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Pathogenetic Characteristics of Infectious Diarrhea among the Elderly Aged ≥60 in Pudong New Area, Shanghai, 2010–2024

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Abstract: This study aimed to characterize the epidemiological characteristics and pathogen distribution of diarrhea among adults aged ≥60 in Pudong New Area, Shanghai. A retrospective analysis was conducted on 4310 diarrhea cases aged ≥60 collected from the ongoing surveillance from January 2010 to December 2024. Specimens were tested for 8 bacterial and 5 viral pathogens using culture and molecular methods. Detection rates were compared across age groups and over time, and age-specific trends were evaluated using joinpoint regression. The overall pathogen-positive rate was 42.20% (1819/4310). Viral infections accounted for the largest proportion (20.26%), mainly norovirus (13.53%) and rotavirus (4.78%). Bacterial infections accounted for 15.99%, predominantly Diarrheagenic *E. coli* (DEC) (5.94%), *non-typhoidal Salmonella* (NTS) (3.57%), and *Campylobacter* spp. (2.60%). Pathogen positivity peaked in 2017, declined after 2020 during the COVID-19 pandemic, and slightly increased thereafter. Viral infections occurred primarily in winter–spring (October–March), whereas bacterial infections peaked in summer–autumn (June–September). Among cases with single infections, the highest viral and bacterial positivity rates were observed in the 60–69 age group (both $p < 0.05$), while DEC was highest in those aged ≥80 (6.57%). Joinpoint regression revealed non-linear age patterns. Viral infections declined with age but rebounded around the early 90s, whereas bacterial infections remained relatively stable before increasing at similar ages. Norovirus, rotavirus, and DEC were the leading pathogens of infectious diarrhea among the elderly in Pudong New Area, Shanghai. Age-specific, temporal, and seasonal patterns underscore the need for targeted prevention strategies, particularly for the extreme elderly.

Keywords: China; diarrhea; pathogen; surveillance; epidemiological characteristics

1. Introduction

Infectious diarrhea remains a major cause of morbidity worldwide and continues to impose a substantial public health burden across all age groups. According to recent Global Burden of Disease estimates, enteric infections account for hundreds of millions of illness episodes annually, resulting in considerable healthcare utilization and socioeconomic impact [1–4]. A broad range of pathogens contributes to infectious diarrhea, including viruses such as norovirus and rotavirus, as well as bacterial agents such as Diarrheagenic Escherichia coli (DEC) and non-typhoidal Salmonella (NTS) [2]. The relative contribution of these pathogens varies markedly

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by geographic region, population structure, and surveillance setting, reflecting the dynamic and heterogeneous nature of the etiological spectrum of infectious diarrhea [2,5,6].

Over the past decades, global improvements in sanitation, vaccination, and case management have led to a substantial reduction in diarrheal mortality [3,7]. While significant progress has been made globally in reducing diarrheal mortality among children, the burden of infectious diarrhea in the elderly is increasingly prominent with the acceleration of population aging [3,8–10]. Elderly individuals are more susceptible to enteric infections due to age-related immunosenescence, a higher prevalence of chronic comorbidities, and increased exposure risks in healthcare and long-term care settings [11–13]. Moreover, infectious diarrhea in older adults is more likely to result in severe clinical outcomes, including dehydration, hospitalization, and prolonged disease courses, thereby placing a disproportionate burden on healthcare systems [14]. Despite these concerns, epidemiological and etiological studies of infectious diarrhea have predominantly focused on pediatric populations, while evidence specific to elderly populations remains comparatively limited.

In China, infectious diarrhea is consistently reported as one of the most common intestinal infectious diseases under the national notifiable disease surveillance system, with a substantial number of cases recorded each year [15]. However, pronounced regional disparities in diarrhea exist due to variations in socioeconomic development, healthcare infrastructure, climate, and population demographics [2,5]. Although routine surveillance provides valuable incidence data, most existing studies rely on aggregated reports or short-term observations and lack long-term, pathogen-specific, and age-stratified analyses. In particular, comprehensive descriptions of pathogen spectra and temporal trends among elderly populations at the subregional or metropolitan level remain scarce, limiting the understanding of pathogen dynamics and constraining the development of targeted prevention and control strategies for this rapidly growing population group.

Long-term, systematic surveillance is essential for elucidating changes in the epidemiological and etiological characteristics of infectious diarrhea, including shifts in dominant pathogens, seasonal patterns, and potential impacts of public health interventions. Such data are critical for improving etiological diagnosis, informing clinical management, and guiding evidence-based allocation of prevention and control resources. Shanghai, as a megacity with a rapidly aging population, faces an urgent need to characterize the evolving pathogen spectrum of infectious diarrhea among its elderly residents. Therefore, using surveillance data collected in Pudong New Area, Shanghai, from 2010 to 2024, this study aims to describe the epidemiological characteristics, pathogen spectrum, seasonal distribution, and long-term trends of infectious diarrhea among elderly individuals, thereby providing a scientific basis for optimizing age-specific and regionally tailored prevention and control strategies.

2. Materials and Methods

The comprehensive diarrhoea surveillance system

From January 2010 to December 2024, a population-based sentinel surveillance program was conducted to monitor the epidemiology and etiological characteristics of acute diarrheal diseases in Pudong New Area, Shanghai, China. The surveillance network consisted of Shanghai Pudong New Area Center for Disease Control and Prevention (Shanghai Pudong New Area Health Supervision Institute) and 47 sentinel hospitals (9 tertiary-level and 4 secondary-level, and 34 primary-level hospitals) with enteric disease services distributed across the district. Sentinel hospitals were selected using the means of surface with non-homogeneity (MSN) method, which considers geographic distribution, population coverage, and healthcare utilization to ensure representativeness.

