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ORIGINAL ARTICLE

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A dynamic platform for global pullorum disease and fowl typhoid

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Abstract

Pullorum disease and fowl typhoid are caused by the *Salmonella* serovars Gallinarum biovars Pullorum and Gallinarum, respectively. The prevalence of these diseases varies across regions and is affected by different risk factors that remain insufficiently documented. To fill this knowledge gap, we have compiled a global dataset for its prevalence, drawing upon a collection of literature from the last seven decades obtained from bilingual databases. However, a more interactive and dynamic platform is still needed for both academics and policymakers to improve biosecurity measures, limit disease transmission, and prevent future outbreaks at the global and local levels. Here, we developed an advanced visualization platform to depict the prevalence of *Salmonella* Pullorum and Gallinarum, especially in China, which is categorized by geographical region and temporal span. The platform offers a user-friendly, efficient, and visually engaging tool to explore the prevalence of pullorum disease and fowl typhoid between 1945 and 2021 in different regions. Additionally, this platform allows users to understand the influence of various factors, such as breed, farm mode, economic usage and even the sex of the primary host, chickens, on the prevalence of this disease. We further provided a detailed overview of individual province within China. In particular, by selecting two different provinces on the interface, users can quickly visualize and grasp the disparities in disease prevalence between the chosen regions. This interactive toolkit enables a dynamic exploration of the patterns and factors contributing to the prevalence of *Salmonella* Pullorum and Gallinarum. This interactive platform is freely available open source at http://139.9.85.208/.

Keywords Pullorum disease, Fowl typhoid, Interactive platform, Prevalence prediction

Introduction

Pullorum disease and fowl typhoid are caused by *Salmonella enterica* subsp. *enterica* serovar Gallinarum biovars Pullorum (bvSP) and Gallinarum (bvSG), respectively, which are considered diseases listed by the World Organization for Animal Health (WOAH) (Terrestrial Manual Online Access, n.d.). Both diseases result in devastating economic losses in the poultry industry worldwide (Chen et al. 2023; Jia et al., 2023; Kang et al. 2022, 2024; Li et al. 2022a). The biovar bvSP mainly infects young chicks with a high mortality rate and adult birds with weight loss, reduced egg laying, diarrhea, lesions, and reproductive tract abnormalities, which can be further transmitted to their offspring

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(Gast & Porter 2020; Wang et al., 2024a). Moreover, bvSG is more often observed in mature poultry birds with signs of septicaemia (Chappell et al. 2009; Jia et al. 2024a). In addition to chickens and turkeys, they also infect game birds, such as pheasants, quail, peacocks, ducks, geese, and pigeons (EFSA Panel on Animal Health and Welfare (AHAW) et al. 2017; Ke et al. 2024).

Pullorum disease and fowl typhoid are both "reportable" diseases in highly developed countries such as the United States, Canada, Australia and the majority of European countries; these diseases were generally eradicated in the 1970s (Barrow & Freitas Neto 2011; Kang et al. 2022). These two prominent diseases are largely unreported in many poultry-intensified countries, particularly in low-income nations (Feng et al., 2023; Wigley 2017). The economic and veterinary importance of *Salmonella* Gallinarum has pushed it to the forefront, necessitating novel mitigation strategies to protect animal welfare (Jia, et al., 2024b; Wang et al., 2024b). Given the absence of documentation regarding the disease's prevalence patterns across different regions during different periods, coupled with a lack of summarized parameters influencing its spread, such as breed, farm mode, and commercial usage, we previously collected and sorted all the literature related to the outbreaks or prevalence of bvSP and bvSG published in the China National Knowledge Infrastructure (CNKI) and in the PubMed database. Finally, we conducted a systematic review to update a dataset that presents the prevalence and epidemiological factors associated with bvSP and bvSG (Kang et al. 2023; Zhou et al. 2022a) and then illustrated a socioeconomic influencing pathway for accelerating disease progression (Zhou et al. 2023).

Despite these attempts, the dataset fails to offer a dynamic "EagleView" picture of the prevalence trends and related parameters; however, an interactive and visualized toolkit can address this gap. Ma *et al.* developed an integrated platform for *Brucella* to track and analyze the incidence and prevalence of brucellosis in both humans and animals (Ma et al. 2022; Zhou et al. 2020). Through rich data, intuitive charts and graphs in this platform, users, including public health experts and policy makers, can gain detailed insights, monitor dynamic changes and trends in brucellosis and further develop more effective disease control and prevention strategies. Motivated by this driving force, we have developed a dynamic platform to empower users to apprehend the entire prevalence landscape of bvSP and bvSG through a straightforward, point-and-click, and user-friendly interface.

