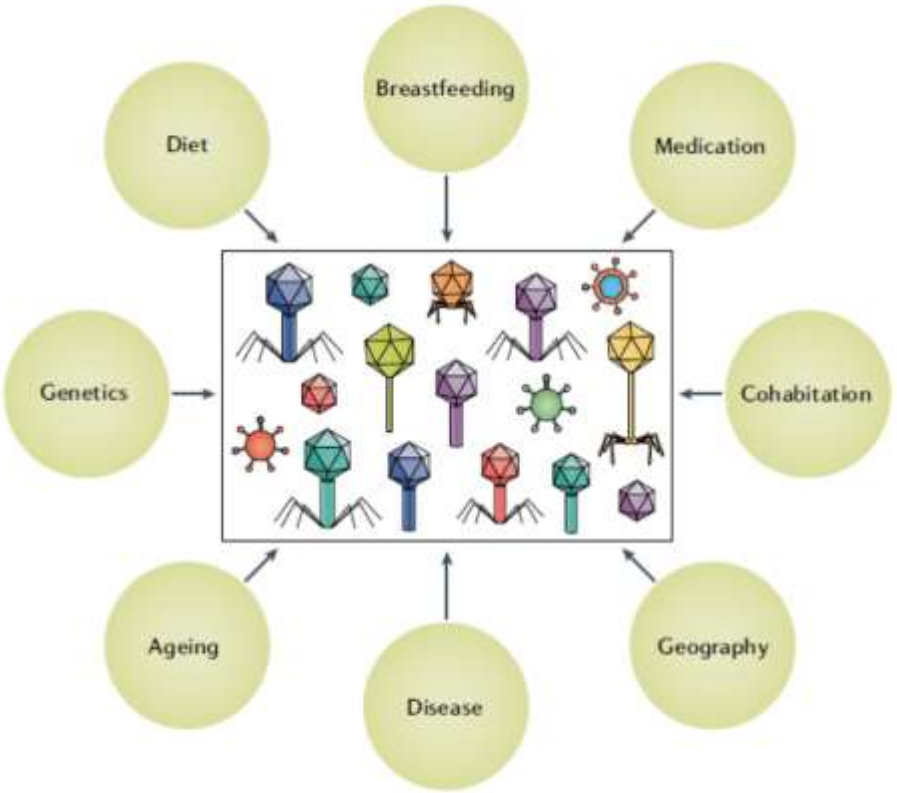




Program Background

- The human virome is large and diverse with >10^{13} particles per person
- The commensal virome is largely understudied and its interactions with the human body and long-term impacts on health and disease are unknown





Liang, G., Bushman, F.D. *Nat Rev Microbiol* **19,** 514–527 (2021)

Program Planning

Human Virome Workshop, April 29, 2022

Goal: To gather information on the current state of the knowledge of the human virome and to identify critical gaps

Concept 1:
Healthy Human Virome

Defining and characterizing the human virome in different tissue compartments in diverse populations across the lifespan.

Concept 2:
Infant Virome

Outlining the establishment of the human virome in the neonatal period, through infancy, and into early childhood.

Concept 3:
Virome & Disease

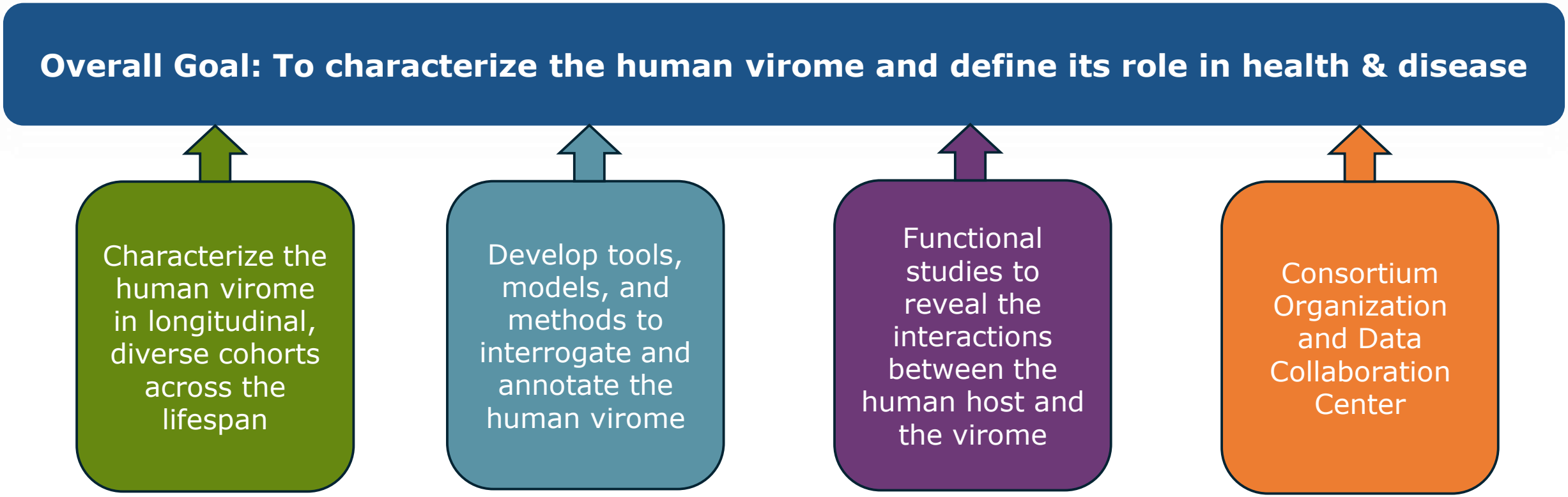
Describing relevant, diverse disease cohorts with appropriate longitudinal samples and clinical data available for the analysis of potential virome/microbiome associations with disease.

https://commonfund.nih.gov/humanvirome/meetings

Critical Knowledge Gaps Identified

- Diversity and dynamics (across tissues, time, populations, and lifespan)
- Establishment (timing and mechanisms)
- Host immune system interactions
- Functional and multi-omic studies
- Impacts of ‘exposome’
- Isolation, quantification, and propagation
- Animal models
- Standardized protocols
- Reference sequence database
- Annotation and contamination detection tools

Program Goal & Initiatives



Four initiatives will work synergistically as a consortium of multidisciplinary and innovative teams who will collaborate to achieve the goals of the program.

Program Deliverables

- Catalog of human commensal viruses across a diverse cohort from multiple body sites
- Tools, technologies, and methods to improve viral detection and annotation
- Functional assays interrogating interactions between the human host and virome
- A human virome research network made up of stakeholders interested in the human virome program and its resources

Thank you!