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ABSTRACT

Introduction

HR-HPV genoprevalence was assessed in cytological specimens co-tested for HR-HPV in a predominantly Midwestern U.S. population, of which there is limited current data. These baseline data will aid in determining future shifts in HR-HPV genoprevalence.

Methods

40,739 cervical/endocervical samples collected in PreservCyt (ThinPrep) media at Mayo Clinic, Rochester underwent HR-HPV co-testing between January 2014 and December 2016 in women ages 30-98. This included 37,656 negative for intraepithelial lesion (NIL), 1,696 atypical squamous cells of undetermined significance (ASC-US), 159 atypical squamous cells, cannot exclude HSIL (ASC-H), 911 low-grade squamous intraepithelial lesion (LSIL), 188 high-grade intraepithelial lesion (HSIL), and 129 atypical glandular cells of undetermined significance (AGUS) cases. Roche cobas® 4800 classified HR-HPV genotypes as 16, 18, or “other” (31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68).

Results

Of 40,739 co-tested specimens, 3,786 were positive for at least one HR-HPV strain. “Other” only genotypes were most prevalent (74.3% of all HR-HPV cases). HPV16 and/or HPV18 were more common in the more significant diagnoses and were present in 59.1% of HSIL. HPV16-only was second most prevalent, with highest prevalence in HSIL (33.3%) and ASC-H (20.6%). HPV16 combined with “other” was third most prevalent, except in AGUS. HR-HPV (all genotypes) was most prevalent in ages 30-39, decreasing with age ($P < 0.0001$). There was a trend toward HPV16 prevalence increasing with age ($P = 0.4244$).

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