Results and discussion

A flexible and advanced platform was established at http://139.9.85.208/. Internal testing demonstrated positive results, confirming the platform's usability and effectiveness. A demonstration video with detailed usage instructions is available in the supplementary material. The homepage of this platform includes three sections: "Overview", "Map data display" and "Support". The "Overview" includes a brief introduction to pullorum disease and fowl typhoid, as well as some common website resources to help users obtain a better understanding of these two diseases. By clicking on the buttons labeled SG, bvSP, and bvSG next to "Home" in the top right corner (Fig. 1A), users can view the prevalence distribution of serovar SG or biovars bvSP and bvSG. Taking bvSP as an example (Fig. 1), the page is divided into four parts after clicking on it. The top two parts consist of different selectors. The top row contains options for geographical locations (continents, countries and China) and periods (five intervals and unavailable data, NA) (Fig. 1B). The bottom row contains four parameters related to chickens (breed, farm mode, economic usage and sex) (Fig. 1C), which are the primary and most significant hosts for these serovars. The above options have a direct impact on map presentation and meta-analysis. Figure 1D illustrates the prevalence trends across different continents, where the chosen continent is highlighted in yellow and the positive rate is displayed. Moreover, the meta-analysis for the prevalence of continents corresponding to the selected scenario, with the upper and lower bounds of the 95% confidence interval, is shown in Fig. 1E.

The data for different countries and provinces in China can also be obtained similarly (Figs. 2 and 3). In contrast, when a particular province is selected from the Chinese map and the "View Detail" button in the lower right corner is clicked, more comprehensive data comprising the meta-analysis, breed, farm mode, gender, economic usage, and related age range are shown (Fig. 4A-H). Above all, the change trend graph in Fig. 4I displays each record, which could provide projections of future prevalence patterns and facilitate the implementation of proactive and effective measures to control future outbreaks.

(See figure on next page.)

Fig. 1 Visualization of the geographical distribution and meta-analysis of bvSP across continents. **A** Selection of serotypes or biotypes. **B** Selection of geographical location and time. **C** Selection of chicken breed, farm mode, economic usage and sex. If not manually selected, the displayed data represent a general overview without considering any of the factors. **D** Geographical distribution of bvSP by continent. **E** Meta-analysis of the prevalence of bvSP by continent. The upper and lower bounds of the 95% confidence interval are displayed after the corresponding dots are clicked

