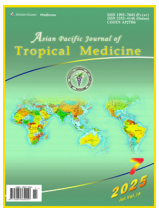

Systematic Review and Meta-Analysis

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Distribution of Group B *Streptococcus* isolated from humans in Southeast Asia: A systematic review and meta-analysis

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ABSTRACT

Objective: To assess the burden of Group B *Streptococcus* (GBS) and analyze the distribution of serotypes in relation to their source. The review highlights data gaps in transmission dynamics and regional food consumption practices, which are essential for designing effective public health strategies and advancing vaccine development.

Methods: Searches were conducted in Web of Science, MEDLINE, Science Direct, PubMed, and Scopus databases to find studies related to GBS during 1990-2025. Eligible studies were those that described prevalence, serotype distribution or sequence type (ST) of GBS in Southeast Asian countries. Random-effects meta-analysis was used to pool data.

Results: A total of 26 studies met the inclusion criteria from eight countries. The pooled estimate of maternal GBS colonization was 15.1%, with serotypes Ⅲ, Ⅴ, Ⅱ, Ⅵ, and Ⅰa accounting for the majority of cases (91.24%) in the Southeast Asia studies. Data on ST was limited; however, ST1 was found to be predominant in Malaysia and Thailand, while ST283 was notably linked to the consumption of raw fish.

Conclusions: The pooled estimate of the maternal colonization with GBS was 15.1% which is equivalent to many other primary and review reports worldwide. Distribution of serotype and ST is needed to be studied in Southeast Asian countries to devise effective preventive measures. These findings underscore the importance of surveillance and tailored prevention strategies to combat GBS infections in Southeast Asia.

KEYWORDS: Group B *Streptococcus*; *Streptococcus agalactiae*; Maternal colonization; Neonatal disease; Serotypes; Sequence type; Southeast Asia

1. Introduction

Group B *Streptococcus* (GBS), also known as *Streptococcus agalactiae*, is a significant pathogen responsible for various infections in both neonates and adults. However, GBS is typically a commensal organism, colonizing the gastrointestinal and genitourinary tracts of healthy adults at rates between 10% and 40%. In pregnant women, the colonization rate can be as high as 30%-70%, with approximately 50% of colonized mothers transmitting the bacteria to their newborns during birth[1].

Summary

Question: What is the burden and serotype distribution of Group B *Streptococcus* (GBS) in Southeast Asia?

Findings: This meta-analysis from eight Southeast Asian countries found a maternal GBS colonization rate of 15.1%, with serotypes Ⅲ, Ⅴ, Ⅱ, Ⅵ, and Ⅰa comprising 91.24% of cases. Sequence type ST1 predominated in Malaysia and Thailand, while ST283 was linked to raw fish consumption.

Meaning: Surveillance of GBS serotypes and sequence types is crucial in Southeast Asia to inform targeted public health interventions and vaccine development to reduce GBS infections.

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In neonates, GBS can lead to two types of invasive diseases which are Early-Onset Disease (EOD) and Late-Onset Disease (LOD). EOD occurs within the first week of life, with symptoms often manifesting as septicaemia or pneumonia. The incidence among infants born to colonized mothers is significantly higher, with about 1%-2% developing EOD, while LOD occurs between 7 and 90 days after birth, with manifestations including bacteremia and meningitis, among other symptoms. LOD is generally associated with horizontal transmission rather than vertical[2]. In adults, GBS can cause serious infections such as endometritis, chorioamnionitis, arthritis, endocarditis, pneumonia, bacteraemia and urinary tract infections, as well as soft tissue, skin, and bone infections particularly in pregnant women and those with underlying health conditions such as diabetes or cancer[3].

In 2015, Singapore experienced a significant foodborne outbreak linked to GBS, specifically the ST283 strain, which resulted from the consumption of contaminated raw freshwater fish dishes, notably known as yusheng. This outbreak affected over 160 individuals, leading to severe health complications, including fever, meningitis, and septic arthritis. Tragically, two fatalities were reported among the victims, highlighting the outbreak's severity and the strain's aggressive nature[4]. The GBS ST283 strain had not previously been recognized as a foodborne pathogen, making this outbreak particularly alarming. The strain was found to be prevalent in various Southeast Asian countries, accounting for significant percentages of human GBS cases: 76% in Laos, 73% in Thailand, 31% in Vietnam, and 23% in Singapore[5]. In Malaysia, a study reported the first two cases of human infection with GBS ST283. Whole genome sequencing showed the Malaysian isolates were closely related to contemporaneous human cases in Singapore, suggesting potential cross-border transmission *via* imported or locally sourced fish[6].

Capsular polysaccharide (cps) is one of the important virulence factors of most GBS isolates that contribute to pathogenicity. Currently, GBS can be categorized into 10 serotypes (Ⅰa, Ⅰb and Ⅱ-Ⅸ)[7]. The distribution and predominance of certain serotypes is susceptible to fluctuations and can change over time. Epidemiological studies show that serotypes Ⅰa, Ⅲ and Ⅴ are frequently associated with invasive disease in pregnant women, newborns and non-pregnant adults[8]. Serotype Ⅲ has been shown to be responsible for more than 70% of cases of early-stage GBS worldwide, while serotype Ⅰa is close behind with around 19% of isolates[7,8]. The distribution of GBS serotypes shows remarkable regional differences[9]. In regions such as Europe and North America, serotypes Ⅲ and Ⅰa dominate. In parts of Africa and Asia, however, the prevalence may shift, with serotype Ⅴ sometimes being more common[7,10]. Understanding the distribution of these serotypes is crucial for developing effective vaccines and prophylactic strategies. Previous studies suggest that a trivalent vaccine targeting serotypes Ⅰa, Ⅰb and Ⅲ could potentially cover a significant proportion of GBS-related disease worldwide[11,12].

Multilocus sequence typing (MLST) has significantly advanced the understanding of the genetic diversity and epidemiology of GBS. This genotypic method allows for the characterization of bacterial populations by analyzing variations in specific housekeeping genes, leading to the identification of distinct sequence types (STs) associated with different clinical outcomes[13]. Certain STs of GBS strains have been identified as having a higher potential for causing invasive diseases. For instance, ST1 and ST19 are predominantly associated with asymptomatic colonization, while ST23 is linked to both carriage and invasive disease[13,14]. Specifically, ST17 has been strongly correlated with neonatal meningitis, indicating its role in severe infections among newborns[15]. The emergence of ST283 has raised concerns as it has been associated with invasive diseases such as septic arthritis and meningitis across various populations, including neonates, pregnant women, and adults[15]. This sequence type has been identified as a major contributor to GBS infections in Southeast Asia, particularly in Thailand and Laos, where it accounted for 73% to 76% of invasive GBS cases from 2000 to 2017. Another notable sequence type, ST7, has also been documented but is less prevalent than ST283 in recent studies. It is often found alongside ST283 in aquatic species and human cases[14]. The genetic profiles derived from MLST not only help in understanding the distribution of strains but also assist in tracking the evolution of virulence among GBS populations. The ability to compare STs across laboratories *via* online databases enhances collaborative research efforts and promotes a better understanding of GBS epidemiology on a global scale[13].

