

Sentinel Surveillance-Based Epidemiological Analysis of Foodborne Diseases in Shengsi County, China, 2019–2024 [Letter]

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Dear editor

We read with genuine interest the sentinel surveillance study by Chen et al documenting foodborne disease (FBD) patterns in Shengsi County, China—a commendable effort to characterise local epidemiological dynamics in a coastal setting where marine food habits create unique pathogen risks.¹ That said, we believe several methodological concerns warrant careful consideration, particularly regarding the authors' claim of a “sharp surge” in *Salmonella* positivity in 2024.

Our first concern relates to statistical significance and sample size. The reported 9.32% *Salmonella* positivity rate in 2024 rests on just 11 positive cases from 118 tested specimens. With such a small denominator, the dramatic-sounding rise from a baseline of 0–1.09% is highly susceptible to stochastic variation. Critically, the authors provide no confidence intervals and perform no significance testing—such as Fisher's exact test—to demonstrate that this apparent increase is not simply a chance finding in a small sample. Characterising this as a “sharp surge” without such validation overstates what the data can reliably support.²

Second, the case definition may introduce meaningful reporting bias. By restricting FBD to individuals with diarrhoea of ≥ 3 bowel movements per day, the study excludes patients who present primarily with fever, nausea, and vomiting—a presentation well-documented in *Salmonella* infections linked to poultry and eggs.³ This rigid criterion likely underestimates the true burden of *Salmonella* in the region and may distort the pathogen profile in ways that obscure actual transmission dynamics.

Third, there is a missed analytical opportunity between clinical and laboratory data. The authors note that the proportion of febrile cases peaked in 2024 at 34.10%, coinciding with the rise in *Salmonella* detections. Yet no cross-tabulation or correlation analysis links confirmed *Salmonella* cases to febrile presentations specifically. Without this step, the suggestion that changes in the clinical profile reflect the *Salmonella* increase remains an assumption—one that the authors' own surveillance dataset could readily test.

Finally, the post-pandemic explanation is premature. The hypothesis that the 2024 surge reflects resumed tourism and the introduction of “new strains” is intuitively plausible, but the study itself acknowledges the absence of molecular subtyping data and food supply chain sampling.¹ Invoking “new strains” without genomic evidence—such as whole-genome sequencing—is a conclusion that runs ahead of what descriptive surveillance alone can establish.⁴

We offer these observations in the spirit of strengthening a surveillance programme that serves a genuinely important public health purpose. Continuous sentinel surveillance of this kind is precisely what coastal communities need—and with confidence intervals, fever–pathogen cross-tabulations, and source attribution data incorporated into future reports, its findings will carry far greater weight for policymakers and clinicians alike.⁵

Disclosure

The author declares no competing interests in this communication.

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