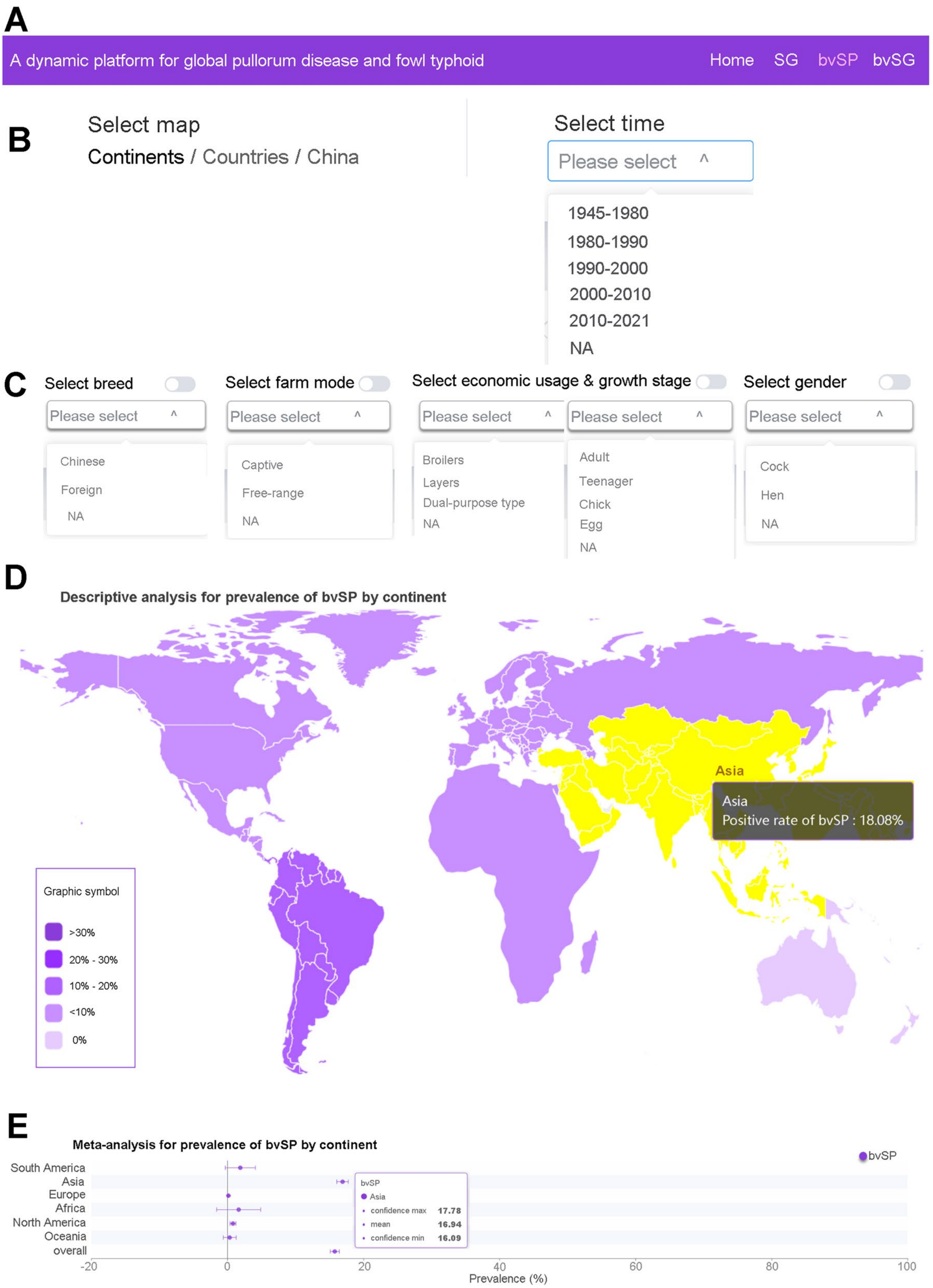

Fig. 1 (See legend on previous page.)