Understanding the prevalence of GBS regarding to serotypes and ST distribution in Southeast Asia is important to design and implement preventive interventions. Therefore, we conducted a systematic literature review and meta-analysis of the incidence of GBS infections and the associated serotypes and ST causing GBS invasive disease.

2. Methods

2.1. Search strategy

A systematic electronic search was conducted using five online databases (Web of Science, MEDLINE, Science Direct, PubMed and Scopus) to identify studies reporting the evaluation of GBS among human in any country in Southeast Asia, which includes 11 countries: Brunei, Myanmar, Cambodia, Timor-Leste, Indonesia, Laos, Malaysia, the Philippines, Singapore, Thailand and Vietnam. We used the following search terms ("Group B *Streptococcus*"

OR "Group B streptococcal" OR "*Streptococcus agalactiae*"). We restricted searches to publications of year 1990-2025, human studies (*e.g.*, fish, bovine and cattle were excluded), research articles or original data (*i.e.*, case reports or reviews or repeated datasets were excluded) and English-language. Studies were included if they report at least one of the following criteria: prevalence of GBS, serotype distribution of GBS and ST distribution of GBS. This systematic review and meta-analysis was registered in PROSPERO (references no. CRD420251013864).

We selected the studies in three phases according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA). First, we excluded the papers based on the titles. Second, we screened the abstracts of the remaining papers and we excluded any papers that do not meet the inclusion criteria. After the initial screening of the titles and abstracts, duplicates were removed and the remaining papers were again screened. Lastly, we assessed the remaining papers by reading the entire text and excluded the papers based on the inclusion and exclusion criteria.

2.2. Study selection

The main author drafted detailed inclusion criteria with experts' guidance from two supervisors to assess the eligibility. One reviewer screened all titles and abstracts of the entries, followed by two additional reviewers scrutinized the text in all selected articles independently in order to ascertain whether they met the inclusion criteria. In case of discrepancies, a third reviewer was asked to express an opinion on whether the study should be included or not. All disagreements were resolved through practical discussion among the reviewers.

2.3. The quality assessment

Two reviewers independently assessed the methodological quality of publications using the Joanna Briggs Institute (JBI) Critical Appraisal Tool for systematic reviews of prevalence/incidence. This tool evaluates nine key domains to identify potential biases and ensure methodological rigor: (1) appropriateness of the sample frame, (2) participant recruitment strategies, (3) adequacy of sample size, (4) detailed description of study subjects and settings, (5) coverage of identified samples, (6) validity of condition identification methods, (7) standardization and reliability of measurements, (8) appropriateness of statistical analyses, and (9) response rates. Each study underwent rigorous appraisal by both reviewers, with discrepancies resolved through discussion to ensure consensus. The process aimed to systematically assess whether studies adequately addressed bias risks in design, execution, and analysis. Results from this appraisal informed decisions about study inclusion and data synthesis, aligning with JBI's evidence-based methodology that emphasizes dual independent assessments to minimize systematic errors.

2.4. Data extraction

Data extraction was performed independently by two reviewers. Data was extracted and recorded on the following characteristics: authors, year, setting, study design (prospective or retrospective), sample size, subject (neonates, pregnant women, non-pregnant adults), isolation (invasive, non-invasive, colonizing sites), prevalence of GBS and venue. Moreover, we gathered results related to serotype and ST distribution. A pre-set Excel abstraction form was used to extract study characteristics and results.

2.5. Data analysis

Meta-analyses were performed with Open Meta (Analyst) using a random-effect model to produce the pooled prevalence of GBS colonization in pregnant women. Random-effects model was used to pool data primarily because it accounts for variability (heterogeneity) across different studies. Additionally, heterogeneity of the studies was evaluated using I^2 and a P-value below 0.05 was considered statistically significant. IBM Statistical Package for Social Science (SPSS) version 29 for Microsoft Windows, (Chicago, USA) was used to analyze and present the data graphically. Percentage and frequency were used to describe the data and facilitate the comparison amid the groups.

3. Results

3.1. Study selection

The selection process is presented visually in Figure 1. A total of 9 238 papers were identified by an extensive literature search as follows: 914 from MEDLINE, 2 330 from Science Direct, 2 037 from Web of Science, 2 905 from Scopus and 1 052 from PubMed, from 1st January 1990 to 1st February 2025. After an initial review of titles and abstracts and the removal of duplicates, we assessed the full text of 83 articles for eligibility, of which 26 met the inclusion criteria[16–41].

3.2. Study characteristics

The characteristics of all 26 studies are summarized in Table 1. The 26 studies included 11 657 participants including neonate (0-28 days), infant (1 month-2 years), pregnant women, non-pregnant

adult (15-≥65 years old). Most identified papers were from Thailand (*n*=8) and Malaysia (*n*=7), followed by five studies from Singapore, two from Vietnam and one from Laos, Indonesia, Thailand and Philippines, and Thai-Myanmar border each. Twelve studies reported the prevalence of GBS[16-18,21,23,27-29,32,34,36,40]. Sixteen studies reported serotypes distribution[19,21,22,24-27,29,31,33,34,36-39,41] and eight reported ST distribution[24,25,27,30,31,35,38,41].

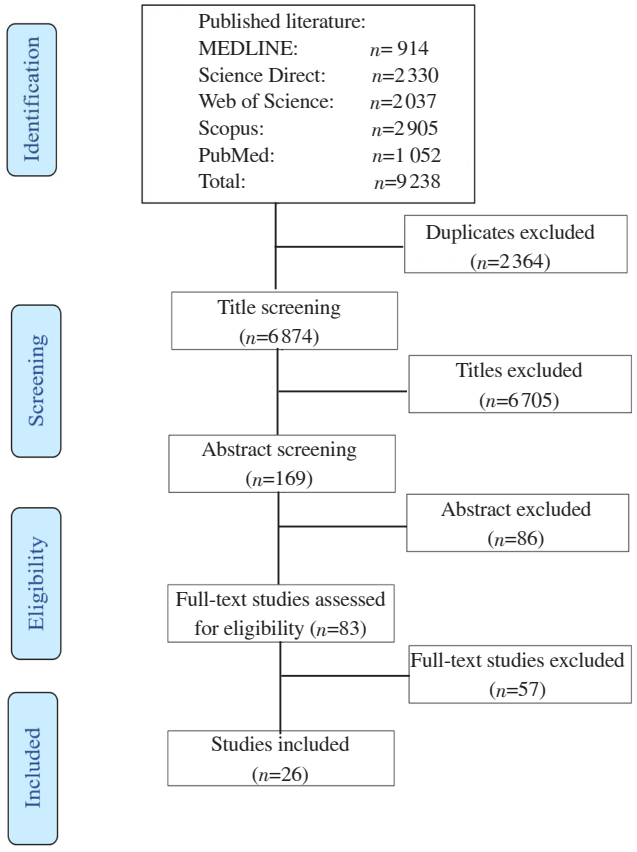

Figure 1. PRISMA flow diagram explaining the methodology to select the eligible studies.

