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Advances in diagnostics of respiratory viruses and insight in clinical implications of rhinovirus infections

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General introduction

RESPIRATORY INFECTIONS

Respiratory infections are among the most common infections in humans and are a major health issue^{1,2}. Overall, they are the cause of high morbidity and mortality, and as such associated with high costs due to absence of work and hospitalization, sometimes even in isolation³⁻⁵.

Respiratory infections can be categorized into upper respiratory tract infections and infections of the lower airways. Although upper respiratory tract infections are usually relatively mild, more serious infections occur in specific high-risk groups. The most prevalent and well known upper respiratory tract infection is the common cold. Infections of the lower airways, mainly bronchiolitis and pneumonias, are in general more serious and the leading infectious cause of death world-wide^{1,6}.

Respiratory infections are caused by a variety of pathogens, but primarily by viruses, with overlapping clinical symptoms. The common cold is a syndrome of upper respiratory tract infections caused by viral pathogens, with rhinovirus being the most prevalent, detected in 40-50% of the cases of the common cold⁶⁻⁸. Other common respiratory viruses are respiratory syncytial virus, adenovirus, para-influenza viruses, bocavirus and metapneumovirus⁶.

Viruses are the most prevalent pathogens detected in hospitalized adults with community acquired pneumonia (Figure 1). As with upper respiratory tract infections, rhinovirus is the most frequent cause, alone or as co-infection with other viruses or bacteria. Strikingly, in up to 62% of the community-acquired pneumonias no causative agent is found with current diagnostic procedures (Figure 1)^{7,8}.

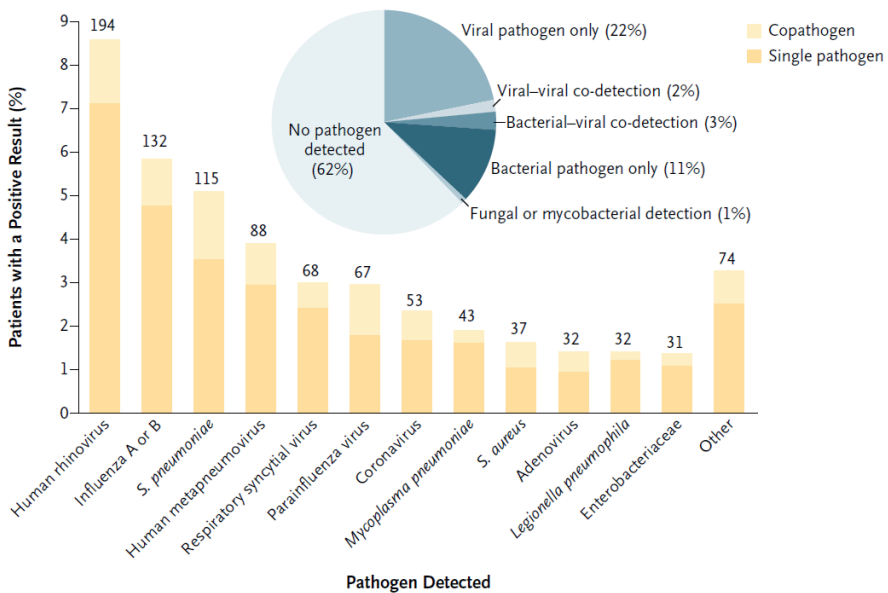


Figure 1. Pathogens detected in adults with community acquired pneumonia requiring hospitalization. (Adapted from Jain et al.⁷)

DIAGNOSTICS OF RESPIRATORY INFECTIONS

Respiratory viral causes of infections are hard to distinguish by their clinical presentation, even so from other pathogens such as bacteria. Therefore, a precise diagnosis is important for adequate therapy and isolation measures. Over the years the diagnostic possibilities have expanded and the conventional routine assays, based on viral culture, antigen detection and serology, have been replaced by molecular methods. A routine diagnostic respiratory assay has to be fast, sensitive, specific, with limited hands-on time, cost-effective and has to be able to detect a wide variety of respiratory pathogens.