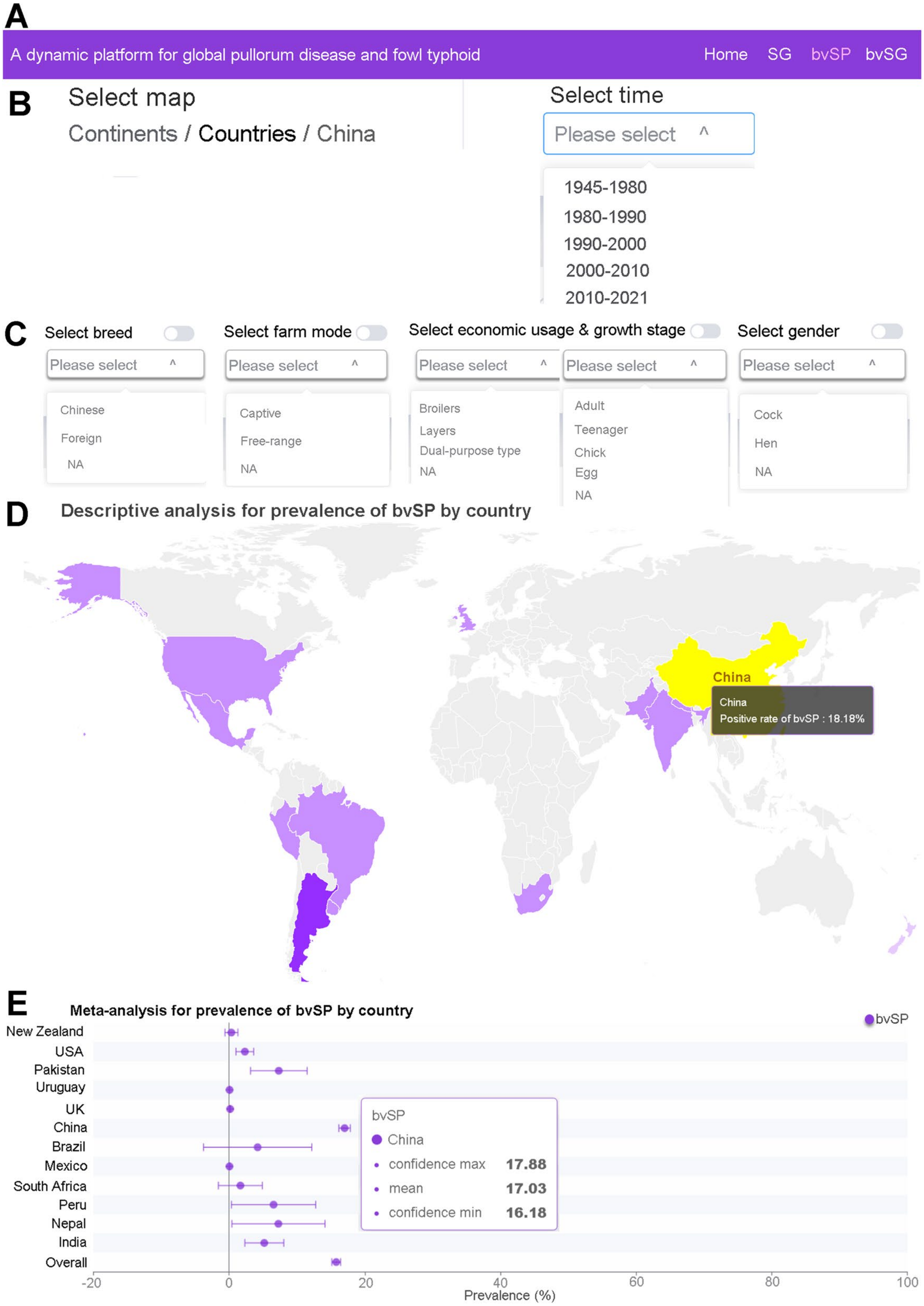

Fig. 2 Visualization of the geographical distribution and meta-analysis of bvSP across countries. **A** Selection of serotypes or biotypes. **B** Selection of geographical location and time. **C** Selection of chicken breed, farm mode, economic usage and sex. If not manually selected, the displayed data represent a general overview without considering any of the factors. **D** Geographical distribution of bvSP by country. **E** Meta-analysis of the prevalence of bvSP by country