3.3. Prevalence of GBS

Nine studies reported the prevalence of GBS colonization in pregnant women, providing sufficient and comparable data to conduct a reliable meta-analysis in this population. In contrast, only three studies addressed invasive GBS infections, each involving different subject groups, which precluded the possibility of a meaningful meta-analysis for invasive cases. Given that GBS colonization is notably more common among pregnant women and poses significant clinical implications for both maternal and neonatal health, this analysis focuses exclusively on the prevalence of GBS in this group, highlighting its importance.

3.3.1. Prevalence of GBS colonization in pregnant women

Nine studies reported the prevalence of GBS colonization in pregnant women[16-18,21,28,32,34,36,40]. A study done by Tor-Udom *et al*.[16] in Thailand reported that the prevalence of colonizing GBS among 406 pregnant women was 16.0%. Another study in Thailand showed 58 (18.1%) pregnant women from 320 cases were colonized with GBS[17]. In addition, two prospective studies in Thailand showed the prevalence of GBS was 15.1% among 421 pregnant women, 4.8% among 421 neonates[28], and 11.3% among 50 intrapartum women[32]. Moreover, Akkaneesermsaeng *et al*.[32] reported that teenage pregnancy, multiparity, and non-Buddhist religions to be significantly associated with GBS colonization. Turner *et al*.[21] found that the GBS colonizing rate was 12.0% in 549 pregnant women at the time of delivery in a refugee population on the Thai-Myanmar border. There is no significant association between GBS colonizing status and the risk factors that form the basis of a GBS risk based IPA strategy (fever, prolonged rupture of membranes, prematurity). Hanh *et al*.[34] reported the prevalence of GBS in an obstetrics and pediatrics hospital in Vietnam was 9.2% among 750 pregnant women. Additionally, a retrospective study among 3 863 pregnant women in Vietnam reported 8.0% colonization rate for GBS[40]. In a study in Indonesia, the prevalence of colonization GBS among pregnant women was 30.0% (53 out of 177). GBS was isolated exclusively from vaginal swabs taken from pregnant women[36]. The highest prevalence (32.1%) of GBS colonization isolates was found in a pilot study in Malaysia among 56 multigravida pregnant women[18]. The overall pooled prevalence of GBS colonization among 7 468 pregnant women from the meta-analysis of nine studies across the five countries was 15.1% (95% *CI* 11.8-18.4, I^2=92.87%) (Figure 2).

A funnel plot was created to assess potential publication bias for

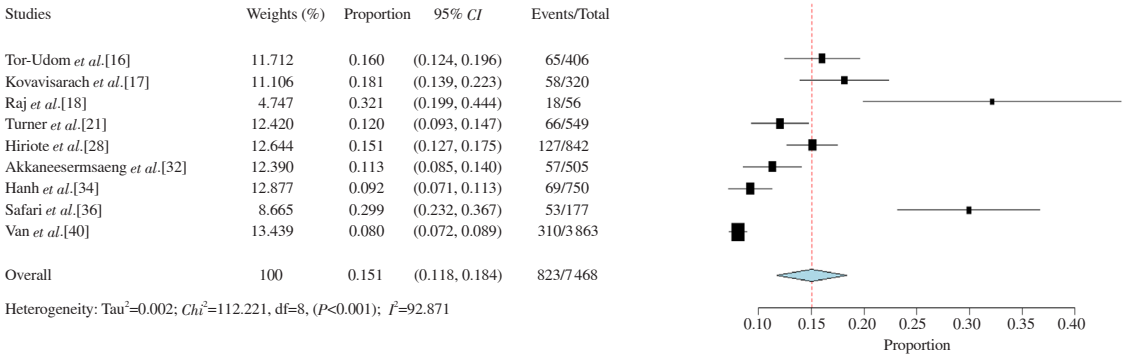

Figure 2. Pooled prevalence of Group B *Streptococcus* colonization in pregnant women.

Table 1. Summary of the characteristics of the included studies.

Author/Year	Setting	Study design	Sample size	Subject	Isolation	Prevalence	Venue	Most common serotypes	Most common ST
Tor-Udom *et al.*, 2006[16]	Thailand	Retrospective study	406 (pregnant women)	Pregnant women	Colonizing isolates	16.0%	Thammasart Hospital	-	-
Kovavisarach *et al.*, 2007[17]	Thailand	Prospective study	320 (pregnant women)	Pregnant women in labor	Colonizing isolates	18.1%	Rajavithi Hospital	-	-
Raj *et al.*, 2009[18]	Malaysia	Prospective study	56 (pregnant women)	Antenatal pregnant women	Colonizing isolates	32.1%	University Malaya Medical Centre (UMMC)	-	-
Karunakaran *et al.*, 2009[19]	Malaysia	Prospective study	49 (65.3% male & 34.6% female)	Neonates, pregnant women and non-pregnant adults	Invasive, non-invasive, and colonizing isolates	-	University Malaya Medical Centre (UMMC)	Ⅰa (22.2%), Ⅵ (17.8%), Ⅲ and Ⅴ (13.3% for each)	-
Chaiwarith *et al.*, 2011[20]	Thailand	Retrospective study	186 (54.8% female & 45.2% male)	Neonates, pregnant women and non-pregnant adults	Invasive, and colonizing isolates (44.1% invasive GBS & 55.9% colonizing GBS)	-	Chiang Mai University Hospital	-	-
Turner *et al.*, 2012[21]	Thai-Myanmar border	Prospective study	549 (pregnant women)	Pregnant women at the time of delivery	Colonizing isolates	12.0%	Shoklo Malaria Research Unit (SMRU) clinic at Maela Camp of refugees	Ⅱ (24.2%), Ⅰa and Ⅵ (each 18.2%), Ⅲ and Ⅴ (each 6%)	-
Eskandarian *et al.*, 2015[22]	Malaysia	Prospective study	103 (10.7% neonates, 47.6%) pregnant women and 41.7% non-pregnant adults)	Neonates, pregnant women and non-pregnant adults	Invasive, non-invasive, and colonizing isolates	-	Universiti Kebangsaan Malaysia Medical Centre (UKMMC)	Ⅵ (22.3%), Ⅷ (21.4%), Ⅲ (20.4%), Ⅰa (17.5%) and Ⅴ (9.7%)	-
Villanueva-Uy *et al.*, 2015[23]	Thailand and Philippines	Prospective study	Not available in Thailand 366 infants aged <3 months in Philippines who culture positive	Infant aged <90 months	Invasive isolates	Not available in Thailand 0.8% in Philippines	Queen Sirikit National Institute of Child Health and Siriraj Hospital in Thailand. Philippine General Hospital and the Governor Celestino Gallares Memorial Hospital in Philippines.	-	-
Rajendram *et al.*, 2016[24]	Singapore	Prospective study	22 (54.5% female & 45.5% male)	Non- pregnant adult	Invasive isolates	-	Tertiary referral hospital	Serotypes Ⅲ (50%) and Ⅱ (22.7%)	ST283 (40.9%)
Tan *et al.*, 2016[25]	Singapore	Retrospective study	36 (52.5% male & 47.5% female)	Non- pregnant adult	Invasive, and non-invasive isolates	-	Six tertiary hospitals	Serotypes Ⅲ (72%), Ⅱ and Ⅵ (11.1%) for each	ST283 (69.4%)
Suhaimi *et al.*, 2017[26]	Malaysia	Prospective study	60 (63.3% female & 36.7% male)	Non- pregnant adult, pregnant women, and neonates	Invasive, non-invasive, and colonizing isolates	-	Two teaching and referral hospitals and one tertiary referral hospital	Serotypes Ⅰa (45%), Ⅲ (16.7%) and Ⅴ (15%)	-
Kalimuddin *et al.*, 2017[27]	Singapore	Retrospective study	408 (57.8% male & 42.4% female)	Non- pregnant adult	Invasive isolates	35.8%	Five public sector hospitals	Serotypes Ⅲ (46.6%), Ⅵ (14.2%) and Ⅴ (13.5%)	ST283 (35.8%)
Hiriote *et al.*, 2017[28]	Thailand	Prospective study	842 (50% pregnant women, 50% neonates)	Pregnant women, and neonates	Invasive, non-invasive, and colonizing isolates	15.1% (Pregnant women) and 4.8% (Neonates)	University Hospital	-	-