History of diagnostics of respiratory viruses

In the 1950's, diagnosing viruses was performed by *in vitro* culture on mono-layer cell lines⁹. Virus culture has been the gold standard for a long time. However, the time to results is considerable and generally too slow for clinical actions. Not only different cell lines and skilled staff are required, but also special safety requirements regarding viable virus¹⁰. Additionally, some viruses as for example rhinovirus species C, are hard or even impossible to propagate in cell-culture.

Later, new diagnostic options were introduced with antigen detection assays and serology. Antigen detection assays, such as rapid lateral-flow immunoassays and direct fluorescent antibody assays, have been designed for several viruses and are rapid but in general less sensitive and specific¹⁰. Serology is often limited by the need to detect seroconversion, IgG antibody titer rise or IgM detection, which is less sensitive in case of repeated exposure to for example rhinoviruses. As the induction of a measurable antibody response may take at least a week, the value of serology in the acute phase is limited¹⁰.

In 1985, an *in-vitro* nucleic acid amplification method was designed. The polymerase chain reaction (PCR) relied on exponential amplification and subsequent detection of specific parts of nucleic acid sequences, with much improved sensitivity and specificity. Initially, after the amplification protocol was completed, the amplified PCR products were visualized by gel electrophoreses, southern-blotting or ELISA-like detection systems. In 1992, the real-time PCR concept was launched, which enabled detection of PCR products while they were generated using fluorescent probes. This greatly enhanced the possibilities as it enabled quantitative detection of targets. Real-time PCR is fast, sensitive, specific and has relative low hands-on time. Initially one virus per run was tested, but, using multiple fluorophores that could be differentiated, also duplex and multiplex PCR assays could be designed. However, the amount of targets that could be detected is limited to a maximum of five (in most platforms) by the number of fluorescent probes that could be differentiated and by applying an efficient workflow with batch-wise testing the time to results could be a day¹¹⁻¹³.

Advances in molecular respiratory viral diagnostics

Recently introduced molecular platforms offer the possibility of syndromic testing, as extended multiplex PCRs detect a wide panel of respiratory pathogens implicated in the clinical syndrome. Another benefit is the random and continuous access resulting in very fast and reliable results throughout the day. Whether these super-fast time to results diagnostic tests have clinical implications needs to be determined in more detail^{14,15}.

Molecular amplification based methods are still limited by the need to pre-define the targets of interest in a diagnostic panel. This is complicated by the high number of possible respiratory pathogens, the genetic diversity of the viruses implicated and the occurrence of new respiratory pathogens. Rare causes are easily overlooked with sometimes great consequences, as encountered for example in the Netherlands during Legionella and Q-fever outbreaks, and MERS-coronavirus in South-Korea¹⁶⁻¹⁸. The emergence of new clinically relevant respiratory viruses is a real threat, which will be clear to anyone after the devastating appearance of SARS-CoV-2 early in 2020 and indeed, NGS played a crucial role in its initial diagnosis and phylogenetic analysis¹⁹⁻²². But in addition, such new viruses may also be present already, without causing a pandemic, like the pigeon paramyxovirus type 1 that was coincidentally found to cause a fatal infection in a stem cell recipient²³. We can never be informed about the role of such viruses without applying NGS as a broad 'catch all' approach.

While for a large proportion of the pneumonias the causative agent is still unknown, it is suspected that the percentage attributed to viral pathogens is higher than currently is assumed. Therefore there is a need for an unbiased catch-all method (see figure 2).

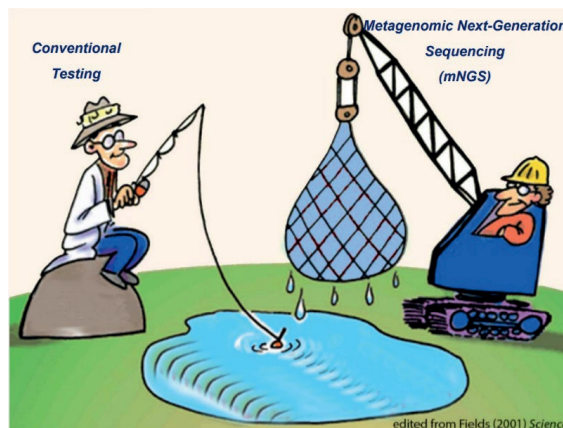


Figure 2. Cartoon representation of selective conventional testing compared to catch-all metagenomic next-generation sequencing.

