UK NEQAS for Microbiology:
First year review of the Molecular detection of respiratory viruses EQA scheme

S. Whitmore[1], B. Kele[1], E. Elenoglou[1], H. Seyedzadeh[1], and S. Rughooputh[1]
[1] **UK NEQAS** for Microbiology, Public Health England, 61 Colindale Avenue, London, NW9 5EQ, United Kingdom

Introduction

Respiratory viruses are among the most common causes of symptomatic infections and are an important cause of morbidity and mortality in humans worldwide . Viral respiratory infections are responsible for about 90% of upper respiratory tract infections and about 30% of lower respiratory tract infections[1].

In April 2016, UK NEQAS for Microbiology introduced the Molecular detection of respiratory viruses EQA scheme into their distribution repertoire. Three distributions are dispatched each year, each consisting of four freeze dried simulated nasopharyngeal aspirates. Participants report on the presence of Influenza viruses, respiratory syncytial virus (RSV), adenoviruses, rhinoviruses, enteroviruses, human metapneumovirus (hMPV), bocavirus, parainfluenza viruses, paraechoviruses and coronaviruses. Participants are scored on reporting the presence of the intended virus from the list above.

As part of ongoing scheme reviews, the data presented is a review of participant results after the first year of the introduction of the Molecular detection of respiratory viruses scheme into the EQA repertoire.

Materials and Methods

In total 314 participant results were reviewed from the first three distributions of the scheme, (distributions 4095, 4167 and 4227). These were distributed between May 2017 and January 2018, consisting in total of 12 simulated specimens being dispatched.
Over the three distributions an influenza A positive specimen was dispatched on five occasions (H3N2 n=3, H1N1 n=2). Influenza B on three occasions, RSV, parainfluenza, rhinovirus and adenovirus on one occasion. Participant results were compared and analysed against the intended results provided by UK NEQAS Microbiology from pre-distribution testing analysis.