At the sentinel hospitals, cluster sampling was implemented, and approximately 10% of monthly diarrhea outpatients were included for pathogen surveillance. This sampling proportion was determined based on surveillance capacity and laboratory workload while ensuring adequate representativeness of circulating enteric pathogens in the study population. Patients were preferentially selected if they presented shortly after symptom onset and had not taken antimicrobial or antiviral medications before the clinical visit.

Diarrhea was defined as the occurrence of three or more loose or watery stools within the previous 24 h according to the Global Enteric Multicenter Study (GEMS). Epidemiologically linked outbreak cases were excluded via inquiry.

Patients recruitment and data collection

Only diarrheal cases aged ≥60 who were enrolled in the surveillance system were included in this study.

For each patient enrolled in the surveillance program, informed consent was obtained prior to conducting a standardized epidemiological investigation, which was performed by trained healthcare professionals using a structured surveillance questionnaire, and was recorded into the dedicated online system. The information collected included demographic characteristics (age, sex, and residence), clinical manifestations (date of symptom

onset, stool frequency and characteristics, presence of fever, and vomiting), treatment history, and vaccination status. All case information was documented using a standardized surveillance case report form and synchronously transmitted to the online registration system.

Sample collection and transport

Fresh fecal specimens were collected when the cases visited the doctor and were recruited to this study, and subsequently transferred to the Microbiology Laboratory of Shanghai Pudong New Area Center for Disease Control and Prevention (Shanghai Pudong New Area Health Supervision Institute), for detection of 13 categories of diarrheal pathogens. Bacteriological testing: Fecal specimens were collected using 5 sterile cotton swabs, then placed in Cary-Blair transport medium and stored at 4 °C. Virological testing: Fecal specimens were collected in sterile sampling boxes and stored at −20 °C. All specimens were transported to the laboratory for testing within 24 h after collection.

Detection of Enteropathogens

All specimens were tested for eight bacterial and five viral enteropathogens. Bacterial pathogens included five categories of Diarrheagenic *E. coli* (DEC) [Enteropathogenic *E. coli* (EPEC), Enterotoxigenic *E. coli* (ETEC), Enteroaggregative *E. coli* (EAEC), Enteroinvasive *E. coli* (EIEC), and Shiga toxin-producing *E. coli* (STEC)], *non-typhoidal Salmonella* (NTS), *Pathogenic Vibrio* spp. (V. cholerae, V. parahaemolyticus, V. mimicus, and V. fluvialis), *Campylobacter* spp., *Aeromonas* spp., *Plesiomonas shigelloides*, *Yersinia enterocolitica*, and *Shigella* spp. Viral pathogens included Norovirus, Rotavirus, Astrovirus, Sapovirus, and Adenovirus.

Bacterial Detection: Specimens were separately inoculated onto Xylose-Lysine-Desoxycholate (XLD) agar, MacConkey (MAC) agar, and Campylobacter-selective agar (Karmali medium) for the isolation and culture of Shigella spp., DEC, and *Campylobacter* spp., respectively. Real-time quantitative PCR (qPCR) was used for the identification and classification of the five DEC categories and *Campylobacter* spp. Concurrently, specimens were inoculated into Selenite Brilliant Green (SBG) sulfa enrichment broth, Alkaline Peptone Water (APW), and modified Phosphate-Buffered Saline (PBS) for enrichment. Following enrichment, the cultures were separately inoculated onto CHROMagar Salmonella agar, Thiosulfate-Citrate-Bile Salts-Sucrose (TCBS) agar, Aeromonas-selective agar (RYAN medium), and Yersinia-selective agar (CIN medium) for the isolation and identification of NTS, pathogenic *Vibrio* spp., *Aeromonas* spp., *Plesiomonas shigelloides*, and *Yersinia enterocolitica*. Positive strains of *Shigella* spp. and *Salmonella* spp. were further serogrouped/serotyped using specific diagnostic antisera.

Viral Detection: DNA or RNA was first extracted from the specimens. Real-time reverse transcription PCR (rRT-PCR) was used to detect Norovirus (Genogroups GI and GII), Rotavirus, Astrovirus, and Sapovirus, while qPCR was used to detect Adenovirus.

A specimen was defined as positive for enteropathogens if at least one of the targeted enteropathogens was isolated or identified. Single infection was defined as the isolation or identification of only one bacterial or viral pathogen. Mixed infection was defined as the isolation or identification of at least two of the targeted enteropathogens.

Statistical Analysis

Data processing was performed using Microsoft Excel 2010 software, and statistical analysis was conducted with R software (version 4.2.1). The age distribution of the study subjects did not conform to a normal distribution, and thus was expressed as M (P_{25}–P_{75}). Categorical variables were summarized in numbers (percentages) and analyzed using the chi-square test or Fisher's exact test. Age-specific positivity rates were calculated for each single-year age group by dividing the number of positive detections by the number of individuals tested.

Joinpoint regression was performed using Joinpoint Regression Program (Version 5.4.0; National Cancer Institute, Maryland, USA) to identify potential inflection points in age-related trends, allowing for a maximum of five joinpoints to avoid overfitting. Annual percentage change (APC) and corresponding 95% confidence intervals (CIs) were calculated for each segment. All statistical tests were two-sided, and $p < 0.05$ was considered statistically significant.

3. Results

Demographic and epidemiological characteristics

From January 1, 2010 to December 31, 2024, a total of 4310 cases of diarrhea were registered in the diarrhea surveillance system in Pudong New Area of Shanghai. Subjects were aged 60–108, and the median age (P_{25}-P_{75})

was 67 (63, 73), with a male-to-female ratio of 0.83:1. The majority of the subjects were elderly people aged 60–69 years (accounting for 63.10%) (Table 1).