Table 1 continues in next page.

Table 1. Continued.

Author/Year	Setting	Study design	Sample size	Subject	Isolation	Prevalence	Venue	Most common serotypes	Most common ST
Kerdsin *et al.*, 2017[29]	Thailand	Prospective study	725 (61.9% male & 38.1% female)	Non- pregnant adult, pregnant women, and neonates	Invasive isolates	28.9%	12 tertiary hospitals	Serotypes Ⅲ (87.15%), Ⅰa (5.24%) and Ⅴ (3.81%)	-
Ong *et al.*, 2018[30]	Singapore	Retrospective study	54 (55.6% male & 44.4% female)	Non- pregnant adult	Invasive isolates	-	Tertiary referral hospital	-	ST283 (42.6%)
Barkham *et al.*, 2018[31]	Laos	Prospective study	38 (75% male & 25% female)	Non- pregnant adult, pregnant women, and neonates	Invasive isolates	-	Tertiary hospital	Serotype Ⅲ (79%)	ST283 (76.3%)
Akkaneesermsaeng *et al.*, 2019[32]	Thailand	Prospective study	505 (pregnant women)	Intrapartum pregnant women	Colonizing isolates	11.3%	University hospital	-	-
Paveenkittiporn *et al.*, 2020[33]	Thailand	Prospective study	1 736 (56.5% female & 43.5% male)	Non- pregnant adult, pregnant women, and neonates	Invasive, non-invasive, and colonizing isolates	-	25 tertiary hospitals	Serotypes Ⅲ (46.4%) and Ⅴ (21%)	-
Hanh *et al.*, 2020[34]	Vietnam	Prospective study	750 (pregnant women)	Pregnant women	Colonizing isolates	9.2%	Obstetrics and Pediatrics Hospital	Serotypes Ⅲ (39.13%), Ⅴ (31.89%) and Ⅰa (11.59%)	-
Ezhumalai *et al.*, 2020[35]	Malaysia	Prospective study	51	Non- pregnant adult, pregnant women, and neonates	Invasive (45.1%), colonizing (54.9%) isolates	-	3 Tertiary hospitals	-	ST1 (42.0%), ST23 (14.0%) and ST19 (8.0%)
Safari *et al.*, 2021[36]	Indonesia	Prospective study	177 (pregnant women)	Pregnant women	Colonizing isolates	30.0%	Primary health centers in Jakarta	Serotype Ⅱ (30%) and serotype Ⅲ (23%)	-
Bahez *et al.*, 2021[37]	Malaysia	Prospective study	62 (pregnant women)	Pregnant women	Non-invasive isolates	-	Hospital Tengku Ampuan Afzan	Serotypes Ⅰa and Ⅰb (16.1% each) Ⅱ, Ⅴ, and Ⅶ (9.7% each), Ⅲ (8.1%), Ⅵ (6.5%), and Ⅷ (1.6 %)	-
Tulyaprawat *et al.*, 2021[38]	Thailand	Prospective study	109 (56.9% males & 43.1% females).	Non-pregnant patients	Invasive isolates	-	Siriraj Hospital	Serotype Ⅲ (52.3%), Ⅴ and Ⅵ (13.8% each), and Ⅰb (11.9%)	ST1 (64.5%), ST283 (16.1%), ST12 (9.7%), ST452 (6.5%) and ST17 (3.2%)
Kam *et al.*, 2021[39]	Singapore	Retrospective study	71 (62.9% males & 37.1% females)	Infants from birth to day 90 of life	Invasive isolates	-	KK Women's and Children's Hospital	Serotype Ⅲ (71.2%), Ⅰa (15.2%), Ⅴ (5.1%), Ⅰb and Ⅱ (3.4% each) and Ⅵ (1.7%)	-
Van *et al.*, 2021[40]	Vietnam	Retrospective study	3 863 (pregnant women)	Pregnant women	Colonizing isolates	8.0%	National Hospital of Obstetrics and Gynaecology	-	-
Muthanna *et al.*, 2023[41]	Malaysia	Prospective study	113 (38.9% males & 61.1% females)	Neonate, infant and adult	Invasive isolates	-	6 Tertiary hospitals	Serotype Ⅴ (23 %), Ⅰa (19.5 %), Ⅱ (18.6 %), Ⅵ (15.9 %), Ⅲ (10.6 %), Ⅶ (4.4 %), Ⅰb and Ⅳ, (3.5% each) and Ⅸ (0.9 %)	ST1 (32.6%), ST17 (13%), ST3, ST12 and ST26 (6.5% for each), ST24 and ST283 (4.3% for each), ST19, ST23, ST28, ST130, ST196, ST335, ST459, ST485 and ST861 (2.2% for each), and lastly three newly identified ST1668, ST1669 and ST1670 (2.2% for each)

-: Not investigated by the authors; ST: Sequence type.

prevalence of GBS colonization among pregnant women (Figure 3). The plot, based on logit-transformed proportions, reveals a fairly symmetrical distribution of studies around the pooled effect estimate, suggesting no strong evidence of publication bias. However, the limited number of included studies restricts the capacity to draw definitive conclusions regarding bias or small-study effects.

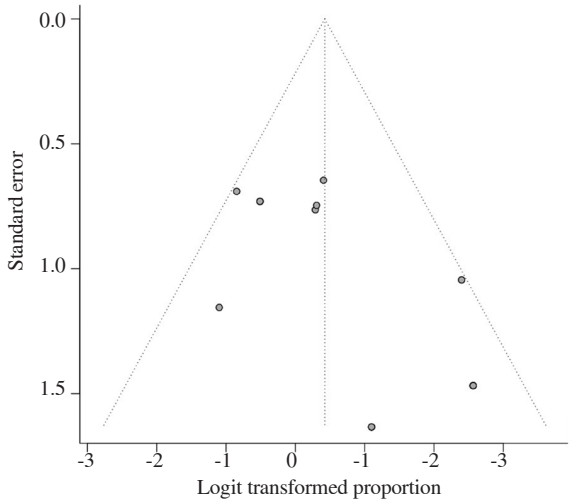

Figure 3. Funnel plot assessing publication bias in studies reporting the prevalence of Group B *Streptococcus* colonization among pregnant women, showing a symmetrical distribution of the studies, indicating no visual evidence of publication bias.

