Campylobacter dixic acid and ciprofloxacin), which are commonly used to treat campylobacteriosis. Whole genome sequencing (WGS) was performed at the Tennessee (TN) State Public Health Laboratory to determine the minimum inhibitory concentration for nine antimicrobial drugs. Whole genome sequencing of Campylobacter isolates provides predicted resistance data. Coupling predicted resistance data with exposure data facilitates better understanding of source attribution of different strains.

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**700. Risk Factors and Molecular Epidemiology of Acute and Chronic Norovirus Infections at a Large Tertiary Care Cancer Center**

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**Session:** P-33. Enteric Infection

**Background.** Norovirus (NoV) is the leading cause of viral diarrhea in patients with cancer. In this study, we describe risk factors associated with acute and chronic NoV infection in this patient population.

**Methods.** We identified 132 patients with NoV diarrhea (using stool RT PCR) between 2016-2020 at University of Texas MD Anderson Cancer Center (MDACC). Patient data, including demographics, clinical characteristics, NoV treatments, and complications were retrospectively extracted from charts. Stool samples were analyzed for NoV genogroups and genotypes. We compared characteristics and outcomes of patients with acute diarrhea (<14 day; AD) versus chronic diarrhea (>14 day or recurrence within 12 weeks; CD) and analyzed the data using Pearson Chi square or Fisher’s exact for categorical variables and Wilcoxon rank-sum test for continuous variables.

**Table 1. Patient Demographics.**

| Characteristic                  | NoV (n=132) | Chronic (n=21) | p-value |
|--------------------------------|-------------|---------------|---------|
| Age at diagnosis in years, median | 25 (14-56) | 25 (14-56) | 0.825   |
| Sex                              |             |               |         |
| Male                            | 66 (49%)    | 12 (57%)     | 0.501   |
| Female                          | 66 (51%)    | 9 (43%)      |         |
| Race                             |             |               |         |
| White                           | 91 (69%)    | 16 (76%)     | 0.825   |
| Hispanic                        | 35 (27%)    | 3 (14%)      |         |
| Other                           | 1 (1%)      | 2 (9%)       |         |
| Other                            | 1 (1%)      | 2 (9%)       |         |
| Non-Hispanic                     | 1 (1%)      | 2 (9%)       |         |
| Histology                        |             |               |         |
| Hematopoietic stem cell recipient | 34 (26%)   | 4 (19%)      | 0.013   |
| Allogeneic hematopoietic stem cell recipient | 98 (75%) | 17 (81%) |         |
| Genetic and microbial transplant | 2 (2%)      | 0 (0%)       |         |
| Parenteral nutrition             | 0 (0%)      | 0 (0%)       |         |
| Immunosuppressants or steroids   | 0 (0%)      | 0 (0%)       |         |
| Graft versus host disease        | 0 (0%)      | 0 (0%)       |         |
| Hematological malignancy         | 85 (65%)    | 18 (86%)     | 0.005   |
| Hematopoietic stem cell recipient | 34 (26%)   | 4 (19%)      |         |
| Allogeneic hematopoietic stem cell recipient | 98 (75%) | 17 (81%) |         |
| Genetic and microbial transplant | 2 (2%)      | 0 (0%)       |         |
| Parenteral nutrition             | 0 (0%)      | 0 (0%)       |         |
| Immunosuppressants or steroids   | 0 (0%)      | 0 (0%)       |         |
| Graft versus host disease        | 0 (0%)      | 0 (0%)       |         |
| Hematological malignancy         | 85 (65%)    | 18 (86%)     | 0.005   |

Of 132 patients identified, 124 had an underlying cancer (39 solid tumor, 85 hematological malignancies, Table 1). On univariate analysis, CD patients were more likely to have a hematological malignancy (p<0.002), be a hematopoietic stem cell recipient (p=0.013), have a history of gastrointestinal graft versus host disease (p=0.011), or have received immunosuppressants or steroids in the 90 days before diarrhea onset (p<0.001, Table 2). CD patients had significantly lower white blood cell counts (p=0.003), absolute neutrophil counts (p=0.049), IgG levels (p=0.001), and serum albumin levels (p=0.002) at the time of NoV diagnosis (Table 3). Patients with CD more often received symptomatic or NoV targeting treatment, including anti-diarrheal (p=0.005), nitazoxanide (p<0.001), intravenous immune globulin (p=0.017), and oral loperamide (p=0.042). CD patients more often had diarrhea recurrence in the first 4 weeks (p=0.001) or the second month (p<0.001) after initial diagnosis and needed enteral or parenteral nutrition (p=0.004). We genotyped NoV in 67 patients (Figure 1), resulting in identification of the following genogroups: GI (n=9, 13%), GII.4 (n=23, 34%), and other types of GII (n=35, 52%). Genotype diversity was higher in patients with CD (p=0.005), nitazoxanide (p<0.001), intravenous immune globulin (p=0.017), and oral loperamide (p=0.042). CD patients more often had diarrhea recurrence in the first 4 weeks (p=0.001) or the second month (p<0.001) after initial diagnosis and needed enteral or parenteral nutrition (p=0.004). We genotyped NoV in 67 patients (Figure 1), resulting in identification of the following genogroups: GI (n=9, 13%), GII.4 (n=23, 34%), and other types of GII (n=35, 52%). Genotype diversity was higher in patients with CD than AD (Figure 1).