Table 1. Demographic characteristics of recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

Characteristic	No. of Cases	Proportion (%)
Total	4310	
Sex		
Male	1956	45.40
Female	2354	54.60
Age group (years)		
60–69	2719	63.10
70–79	1119	26.00
≥80	472	11.00
Season		
Spring (March–May)	913	21.20
Summer (June–August)	1287	29.90
Autumn (September–November)	1272	29.50
Winter (December–February of the following year)	838	19.40

Etiological Agent Detection

Among the 4310 cases, the overall pathogen positive rate was 42.20% (1819/4310) (Table 2).

Overall pathogen positivity did not differ between females and males (42.14% vs. 42.28%, $p = 0.951$). However, the positivity rate of single-bacterial infection was higher in females than in males (17.33% vs. 14.37%, $p = 0.009$), whereas no significant sex differences were observed for single-viral infection, mixed infection, or any individual pathogen examined (both $p > 0.05$) (Table A1). Specifically, single-virus infection was the predominant type, with a positive rate of 20.26% (873/4310); the positive rate of single-bacterial infection was 15.99% (689/4310); and the positive rate of mixed infection stood at 5.96% (257/4310) (Table 2).

Among the cases of single-viral infections, a significantly higher positive rate was observed for norovirus (13.53%, 583/4310), while it was observed for rotavirus followed, with a positive rate of 4.78% (206/4310). Among the cases of single-bacterial infections, DEC showed the highest positive rate of 5.94% (256/4310); NTS and *Campylobacter* spp. were the next most, with positive rates of 3.57% (154/4310) and 2.60% (112/4310), respectively. Among coinfection, virus-bacteria co-infection was the dominant type, with a positive rate of 2.65% (114/4310) (Table 2).

Table 2. Etiological Agent Detection among recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

	Positives	Positive Rate (%)	Positive Rate by Age Group (%)			χ^2	*p* Values
			60–69	70–79	≥80		
total	1819	42.20	45.72	35.84%	37.08	37.437	<0.001 *
single-virus infections	873	20.26	21.99	16.89	18.22	14.141	<0.001 *
Norovirus	583	13.53	14.27	11.97	12.92	3.084	0.226
Rotavirus	206	4.78	5.55	3.49	3.39	3.016	0.234
Astrovirus	35	0.81	0.96	0.54	0.64	0.581	0.858
Sapovirus	29	0.67	0.81	0.45	0.42	0.772	0.791
Adenovirus	20	0.46	0.40	0.45	0.85	2.791	0.202
single-bacterial infections	689	15.99	17.10	14.30	13.56	6.963	0.031 *
DEC	256	5.94	5.81	5.99	6.57	7.025	0.031 *
NTS	154	3.57	3.90	3.31	2.33	1.091	0.604
Pathogenic Vibrio	88	2.04	2.35	1.52	1.48	1.266	0.577
Campylobacter spp.	112	2.60	2.98	2.14	1.48	1.978	0.402
Aeromonas	46	1.07	1.14	0.98	0.85	0.029	0.986
Plesiomonas shigelloides (P. shigelloides)	16	0.37	0.48	0.18	0.21	1.433	0.660
Yersinia enterocolitica (Y. enterocolitica)	8	0.19	0.22	<0.001	0.42	4.098	0.096
Shigella	9	0.21	0.22	0.18	0.21	0.037	0.876
coinfections	257	5.96	6.62	4.65	5.30	5.923	0.052
virus-virus	77	1.79	1.99	1.07	2.33	3.523	0.168
bacteria-bacteria	66	1.53	1.62	1.61	0.85	3.547	0.176
virus-bacteria	114	2.65	3.02	1.97	2.12	0.386	0.845

* $p < 0.05$.

Temporal trends of Multiple etiologies

From 2010 to 2024, the overall pathogen positivity rate showed a fluctuating pattern, with an increase before 2017, a decline thereafter, and a modest rebound beginning in 2023. Viral pathogens remained the predominant etiological agents throughout the study period and largely contributed to the overall trend. Viral detection increased from 2011, decreased after 2017, reached the lowest levels during 2020–2023, and rose slightly in 2024, with norovirus accounting for most of the observed variation. Rotavirus showed occasional increases, whereas other viral pathogens were detected infrequently. Bacterial infections displayed a comparable temporal pattern, remaining relatively stable before 2020, declining during the pandemic period, and increasing modestly thereafter. Among bacterial pathogens, DEC was detected more frequently during the earlier years of surveillance, while NTS and *Campylobacter* exhibited variable detection across years without consistent long-term patterns (Figure 1). No clear temporal trend was observed for other viral infections, which may be attributable to their lower detection rates (Table A2).

