Background. Human coronaviruses (HCoV) OC43, 229E, NL63 and HKU1 commonly cause upper respiratory tract infections, but can also cause severe lower respiratory tract disease. Increased use of diagnostic assays for respiratory viruses has facilitated detection and, since 2014, voluntary reporting of HCoV to the National Respiratory and Enteric Virus Surveillance System (NREVSS).

Methods. We reviewed weekly aggregate test results for HCoV OC43, 229E, NL63 and HKU1 voluntarily reported to NREVSS by U.S. hospital and clinical laboratories from July 1, 2014–April 30, 2017. Laboratories reporting any HCoV result using PCR were included, and the weekly percentage of positive HCoV tests by type was calculated. For a subset of HCoV detections reported to NREVSS via the Public Health laboratory Interoperability Project (PHLIP), which collects individual-level demographic data, we described age distribution and sex. Age distribution by HCoV type was compared using the Kruskal–Wallis test.

Results. 154 laboratories, across all 9 U.S. census divisions, reported 834,742 tests for HCoV; 18,514 (2.2%) were positive for HCoV-OC43, 8,363 (1.0%) for HCoV-NL63, 6,828 (0.8%) for HCoV-229E, and 5,170 (0.6%) for HCoV-HKU1. The percentage of tests positive for HCoV generally peaked between December and March (Figure 1). HCoV-OC43 showed distinct annual peaks with variation in magnitude by year. HCoV-HKU1 and NL63 had similar patterns, each with notable peaks during winter 2016 compared with 2015 or 2017. HCoV-229E showed a discernable peak in 2017 compared with the previous 2 years. Of 20,533 individuals with HCoV test results reported via PHLIP, 1,589 (7.7%) tested positive for any HCoV; 50% of HCoV-positive individuals were male, and the median age was 22 (range 0–96) years. Age distribution differed between HCoV types ($P < 0.01$, Figure 2).

Conclusion. Over approximately 3 seasons, peak positivity for HCoV occurred during winter months, and annual differences in circulation by HCoV type were observed. Continued testing and surveillance for HCoV will allow for further characterization of circulation trends over time and by geographic region, and improved understanding of the contribution of HCoV to the winter respiratory virus season.
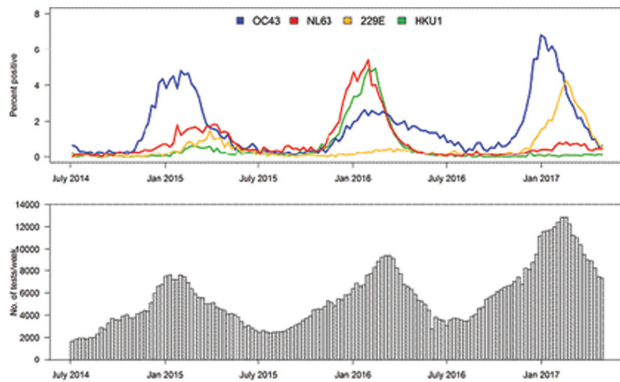

Figure 1. (A) Percentage of tests positive for human coronaviruses (HCoV) OC43, NL63, 229E, and HKU1 reported to the National Respiratory and Enteric Viruses Surveillance System (NREVSS) by week, July 1, 2014 – April 30, 2017. (B) Number of tests performed for HCoV reported to NREVSS by week, July 1, 2014 – April 30, 2017
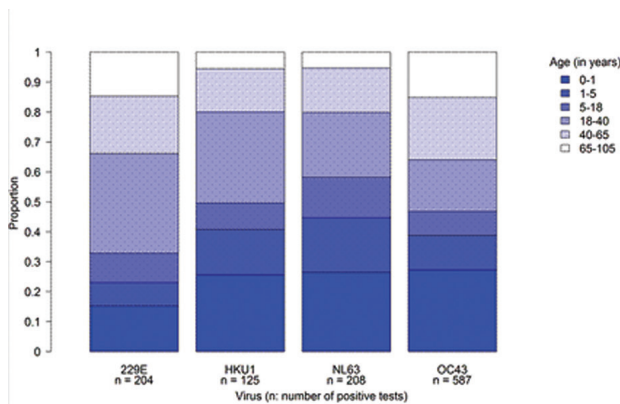

Figure 2. Age distribution of human coronaviruses 229E, HKU1, NL63 and OC43 positive tests reported to Public Health Laboratory Interoperability Project (PHLIP), October 2014 – April 2017.