(adapted from Chiu et al.²⁴).

The newest diagnostic development, metagenomic next-generation sequencing (mNGS) is such an unbiased catch-all method, detecting all the genetic material in a sample. Standardized protocols for application of mNGS in the diagnostic field are still lacking and also the time to results and the cost of this approach are reason for concern, although the latter is rapidly declining (figure 3). To use mNGS as routine diagnostic tool, there is a need for fast, automated, combined DNA and RNA pre-treatment and analysis protocols with high sensitivity and specificity.

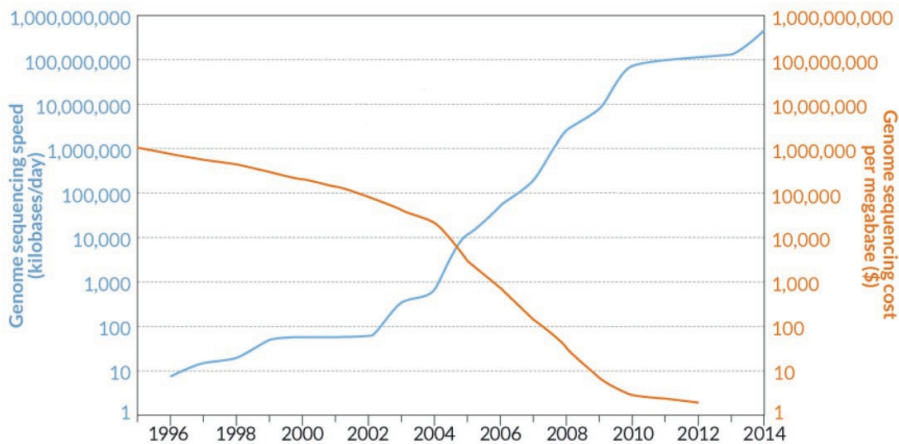


Figure 3. Improvements in costs and speed of genome sequencing.
(adapted from Otwell²⁵).

Another advantage of this catch-all technique is that additional information is provided on strain characteristics, genotyping, susceptibility and virulence markers, pathogen evolution and the virome in health and disease. The respiratory virome and its correlation to clinical data is not yet studied extensively.

RHINOVIRUSES

Rhinoviruses are single stranded positive-sense RNA viruses in the family Picornaviridae and the genus *Enterovirus*. Since their discovery in the 1950s over 160 types, subdivided in species A, B and C, have been discovered^{26,27} (Figure 4).