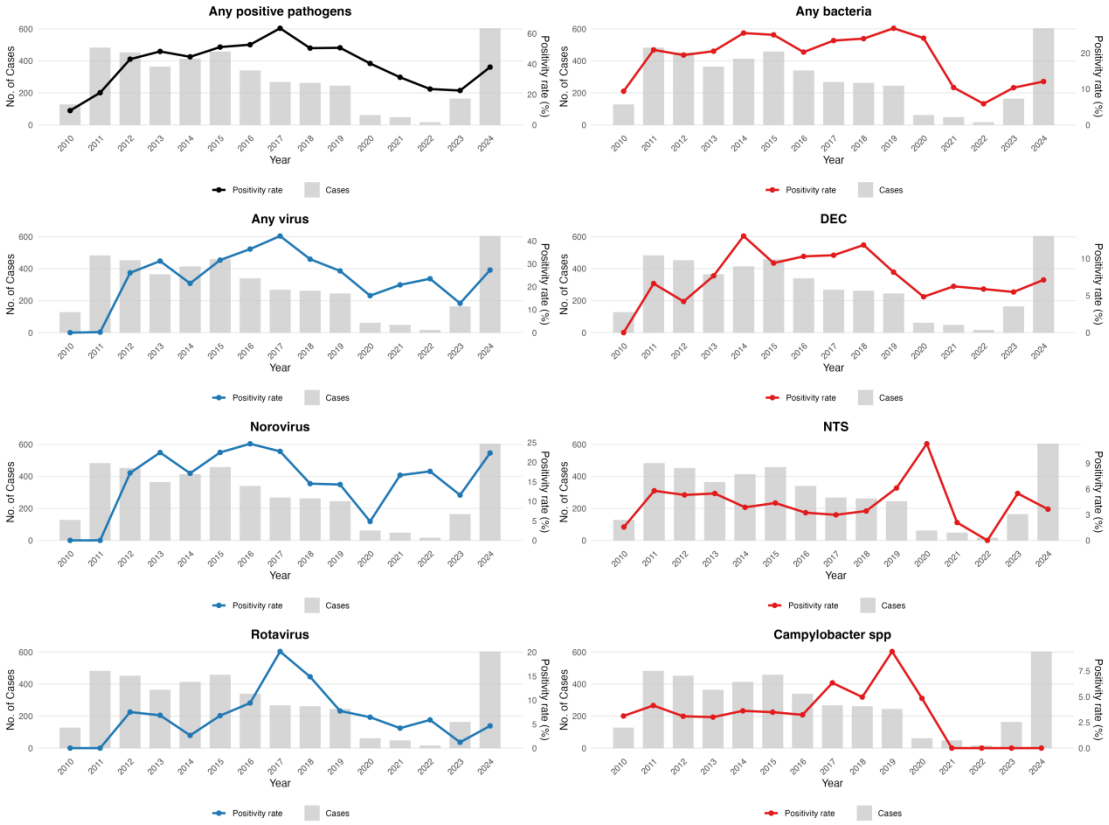

Figure 1. Annual trends in the positivity rates of multiple etiologies among recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

Seasonal trends of Multiple etiologies

The overall pathogen spectrum of diarrheal outpatients aged ≥60 did not show a distinct seasonal trend. Overall, viral pathogens predominated from October through March of the following year, while bacterial pathogens were dominant from June through September. The periods of April-May and September-October represented transitional phases where viral activity shifted to bacterial, and bacterial to viral, respectively. Both norovirus and rotavirus exhibited significant seasonal fluctuations. Rotavirus peaked distinctly during the winter months, particularly in December, January, and February. In contrast, the seasonal pattern for norovirus was less pronounced and spanned a broader period, primarily concentrated in autumn and winter (Figure 2).

The positive rate of DEC peaked between July and September, whereas *Campylobacter* spp. and NTS exhibited less distinct and more diffuse seasonal patterns, likely due to their overall lower detection rates (Figure 2).