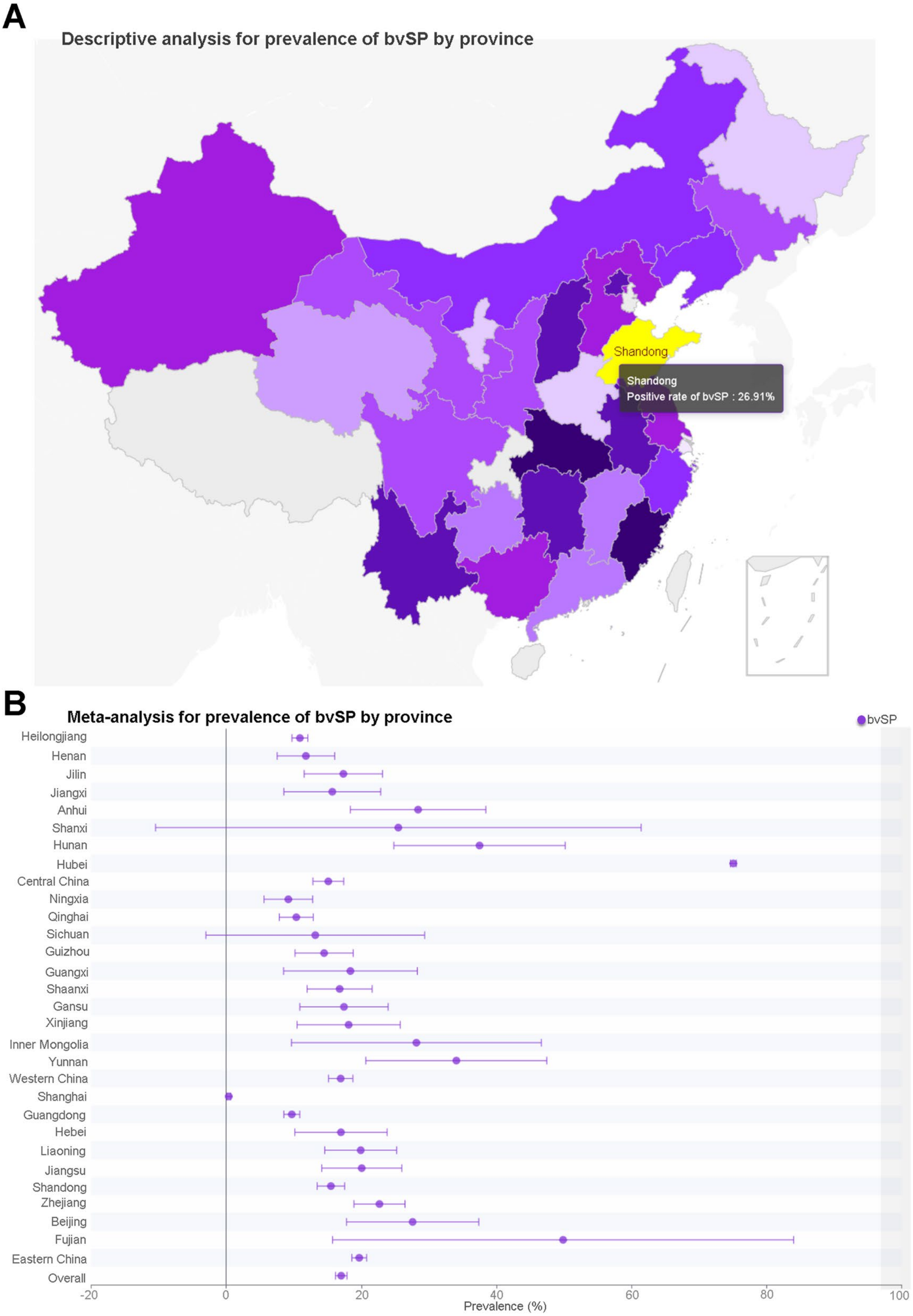

Fig. 3 Visualization of the geographical distribution and meta-analysis of bvSP in provinces of China. **A** Geographical distribution of bvSP by country. **B** Meta-analysis of the prevalence of bvSP by country

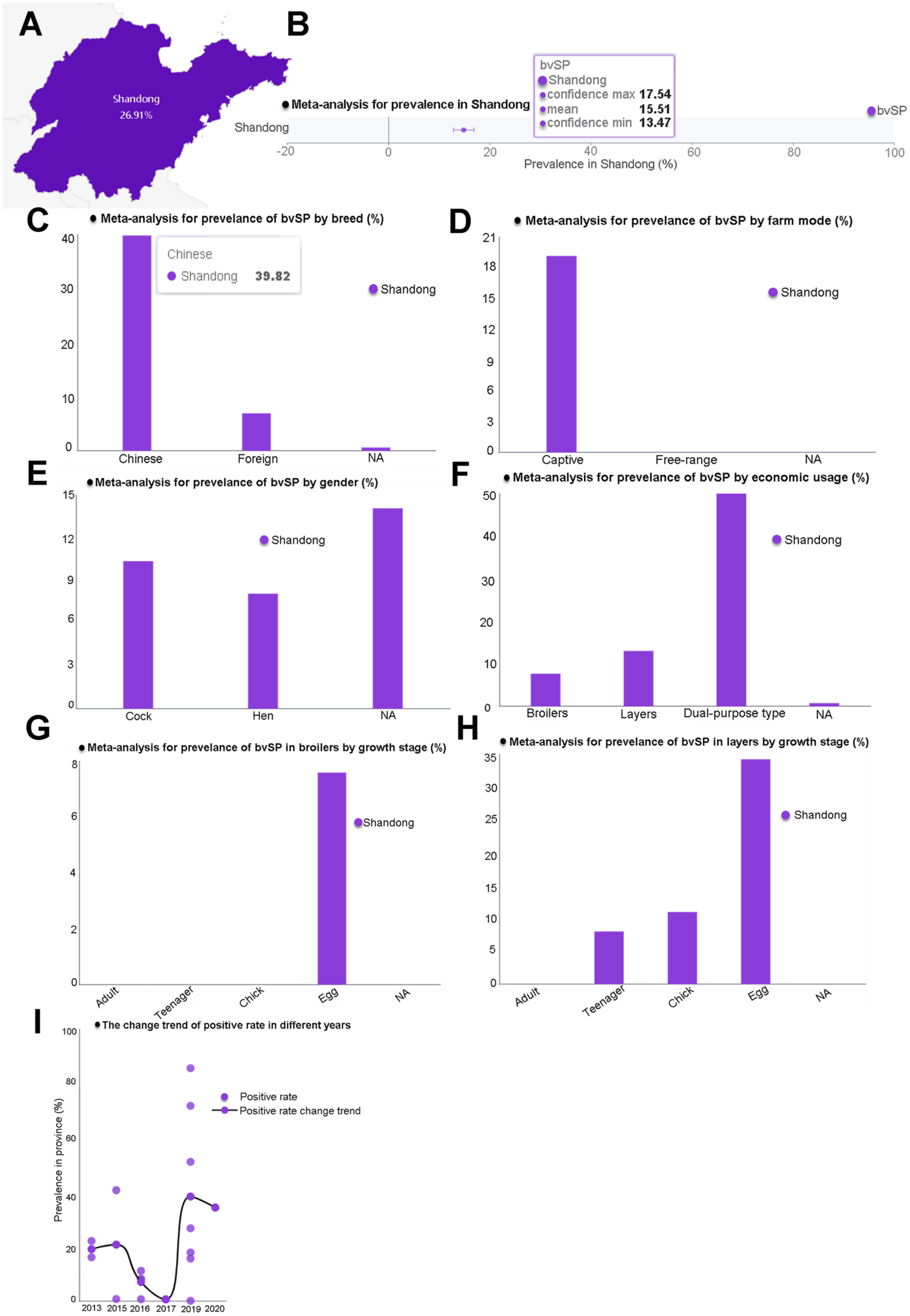

Fig. 4 Visualization of the prevalence of bvSP in Shandong province. **A** The prevalence rate of bvSP in Shandong province. **B** The meta-analysis for the prevalence of bvSP in Shandong (95% confidence interval: 13.47--17.54). **C**-**F** The prevalence of bvSP by breed, farm mode, gender or economic usage, respectively. **G**, **H** The prevalence by growth stage of broilers and layers, respectively; **I** The change trend of the positive rate in different years