3.3.2. Prevalence of Invasive GBS

Three studies reported the prevalence of invasive GBS[23,27,29]. A study in Thailand and Philippines among infants aged <90 months found that the prevalence of GBS was 0.8% among the positive cultures in the Philippines; while in Thailand, the prevalence was not reported due to the total number of cultures taken for further investigation was not available. In the Philippines, all the cases were of early-onset disease (EOD) in infants. Two babies died, and the other recovered from infection and was released from hospital. In Thailand cases, there are two cases: the first one was a boy who died 14 hours after birth, and the second case was a girl born at 35 weeks who recovered and was released from hospital[23].

The prospective study by Kerdsin *et al.*[29] showed a prevalence of GBS of 28.9% (210 out of 725) among non-pregnant adult, pregnant women, and neonates in Thailand. The prevalence was higher among male (*n*=130, 61.9%) than female (*n*=80, 38.1%). Of the 149 patients with the clinical manifestation, septicemia was the most common invasive condition (*n*=135, 90.6%), followed by meningitis (*n*=10, 6.7%) and septic arthritis (*n*=4, 2.7%) among the cases. The highest prevalence of invasive GBS (35.8%) was reported by Kalimuddin *et al.*[27] in five public sector hospitals in Singapore among 408 non-pregnant adults who consumed raw fish during 2015 GBS outbreak. Most of the patients were young adults, male (*n*=236, 57.8%) and Chinese ethnicity (*n*=316, 77.5%). The GBS infections were associated with meningoencephalitis, native joint septic arthritis, and spinal infection.

3.4. Serotype distribution of GBS

A total of 16 studies of serotype distribution with a total of 3151 samples are shown in Figure 4. In general, serotype Ⅲ was the most common in nine studies, followed by serotype Ⅰa in three studies and serotype Ⅱ in two studies, and Ⅵ and Ⅴ in one study each. In addition, serotypes Ⅰb, Ⅳ, Ⅶ and Ⅷ were reported; a small proportion of serotypes were non-typeable. Serotype Ⅸ only reported in one study among invasive isolates. Figure 2 presents the overall pooled distribution of GBS serotypes in Southeast Asia. Serotype Ⅲ is the most common, accounting for 44.84% of cases, followed by serotype Ⅴ (17.01%), serotype Ⅱ (11.62%), serotype Ⅵ (9.01%), and serotype Ⅰa (8.76%). The remaining serotypes, including Ⅰb, Ⅳ, Ⅶ, Ⅷ, Ⅸ, and NT (non-typable), are much less frequent, each representing less than 5% of the total isolates. In addition, it shows the distribution of each serotype by country, highlighting geographical variations. Serotype Ⅲ was particularly dominant in Singapore and Thailand, while serotype Ⅴ is more prevalent in Vietnam and Thailand. Other serotypes, such as Ⅵ and Ⅱ, show higher percentages in Malaysia and Indonesia, respectively.

Information on serotypes associated with colonizing and non-invasive GBS among pregnant women was available from four studies[21,34,36,37]. Turner *et al.*[21] study, among 66 GBS isolates, eight of the ten currently known GBS serotypes were identified, the most common serotype was Ⅱ, identified in 16 isolates (24.2%), followed by serotype Ⅰa and serotype Ⅵ, each found in 12 isolates and accounting for 18.2% of the total samples. Other serotypes detected included Ⅲ and Ⅴ (6 isolates each, 9.1%), Ⅳ (4 isolates, 6.1%), Ⅶ (5 isolates, 7.6%), and Ⅰb (1 isolate, 1.5%), while no isolates were found for serotypes Ⅷ and Ⅸ; additionally, 4 isolates (6.1%) were non-typeable. Hanh *et al.*[34] found that mothers colonized with serotypes Ⅲ (*n*=27, 39.13%) and Ⅴ (*n*=22, 31.89%) were the most frequent, followed by serotype Ⅰa and Ⅵ (*n*=8, 11.59% for each), Ⅰb (*n*=2, 2.90%), Ⅱ and Ⅶ (*n*=2, 1.45% for each), respectively. Serotypes Ⅳ, Ⅷ and Ⅸ were not found. Safari *et al.*[36] reported that serotype Ⅱ was the most common (*n*=16, 30%), followed by serotype Ⅲ (*n*=12, 23%), Ⅰa and Ⅳ (*n*=7, 13% each), Ⅵ (*n*=4, 8%), Ⅰb and Ⅴ (*n*=3, 6% each), and one non-typeable strain. GBS serotype Ⅲ was more resistant to erythromycin, clindamycin, and levofloxacin. In addition, six out of ten multidrug-resistant isolates were serotype Ⅲ followed by serotype Ⅰb (2/10), serotype Ⅰa (1/10), and serotype Ⅳ (1/10). Bahez *et al.*[37] found that among 62 colonizing GBS isolates, 48 (77.4%) were serologically