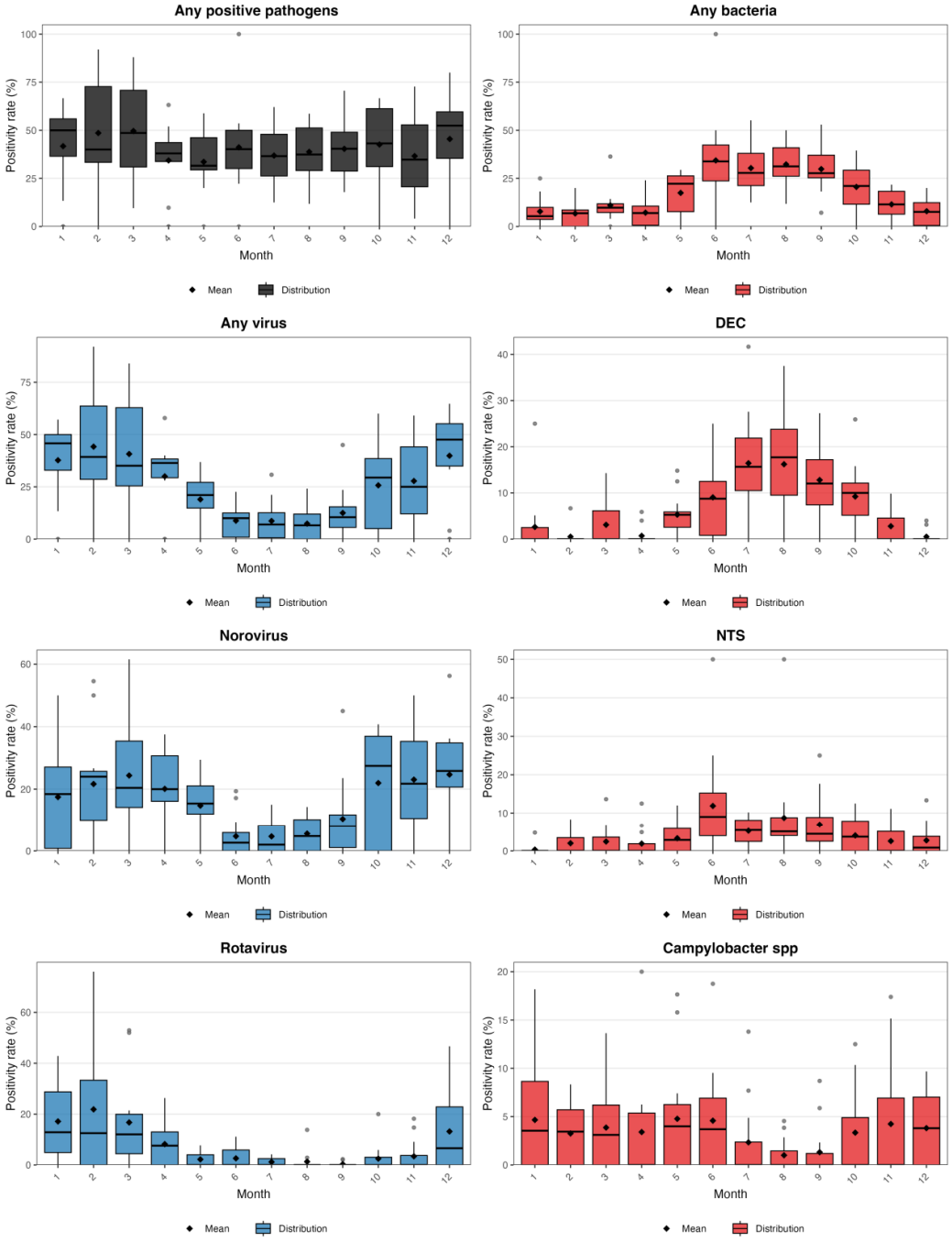

Figure 2. Seasonal trends in positivity rates of multiple etiologies among recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

Age-Associated Patterns of Viral and Bacterial Infections

Overall pathogen positivity was highest in the 60–69 age group (45.72%), followed by the ≥80 age group (37.08%), and lowest in the 70–79 age group (35.84%) ($p < 0.001$; Table 2). Among cases with single-viral infections, the highest positivity rate was observed in the 60–69 age group (21.99%), followed by the ≥80 age group (18.22%), and the lowest in the 70–79 age group (16.89%). The differences among age groups were statistically significant ($p < 0.001$). For single-bacterial infections, the highest positivity rate was also found in the 60–69 age group (17.10%), followed by the 70–79 age group (14.30%), and the lowest in the ≥80 age group (13.56%), with statistically significant differences among groups ($p = 0.031$). No statistically significant difference was observed in the distribution of mixed infections across age groups ($p = 0.052$) (Table 2).

No statistically significant differences were found in the positivity rates of norovirus ($p = 0.226$) or rotavirus ($p = 0.234$) across age groups. No significant age-related differences were observed for NTS or *Campylobacter* spp. Other pathogens, including *Aeromonas*, *Plesiomonas shigelloides*, *Yersinia enterocolitica*, and *Shigella*,

showed consistently low positivity rates across all age subgroups (≤1.30%) (Tables 2 and A3). Notably, the positivity rate of DEC differed significantly among age groups ($p = 0.031$), with the highest rate in the ≥80 age group (6.57%) (Tables 2 and A3).

Overall enteropathogen positivity and viral infections declined progressively from age 60 to the late 80s, whereas bacterial infections remained relatively stable. At the pathogen-specific level, rotavirus showed a gradual decline with increasing age and turn point observed in the 80s, while norovirus positivity remained largely unchanged before 90s. NTS and *Campylobacter* spp. were consistently detected at low levels with only minor fluctuations. After approximately 90, a transient rebound in pathogen positivity was observed. Both overall and viral infections increased around this age before declining again in the extremely age groups. Bacterial infections showed a more pronounced rise near 90s, mainly driven by an increase in DEC, which subsequently declined in older age groups (Figure 3). The pronounced fluctuations observed in the group aged >90 may partly reflect the relatively small sample size in these strata.

