

VIRUS SECRET REVEALED BY THERMODYNAMICS

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ABSTRACT

In regard to recent viral outbreaks, transmissibility is of huge public health concern. Although many variables contribute to how transmissible or infectious a virus is, viral stability plays a critical role. In an effort to decipher the stability of viruses based on their structural properties, we gathered data on various kinetic parameters surrounding the stability of viruses with respect to temperature. Specifically, eleven viruses with single-stranded RNA genomes and human hosts were chosen. From this data, the van't Hoff relationship was used to extrapolate thermodynamic parameters. On the basis of our analysis, we discovered two characteristics of virus stability that have not previously been reported. Results show that enthalpy-entropy compensation holds true for viral stability indicating that there is limited variability in the stability with respect to condition. It is also found that a weak correlation exists between thermodynamic parameters and genome length. We expect that the insight obtained from this research will be directly applicable to new emerging pathogenic viruses.

BACKGROUND

Assessing the stability of viruses is crucial, as their stability can differ greatly based on the surfaces they come in contact with. While some viruses last several hours as aerosols, they can last up to several days on certain surfaces. Therefore it is important to assess the basis behind viral stability, so that viral stability can be quickly determined.

MATERIALS AND METHODS

Twenty papers were gathered from PubMed using various search terms such as “virus stability” and “Arrhenius”. From these papers, rate constants and their corresponding temperatures were obtained. Rate constants that were not explicitly listed were obtained by taking the natural log of the change in concentration over the duration of change. Software such as ImageJ were used to obtain such data points. From this, a rearranged form of the Eyring equation (equation 1) was used to obtain the free energy parameter. Equation 2 was then used to obtain the enthalpy and entropy parameters.

Genome lengths and envelope presence for each virus were noted in order to assess their affect on viral stability.

RESULTS

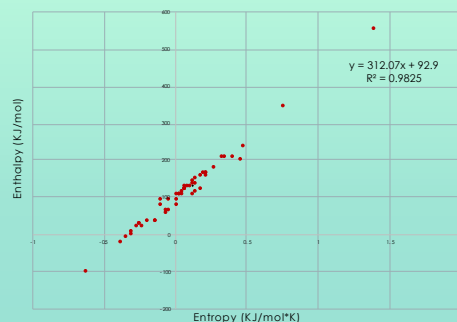


Figure 1. Entropy-Enthalpy Compensation

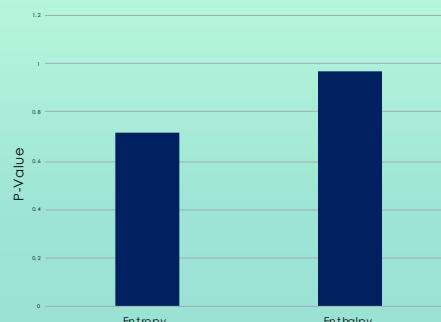


Figure 2. T-Test for Enveloped and Non-Enveloped Viruses

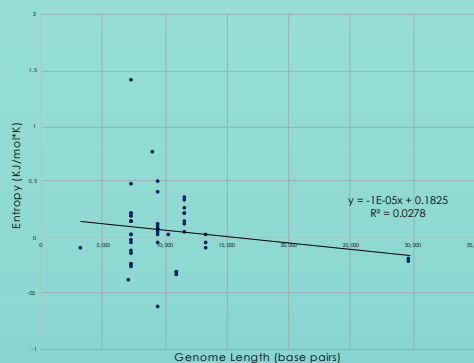


Figure 3. Effect of Genome Length on Entropy

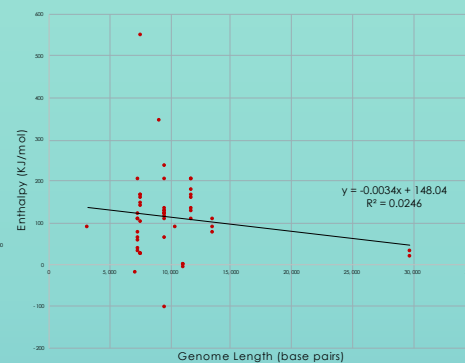


Figure 4. Effect of Genome Length on Enthalpy

$$\Delta G = -RT \ln \left(\frac{k * h}{K_b * T} \right)$$

ΔG : Gibbs Free Energy
 R : Ideal Gas Constant (8.314 J/mol*K)
 T : Temperature
 k : Rate Constant (s⁻¹)
 h : Planck's Constant (6.626 * 10⁻³⁴ J*s)
 K_b : Boltzmann's Constant (1.381 * 10⁻²³ J/K)

Equation 1. Rearranged Eyring Equation

$$\Delta G = \Delta H - T\Delta S$$

ΔG : Gibbs Free Energy
 ΔH : Enthalpy
 ΔS : Entropy
 T : Temperature

Equation 2. Gibbs Free Energy Equation

VIRUSES INCLUDED IN THE STUDY

- Hepatitis A Virus
- Hepatitis B Virus
- Hepatitis C Virus
- Hepatitis E Virus
- SARS Coronavirus
- Influenza Virus
- Poliovirus
- Sindbis Virus
- Yellow Fever Virus
- Alkhurma Hemorrhagic Virus
- Human Immunodeficiency Virus

CONCLUSION

Results showed that enthalpy-entropy compensatory behavior was present. For the first time, it is found that the stability of the examined pathogenic viruses are similar in various conditions at human physiological temperature, despite the wide variation in both enthalpy and entropy. Regarding other factors that affect stability, it is seen that the presence of an envelope does not affect both the enthalpy and entropy of inactivation ($P > 0.05$). A weak correlation was also present between genome length and the two thermodynamic parameters. Therefore it is concluded that thermodynamics may be the guiding principle in the evolution of viral stability.

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