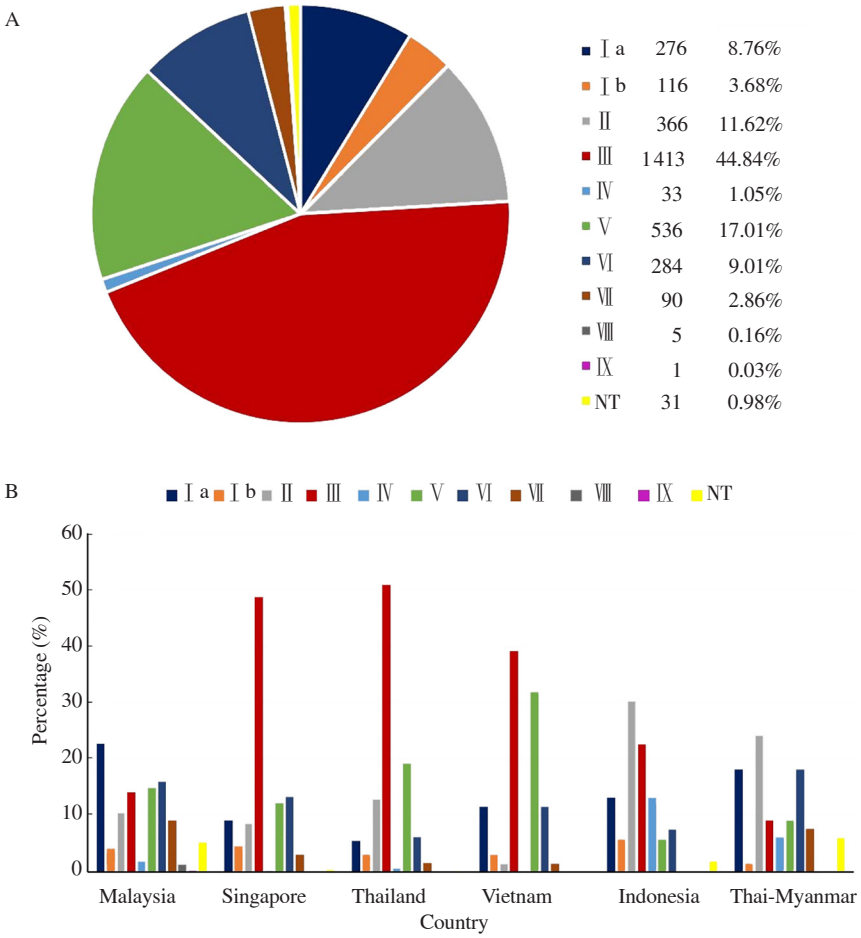

Figure 4. Distribution of Group B *Streptococcus* serotypes in Southeast Asian Countries. (A) Distribution of Group B *Streptococcus* serotypes; (B) Distribution of Group B *Streptococcus* serotypes by country.

typeable, and 14 (22.6%) were non-typeable. Serotypes Ⅰa and Ⅰb (*n*=10, 16.1% each) were the most common, followed by Ⅱ, Ⅴ, and Ⅶ (*n*=6, 9.7% each), Ⅲ (*n*=5, 8.1%), Ⅵ (*n*=4, 6.5%), and Ⅷ (*n*=1, 1.6%).

Information on serotypes associated with invasive and non-invasive isolates was available in 11 studies[19,22,24,25,27,29,31,33,38,39,41]. Meta-analyses could not be performed on Barkham *et al.*[31] because data on serotypes other than serotype Ⅲ were not reported. Barkham *et al.*[31] reported that among 38 of GBS isolates, 30 (79%) were serotype Ⅲ with 32% had meningitis.

In Malaysia, Karunakaran *et al.*[19] found that serotyping of 45 GBS isolates using a commercial serotyping kit revealed that the most common serotype was Ⅰa (*n*=10, 22.2%), followed by Ⅵ (*n*=8, 17.8%), and both Ⅲ and Ⅴ (*n*=6, 13.3% each). Other serotypes identified included Ⅰb, Ⅱ, Ⅳ, and Ⅷ (*n*=2, 4.4% each), Ⅶ (*n*=1, 2.2%), while 6 isolates (13.3%) were non-typeable. Eskandarian *et al.*[22] reported that among 103 GBS serotype Ⅵ was the most common capsular type (*n*=23, 22.3%) followed by Ⅶ (*n*=22, 21.4%), Ⅲ (*n*=21, 20.4%), Ⅰa (*n*=18, 17.5%), Ⅴ (*n*=10, 9.7%), Ⅱ (*n*=8, 7.7%) and Ⅳ (*n*=1, 1%). No serotype Ⅰb isolates were found in the study. Suhaimia *et al.*[26] reported that serotype Ⅰa was the most common serotype (*n*=27, 45%), followed by Ⅲ (*n*=10, 16.7%), Ⅴ (*n*=9, 15%), Ⅵ (*n*=8, 13.3%), Ⅷ (*n*=2, 3.3%) and Ⅶ (*n*=1, 1.7%). Serotype Ⅰb, Ⅳ and Ⅸ were not found in the study. No significant association was found between serotypes and isolation sites in the study (*P*>0.05). A study by Muthanna *et al.*[41] reported that among 113 invasive GBS isolates the most common serotype was serotype Ⅴ (*n*=26, 23%), followed by Ⅰa (*n*=22, 19.5%), Ⅱ (*n*=21, 18.6%), Ⅵ (*n*=18, 15.9%), Ⅲ (*n*=12, 10.6%), Ⅶ (*n*=5, 4.4%), Ⅰb and Ⅳ, (*n*=4, 3.5% each) and Ⅸ (*n*=1, 0.9%).

While the seven remaining studies reported serotype Ⅲ to be the most common serotype which associated with invasive isolates[24,25,27,29,33,38,39]. In Thailand, Paveenkittiporn *et al.*[33] reported that of the 1 736 isolates, multiplex PCR revealed 805 isolates of serotype Ⅲ (46.4%), 365 isolates of serotype Ⅴ (21%), 248 isolates of serotype Ⅱ (14.3%), 118 isolates of serotype Ⅵ (6.8%), 96 isolates of serotype Ⅰa (5.5%), 57 isolates of serotype Ⅰb (3.3%), 31 isolates of serotype Ⅶ (1.8%), 12 isolates of serotype Ⅳ (0.7%), and 4 isolates that were untypeable (0.2%). Serotype Ⅲ was strongly significantly (*P*=0.001) correlated with meningitis, sepsis and septic arthritis, while serotype Ⅴ was more associated with urinary tract infection than other serotypes (*P*=0.005). Additionally, in Thailand, Kerdsin *et al.*[29] reported that among a total of 210 GBS samples, serotype Ⅲ was the most common serotype (*n*=183,

87.15%) and it was mainly detected in septicemia cases (73.8%), followed by serotype Ⅰa (*n*=11, 5.24%), Ⅴ (*n*=8, 3.81%), Ⅱ and Ⅵ (*n*=3, 1.43% each) and Ⅰb and Ⅶ each in just 1 case (0.47%). Additionally, a study by Tulyaprawat *et al*.[38] in Siriraj Hospital in Thailand reported that, 57/109 isolates (52.3%) of the total isolates belonged to serotype Ⅲ, followed by serotypes Ⅴ and Ⅵ (13.8%, 15/109 isolates for each serotype). Serotype Ⅰb was the next most prevalent serotype (11.9%, 13/109 isolates). Serotypes Ⅰa (3.7%, 4/109 isolates), Ⅶ (2.7%, 3/109 isolates), and Ⅳ (1.8%, 2/109 isolates) were additional serotypes. Serotypes Ⅱ, Ⅷ, or Ⅸ were not found. In Singapore, the four retrospective studies[24,25,27,39] were among patients with consumption of raw fish and infants from birth to day 90 of life. Tan *et al*.[25] found a significant association between eating raw fish and serotype Ⅲ bacteremia, where all the patients who ate raw fish (*n*=19) were associated with serotype Ⅲ. Those who did not eat raw fish (*n*=17) had various serotypes: Ⅲ (*n*=7, 41.2%), Ⅱ and Ⅵ (*n*=4, 23.5%) of each, Ⅰa and Ⅶ (*n*=1, 5.9%) of each. However, serotype Ⅲ was the most common in both groups. Rajendram *et al*.[24] reported that among 22 GBS cases, serotype Ⅲ found in 11 (50%) of the cases, followed by serotypes Ⅱ (*n*=5, 22.7%), Ⅰa (*n*=3, 13.6%), Ⅴ (*n*=2, 9.1%), and Ⅶ (*n*=1, 4.6%). Serotype Ⅲ was found to be associated with bacteremia. Kalimuddin *et al*.[27] reported that among 408 GBS isolates, serotype Ⅲ (*n*=190, 46.6%) to be the most common, followed by Ⅵ (*n*=58, 14.2%), Ⅴ (*n*=55, 13.5%), Ⅰa (*n*=38, 9.3%), Ⅱ (*n*=35, 8.6%), Ⅰb (*n*=17, 4.2%), Ⅶ (*n*=12, 2.9%) Ⅳ (*n*=1, 0.2%) and 2 isolates (0.5%) were non-typeable. Patients with serotype Ⅲ infection were younger and had fewer comorbidities but were more likely to develop meningoencephalitis, septic arthritis, and spinal infection. A study by Kam *et al*.[39] in KK Women's and Children's Hospital in Singapore among 71 infants from birth to day 90 of life reported that out of the 71 cases of invasive GBS, 59 isolates were serotyped, and serotype Ⅲ was the most prevalent serotype in both the EOD (*n*=6, 37.5%) and LOD groups (*n*=36, 65.5%; total *n*=42, 71.2%). Serotype Ⅰa was the second most common serotype identified (*n*=9, 15.3%) followed by serotype Ⅴ (*n*=3, 5.1%). Serotypes Ⅰa, Ⅰb, Ⅱ, Ⅲ, and Ⅴ accounted for 98.3% (*n*=58) of the serotypes while serotypes Ⅰa, Ⅰb and Ⅲ (*n*=53) were seen in 89.8% of the GBS isolates. All the cases of meningitis (with or without concomitant bacteremia) were caused by serotype Ⅲ.