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**699. Case-Case Comparison of Exposures among Fluoroquinolone-Resistant and Pan-Susceptible Campylobacter Cases, Tennessee, 2016-2018**

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**Session:** P-33. Enteric Infection

**Background.** Campylobacter causes an estimated 1.5 million infections each year in the United States. Of those, approximately 48,000 infections are caused by antibiotic-resistant strains, including strains resistant to fluoroquinolones (e.g., nalidixic acid and ciprofloxacin), which are commonly used to treat campylobacteriosis. Campylobacter infection is commonly attributed to consuming poultry products. Exposure data was collected through routine case interviews. We compared exposure data between fluoroquinolone-resistant and pan-susceptible Campylobacter cases reported in 2016-2018 to assess attribution.

**Methods.** Broth microdilution was performed on Campylobacter isolates at CDC to determine the minimum inhibitory concentration for nine antimicrobial drugs. Whole genome sequencing of Campylobacter isolates from Tennessee were submitted to CDC NARMS. Of those, 123 (20%) isolates were resistant to fluoroquinolones and 304 (50%) isolates were pan-susceptible. The gyr A (86) resistance gene was detected in 46/54 (85%) of resistant isolates. Exposure data were available for 59 (48%) fluoroquinolone-resistant cases and 186 (61%) pan-susceptible cases. Consumption of chicken (OR 2.1, p-value 0.03) and handling raw seafood (OR 3.1, p-value 0.03) were significantly associated with fluoroquinolone resistance. More fluoroquinolone-resistant cases reported international travel compared to pan-susceptible cases (15% versus 4%) with OR 4.6, and p-value 0.004. A total of 606 Campylobacter isolates from Tennessee were submitted to CDC NARMS. Of those, 123 (20%) isolates were resistant to fluoroquinolones and 304 (50%) isolates were pan-susceptible. The gyr A (86) resistance gene was detected in 46/54 (85%) of resistant isolates. Exposure data were available for 59 (48%) fluoroquinolone-resistant cases and 186 (61%) pan-susceptible cases. Consumption of chicken (OR 2.1, p-value 0.03) and handling raw seafood (OR 3.1, p-value 0.03) were significantly associated with fluoroquinolone resistance. More fluoroquinolone-resistant cases reported international travel compared to pan-susceptible cases (15% versus 4%) with OR 4.6, and p-value 0.004.}

**Conclusion.** Fluoroquinolone-resistant Campylobacter infections were acquired domestically and internationally. Exposure to chicken products and handling raw seafood were associated more often among fluoroquinolone-resistant cases. Whole genome sequencing of Campylobacter isolates provides predicted resistance data. Coupling predicted resistance data with exposure data facilitates better understanding of source attribution of different strains.

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

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**Table 3. Microbiological features of pediatric Shigella and Campylobacter infections.**

| Characteristic | Shigella (n=59) | Campylobacter (n=18) |
|---------------|----------------|----------------------|
| Species       | S. sonnei (57/66.6) | C.jejuni (16/100); C. coli (2/3.4) |
| Source        | Stool           | Stool                 |
| Urine         | 55 (93.2)       | 16 (100); 4 (6.8)   |
| Resistance1   | Ampicillin (n=31) | 4 (12.9); 40 (72.7) |
| (Not tested)  |                | (Not tested)         |

1 Number of Shigella isolates tested indicated in parentheses. Exposure data were available for 59 (48%) fluoroquinolone-resistant cases and 186 (61%) pan-susceptible cases. Consumption of chicken (OR 2.1, p-value 0.03) and handling raw seafood (OR 3.1, p-value 0.03) were significantly associated with fluoroquinolone resistance. More fluoroquinolone-resistant cases reported international travel compared to pan-susceptible cases (15% versus 4%) with OR 4.6, and p-value 0.004.

**Conclusion.** Fluoroquinolone-resistant Campylobacter infections were acquired domestically and internationally. Exposure to chicken products and handling raw seafood were associated more often among fluoroquinolone-resistant cases. Whole genome sequencing of Campylobacter isolates provides predicted resistance data. Coupling predicted resistance data with exposure data facilitates better understanding of source attribution of different strains.

**Disclosures.** All Authors: No reported disclosures
beneficial patient outcomes, including low rates of recurrence. These results support the continued clinical development of ibezapolstat.

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