Development of a reference method to quantify the viral load

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BACKGROUND

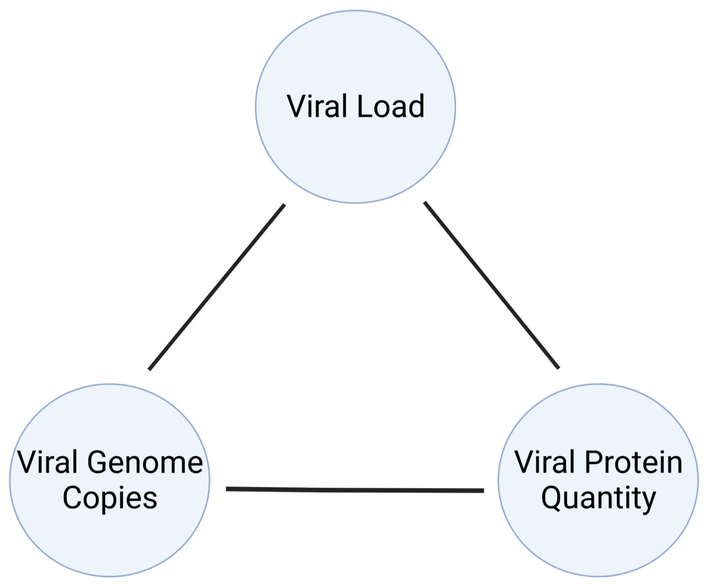
Accurate and comparable measurements are essential to support the diagnosis of viral disease. Consistent measurement results can be achieved by making them SI-traceable through the development of reference measurements. DNA and Protein serve as measurands of interest.

IMPACT

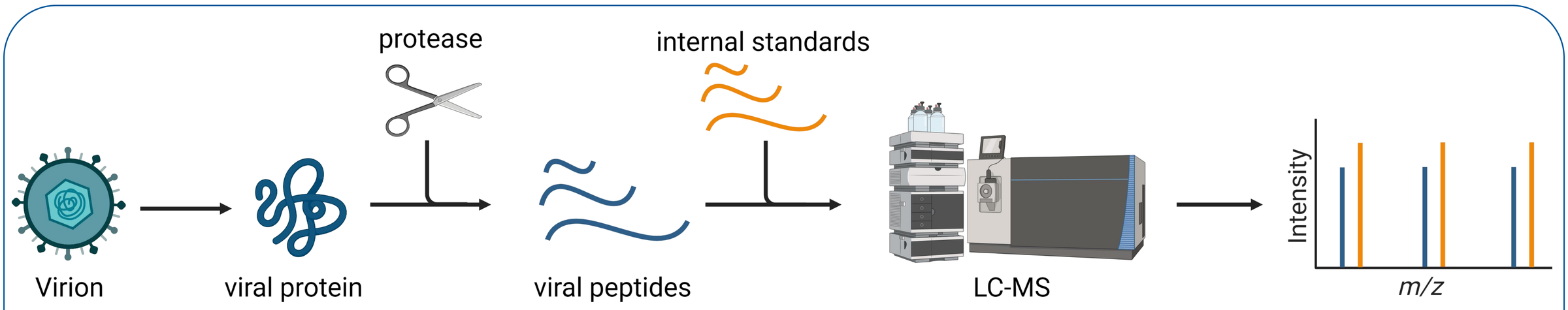
- SI-traceable method enables comparable measurements
- Alternative method to
  - diagnose viral disease and to determine viral load
  - identify false positve/negative results from already existing methods

ASSUMPTION

Viral Load / ml
≙
Viral Particle Amount / ml
≙
Viral Genome Copies / ml
≙
Viral Protein Quantities / ml



PROJECT OUTLINE



Virus Preparation

- Virus production
- Virus purification
- Virus titration using qPCR

Proteomics Study

- Protein sample preparation
- LC-MS measurements
- Bioinformatically analysis to choose peptide of interest

Method Development

- Internal standard calibration
- Choose/test labeling method
- Assay verification
- Uncertainty measurements

References:
Arsene, Cristian G., et al. “Protein Quantification by Isotope Dilution Mass Spectrometry of Proteolytic Fragments : Cleavage Rate and Accuracy.” *Analytical Chemistry*, vol. 80, no. 11, 2008, pp. 4154–60.
Burkitt, William I., et al. “Toward Système International d’Unité-Traceable Protein Quantification: From Amino Acids to Proteins.” *Analytical Biochemistry*, vol. 376, no. 2, 2008, pp. 242–51, doi:10.1016/j.ab.2008.02.010.
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