# Epidemiology of viral respiratory infections with focus on inhospital influenza transmission

Akademisk avhandling

Som för avläggande av medicine doktorsexamen vid Sahlgrenska akademin, Göteborgs universitet kommer att offentligen försvaras i hörsal Arvid Carlsson, Medicinaregatan 3, Göteborg,

## Fredagen den 12 juni 2020 klockan 13.00 av Martina Sansone

Fakultetsopponent:

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## Avhandlingen baseras på följande delarbeten:

- I. Sansone M, Andersson M, Brittain Long R, Andersson LM, Olofsson S, Westin J, Lindh M. Rhinovirus infections in western Sweden: a four-year molecular epidemiology study comparing local and globally appearing types. *Eur J Clin Microbiol Infect Dis. 2013 Jul;32(7):947-54*
- II. Sansone M, Wiman Å, Karlberg ML, Brytting M, Bohlin L, Andersson LM, Westin J, Nordén R. Molecular characterization of a nosocomial outbreak of influenza B virus in an acute care hospital setting. J Hosp Infect. 2019 Jan;101(1):30-37
- III. Sansone M, Andersson M, Gustavsson L, Andersson LM, Nordén R, Westin J. Extensive hospital in-ward clustering revealed by molecular characterization of influenza A virus infection. Clin Infect Dis 2020. Feb 3 [Epub ahead of print]
- IV. Sansone M, Holmström P, Hallberg S, Nordén R, Andersson LM, Westin. Antiviral prophylaxis was the most effective preventive measure identified by system dynamic modelling of healthcare-associated influenza. In manuscript.

## SAHLGRENSKA AKADEMIN INSTITUTIONEN FÖR BIOMEDICIN



# Epidemiology of viral respiratory infections with focus on inhospital influenza transmission

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#### ABSTRACT

Human Rhinovirus (HRV) and influenza virus are respiratory pathogens which represent a major global disease burden. Healthcare-associated infections (HCAIs) are increasingly recognized as a public health concern, but limited data has been published on the characteristics and epidemiology of HCAIs caused by respiratory viruses. The aim of this thesis was to investigate the molecular epidemiology of HRV and influenza virus with special focus on in-hospital influenza transmission. In paper I, 114 stored respiratory samples positive for HRV, collected over a four-year period, were sequenced and compared with HRV sequences identified in other parts of the world. In paper II, a nosocomial outbreak involving 20 cases with influenza B virus infection were retrospectively investigated by combining clinical and epidemiological data with molecular methods. In paper III, the characteristics of 435 hospitalized adult patients with Influenza A virus infection throughout an entire year were described, whereof 114/435 (26%) were classified as HCAI. Suspected in-ward transmission was investigated by combining epidemiological investigations and whole-genome-sequencing. In paper IV, a system dynamic model for healthcareassociated influenza transmission was developed and used to identify factors promoting transmission as well as effective control interventions. *Conclusions:* HRV infections are represented by many subtypes. Epidemics are highly globalised, and subtypes may circulate locally for extended time periods. Influenza B may spread rapidly within an acute-care hospital, and molecular methods can be used for outbreak analysis. In-ward transmission of influenza A occurs frequently, and healthcareassociated influenza may have a severe outcome. System dynamic modelling may be a valuable tool to illustrate in-hospital transmission of influenza. Antiviral prophylaxis seemed in our model to be the most effective control measure.

**Keywords**: influenza, rhinovirus, infection-control, hospital outbreak, nosocomial, phylogeny, polymerase chain reaction, viral transmission, whole-genome sequencing, system dynamics.

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