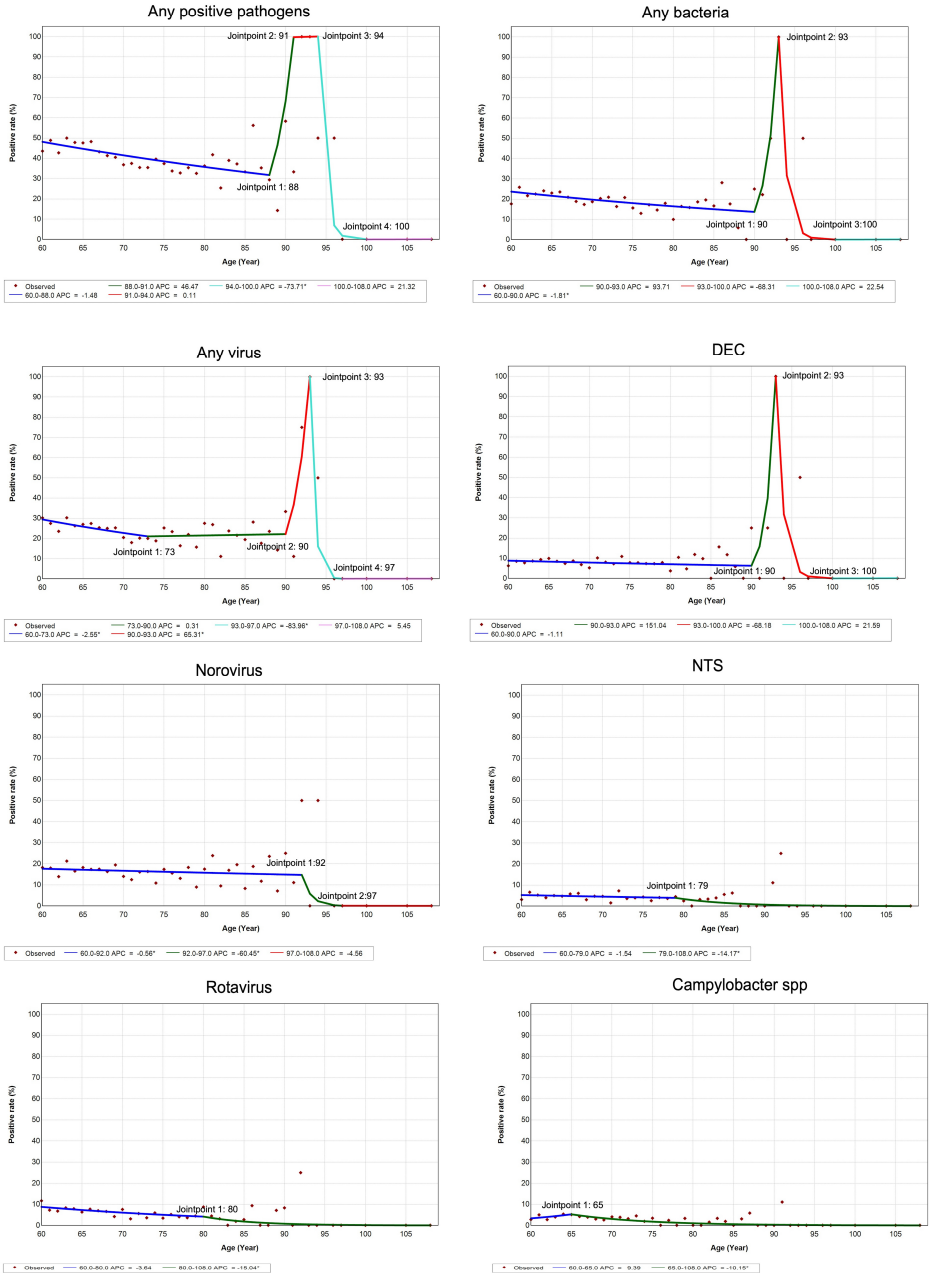

Figure 3. The joinpoint regression of the positive rates of multiple etiologies by age of the recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024. (Joinpoint regression analysis was performed to evaluate age-specific trends in pathogen positivity rates. The red diamonds represent observed the positivity rates of recruited cases by age, and the colored curves indicate the fitted joinpoint regression patterns. Annual percent change (APC) and corresponding 95% confidence intervals were estimated for each segment. * Indicates that the APC is significantly different from zero at $p < 0.05$).

4. Discussion

This 15-year surveillance study included 4310 diarrheal outpatients aged ≥60 in Pudong New Area, Shanghai, with an overall pathogen positivity rate of 42.20% (1819/4310), whereas no detectable pathogen was identified in 57.80% of cases (2491/4310). Negative results may reflect delayed presentation, prior pathogen clearance, limited assay sensitivity, or causes not covered by the surveillance panel. Viral infections predominated, accounting for 20.26% of cases, followed by bacterial infections (15.99%) and mixed infections (5.96%). Norovirus and rotavirus were the leading viral pathogens, while diarrheagenic Escherichia coli (DEC) was the most frequently detected bacterial pathogen. Although overall viral predominance was observed across age groups, DEC positivity differed significantly by age and was highest among individuals aged ≥80. Long-term surveillance revealed dynamic fluctuations in pathogen detection from 2010 to 2024, including temporal peaks in norovirus and DEC, as well as a post-2023 rebound. Seasonally, viral pathogens predominated in autumn–winter, whereas bacterial pathogens were more common in summer.

Our study revealed that the overall pathogen positivity rate among the elderly aged ≥60 in Pudong New Area, Shanghai, 2010–2024, was 42.20%, which was lower than those reported in general population surveillance studies in Shanghai (≥18 years old; 46.44%), Pudong New Area (the general population, 55.7%), and Yantai City, Shandong Province (43.92%). Conversely, it is higher than rates reported in Wuxi City, Jiangsu Province (27.76%) and Jiangsu Province as a whole (17.97%) [16–20]. The high prevalence of viral infections, mirrors results from other Chinese studies. Its high positive rate may be associated with age-related decline in immunity among the elderly and the heightened risk of contact transmission and outbreaks in collective living environments such as nursing homes [19]. Among the identified pathogens, single viral infections constituted the highest, followed by single bacterial infections. This indicates that viruses are the predominant etiological agents of infectious diarrhea in the elderly, which aligns with surveillance findings from other regions in China [19]. Norovirus and rotavirus were the primary viral pathogens identified, consistent with conclusions from multiple domestic studies on the spectrum of diarrheal pathogens [2,20–22]. Sex-related differences were comparatively limited, with only a modestly higher positivity rate of single-bacterial infection observed in females.

An important finding of this study is the age-related heterogeneity in pathogen distribution within the elderly population. While grouped analysis revealed a significantly higher positivity rate of DEC among individuals aged ≥80 years, continuous age modeling further uncovered non-linear dynamics for several pathogens. Overall and viral infection rates declined gradually from 60 to the late 80s, followed by a transient increase in the early 90s and subsequent decline in the most advanced age groups. Bacterial infections remained relatively stable across most ages, with a pronounced increase around the early 90s before declining thereafter. Norovirus positivity remained largely stable until approximately age 90, whereas rotavirus exhibited a gradual decline across ages without a clear inflection point. DEC showed a late-age increase with the highest positivity in individuals aged ≥80, while NTS and *Campylobacter* spp. remained low with only minor fluctuations. These findings suggest that susceptibility patterns evolve progressively rather than uniformly throughout older adulthood [23]. Advanced aging is characterized by immunosenescence, impaired mucosal immunity, and age-related alterations in gut microbiota and intestinal barrier integrity, all of which may reduce colonization resistance and increase vulnerability to enteric bacterial pathogens [24,25]. The late-age rebound observed in overall or specific infections may also reflect cumulative physiological decline, increased frailty, shifts in exposure patterns, or small sample sizes in the most advanced age, whereas reduced social contact and mobility may differentially affect viral transmission dynamics [26]. Together, these findings indicate that adults aged ≥80 represent a distinct epidemiological subgroup, highlighting the need for age-stratified surveillance, pathogen-specific monitoring, and tailored clinical considerations within aging populations.

