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*HPV Type Replacement and Spatial Within-Host Modelling*

The human papillomavirus (HPV) is a ubiquitous, multi-type virus that affects many Canadians. Most infections with HPV are transient and cleared by the body naturally. However, persistent infection may lead to pre-cancerous and cancerous lesions. Vaccines against two cancerous types (HPV-16 and -18) have been developed recently. However, researchers are concerned about the possibility of type replacement occurring. This is a phenomenon wherein the vaccination against certain vaccine types of a pathogen causes the niche space for non-vaccine types to be expanded due to the decreased prevalence of these vaccine types. This can result in the increased prevalence of other cancerous non-vaccine HPV types, which may lessen the benefits of the vaccine. Previous mathematical models have been used to examine the potential for type replacement occurring. These models show that HPV type replacement hinges on HPV type interactions. Spatial within-host models can be used to examine HPV types interactions in more detail. This can give researchers and epidemiologists more insight into the potential for HPV type replacement and its implications.

In this talk, I will quickly review some ecological considerations that must be made when developing spatial within-host models for HPV. I will then showcase a spatial model, outlining the important mechanisms of the model. I will wrap up by discussing some analytical results of the model.