**Background.** Latin America has some of the highest rates of multi-drug resistant gram-negative bacteria worldwide. However, local surveillance registries to compare rates of resistance among countries are lacking, particularly in Central America. Awareness of local resistance patterns in this region is critical to improve antibiotic use and patient outcomes. We sought to measure the prevalence of resistant gram-negative bacteria (GNB) at a tertiary hospital in Guatemala.

**Methods.** We retrospectively conducted a single-center study to measure the percentage of GNB that were non-susceptible to various antibiotics between April and October of 2017. All cultures (blood, urine, cerebrospinal fluid, and other body fluids) were collected as part of routine clinical care during the study period. Duplicate results from multiple specimens with the same organism from the same patient, were excluded. Antibiotic susceptibility testing was performed by disk diffusion method. Bacterial isolates were categorized as susceptible, intermediate, or resistant based upon the Clinical Laboratory Standard Institute 2015 edition per guidance from the National Laboratory of Guatemala.

**Results.** A total of 969 unique gram-negative isolates from 818 patients were included. Urine was the most common culture type. The most frequently isolated bacteria were *Escherichia coli* and *Klebsiella* species. The percentage of GNB which were non-susceptible to individual antibiotics are detailed in Table 1. Of the isolates tested, 12% – 66% of GNB were non-susceptible to cephapirinols, 7% – 31% were non-susceptible to carbapenems, and 14% – 44% were non-susceptible to fluoroquinolones.

**Conclusions.** The prevalence of multi-drug resistant GNB is high in Escuintla, Guatemala. Continued surveillance is vital to guide judicious and appropriate empirical antibiotic use in the setting of rising rates of antibiotic resistance. Local and regional resistance rates are known to vary, underlying the importance of developing more regional and national antibiotic resistance surveillance networks within Guatemala and other countries in Central America where there is a paucity of data.

**#5: Trends in Seasonal Prevalence of Respiratory Pathogens Among Children in the United Arab Emirates: A Multi-Center Study.** Sara Salim1, Handan Celiloglu1,2, Farah Tayyab2, Zainab A. Malik3,4, College of Medicine, Mohammed Bin Rashid University of Medicine and Health Sciences, Dubai, United Arab Emirates; 2Microbiology Laboratory, Mediclinic City Hospital, North Wing, Dubai, United Arab Emirates; 3Department of Pediatrics, Mediclinic City Hospital, Dubai Healthcare City, Dubai, United Arab Emirates; 4Pediatric Infectious Diseases, Mediclinic City Hospital, Dubai, United Arab Emirates.

**Background.** Pediatric respiratory infections cause a high disease burden globally. Their seasonality and molecular epidemiology in the United Arab Emirates (UAE) are not well understood. This data is important for clinical practice, to monitor disease outbreak and to optimize for vaccine and antibiotic combinations.

**Methods.** Children 0–18 years of age who presented to multiple hospitals and clinics within a large private healthcare group in Dubai between January 1st and December 31st, 2019, and had upper respiratory samples positive for any pathogen on multiplex polymerase chain reaction (mPCR) were included in this retrospective analysis. Socio-demographic, clinical, and molecular data were collected.

**Results.** Two thousand four hundred and twenty-two children had mPCR sample positive for at least one pathogen. The median age of our population was 39 months, and 56.8% were male. Emergency room was the most common site (32.3%) of sample collection and the vast majority presented with fever (85.7%). Rhinovirus/Enterovirus – 39% months, and 56.8% were male. Emergency room was the most common site (32.3%) of sample collection and the vast majority presented with fever (85.7%). Rhinovirus/Enterovirus – 39% months, and 56.8% were male. Emergency room was the most common site (32.3%) of sample collection and the vast majority presented with fever (85.7%). Rhinovirus/Entero – Human rhinovirus/Enterovirus; Para – Parainfluenza virus; RSV – Respiratory Syncytial Virus; Mycoplasma – Mycoplasma pneumoniae; Bordetella para – Bordetella parapertussis; Bordetella Per – Bordetella pertussis; Chlamydia – Chlamydia pneumoniae.

**Figure 1: Monthly Distribution of Pathogens**

- **Adeno – Adenovirus; Corona – Coronavirus; MPV – Human Metapneumovirus; Infla A – Influenza A; Infla B – Influenza B; Rhino/Entero – Human rhinovirus/Enterovirus; Para – Parainfluenza virus; RSV – Respiratory Syncytial Virus; Mycoplasma – Mycoplasma pneumoniae; Bordetella para – Bordetella parapertussis; Bordetella Per – Bordetella pertussis; Chlamydia – Chlamydia pneumoniae.**