# Epidemiologic Trends in Non-Vaccine-Type HPV after Vaccine Introduction: No Evidence for Type Replacement but Evidence for Cross-Protection

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## Introduction

The introduction of HPV vaccines has led to a substantial decline in the prevalence of vaccinetype HPV in community settings. However, the impact of vaccination on non-vaccine-type HPV is not well understood.

# **Hypotheses**

An increase in non-vaccine-type HPV after vaccine introduction may suggest type replacement (a decrease in prevalence of vaccine-type HPV creates an ecological niche other types could occupy), which could adversely impact vaccine effectiveness. Conversely, a decrease in non-vaccine HPV types genetically related to vaccine-type HPV suggests cross-protection, which would enhance vaccine effectiveness.

### **Methods**

Three cross-sectional HPV surveillance studies were conducted in 2006-2007 (N=371), 2009-2010 (N=409) and 2013-2014 (N=400). Participants were sexually active 13-26 year-old women who completed a survey and underwent cervicovaginal HPV DNA testing. We determined trends in non-vaccine-type HPV prevalence across the three waves, using logistic regression and propensity score analysis to adjust for differences in participant characteristics. Outcome variables were: 1) prevalence of all 28 non-vaccine-type HPV and 2) prevalence of HPV types genetically related to HPV16 (HPV31, 33, 35, 52, 58, 67) and HPV18 (HPV39, 45, 59, 68, 70).

#### Results

Vaccination rates increased from 0% to 71.3% across the three waves. Adjusted logistic regression models demonstrated that from waves 1 to 3, there was no significant increase in non-vaccine-type HPV among all women (AOR 1.17, 95% CI 0.87-1.58) or vaccinated women (AOR 1.02, 95% CI 0.73-1.42), but there was a significant increase among unvaccinated women (AOR 1.88, 95% CI 1.16-3.04). Conversely, from waves 1 to 3, there was a significant decrease in HPV types genetically related to HPV16 among all women (AOR 0.62, 95% CI 0.43-0.90) and vaccinated women (AOR 0.57, 95% CI 0.38-0.88) but not unvaccinated women (AOR 1.33, 95% CI 0.81-2.17). Genetically-related types decreased 36.1% among vaccinated women. There was no decrease from waves 1 to 3 in HPV types genetically related to HPV18.

#### Conclusions

These data do not demonstrate evidence of type replacement. However, the decrease in the prevalence of HPV types genetically related to HPV16 among vaccinated (but not unvaccinated) women suggests cross-protection against these types.

## **Acknowledgements**

This study was supported by two R01s (NIAID R01 073713 and R01 Al1P4709) and NIH Grant T35DK060444.