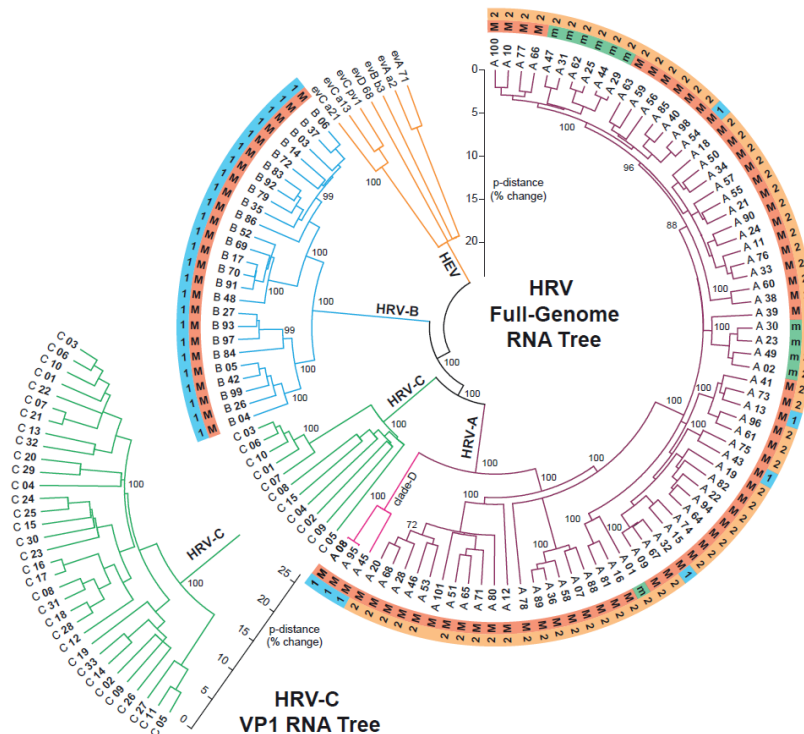


Figure 4. Phylogenetic tree of rhinovirus.

(adapted from Fields et al.²⁸)

The genome of rhinoviruses is approximately 7,200 bp long and consists of a single open reading-frame that encodes a large polyprotein of nearly 2200 amino acids, which is cleaved to produce 11 viral proteins (VP). VP1, VP2, VP3 and VP4 compose the viral capsid that embeds the RNA, while the non-structural proteins are involved in replication and assembly. At the 5' end of the genome the rhinoviruses have a long untranslated region (UTR), with internal ribosome entry sites (IRES), for initiation of translation. The 3' end untranslated region is much shorter and enables efficient replication^{26,29}, figure 5.

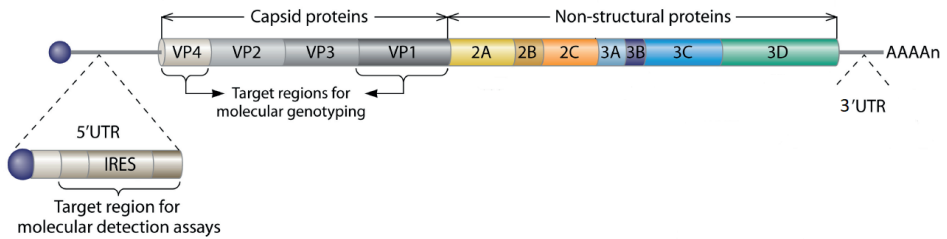


Figure 5. The genome structure of rhinoviruses.

UTR, untranslated region. IRES, internal ribosome entry site (Adapted from Jacobs et al.²⁶)

Epidemiology of rhinoviruses

Rhinoviruses have a worldwide distribution with a high prevalence, especially in young children. Although rhinovirus infections occur all year round, they have a peak incidence in early fall and spring³⁰⁻³³.

Rhinoviruses are transmitted by direct contact, droplets or aerosols, but most important experimental evidence supports efficient transmission occurring through (in)direct contact mainly through hands, after which the virus attaches and replicates in the nasal mucosa, with an additional role for aerosol transmission³⁴⁻³⁹.

Clinical manifestations of rhinoviruses

Rhinoviruses can cause a wide variety of respiratory symptoms, but asymptomatic shedding does occur as well. Asymptomatic infection tends to be more prevalent in younger patients and was even found in 12-32% of children under the age of four⁴⁰⁻⁴⁵.

The most frequently encountered symptomatic presentation of rhinovirus infection is the, self-limiting, common cold. This usually starts with a sore throat followed by nasal obstruction and rhinorrhea, but a variety of symptoms has been observed. Rhinoviruses can also cause (rhino)sinusitis and otitis media, but in those cases co-infection with bacteria is common. Although rhinoviruses have long been considered relatively mild viruses, causing benign upper respiratory tract infections, they are now implicated in more serious lower respiratory tract infections in high-risk groups. They have been associated with the development of asthma, asthma and COPD exacerbations, bronchiolitis and life-threatening pneumonia, mainly in children and the elderly^{7,26,46-48}.

The development of more serious infections by rhinovirus is probably multifactorial and dependent on both host and environmental factors (Figure 6). Though several factors associated with more severe disease are known, much remains unknown.

