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Streptococcus agalactiae (GBS) causes neonatal sepsis, meningitis, and adult invasive disease. We analyzed the entire genomes of 25 GBS clinical isolates from Songklanagarind Hospital, Thailand. All isolates were susceptible to penicillin, ampicillin, ceftriaxone, vancomycin, linezolid, and co-trimoxazole, but some of them were resistant to tetracycline (63.6%) and tigecycline (45.5%). Out of 25 isolates, 5 were multidrug-resistant. Genomic analysis revealed key virulence genes (*cyl* operon, *cfb*, *neuA/B/C*, *hylB*). Findings highlight the genetic and phenotypic diversity of invasive GBS in Southern Thailand and stress the need for ongoing genomic surveillance.

To phenotypically and genotypically characterize the *S. agalactiae* from clinical isolates

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graph TD; A[Sample Collection] --> B[Isolation & Identification]; B --> C[Antimicrobial Susceptibility Testing]; C --> D[DNA Extraction & Whole-Genome Sequencing]; D --> E[Bioinformatics Analysis];
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The flowchart illustrates the study workflow for GBS clinical isolates, consisting of five sequential steps:

- Sample Collection**: GBS clinical isolates will be collected from Songklanagarin Hospital.
- Isolation & Identification**: MALDI-TOF and species-specific PCR amplification confirm.
- Antimicrobial Susceptibility Testing**: MICs of 13 antibiotics were determined by broth microdilution.
- DNA Extraction & Whole-Genome Sequencing**: Genomic DNA was extracted using DNA extraction kits.
- Bioinformatics Analysis**: MLST typing, resistance genes, virulence genes, plasmid, Pan-genome and phylogeny.

Stacked bar chart showing the percentage of S (green), I (yellow), and R (red) for 13 antibiotics. The y-axis represents the percentage from 0% to 100%.

Antibiotic	S (%)	I (%)	R (%)
PEN	100	0	0
AMP	100	0	0
CRO	100	0	0
VAN	100	0	0
LZD	100	0	0
ERY	76	4	20
AZM	76	0	24
CLI	84	0	16
LVX	96	0	4
TET	24	24	52
TGC	60	0	40
SXT	100	0	0
CHL	92	0	8

	SA_1031	SA_1063	SA_1075	SA_1075	SA_1142	SA_1223	SA_1454	SA_1454	SA_1600	SA_2303	SA_2609	SA_2919	SA_3326	SA_3339	SA_3912	SA_4029	SA_4248	SA_4674	SA_6720	SA_7168	SA_7650
SA_1031																					
SA_1063	99.96																				
SA_1075	98.67	98.86																			% ANI
SA_1142	98.90	98.97	98.89																		99.5 = Intra-specific
SA_1223	98.93	98.94	98.77	99.26																	83.95 = Inter-species
SA_1454	98.86	98.96	98.88	99.64	99.43																98.3 = Interspecific
SA_1548	98.77	98.83	98.88	99.23	99.47	99.31															
SA_1800	99.94	99.92	98.96	98.93	98.96	98.83	98.83														
SA_2303	98.77	98.98	98.84	98.83	98.94	99.47	99.39	98.93													
SA_2609	98.81	98.81	99.00	99.21	99.12	99.15	99.09	99.39	98.93												
SA_2919	98.97	99.02	99.01	99.07	99.21	98.92	99.14	99.15	98.94												
SA_3326	98.78	98.88	98.77	98.62	98.83	98.70	98.80	98.77	98.71	98.90	98.77										
SA_3339	98.80	98.92	98.77	98.93	99.41	99.48	99.16	98.88	99.20	98.98	98.95										
SA_3912	98.86	98.95	98.83	99.02	99.39	99.51	99.33	98.83	98.92	99.21	98.91	99.07									
SA_4029	98.77	98.90	98.91	99.22	98.93	99.15	98.92	98.80	98.80	98.87	98.97	99.19									
SA_4248	98.83	98.82	98.80	98.89	98.75	98.84	98.87	98.96	98.83	99.00	98.89	98.77	98.72	98.83	98.88						
SA_4674	98.80	98.85	98.74	98.62	98.81	98.71	98.62	98.78	98.74	98.80	98.69	99.22	98.62	98.70	98.73	98.77					
SA_6720	98.88	98.96	98.90	98.98	99.62	99.20	98.84	98.84	99.41	99.01	98.82	99.96	99.99	99.01	98.88	98.62					
SA_7168	98.87	98.92	98.91	99.23	99.15	99.24	98.88	98.98	99.20	98.97	99.21	99.81	99.89	99.21	99.81	99.89	98.96	98.74			
SA_7650	98.85	98.78	98.94	99.10	99.20	99.23	99.19	99.22		98.96	99.22	99.04	99.23	99.07	99.19	99.19	99.09	99.07			
SA_6848	98.88	98.92	98.95	99.21	99.51	99.38	99.58	98.99	99.35	99.07	98.96	98.86	99.20	99.29	99.84	98.95	98.89	99.23	99.39	99.23	
SA_67	98.90	98.95	98.91	98.98	99.43	99.61	99.35	98.84	99.87	99.31	99.19	98.81	99.95	99.96	99.19	98.90	98.80	99.98	99.62	99.23	99.38
SA_6720	99.92	99.72	99.84	98.92	98.84	99.06	99.83	99.87	98.83	100.00	98.70	98.95	99.98	100.00	98.82	98.82	98.98	99.99	99.96	98.94	99.91
SA_7650	98.99																				

[illegible]

	lin(B)	isa(E)	spw	ant(6-1a)	eml(B)	tei(S)	cstA	tei(M)	tei(O)	sst4	tei(L)	tei(O/W)	em(A)	mef(A)	msr(D)	cstA16
SA_1031	Present															
SA_1063	Present															
SA_1075								Present								
SA_1142									Present							
SA_1223										Present						
SA_1454								Present								
SA_1548											Present					
SA_1800				Present						Present						
SA_2919								Present								
SA_3326									Present							
SA_3339	Present			Present	Present		Present				Present	Present				
SA_3912								Present								
SA_4029								Present								
SA_428									Present							
SA_5175									Present							
SA_5974										Present						
SA_6108				Present							Present					
SA_6208													Present	Present	Present	Present
SA_67								Present								
SA_6720								Present								
SA_7163									Present							
SA_7850													Present			

- **AST:** All isolates susceptible to PEN, AMP, CRO, VAN, LZD, SXT; resistance mainly to TET (52%) & TGC (40%). MDR in ~20%.
- **ARGs:** *tet(M)* most common; one isolate carried multiple ARGs.
- **Virulence:** All carried *cyl* operon + *acpC*, *cfa/cfb*, CPS cluster; *hylB* absent in one isolate.
- **Genomics:** High ANI similarity. MLST: ST1 most frequent; diverse STs incl. novel ST (SA_1548). ST283 absent.

- GBS isolates were fully susceptible to first-line β -lactams, but resistant to tetracycline/tigecycline.
- 20% were multidrug-resistant.
- Virulence genes were widespread; one novel ST identified, ST283 absent.
- Highlights need for continuous AMR and genomic surveillance.

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2. Vornhagen, Jay, Kristina M. Adams Waldorf, and Lakshmi Rajagopal. "Perinatal group B streptococcal infections: virulence factors, immunity, and prevention strategies." *Trends in microbiology* 25.11 (2017): 919-931.