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1031. PCR Array Profiling of Antiviral Genes in Human Embryonic Kidney Cells Expressing Human Coronavirus OC43 Structural and Accessory Proteins

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Background. Human coronavirus OC43 (HCoV-OC43) causes common cold, and is associated with severe respiratory symptoms in infants, elderly and immunocompromised patients. HCoV-OC43 is a member of *Betacoronavirus* genus that includes also the Severe Acute Respiratory Syndrome (SARS) and the Middle East Respiratory Syndrome (MERS) coronaviruses. Both SARS-CoV and MERS-CoV were shown to express proteins with the potential to evade early innate immune responses. However, the ability of HCoV-OC43 to antagonise the intracellular antiviral defences has not yet been investigated. The objective of this study was to investigate the role of HCoV-OC43 structural (membrane and nucleocapsid) and accessory (ns5a and ns2a) proteins in the modulation of antiviral gene expression profile in human embryonic kidney 293 (HEK-293) cells using PCR array analysis.

Methods. HCoV-OC43 membrane (M), nucleocapsid (N), ns5a and ns2a mRNA were amplified and cloned into the pAcGFP1-N expression vector (Clontech), followed by transfection in HEK-293 cells. Expression of M, N, ns5a and ns2a proteins were confirmed by indirect immunofluorescence test. Three days post-transfection, the cells were challenged by Sendai virus. The Human Antiviral Response PCR array system (Qiagen) was used to profile the antiviral gene expression in HEK-293 cells, using the fold regulation comparison and the manual normalisation methods.

Results. Around 50–60 genes were downregulated by HCoV-OC43 proteins, the most prominent genes being those critical for the activation of transcription factors involved in the antiviral response like interferon regulatory factors (IRFs) and activator protein 1 (AP-1). Among the most important downregulated genes were those coding for Interferons (IFNs) mitogen-activated protein kinases (MAPKs), pro-apoptotic and pyroptotic proteins (Caspases, cathepsins, tumour necrosis factor), pro-inflammatory cytokines (Interleukins), pattern recognition receptors (PRRs; toll-like receptors and NOD-like receptors) and their signaling transduction proteins (TICAM1, MAVS).

Conclusion. This study shows for the first time that similarly to SARS-CoV and MERS-CoV, HCoV-OC43 has the ability to downregulate the transcription of genes critical for the activation of different antiviral signaling pathways.

Disclosures. **All authors:** No reported disclosures.

1032. Human Coronavirus (HCoV) Infection Among Adults in Cleveland, Ohio: An Increasingly Recognized Respiratory Pathogen

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Background. Human Coronaviruses (CoV) have been long recognized as a common cause of respiratory tract disease including severe respiratory tract illness, yet there are few recent studies characterizing disease among adults in the United States. Here, we describe CoV infections and clinical characteristics among adults (>18 years) presenting with respiratory illness in Cleveland, Ohio.

Methods. Between February 1, 2016 and April 30, 2017, 2949 nasopharyngeal swab specimens were analyzed by NxTAG Respiratory Pathogen Panel in adults presenting with respiratory illness at MetroHealth Medical Center. Clinical data were collected on adults whose samples screened positive for CoV-HKU1, CoV-OC43, CoV-229E or CoV-NL63.

Results. Coronaviruses were detected in 192 (6.5%) adults including 105 (3.5%) OC43, 67 (2.3%) 229E, 13 (0.4%) HKU1 and 7 (0.2%) NL63. The majority of adults with coronavirus infection were females (66.2%) with a median age of 53 years. Common comorbidities included smoking (40.0%), asthma (38.0%), COPD (35.4%), and inhaled corticosteroid use (28.6%). Eighty-five (46.4%) required admission to the hospital. Common presenting symptoms included shortness of breath (42.7%) and cough (31.0%) whereas fever was uncommon (12.5%). Gastrointestinal symptoms were more common in HKU1 and NL63 infected adults. Seventy-three percent of coronavirus disease occurred between the months of January and March. Despite the recognition of coronavirus infection, 70 (36.5%) received antibiotics for their disease.

Conclusion. This study provides needed insight into clinical characteristics and severity associated with coronavirus infection in adults. Coronavirus infection should be considered in differential diagnosis of respiratory tract illness in adults including those that require hospitalization, have a history of smoking and have pulmonary comorbidities.

Disclosures. **All authors:** No reported disclosures.

1033. Evaluation of Serum TNF-alpha, IL-6, IL-10, and IFN-gamma Levels in Patients with Crimean–Congo Hemorrhagic Fever

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