Meningococcal Disease Risk Among Men Who Have Sex with Men – United States, 2012-2015

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Background

- From 2010-2016, clusters of meningococcal disease were reported in the US among men who have sex with men (MSM) in New York City (NYC), Los Angeles County (LAC), and Chicago.
- MSM have not previously been considered at increased risk for meningococcal disease.

Methods

Data Sources and Analysis

- All meningococcal disease cases among males aged 18-64 years reported to the National Notifiable Disease Surveillance System (NNDSS) between January 2012 and June 2015 were reviewed.
- MSM status, HIV status, and demographic information were collected by state and local health departments through retrospective review of reported meningococcal cases.
- Cases were classified as either MSM or not known to be MSM (non-MSM). MSM cases were further classified as sporadic cases or into jurisdiction-specific groups (NYC, LAC, Chicago) if an outbreak or cluster of MSM cases was reported during the observation period.
- Annualized incidence rates among MSM and non-MSM were compared.
- Denominators were estimated using 2012 census data and published estimates of the proportion of MSM in the US.
- Available isolates from clusters and sporadic cases were characterized using standard microbiological methods and PCR; genetic similarity of these isolates was assessed using whole genome sequencing.
- Data were analyzed using SAS software version 9.3 (SAS Institute, Cary, North Carolina)

Ethical considerations

All data was de-identified prior to transmission and analysis at CDC. This evaluation was approved by the CDC Human Research Protections Office as public health practice and exempted from full review by the CDC Institutional Review Board.

Results

Demographic. Surveillance and Clinical Characteristics

- From Jan 2012-June 2015, 527 cases of meningococcal disease in men aged 18-64 years were reported through NNDSS.
- 74 (14.0%) were reported as MSM: 23 NYC, 14 LAC, 11 Chicago, and 26 sporadic. 453 (86%) were reported as non-MSM.
- The median age of MSM and non-MSM case-patients was 31 and 34 years respectively.
- Serogroup C accounted for 62 (83.8%) MSM cases and 98 (21.6%) non-MSM cases (p<0.05). All cluster-associated serogroup C cases among MSM</p> were due to sequence type (ST)-11.
- 38 (59.4%) MSM had known HIV infection.
- Death occurred among 24 (32.4%) of the 74 MSM and 90 (23.5%) of the 383 non-MSM with known outcome (p=0.11).
- No association was found between HIV-infection and death (p=0.56).
- Cases with serogroup C disease had 1.5 times the risk of death than those with disease due to other serogroups.



Figure 1. Number and proportion of meningococcal disease cases by MSM status and month among men aged 18-64 years, January 2012-June 2015

Table 1. Annualized meningococcal disease incidence rate and relative risk					
among MSM and non-MSM aged 18-64 years, January 2012-June 2015.					
Category	Cases (N)	Estimated	Annualized Incidence rate per 100,000	Relative Risk (95% Cl)	p-value
Overall Estimates: Clusters (NYC, LAC, Chicago) and sporadic cases					
Non-MSM	453	92,849,904	0.15	Ref	
MSM	74	3,768,102	0.59	4.0(3.6-4.5)	<0.001
HIV-uninfected MSM	26†	3,290,927	0.24	1.6(1.1-2.4), Ref	0.015
HIV-infected MSM	38†	477,175	2.33	10.1(6.1- 16.6)*	<0.001
Sporadic cases only					
Non-MSM	414	86,940,086	0.14	Ref	
MSM	26	3,040,442	0.26	1.8(1.2-2.7)	<0.001
HIV-uninfected MSM	6‡	2,652,873	0.07	0.5(0.2-1.1), Ref	0.064
HIV-infected MSM	12‡	387,569	0.93	13.7(5.1- 36.5)*	<0.001
HIV status unknown in +10/74 MSM overall, and in +8/26 sporadic MSM cases.					

*Relative risk compared to HIV-uninfected MSM



Legend: MSM-Location of outbreak-Year collecte

Figure 2. Phylogenetic analysis of meningococcal isolates among MSM aged 18-64 years, January 2012-June 2015.

Conclusions

- Although the absolute incidence is low, the risk of meningococcal disease among MSM is higher than the non-MSM male population in the US.
- HIV appears to be the primary driver of this increased risk in non-outbreak settings.
- All cluster-associated NmC cases among MSM were due to ST-11, though whole genome sequencing showed marked genetic differences, indicating that the strains responsible for the MSM clusters may have come from a common ancestor and further diverged substantially over time.
- Further evaluation is needed to better understand transmission and risk factors in this population in order to inform public health prevention and response strategies.

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