3.5. Sequence type distribution of GBS

A total of eight studies reported the ST distribution among GBS isolates[24,25,27,30,31,35,38,41]. However, meta-analyses could not be performed because the required data about ST distribution were not available in five studies[24,25,27,30,31]. Ezhumalai *et al*.[35] in Malaysia identified 15 STs among 50 invasive and non-invasive GBS isolates, with ST1 being the most prevalent (*n*=21, 42.0%), followed by ST23 (*n*=7, 14%), ST19 (*n*=4, 8%), ST103 (*n*=3, 6%), ST167, ST335, ST28, ST24 (*n*=2, 4% for each), and ST14, ST17, ST144, ST314, ST651, ST635, ST485 (*n*=1, 2% for each). Another study in Malaysia[41] found that among 113 GBS isolates, ST1 (*n*=15, 32.6%) made up the majority of GBS invasive isolates, followed by ST17 (*n*=6, 13%), ST3, ST12 and ST26 (*n*=3, 6.5% for each), ST24 and ST283 (*n*=2, 4.3% for each), ST19, ST23, ST28, ST130, ST196, ST335, ST459, ST485 and ST861 (*n*=1, 2.2% for each), and lastly three newly identified ST1668, ST1669 and ST1670 (*n*=1, 2.2% for each). This study reported ST283 in humans for the first time in Malaysia in two cases, which were associated with Chinese ethnicity, non-pregnant patients and susceptibility to antibiotics[41]. In Laos, Barkham *et al*.[31] reported that ST283 accounted for the majority of invasive GBS (*n*=29, 76.3%). The study did not report the other ST of the remaining samples. ST283 was associated with meningitis among young adults without comorbidities. In Singapore, studies by Tan *et al*.[25], Rajendram *et al*.[24], Kalimuddin *et al*.[27] and Ong *et al*.[30] reported that ST283 was more associated with eating raw or undercooked fish, Chinese ethnicity and patients without significant comorbidities. In Thailand, Tulyaprawat *et al*.[38] reported that among 109 of GBS isolates, ST1 (64.5%) was the most common ST, followed by ST283 (16.1%), ST12 (9.7%), ST452 (6.5%) and ST17 (3.2%).

4. Discussion

Currently, the prevalence of invasive and colonizing GBS, serotype distributions and ST distributions of the isolates in the Southeast Asia setting is investigated in small and fragmented ways. Therefore, this is the first meta-analysis of its kind to summarize the pooled proportion of invasive and colonizing GBS regarding to serotype and sequence type distributions reported in 26 studies among eight countries.

In the current meta-analysis, the overall estimate average of the maternal GBS colonization proportion among pregnant women was 15.1% (95% *CI* 11.8%-18.4%). This finding is comparable with the meta-analysis study conducted worldwide in 2016[42]. In the sub-group analysis of the maternal rectovaginal colonization, Southeast Asia was represented by only seven studies involving 3749 women, of whom 389 were GBS positive, resulting in an 11.1% colonization rate (95% *CI* 6.8%-15.3%)[42]. However, the overall estimates of maternal rectovaginal GBS colonization proportion from 78 studies with 73791 pregnant women was 17.9% (95% *CI* 16.2%-19.7%). Southeast Asia had the lowest estimated proportion of colonization compared to other regions, with Africa at 22.4% (95% *CI* 18.1%-26.7%), the Americas at 19.7% (95% *CI* 16.7%-22.7%), Europe at

19.0% (95% *CI* 16.1%-22.0%), the Eastern Mediterranean at 16.7% (95% *CI* 11.7%-21.7%), and the Western Pacific at 13.3% (95% *CI* 7.8%-18.8%)[42].

Another meta-analysis study analyzed the maternal colonization dataset, which included 390 articles, 85 countries and a total of 299 924 pregnant women, and found that the global adjusted estimate for maternal GBS colonization was 18% (95% *CI* 17%-19%), with regional differences, with 12.5% (95% *CI* 10%-15%) GBS colonization in Southeast Asia and 11% (95% *CI* 10%-12%) GBS colonization in East Asia[43]. Moreover, a South Indian cohort study found that among 310 mothers, 12.9% (95% *CI* 9.2%-17.6%) were GBS colonized, linked with neonatal systemic illness and premature rupture of membranes[44]. These results are slightly closer to the overall estimate of the colonization proportion reported in the current meta-analysis.

The reported colonization rate is subject to variation due to a multitude of factors including geographic location, genetic variations in host responses, and differences in sampling and processing techniques. Furthermore, methodological choices such as the timing of sample collection during pregnancy, the utilization of enriched selective culture media, and the specific identification method employed (serological, molecular, or presumptive tests) can also significantly influence the observed variability across different studies. Universal screening and localized surveillance are critical, given the absence of consistent country-level data and the risk of neonatal complications linked to GBS colonization[45].

