Literature Review

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Below is the email I received from Norman about the project.

Hi guys,

I played around a bit with the virusmentha data that already has grouped virus-host ppis accroding to virus families. Here are the stats (number are the ppis, then family):

**2987 Herpesviridae**

**1593 Retroviridae**

**1305 Orthomyxoviridae**

**820 Paramyxomyxoviridae**

**569 Flaviviridae**

246 Adenoviridae

200 Poxviridae

162 Polyomaviridae

159 Bunyaviridae

114 Filoviridae

59 Reoviridae

56 Arterieviridae

56 Togaviridae

36 Hepadnaviridae

14 Rhabdoviridae\_

11 Arenaviridae

5 Coronaviridae

3 Hepeviridae

1 Baculoviridae

1 Siphoviridae

With those numbers  I guess we should do the analysis with the first 5:

Alternatively, we can skip Paramoxyviridae, as the remaining 4 groups provide the best investigated viruses in terms of their interactions and have a large(r) set of PPIs.

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**Diversity of human viruses**

Statistics of viruses known to infect humans, genomes sequenced, genetic diversity?

Statistics of human disease caused by these viruses, case numbers, mortality, economic damage etc.

* Herpesviridae (mostly Herpes simplex, HSV)
  + viruses known to infect humans
  + genomes sequenced
  + genetic diversity
  + human disease caused by these viruses
    - case numbers
    - mortality
    - economic damage
    - vaccine
* Retroviridae (mostly HIV)
  + viruses known to infect humans
  + genomes sequenced
  + genetic diversity / origin
    - Sharp, Paul M., and Beatrice H. Hahn. "Origins of HIV and the AIDS pandemic." Cold Spring Harbor perspectives in medicine 1.1 (2011): a006841. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3234451/>)

AIDS is caused by two lentiviruses, HIV-1 ad HIV-2, originated at around the same time from multiple cross-species transmission of SIVs in African primates, specifically from SIVcpz in chimpanzees to HIV-1 group M in human. These genetic changes are needed to accommodate cross-species. SIV newly introduced and accumulated in the new host, and there need to be enough accumulation to adapt to host proteins and restriction factors, and for further human-to-human spread.

* + human disease caused by these viruses
    - case numbers
      * CDC reports (<https://www.cdc.gov/hiv/basics/statistics.html> )
        + Since the beginning of epidemic (which was officially began on June 5, 1981
        + 37,600 new HIV infections in 2014
        + 39,513 were diagnosed in 2015
        + 2.1 million new cases in HIV in 2015
        + 1.1 million died from AIDS-related illnesses in 2015
        + Annual number of new diagnoses has been declining
        + 1.1 million people living with HIV at the end of 2014
        + 36.7 million living with HIV around the world as of June 2016
    - mortality
    - economic damage
    - vaccine
* Orthomyxoviridae (mostly Influenza)
  + viruses known to infect humans
  + genomes sequenced
  + genetic diversity
  + human disease caused by these viruses
    - case numbers
    - mortality
    - economic damage
    - vaccine
* Paramyxoviridae (mostly measles)
  + viruses known to infect humans
  + genomes sequenced
  + genetic diversity
  + human disease caused by these viruses
    - case numbers
    - mortality
    - economic damage
    - vaccine
* Flaviviridae (Hepatitis C)
  + viruses known to infect humans
  + genomes sequenced
  + genetic diversity
  + human disease caused by these viruses
    - case numbers
    - mortality
    - economic damage
    - vaccine

Chen, Chien-Jen, et al. "Epidemiology of virus infection and human cancer." *Viruses and Human Cancer*. Springer Berlin Heidelberg, 2014. 11-32.

The International Agency for Research (IARC) is part of the World Health Organization and its main research focus is on human cancer and causes based on their epidemiological and laboratory data. There are viruses that cause cancer in human and identified as Group 1 carcinogen (Group 1 is classified as “known to be human carcinogens”) by IARC. The 7 viruses that fall into Group 1 category are: Epstein-Barr virus (EBV), human papillomavirus (HPV), human T cell lymphotrophic virus, type-1 (HTLV-1), Kaposi’s sarcoma herpes virus (KSHV) (4 direct chronic carcinogens), hepatitis B virus (HBV), hepatitis C virus (HCV) (2 indirect carcinogens through chronic inflammation), and human immunodeficiency virus, type-1 (HIV-1) (indirect carcinogen through immune suppression).

References:

Chen, Chien-Jen, et al. "Epidemiology of virus infection and human cancer." *Viruses and Human Cancer*. Springer Berlin Heidelberg, 2014. 11-32.