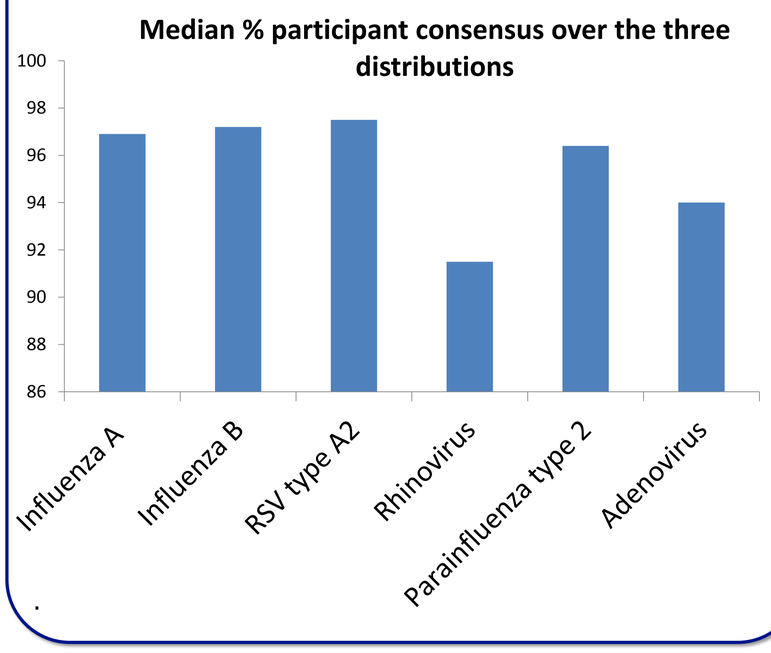
Results

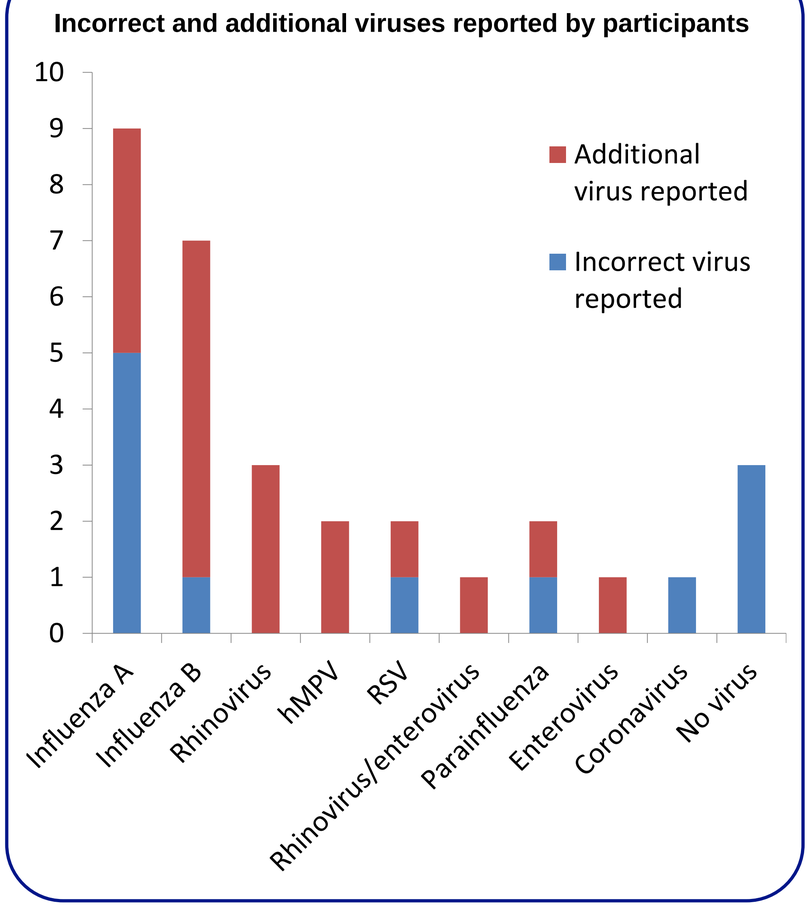
- Over the three distributions, participants' results return rates were 93.0%, 94.3% and 99.1% respectively.
- In total over the three distributions, there was a median consensus of 96.9% (95.3-99.1% range) identified for Influenza A positive specimens, as shown in Table 1
- 97.2% (96.5-97.9% range) consensus with Influenza B positive specimens, 97.5% consensus with RSV positive specimens, 91.5% consensus with rhinovirus positive specimens, 94.0% consensus with adenovirus positive specimens and 96.4% consensus for parainfluenza positive specimens.
- An incorrect virus was reported by participants on 8/12 (66.7%) specimens dispatched.
- 12 incidents of participants reporting an incorrect virus was identified over the three distributions.
- Influenza A was incorrectly reported on 5/12 (41.7%), with the majority (n=4) occurring on an influenza B positive intended result.
- Influenza B, RSV, parainfluenza and coronavirus were all reported incorrectly on 1/12 occasions respectively by participants.
- Participants incorrectly reported a 'No virus detected' result on 3/12 (25.0%) occasions. All incorrect false negative reports occurred on Influenza B positive specimens.
- An incorrect additional virus was reported on 8/12 (66.7%) specimens by participants.
- 22 incidents of participants reporting incorrect additional viruses were identified.
- Influenza B (6/22) was the most frequently reported additional virus, with 4/6 occurrences observed with an Influenza A positive specimen.
- Influenza A was incorrectly reported on four occasions as an additional virus, rhinovirus on three, hMPV on two, RSV, parainfluenza and enterovirus each on one occasion.

- An median increase in correct Influenza A reporting was observed over the 3 distributions, from 95.3% to 98.6% (+3.3%). With pre distribution typing Ct values of 28, 22, 23, 29 and 24 identified.
- A median of 93.8% (92.5-95.7% range) of participants are typing Influenza A positive specimens
- 99.6% of these participants reported a correct typing result.
- All incorrect typing results (2/2) were identified for Influenza A H3N2 positive specimens, with H1N1 and H1N3 being reported incorrectly by participants.
- 100% of Influenza A H1N1 positive specimens were correctly typed by participants.

Table 1.

	Return rate %	Intended virus	% participant consensus
4095	93.0	Influenza A H3N2	95.3
		Influenza B	96.5
		RSV type A2	97.5
		Parainfluenza type 2	96.4
4167	94.3	Influenza A H1N1	96.9
		Influenza B	97.9
		Influenza A H3N2	96.9
		Rhinovirus type 2	91.5
4227	99.1	Influenza A H1N1	99.1
		Influenza B	97.2
		Influenza A H3N2	98.1
		Adenovirus type 2	94.0





Intended result (number dispatched)	Incorrect virus reported	Additional virus reported
Influenza A H3N2 (n=3)	Influenza B (n=1)	Influenza B (n=3) Rhinovirus (n=2) hMPV (n=1)
Influenza A H1N1 (n=2)		Influenza B (n=1) RSV Rhinovirus/enterovirus Rhinovirus
Influenza B (n=3)	Influenza A (n=4) No virus (n=3)	Influenza A (n=1)
RSV A2 (n=1)	Parainfluenza (n=1)	hMPV (n=1)
Rhinovirus (n=1)		Influenza B (n=2)
Parainfluenza 2 (n=1)	RSV (n=1)	Parainfluenza 4 (n=1) Enterovirus
Adenovirus type 2 (n=1)	Influenza A (n=1) Coronavirus	Influenza A (n=3)

Conclusions

- Overall an excellent participant return rate was recorded for the scheme distributions despatched between May 2017 and January 2018.
- An excellent consensus to the intended results was identified over the three distributions. A low incidence of incorrect viruses reported by participants was observed.
- On few occasions participants reported additional viruses to the intended result (false positive results). With Influenza B being reported most commonly.
- A low incidence of participants reporting false negative results was observed.
- The majority of participants are typing Influenza A positive specimens and reporting the correct typing results as recommended by the WHO [2].
- The majority of participants are using commercial assays over in-house assays for respiratory virus testing.

The new UK NEQAS for Microbiology scheme for the molecular detection of respiratory viruses has become a popular EQA tool and has seen an increase in uptake over the three distributions

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References

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2. WHO Global Influenza Surveillance Network **Manual for the laboratory diagnosis and virological surveillance of influenza** 2011, ISBN: 9789241548090