**Efficiency of RNA isolation from respiratory samples using the NucliSens miniMAG and easyMAG extraction procedures**

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**Objectives:** The semi-automated NucliSens miniMAG (MM) and the automated NucliSens easyMAG (EM) (bioMérieux, Durham, NC) are platforms for the extraction of total nucleic acids (NA) from clinical samples. The method used by both is based on the established Boom chemistry but utilises magnetic silica particles. The purpose of this study was to evaluate both systems for the removal of inhibitors and the efficiency of isolation of respiratory syncytial virus (RSV) and human metapneumovirus (hMPV) RNA from paediatric respiratory samples.

**Methods:** Nasal swabs or respiratory specimens were collected from children with respiratory tract infections. A comparative analysis was conducted between the NucliSENS miniMAG and easyMAG extraction procedures; (1) no pre-incubation and MM protocol, (2) no pre-incubation and EM protocol, (3) no pre-incubation and Specific A extraction protocol, and (4) pre-incubation with proteinase K and Specific A extraction protocol. A panel of 12 samples, including 4 standards (obtained from VQCo, Uppsala, Sweden) was tested with five different extraction protocols. Each NA extract was tested for RSV and hMPV using a laboratory validated protocol and NucliSens analyte specific reagents (bioMérieux). Sensitivity of each method was compared using aliquots of serially diluted in vitro transcribed RNA-reference.

**Results:** For RSV testing, initial inhibition rates for samples extracted with MM were 0% (0/266) and for MM 2.11% (10/475). For hMPV testing, initial inhibition rates for samples extracted with MM were 2.11% (10/475). Inhibition was resolved for all samples after repeat MM extraction from an aliquot for a final inhibition rate of 0%.

**Conclusions:** The NucliSENS easyMAG platform (bioMérieux) is designed for nucleic acid extraction from a broad range of different sample types. For the samples scored positive with all five methods the mean Ct values were 32.8, 31.0, 32.9, 30.5, and 31.3, respectively.

**Conclusion:** Best results for both HBV DNA and control PhHV DNA detection, were obtained in combination with protocol 4 that uses proteinase K pre-incubation, followed by extraction with the NucliSENS easyMAG platform using the Specific A protocol. The Protein Recovery system contributed minimal (on average −0.2 Ct) to the overall measurement error. Extracted samples were analysed by real time PCR.

**Results:** PhHV DNA was detected in all samples. Mean Ct values were 29.6, 29.8, 29.5, 29.3, and 31.4 for protocols 1, 2, 3, 4, and 5, respectively. HBV DNA was not detected in the negative control samples. For the remaining samples HBV DNA was detected in 100% (protocols 1, 2, 3, 4, and 5) and 91% (protocol 3). For the samples scored positive with all five methods the mean Ct values were 23.8, 31.0, 32.9, 30.5, and 31.3, respectively.

**Conclusion:** Best results for both HBV DNA and control PhHV DNA detection, were obtained in combination with protocol 4 that uses proteinase K pre-incubation, followed by extraction with the NucliSENS easyMAG platform using the Specific A protocol. The Protein Recovery system contributed minimal (on average −0.2 Ct) to the overall measurement error.
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