

Type: Poster Presentation

Final Abstract Number: 57.030

Session: *Virology and Viral Infections (Non-HIV) I*

Date: Friday, April 4, 2014

Time: 12:45–14:15

Room: Ballroom

Household transmission of influenza in a developing country setting—South Africa, 2013

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Background: The household is an important factor in influenza transmission due to high frequency and intensity of contact. Few reports describe household secondary attack rates (SAR) of influenza in developing country settings with high HIV prevalence.

Methods & Materials: We performed a case-ascertained household transmission study during May–October 2013. Index cases were patients presenting with influenza-like-illness (ILI), defined as cough and fever ($\geq 38^\circ\text{C}$) with onset in the last 3 days, at clinics in two peri-urban areas in South Africa. Household contacts of index cases with laboratory-confirmed influenza and no previously sick household members were followed for new onset ILI symptoms for 12 days.

Results: Thirty-three index cases and 124/137 (91%) of eligible household members in 33 households were enrolled. Households had a median of 4.5 (range 1–16) members. Index cases were 71% female with a median age of 21 years (interquartile range (IQR) 8–35); 11/33 (33%) were HIV-infected. Household members were 44% female with a median age of 20 years (IQR 12–40); 13/124 (10%) were HIV-infected (10 by report, 3 tested). In the preceding year, 75% of household members reported a history of ILI; 8/124 (6%) had received the influenza vaccine. Risk factor questionnaires were completed for 100/124 (81%) household members. Most (68/100; 68%) never avoided contact with the index patient and 47/100 (47%) shared a bed with them. Symptom diaries were filled for all eligible household members (by proxy if not enrolled); 89/137 (65%) were completed. Assuming non-responders did not have ILI, 22/137 household members in 14/33 households reported new onset ILI symptoms during the study, yielding a SAR of 16%; the median age was 24 years (IQR 10–39). Of those, 20/22 (91%) completed additional risk factor questions; 18/20 (90%) never avoided interacting with household members or attending work or school and 15/20 (75%) still slept with other household members.

Conclusion: Household members of influenza-infected persons reported low influenza vaccination rates and not changing behavior to reduce influenza transmission when another household member is sick, which may contribute to the SAR. Education on transmission-reducing behaviors and increasing vaccination rates should guide public health measures to improve influenza transmission control in households in peri-urban settings.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1091>

Type: Poster Presentation

Final Abstract Number: 57.031

Session: *Virology and Viral Infections (Non-HIV) I*

Date: Friday, April 4, 2014

Time: 12:45–14:15

Room: Ballroom

Screening of 100 women for HPV infection and HPV genotyping

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Background: Human papillomaviruses (HPV) infect only humans, there are more than 100 types of HPV and these viruses are highly species specific. HPV is associated to different diseases, there are 2 group HPV genotype: Low grade (6, 11), High grade (16, 18). Evidence linking HPV to cervical carcinoma is extensive, with HPV-16 accounting for approximately 60 percent of cases and HPV-18 for 10 percent. The worldwide prevalence of HPV infection among females is approximately 10 percent. Worldwide, the most serious HPV infections are caused by high-risk types HPV 16 and 18, both of which are preventable by vaccination. The aim of this study is to determine the prevalence of HPV in women without any symptom of HPV attending to screening clinics and its genotyping in Iran.

Methods & Materials: One hundred liquid cervical cell samples from 100 women, resident of Iran participating in HPV screening, based on the liquid-based, thin layer preparation with inserting the endocervical brush into the endocervix were taken. Were assessed HPV with a HPV multiplex real-time PCR using primers for 16–18–52–31–45–56–33–39–58–35–59 66 genotypes based on DNA extraction. Correlations of HPV infection with age, geographic area, socioeconomic, contraception, age of marriage were assessed.

Results: From one hundred specimens, 53 (53%) was positive for HPV infection. The frequency of high-risk HPV infection was genotype 16 (24%), 18 (14%), co infection 16&18 (7%), 39 (20%), 59 (7%), 56 (4%), 35 (5%), 31 (3%). The prevalence of low-risk HPV infection was zero.

Conclusion: Compared to other studies, the prevalence of high risk HPV infection in our study was higher about 38%. These differences could be due to the use of a PCR with high analytic sensitivity. These data are relevant for using vaccine protection for girls.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1092>