For example, the average prevalence rate (38.34%) of bvSP in 2019 in Shandong province was nearly twice that of the highest year (2015, 20.67%) in previous years (F ig. 4I). We assume that this is due to a severe outbreak of African Swine Fever in Shandong province, a major poultry-raising province (Bingsheng & Yijun 2008; *China*, 2020; Li et al., 2022b; YANG, 2021), which resulted in a decrease in the pig population and an increase in poultry numbers (Huang et al. 2024; Jia et al. 2024c; Liu et al. 2020; You et al. 2021).

Furthermore, this website allows users to compare the prevalence disparities of two selected provinces from different perspectives. Figure 5A-C shows that the prevalence of bvSP is greater in Shandong chickens than in Guangdong chickens, the former of which is associated primarily with free-range indigenous Chinese chickens (Fig. 5D, E). In Shandong rovince, bvSP was detected in both cocks and hens (Fig. 5F), as well as in chickens with different economic uses (Fig. 5G). Similarly, in both provinces, bvSP was detected in the eggs of broilers (Fig. 5H). However, concerning layers, only Shandong province presented bvSP in young chicks and eggs, whereas adult laying hens presented no bvSP in either province (Fig. 5I). Furthermore, the prevalence trend changes in the two provinces are consistent, with only the time frames shifting (Fig. 5J). This discrepancy might be attributed to the provinces' disease prevention and control measures and the differences in farming scales. Additionally, the prevalence patterns in other provinces and comparisons between any two provinces can be obtained in the same manner.

In addition to the aforementioned features, the platform also supports updates. Once new epidemiological survey data, including bvSP and bvSG data, are integrated into the dataset, the platform accordingly displays new information, which meets the needs for long-term monitoring of pathogens (Zhou et al. 2022a). Nevertheless, our study is subject to the following limitations or considerations: (1) It focuses on individual-level prevalence without considering differences between farms, which may impact decisions regarding pathogen eradication and animal disease control. (2) Despite efforts to reduce heterogeneity within the literature structure, there remains high heterogeneity of over 90%, indicating significant variations among the included studies. Various subgroup analyses have been conducted to better explore the sources of heterogeneity and understand how different factors affect the epidemiological characteristics of diseases. However, we did not perform meta-regression to assess the influence of multiple covariates, which could provide deeper insights into the observed variations. (3) A lack of inclusion criteria on the basis of study design may introduce bias. For example, combining case reports, which focus on individual cases, with cross-sectional studies, which provide a population-level snapshot, could lead to inaccurate interpretations. Establishing clear inclusion criteria to combine studies with similar methodologies would help mitigate this bias in future analyses. (4) We retrieved all relevant articles only from the CNKI (Chinese) and PubMed (English) databases, potentially excluding literature published in other languages. Although this may lead to data bias, we believe our study remains robust, as it focuses on the two most widely spoken languages, English and Mandarin Chinese, with English being the dominant language in global scientific texts. (5) Not all tests and reports were recorded and published, resulting in incomplete data. Addressing these gaps through a systematic review and developing a visualization platform would help raise public awareness and improve data transparency.

Conclusion

We first developed an updatable visualization platform for the global prevalence of pullorum disease and fowl typhoid. Particularly, we displayed essential data on serotypes (biotypes), geographical regions, and periods by using their dynamic and flexible features. Users can obtain a detailed overview of the prevalence of bvSP and bvSG and predict the progression of the disease burden. Notably, considering that the outbreak of *S.* Gallinarum in China was severe, more dynamic presentations of each province in China are provided, including a comparison of prevalence patterns among the two provinces at the same time.

