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Outbreak of Rotavirus in a Long-term Care Facility

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Background: Nosocomial viral gastroenteritis is common during the winter season but the pathogen involved does not always belong to the family Caliciviridae such as *Norovirus*. We report an outbreak of rotavirus infection among elderly patients in a long-term care facility of our hospital.

Outbreak: On 3 March 2006, four cases of rapid onset gastroenteritis since 28 February were reported among elderly patients in a long-term care facility ward and subsequently spread to patients on all other floors of the same building. The prolonged symptomatic phase was atypical for *Norovirus* infection. The outbreak was controlled by: strict contact isolation and, when necessary, cohorting; attribution of dedicated toilets and places of common meals for infected patients; restriction of the number of external visits; enhanced promotion of hand hygiene as the cornerstone of countermeasures; and enhanced cleaning and disinfection of surfaces, floors, rooms and sanitary facilities twice daily. On 13 March, the last symptomatic case day was noted and on 20 March the outbreak was declared over.

Results: Twenty-five of 108 elderly patients became ill for an attack rate of 23%; there was no mortality attributable to the outbreak. No healthcare worker developed gastroenteritis. *Rotavirus* was found in 10 of 17 viral coprocultures and one patient had a co-infection with adenovirus. No cases of *Clostridium difficile* toxin or *Norovirus* were detected. The median duration of symptoms was 4 days. Three patients were infected directly by an infected patient sharing the same room, and eight had an infected patient in the neighbouring room. In contrast to this presumed transmission by close contact, 11 symptomatic patients were infected within the same ward as the index cases but without obvious vicinity to them, and 11 patients sharing a room with diarrheic patients remained asymptomatic.

Conclusion: *Rotavirus* outbreaks occur not only among children, but also among elderly patients in long-term care facilities. The infection seems to last longer than gastroenteritis due to *Norovirus*. Because of substantial attack rates, a high index of suspicion is warranted in order to implement infection control measures at the very onset of an outbreak.

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Epidemiology of Nontuberculous Mycobacteria in the USA: Pilot Study Utilizing Closed Healthcare Systems

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Background: The nontuberculous mycobacteria (NTM) are ubiquitous environmental organisms increasingly reported in association with human disease. The prevalence of this disease is thought to be increasing but current epidemiologic data in the USA is lacking. These organisms cause systemic infection in immunocompromised hosts and more commonly are associated with lung disease. Since the late 1980s there has been a change in reported presentation from fibrocavitary disease in elderly males with emphysema to a slowly progressive nodular bronchiectatic lung disease in postmenopausal women with no apparent predisposing conditions. Prior epidemiologic studies in the USA in the 1980s relied on surveys of state referral labs and estimated a case prevalence of 1–2/100,000 population. These studies likely underestimated prevalence due to incomplete ascertainment. Current widespread use of DNA probes for isolate identification has decreased referral to these labs making this methodology impractical to repeat. Closed healthcare systems serving a geographically stable population who receive the entirety of their healthcare within the system offer a conducive setting for rapidly searching databases to assess isolate prevalence and linking this to demographic and comorbid host characteristics.

Objectives: Assess changing prevalence and associated host characteristics of nontuberculous mycobacterial disease in a geographically diverse network of closed healthcare systems.

Methods: Representative closed systems (Kaiser Permanente Southern California, KPSC – n = 3.1 million; Geisinger Health System Pennsylvania, GHSCP – 1.5 million; Walter Reed Army Medical Center DC, WRAMC – 20,000) conducted a feasibility screen by querying lab databases for all mycobacterial isolates during 2005.

Source	% positive specimens	(+) Isolates ^a	(+) Patients ^a
KPSC	7	37	
GHSP	5	5.7	4.5
WRAMC	6	220	

^aPer 100,000 source population.

Results: See the table.

Mycobacterium avium complex (65% KPSC, 51% GHSP, 56% WRAMC) was the most common species followed by *M. goodii* and the rapid-grower mycobacteria. The most common body site source was the lung (40% GHSP, 72% WRAMC).

Conclusions: Rapid screening of electronic lab data can be used to identify individuals with NTM who

can be assessed for disease criteria and demographic and comorbid conditions. Closed health care systems afford linked databases and settings with defined source populations for assessment of prevalence over time.