From 2010 to 2024, infectious diarrhea among adults aged ≥60 in Pudong exhibited a fluctuating yet structured trajectory, with high incidence during 2010–2018, a decline in 2019–2022, and a rebound in 2023–2024. The temporary decrease coincided with the COVID-19 pandemic, but longer-term trends likely reflect shifts in pathogen ecology. Following the introduction and uptake of rotavirus vaccination in China, rotavirus-associated gastroenteritis declined, and reduced viral circulation in vaccinated children may have indirectly lowered transmission to cohabiting elderly individuals [27,28]. Post-2017, as rotavirus detections declined, norovirus activity relatively increased, suggesting ecological niche replacement. Norovirus peaks in 2013 and 2016 align with the periodic emergence of novel GII.4 variants [29]. Bacterial pathogens showed heterogeneous dynamics, with a sustained decline in DEC after 2020 and a transient NTS peak in 2020, highlighting pathogen-specific responses [30]. Overall, vaccination-driven viral shifts, viral evolution, and inter-pathogen competition appear to have reshaped infectious diarrhea epidemiology among older adults.

Seasonality analysis revealed a distinct bimodal pattern characterized by winter-spring predominance of viral pathogens (December–March), particularly rotavirus, and summer-autumn predominance of bacterial pathogens (June–September), notably DEC. This pattern is largely consistent with findings from multiple studies conducted in temperate regions of China, particularly in the Yangtze River Delta region, and is likely mediated by climatic factors—temperature and humidity—that differentially modulate pathogen survival, transmission efficiency, and human exposure risks [31–34]. The seasonal prevalence of norovirus in this study exhibited a broader range compared to rotavirus, spanning autumn, winter, and spring. This pattern aligns with previously reported characteristics in Shanghai, which describe a "peak in autumn and winter, with a plateau period extending into spring" [35]. This distinct seasonal pattern may provide a scientific basis for implementing differentiated prevention and control strategies across different periods. For instance, emphasis should be placed on reinforcing food safety and drinking water hygiene education during summer, while increased attention should be given to the prevention and control of viral gastroenteritis in collective settings such as nursing homes during winter.

Importantly, our study has several strengths. It is based on a large, long-term and multi-site sentinel surveillance dataset spanning 15 years (2010–2024), which enhances the robustness of temporal trend analyses. Standardized laboratory testing for both viral and bacterial pathogens provides comprehensive pathogen coverage. In addition, the use of joinpoint regression allows more precise characterization of non-linear age-specific and temporal trends in infectious diarrhea among older adults, providing valuable evidence for targeted prevention strategies. Our study also has several limitations. First, as a sentinel surveillance, selection bias may exist, wherein patients with more severe symptoms or stronger healthcare-seeking behavior were more likely to be included. This may limit the generalizability of the findings to all older adults with infectious diarrhea in the community. Second, pathogen detection depended on clinical sampling and laboratory testing methods. Updates in diagnostic techniques over time (e.g., the transition from traditional culture to molecular diagnostics) may have affected the detection rates and comparability of pathogens, particularly viruses and atypical bacteria. Third, although age- and sex-stratified analyses were performed, detailed information on comorbidities, living arrangement, and long-term care residence was unavailable, precluding further risk-factor assessment. Finally, the study was conducted in a single geographic area, which warrants caution when extrapolating the findings to other regions.

Overall, the overall pathogen positive rate among diarrheal outpatients aged ≥60 in Pudong New Area, Shanghai from 2010 to 2024 was high. Norovirus, rotavirus, and DEC were identified as the predominant pathogens. While differences in the distribution of single viral and bacterial infections were observed across different age groups, the overall pathogen profile remained relatively consistent, with the exception of DEC. The overall spectrum of pathogens among diarrheal outpatients aged ≥60 did not show a distinct seasonal variation trend; however, a clear bimodal pattern was evident, with viral pathogens peaking in autumn and winter, and bacterial pathogens being more active in summer and autumn. Moving forward, continuous long-term surveillance in this area is essential to evaluate the prolonged impact of macro-level factors, such as climate change and public health policies, on the epidemiological characteristics of diarrheal pathogens in the elderly.

Author Contributions

W.Z.: conceptualization, methodology, formal analysis, and writing—original draft preparation. J.C.: surveillance coordination, conceptualization, methodology, writing—review and editing. A.Z. and G.S.: surveillance coordination, data curation and investigation. C.Y: conceptualization and writing—review and editing. X.W.: laboratory testing and validation. L.Z.: supervision, project administration, and writing—review and editing. All authors have read and agreed to the published version of the manuscript.

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Institutional Review Board Statement

Ethical approval for this study was granted by the Ethical Review Board of Shanghai Pudong New Area Center for Disease Control and Prevention (Shanghai Pudong New Area Health Supervision Institute). All procedures involving human participants complied with the ethical standards of the Declaration of Helsinki.

Informed Consent Statement

Patient consent was waived due to the following reasons: (1) the study involved the analysis of existing surveillance data collected through the Pudong New Area Diarrheal Disease Surveillance Program as part of routine public health surveillance activities; (2) the research posed minimal risk to participants, as all data were de-identified and analyzed in aggregate form to ensure confidentiality; and (3) the waiver of informed consent is

consistent with national regulations and ethical guidelines for public health surveillance research in China, which permit the use of surveillance data for research purposes without individual consent when the research serves public health interests and privacy protections are ensured.