Methods

Data collation

The data on this platform are derived from a systematic meta-analysis following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (a checklist is shown in Table S1), which is based on epidemiological surveys and case reports spanning nearly 80 years on pullorum disease and fowl typhoid retrieved from two major databases, China National Knowledge Infrastructure (CNKI, http://www.cnki.net/) and PubMed (https://pubmed.ncbi.nlm.nih.gov/) (Zhou et al. 2022a). A total of 8,631 articles were retrieved after the initial search using the keywords "鸡白痢" or "鸡伤寒", "Pullorum" or "Gallinarum" in the two databases for articles published before May 1, 2021. After 1,212 duplicates were removed via EndNote, 7,032 articles unrelated to epidemiological investigations were excluded on the basis of the titles and abstracts. Furthermore, 29 articles with unavailable full text, 12 unrelated to *Salmonella* Pullorum or *Salmonella* Gallinarum, 51 not relevant to epidemiological surveys in the full-text content, and 94 with

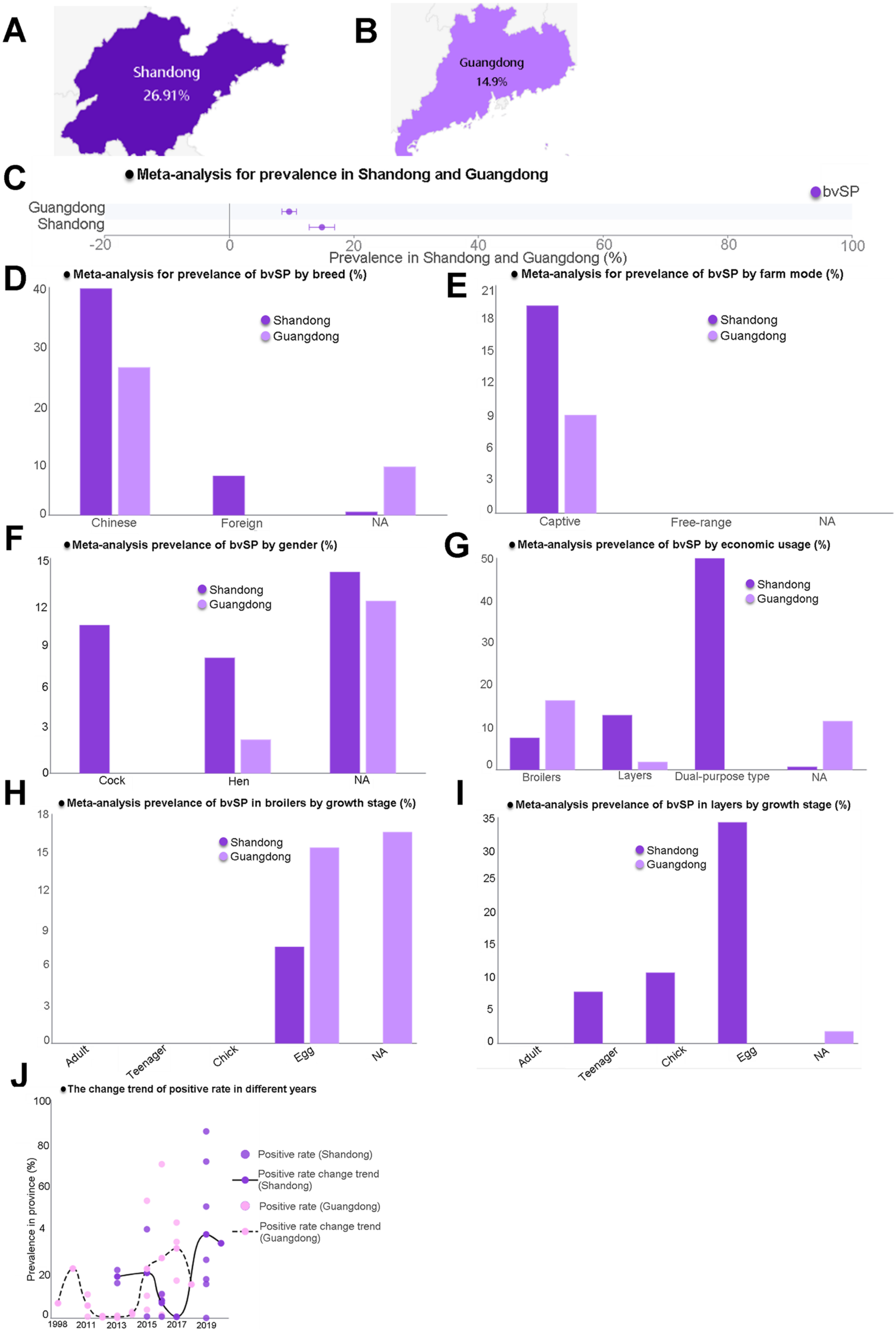

Fig. 5 Visualization comparison of bvSP prevalence between Shandong and Guangdong provinces. **A**, **B** The prevalence rates of bvSP in Shandong and Guangdong. **C** The meta-analysis for the prevalence of bvSP in Shandong and Guangdong. **D**-**G** The prevalence of bvSP by breed, farm mode, gender or economic usage. **H**, **I** The prevalence by growth stage of broilers and layers. **J** The change trend of the positive rates for Shandong and Guangdong in different years

unclear sample sizes were also excluded. A total of 201 articles after strict validation were ultimately selected for subsequent analyses (Supplementary Tables) (Zhou et al. 2022a). The included and excluded studies were verified via a random sampling method. The individual-level prevalence (positive rate) of each record is displayed in each table.

