Table 1. Mucosal cytokine concentrations in children with RSV infection

	RSV-OP(n=78)	RSV-IP (n=141)	RSV-Ward (n=101)	RSV-PICU (n=40)	OP vs Ward vs PICU (p-value)
Type-I IFN					
IFN-α2	1.6 (0.9-2.2)	0.7 (0.3-1.2)	0.7 (0.5-1.2)	0.7 (0.1-1.2)	<0.0001
IFN-β	3.6 (1.5-7.9)	2.4 (1.1-5.8)	2.4 (1.8-6.0)	1.8 (0.7-3.9)	0.1
Type-II IFN					
IP-10	268.6 (118.5-825.6)	87.6 (15.3-221.2)	116.2 (28.4-234.9)	34.8 (4.5-124)	<0.0001
IFN-γ	1.6 (0.8-3.5)	1.2 (0.5-1.9)	1.2 (0.7-2.3)	1.1 (0.4-1.3)	0.05
Type-III IFN					
IFN-λ1	5.2 (2-14.1)	3.4 (1.9-9.1)	3.4 (1.9-9.1)	3.3 (1.9-9.1)	0.2
IFN-λ2/λ3	14.3 (4.4-24.8)	8.9 (3.4-12.7)	8.9 (3.7-12.7)	8.9 (1.4-12.7)	0.0007

IP: inpatients; OP: outpatients. Values represent absolute numbers and medians (25%-75% interquartile range-IQR). Cytokine conc. expressed in pg/mL. Mann-Whitney test was used to determine differences between two groups; Kruskal-Wallis was used to determine differences between three groups (p-values*).

Conclusion: Infants with mild RSV infection had higher RSV VL and higher conc. of IP-10 and type-I, III IFN than those hospitalized with severe disease. These findings suggest that IP-10 and mucosal IFNs are associated with protection against severe RSV disease and could be used as biomarkers for patient stratification in the clinical setting.

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132. Emergence and Spread of Multidrug-resistant salmonella Serotype Infantis Infections in the United States, 2003–2018

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Session: O-25. Hot Topics in Bacteria and Viral Infections

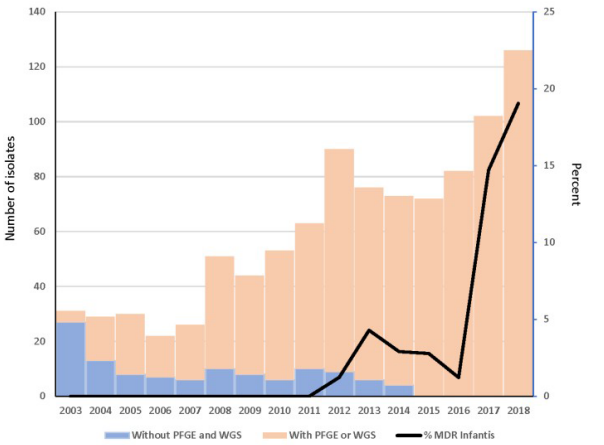
Background: Infantis re-emerged as a leading *Salmonella* serotype when a multidrug-resistant (MDR) strain with a rare extended spectrum β-lactamase (ESBL) $bla_{\text{CTX-M-65}}$ gene emerged among returned travelers from Peru in 2012 and then spread domestically. This strain has been isolated from chickens at slaughter and retail, and humans in outbreaks traced to chicken. We reviewed national surveillance data to determine incidence trends and antibiotic resistance among Infantis infections.

Methods: We reviewed data from 2003–2018 from the Foodborne Diseases Active Surveillance Network to determine the incidence and epidemiology of infections in 10 sites under surveillance; PulseNet to determine pulsed-field gel electrophoresis (PFGE) patterns; and National Antimicrobial Resistance Monitoring System (NARMS) to determine antimicrobial susceptibility testing (AST) results and resistance genes of isolates identified by whole genome sequencing (WGS). We defined MDR Infantis as having ceftriaxone resistance by AST and either the $bla_{\text{CTX-M-65}}$ gene or one of 18 PFGE patterns linked to that gene by WGS.

Results: The 2,154 patients with Infantis infection had a median age of 36 years and 57% were female; 86% had isolates from stool, 9% from urine, and 3% from blood. Only 10% reported foreign travel and 27% were hospitalized. The incidence of infections began increasing in 2010 and by 2017–2018 was 2-fold higher than the average during 2003–2009. During 2003–2018, 856 (88%) of 970 NARMS isolates had PFGE or WGS data; 48 isolates were MDR Infantis, and in addition to ceftriaxone and ampicillin resistance (by definition), all 48 were resistant to 3 or more antibiotic classes, 94% had decreased susceptibility to ciprofloxacin, and 67% were resistant to cotrimoxazole. During 2012–2016, 2% of isolates were MDR Infantis; this increased to 17% during 2017–2018 (Figure).

Conclusion: During the past decade, the incidence of Infantis infections markedly increased. This was likely driven by the emergence of an ESBL-producing strain that was initially associated with travel, and is now mostly domestically acquired and associated with consuming chicken. MDR Infantis now accounts for 1 in 5 Infantis infections. Public health strategies to reduce *Salmonella* contamination of chicken could help prevent these infections.

Number of *Salmonella enterica* Infantis isolates and percentage MDR Infantis* by year—United States, 2003–2018†



*MDR Infantis isolates were defined as having ceftriaxone resistance by antimicrobial susceptibility testing and either the $bla_{\text{CTX-M-65}}$ gene or one of 18 pulsed-field gel electrophoresis (PFGE) patterns linked to that gene; % MDR Infantis was calculated among isolates with PFGE or whole-genome sequence (WGS) data.

†Since 2003, 50 state and 3–4 local health departments have participated in the National Antimicrobial Resistance Monitoring System. Isolates were tested for antimicrobial susceptibility, PFGE, and WGS (since 2014).

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133. validation of a Global Respiratory Severity Score in Infants with Primary RSV Infection

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Session: O-25. Hot Topics in Bacteria and Viral Infections

Background: We recently developed a global respiratory severity score (GRSS) as a research tool from (n=139) infants with primary respiratory syncytial virus (RSV) infection enrolled prospectively in the Assessing Predictors of Infant RSV Effects and Severity (AsPIRES) study. The objective of the present study was to validate our original findings that the GRSS correlates well with clinical outcomes including hospitalization and length of stay (LOS) utilizing an independent cohort.

Methods: Clinical and demographic data on infants with primary RSV infection were abstracted from the electronic medical record. The GRSS was calculated by applying the original training data formula to the new data set. We compared the mean GRSS between the hospitalized and non-hospitalized group with Welch two sample t-test, and correlated it with hospitalization and LOS using Pearson's correlation test.

Results: A total of 184 (98 hospitalized and 86 non-hospitalized) subjects were enrolled. The hospitalized and non-hospitalized infants were different in general appearance, the percentage with rales, retractions, lethargy, respiratory rate and oxygen saturation. The hospitalized group had a significantly ($t=9.334$, $p< 0.0001$) higher GRSS (4.20±2.10) than the non-hospitalized group (1.76±1.41). Using GRSS ≤3.5 as the classification criterion, we correctly predicted the hospitalization status of 131 (71.2%) subjects. The area under the ROC curve of the GRSS as a classifier of hospitalization is AUC=0.8265 ($p< 0.0001$). Pearson correlation between the GRSS and LOS is ($p< 0.0001$).

Area under the ROC curve of the GRSS