Data Availability Statement

The dataset analyzed during the current study is not publicly available due to privacy and ethical restrictions, but is available from the corresponding author on reasonable request.

Acknowledgments

The authors would like to acknowledge the 47 sentinel hospitals (nine tertiary-level and four secondary-level, and thirty-four primary-level hospitals) for their help with conducting this survey.

Conflicts of Interest

The authors declare no conflict of interest.

Use of AI and AI-Assisted Technologies

No AI tools were utilized for this paper.

Appendix A

Table A1. Etiological Agent Detection by gender among recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

	Positive Rate by Gender (%)		χ^2	*p* Values
	Female	Male		
total	42.14	42.28	0.004	0.951
single-virus infections	19.41	21.27	2.160	0.142
Norovirus	4.80	4.75	0.554	0.426
Rotavirus	0.51	0.87	1.028	0.260
Astrovirus	12.62	14.62	1.224	0.250
Sapovirus	0.47	0.46	0.000	0.826
Adenovirus	1.02	0.56	3.199	0.058
single-bacterial infections	17.33	14.37	6.779	0.009 *
DEC	6.63	5.11	0.393	0.521
NTS	3.61	3.53	1.122	0.265
Pathogenic Vibrio	0.25	0.15	0.014	0.745
Campylobacter spp.	2.34	1.69	0.308	0.562
Aeromonas	1.23	0.87	0.153	0.643
Plesiomonas shigelloides (P. shigelloides)	0.42	0.31	0.000	1.000
Yersinia enterocolitica (Y. enterocolitica)	2.63	2.56	0.645	0.401
Shigella	0.21	0.15	0.000	1.000
coinfections	5.40	6.65	2.763	0.096
virus-virus	1.40	2.25	1.536	0.176
bacteria-bacteria	1.57	1.48	1.231	0.254
virus-bacteria	2.42	2.91	0.002	0.901

* $p < 0.05$.

Table A2. Annual number of positive detections of other pathogens among recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

Year	Total	No. of Cases							
		Sapovirus	*Adenovirus*	*Astrovirus*	*Shigella* spp.	*Pathogenic Vibrio* spp.	*Aeromonas* spp.	*Plesiomonas shigelloides*	*Yersinia enterocolitica*
2010	128	0	0	0	0	6	1	0	0
2011	483	1	0	0	4	13	6	3	0
2012	452	4	1	6	3	7	26	4	2
2013	365	3	3	8	0	5	10	7	1
2014	414	2	4	4	0	10	14	9	2
2015	458	12	4	11	1	26	10	5	3
2016	340	4	8	15	0	6	6	6	1
2017	268	8	2	13	1	7	4	0	2
2018	262	7	3	4	1	8	5	2	2

Table A2. *Cont.*

Year	Total	No. of Cases							
		Sapovirus	*Adenovirus*	*Astrovirus*	*Shigella* spp.	*Pathogenic Vibrio* spp.	*Aeromonas* spp.	*Plesiomonas shigelloides*	*Yersinia enterocolitica*
2019	245	4	5	5	1	7	1	0	4
2020	62	1	1	1	0	2	0	0	0
2021	48	0	0	0	0	1	0	0	0
2022	17	0	0	0	0	0	0	0	0
2023	164	0	0	0	0	0	0	0	0
2024	604	6	0	0	0	13	2	1	0

Table A3. Detailed Etiological Agent Detection by Pathogen Subgroups among recruited cases aged ≥60 in Pudong New Area, Shanghai, 2010–2024.

	Positives	Positive Rate (%)	Positive Rate by Age Group (%)			*p* Values
			60–69	70–79	≥80	
Norovirus	583	13.53	14.27	11.97	12.92	0.226
GI	50	1.16	1.47	0.71	0.42	
GII	514	11.93	12.32	10.9	12.08	
GI and GII	10	0.23	0.26	0.27	0	
Others	9	0.21	0.22	0.09	0.42	
Rotavirus	206	4.78	5.55	3.49	3.39	0.2338
A	202	4.69	5.41	3.49	3.39	
B	3	0.07	0.11	0	0	
C	1	0.02	0.04	0	0	
DEC	256	5.94	5.81	5.99	6.57	0.0308 *
ETEC	140	3.25	3.13	2.95	4.66	
EPEC	56	1.3	1.25	1.79	0.42	
EAEC	44	1.02	1.18	0.8	0.64	
EIEC	5	0.12	0.07	0	0.64	
EAEC/ETEC	6	0.14	0.04	0.45	0	
EPEC/ETEC	5	0.12	0.15	0	0.21	
NTS	154	3.57	3.9	3.31	2.33	0.6039
S. enteritidis	55	1.28	1.21	0.63	0.85	
S. typhimurium	44	1.02	1.29	1.61	0.42	
Others	55	1.28	1.4	1.07	1.06	
Pathogenic Vibrio	88	2.04	2.35	1.52	1.48	0.5774
V. parahaemolyticus	85	1.97	2.28	1.52	1.27	
Others (non-O1/non-O139 *V. cholerae*)	3	0.07	0.07	0	0.21	
Campylobacter spp.	112	2.6	2.98	2.14	1.48	0.4021
Campylobacter jejuni (C. jejuni)	12	0.28	2.57	1.79	0.85	
Campylobacter coli (C. coli)	94	2.18	0.29	0.18	0.42	
C. jejuni/coli	1	0.02	0	0.09	0	
Others	5	0.12	0.11	0.09	0.21	
Shigella	9	0.21	0.22	0.18	0.21	0.8761
Shigella sonnei (S. sonnei)	8	0.19	0.22	0.18	0	
Shigella flexneri (S. flexneri)	1	0.02	0	0	0.21	

* $p < 0.05$.

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