The data for the descriptive analysis (referring to a systematic review) were obtained from Table S2, providing an overview of the essential characteristics and trends of the included studies, whereas the remaining data were derived from Tables S3 to S7, with Tables S4 to S7 representing breed, farm mode, economic usage (including the growth stages of broilers and layers), and gender, respectively. The supplementary file is shared at figshare (https://doi.org/10.6084/m9.figshare.19519402.v1) (Zhou et al. 2022b). For all meta-analyses, the binary random-effects model (DL: DerSimionian–Laird method) was used through Open Meta-Analyst, which accounts for between-studies heterogeneity and includes the variation in this heterogeneity in the weight calculations (DerSimonian & Laird 1986; Fekih-Romdhane et al. 2022; Paudyal et al. 2018; Takkouche et al. 1999).

Platform development

The platform employs a browser/server (C/S) architecture, a network architecture model where the users access server resources through a web browser (Wang et al. 2021). The backend is developed *via* Java (V. 8.0) and Spring Boot (V. 2.7.8), whereas the frontend uses Vue 3 (V. 3.2.45) with the TypeScript (V. 4.9.3) framework. The MySQL database (V. 8.0.20) is adopted to store data uploaded through application programming interface (API) calls, allowing different software systems or applications to communicate and exchange data seamlessly (Woody et al. 2020). The network request library Axios (V. 1.3.3) is utilized to access backend API data. The process involves initiating hypertext transfer protocol (HTTP) requests, managing cross-origin issues via route forwarding mechanisms, and processing the obtained responses. Pinia (V. 2.0.30), a storage solution for Vue, is used to store specific frontend data and facilitates sharing across components and pages.

The graphical representation, created by Echarts (V. 5.4.2), is further upgraded by using the Vue-Echarts component (V. 6.6.0) to improve rendering and adaptability. Geospatial data are incorporated by loading GeoJSON data, followed by API queries to obtain corresponding data for provinces, countries, and continents. The specific components were developed *via* the UI Kit Element-Plus (V. 2.3.7). The cascading style sheet (CSS) styles, which are used to describe and define the visual appearance and layout of web pages, were adjusted to match the design requirements of the layout. The vue router facilitates navigation between pages. Front-end interaction involves toggling switches to modify corresponding API endpoints. The distinct datasets are acquired and rendered within front-end components by selecting various filtering criteria.

To evaluate the platform's usability, we conducted internal tests involving 20 group members, including master's students, Ph.D. students, and postdoctoral researchers. Among them, four focused on *S. Gallinarum*, and six specialized in epidemiology, with three working specifically on *Salmonella* Gallinarum-related topics. The remaining 13 participants were from unrelated fields. The tasks assigned included determining the prevalence of bvSP in Asia from 1990--2000; the prevalence of bvSG in eggs in South Korea; and the prevalence of SG, bvSP and bvSG across different farming models in Guangxi province, China.

Abbreviations

bvSP	*Salmonella enterica* subsp. *enterica* serovar Gallinarum biovar Pullorum
bvSG	*Salmonella enterica* subsp. *enterica* serovar Gallinarum biovar Gallinarum
WOAH	the World Organization for Animal Health
CNKI	China National Knowledge Infrastructure
C/S	Browser/server
API	Application programming interface
HTTP	Hypertext Transfer Protocol
CSS	Cascading Style Sheets

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s44149-024-00145-8.

Additional file 1: Supplementary Tables S1-S7

Additional file 2. Supplementary demonstration video showing detailed usage instructions

Acknowledgments

Not applicable.

Authors' contributions

XMK and CHJ created the search strategy. CHJ, PKG, SW, ZJG and CYD developed the platform. XMK and XZ retrieved and screened the publications and extracted the data for meta-analysis. HYZ and LLH detailed the platform. XMK created the graphics and wrote the original draft. AS and YL reviewed and edited the draft. MY conceived the work.

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Data availability

All data are included in this article, the supplementary video and the figshare (https://doi.org/10.6084/m9.figshare.19519402.v1).

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The figures were edited with Snagit software. All contributing authors declare that they have no competing interests. Author Min Yue was not involved in the journal's review or decisions related to this manuscript.

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