Folding of viral DNA in a capsid yields a highly ordered liquid crystal phase subject to extreme pressures. Two main mechanisms contribute to the large pressure as well as shearing stress in the domain: high bending resistance of the DNA and electric effects due to the large negative charge of the DNA molecule and environmental ions.

We construct a phenomenological model of genome packing and show that it yields qualitative and quantitative agreement with the packing configurations of known viruses. First, we rely on cryogenic images of viruses and molecular dynamics simulations to argue that the packed genome forms a biaxial smectic arrangement with an isotropic core, this being the result of the high bending resistance of the DNA molecule. The liquid crystal director field obtained from the analysis is now the tangent field of a filament representing the axis of the DNA ribbon. We study the role of liquid crystal defects and knots in the packing. Available information to determine the material parameters of the model include: length of the genome, capsid geometry, cryogenic imaging, density curves, pressure and ejection speeds measurements. However, the mechanical model alone is not sufficient to capture all the packing features. Additionally assuming that the DNA and the surrounding water, that sustains the ions, are in a gel state, allows us to incorporate the chiral charge distribution of the viral genome and the environmental electric charges, all of which, together with the mechanical forces, contribute to the large osmotic pressure observed (about 60 atmospheres). These configurations, corresponding to gels with high residual stress, yield free boundary problems that bear analogies with those of liquid crystal droplets and elastomers.

This is joint work with Javier Arsuaga and Mariel Vazquez.