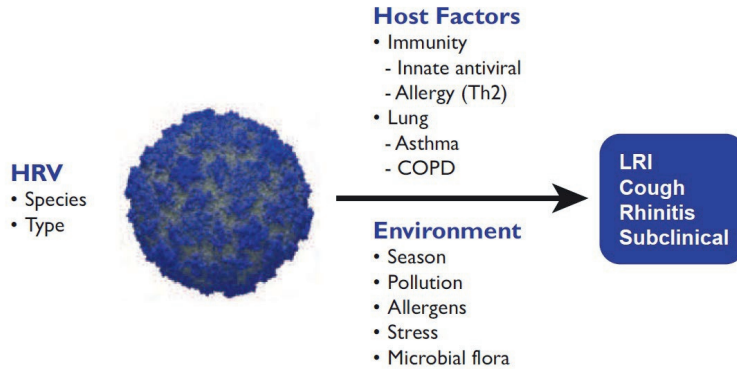


Figure 6. Spectrum of human rhinovirus infections and factors involved.

(adapted from Fields' Virology ²⁸)

More severe rhinovirus infections have been shown in elderly patients, immunocompromised patients and patients with underlying chronic lung disease⁴⁹⁻⁵³. In children, risk factors for more serious infections are prematurity, congenital heart disease, respiratory syncytial virus co-infections, and non-infectious underlying respiratory disease. Finally, rhinoviruses have been associated with a complicated post-operative course after cardiac surgery⁵⁴⁻⁵⁶. In children, higher viral loads and viremia have been found in association to higher disease severity and more extensive clinical symptoms⁵⁷⁻⁶⁵. Whether rhinovirus viremia does occur in adults and is associated with more severe disease is still unknown.

Another gap in knowledge exists on whether rhinovirus infection can lead to serious complications in case of extreme stress and special circumstances, for example in children undergoing cardiac surgery.

In addition, the association of specific rhinovirus types to more serious disease is still open for debate. Some studies showed rhinovirus type C to cause more severe illness, while others failed to demonstrate a difference between the rhinovirus types^{48,66-70}. A longitudinal study with a large number of patients with a variety of rhinovirus types is needed to determine the influence of rhinovirus species on disease severity.

Although rhinovirus infections have been associated with mortality, the major disease burden is caused by the high frequency of infections, the duration of illness (a median of 7 days) and the associated economic burden^{29,46,71}.

Treatment and prevention

There is currently no licensed treatment available for rhinovirus infections, although several antiviral treatments have been described or are under development^{26,72}. Therefore, at the moment, the best way to prevent rhinovirus infections is adequate hand hygiene measures⁷³.

SCOPE OF THIS THESIS

The research presented in this thesis aims to determine the implications and performance of new viral respiratory diagnostic methods and the aspects of the disease severity of the most common respiratory virus, rhinovirus.

Part I: Application and added value of advanced respiratory viral diagnostic methods

In this part, advanced diagnostic methods for respiratory infections were studied to determine their clinical implications and their performance, when applied to routine diagnostics.

An in-house developed diagnostic mNGS protocol, with simultaneous RNA and DNA detection, was developed and compared with real-time PCR (chapter two). This protocol was used to study respiratory infections and the respiratory virome in patients with COPD exacerbations and to correlate these results with clinical data and real-time PCR (chapter three).

Rapid molecular syndromic testing by an innovative automated amplification platform was compared to lab-developed multiplex real-time PCR assays, focusing on the difference in time to results and its implications for clinical decision making, regarding isolation, and antimicrobial therapy (chapter four).

Part II: Clinical implications of rhinovirus

In this part, rhinovirus is studied in different patient populations to determine the clinical impact and factors influencing the course of the disease. To determine whether rhinovirus infections, symptomatic or asymptomatic, have a negative effect on the post-operative course of children undergoing cardiac surgery, a large prospective study screening all children at the time of their operation was performed (chapter five).

A retrospective study to detect rhinovirus viremia and its association with disease severity was performed in adult patients with high rhinovirus loads in bronchoalveolar lavage (chapter six). The difference in disease severity between different rhinovirus species and types was studied in a prospective study in an adult population in general practices throughout Europe (chapter seven).

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