Determination of GBS serotypes is important to understand the epidemiology of GBS[46]. To date, based on capsular polysaccharide (CPS), which is one of the major virulence factors underlying invasive GBS disease, a total of 10 GBS capsular serotypes (Ⅰa, Ⅰb, and Ⅱ-Ⅸ) have been characterized[47]. The distribution of GBS serotypes in Southeast Asia shows distinct regional patterns compared to global trends. In this meta-analysis, serotype Ⅲ dominated, comprising nearly half of all isolates, followed by serotypes Ⅴ, Ⅱ, Ⅵ, and Ⅰa across the included studied countries. This contrasts with global systematic reviews, where serotypes Ⅰa, Ⅰb, Ⅱ, Ⅲ, and Ⅴ collectively account for over 94% of cases, with Ⅰa often reported as the most prevalent in many regions[48-51]. While Southeast Asian data aligns broadly with the global prominence of serotypes Ⅲ, Ⅰa, and Ⅴ, the regional predominance of serotype Ⅲ diverges from patterns seen in parts of Europe, Africa, and the Americas where Ⅰa typically leads[52]. Notably, serotype Ⅸ-occasionally reported in African and European studies-was almost absent from the Southeast Asian dataset, suggesting potential geographical variations in serotype distribution. The analysis also identified a small but significant proportion (0.2%) of non-typeable (NT) GBS strains, a finding with implications for vaccine development as current capsular polysaccharide-based strategies may not cover these unclassified variants. This NT prevalence, though low, mirrors challenges observed in other regions where antigenic diversity complicates vaccine formulation. The Southeast Asian serotype hierarchy (Ⅲ > Ⅴ > Ⅱ > Ⅵ > Ⅰa) differs from the global pattern (Ⅰa > Ⅲ > Ⅴ > Ⅰb > Ⅱ), highlighting the need for region-specific surveillance. These variations may reflect differences in population immunity, environmental factors, or circulating clones across geographical regions. The consistency in core serotype prevalence (Ⅲ, Ⅰa and Ⅴ) across studies supports their inclusion in multivalent vaccine candidates, while the regional disparities underscore the importance of tailoring prevention strategies to local epidemiological patterns.

The findings from this systematic review reveal notable differences in the distribution of GBS STs across Southeast Asia compared to other regional studies. ST1 emerged as the most prevalent strain across multiple countries, consistent with regional trends. In Malaysia, ST1 accounted for 42.0% of overall isolates and 60.9% of invasive isolates, while Thailand reported an even higher ST1 prevalence (64.5%). This aligns with broader Southeast Asian patterns where ST1 dominates due to its association with severe human infections, suggesting regional coexistence of both widespread and niche strains. The disparity in ST1 prevalence among the studies may reflect differences in surveillance focus, sampling biases toward clinical *vs*. environmental isolates, or host population dynamics[13,53,54]. ST283 displayed significant cross-border prevalence, appearing in Malaysia, Laos, Singapore, and Thailand. However, in Malaysia, ST283 representing only 4.3% (2 cases) of invasive isolates[41]. This contrasts sharply with data from Laos and Thailand, where ST283 accounted for 76.3% and 16.1% of invasive human GBS cases, respectively, as reported in prior studies[31,38]. Similarly, in Singapore, ST283 comprised 35.8% to 69.4% of invasive GBS isolates during outbreak periods[24,25,27,30], highlighting its regional significance as a hypervirulent clone linked to raw freshwater fish consumption[5]. The lower prevalence of ST283 in Malaysian study may reflect geographical variations in dietary practices or differences in aquaculture exposure, as ST283 is strongly associated with tilapia farming and raw fish consumption[55].

The study in Thailand, showing ST283 at 16.1%[38], differ from earlier reports of 73% prevalence[5], potentially due to methodological factors such as inclusion criteria (*e.g.*, mixing invasive and non-invasive isolates) or sampling from populations with lower exposure to raw fish. This discrepancy underscores the importance of stratifying analyses by clinical severity and exposure risks. The variability in ST283 detection across reviews may also stem from temporal trends. For instance, Singapore's 2015 raw fish sales ban correlated with reduced ST283 cases[56], implying that public health interventions could alter strain prevalence over time. Furthermore, differences in genomic surveillance scope—some studies focused exclusively on invasive isolates or aquaculture-linked outbreaks[5]—might amplify ST283's perceived dominance compared to broader systematic reviews. These findings emphasize the need for standardized reporting of ST distributions stratified by clinical context, exposure history, and geographical subregions to clarify transmission dynamics in Southeast Asia.

Divergence in other STs between Malaysia and Thailand is notable in this review[35,38,41]. Malaysia exhibited higher proportions of the ST23 strain, accounting for 14.0% overall and 8.7% of invasive cases[35], a strain that is less prominent in Thailand[38]. In contrast, Thailand reported higher levels of ST12 (9.7%) and ST452

(6.5%), strains that were minimally represented in Malaysian data. Additionally, ST17, which is associated with antimicrobial resistance, comprised 13.0% of invasive isolates in Malaysia but only 3.2% in Thailand. Three novel STs that were identified in a Malaysian study (ST1668-1670) highlight a genetic diversity understudied in the region, which may be affected by antimicrobial use in the local area or animal husbandry[41]. In Southeast Asia, the regional dominance of ST1 and ST283 highlights shared zoonotic risks, advocating for standardized One Health surveillance. However, country-specific strain distributions (*e.g.*, Thailand's ST452 *vs.* Malaysia's ST23) suggest tailored control measures may be necessary. The limited data from Laos and Singapore underscores the need for expanded genomic epidemiology efforts to map reservoirs and transmission pathways. These findings align with global trends where ST1 and ST7 dominate in Asia but contrast with European profiles dominated by ST1 and ST123, emphasizing the need for region-specific vaccine development and antimicrobial stewardship programs[57].

The limitations in this review regarding GBS in Southeast Asia are primarily due to the scarcity of data on its prevalence, serotypes, and STs. There is a notable lack of comprehensive epidemiological data on GBS in Southeast Asia, particularly concerning invasive disease and specific serotypes or STs. The distribution of GBS serotypes and STs varies globally, but detailed information from Southeast Asia is limited, making it difficult to understand the regional epidemiology. Moreover, the heterogeneity in study findings is partly due to differences in methodologies and data quality across various studies, which complicates the synthesis of results. Improving surveillance and data collection on GBS infections, especially in Southeast Asia, is crucial for understanding the disease burden and developing effective prevention strategies. Standardizing methodologies across studies could help reduce heterogeneity and provide more consistent insights into GBS epidemiology.

In conclusion, data from this systematic review and meta-analysis provided important epidemiological information on GBS isolated from the 11 657 patients, neonates and pregnant women in five Southeast Asia countries. Overall, the pooled prevalence of maternal GBS colonization was 15.1% in this meta-analysis. Serotypes Ⅲ, Ⅴ, Ⅱ, Ⅵ and Ⅰa were found to be the most common serotypes in Southeast Asia that accounted for 91.24% of the total. The distribution of GBS-ST, predominance of ST1 and ST283, and the need for surveillance and tailored prevention strategies were emphasized. These findings may contribute to the development of GBS vaccine suited for disease prevention and treatment in Southeast Asia.

Conflict of interest statement

The authors report no conflict of interest.

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Availability of data and materials

The datasets that are used and analyzed in this study can be made available upon reasonable request.

Authors' contributions

AM and MNMD conceived and designed the methodology and data analysis, prepared figures and tables, authored and reviewed drafts of the paper, and approved the final draft. NS, NDD and MMJA analyzed the data, authored and reviewed drafts of the paper, and approved the final draft. SAN and MNAA reviewed drafts of the paper, and approved the final draft.

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