

Table 1. DHPLC and sequencing result of all 206 isolates of *S. Typhi* and *S. ParatyphiA*

S. No.	Phenotype	No of Isolates	CIP MIC range (µg/ml)	CIP MIC average/mean	NAL MIC range (µg/ml)	NAL MIC average/mean	<i>gyrA</i>	<i>gyrB</i>	<i>parC</i>
<i>S.Typhi</i> (N=162)									
1.	NAL ^S CIP ^S	16	0.006-0.023	0.0126	1.5-3	2.3333	—	—	—
2.	NAL ^R CIP ^{DS}	57	0.064-1	0.301333	96-256	250.947	Ser83 Phe (N=25) Ser 83 Tyr (N=26) Asp 87 Asn (N=5) Asp 87 Gly (N=1)	—	Ser 80 Iso (N=3)
3.	NAL ^R CIP ^R	53	2->32	20.320	256	256	Ser 83 Phe Asp 87 Asn	—	Ser 80 Iso
4.	NAL ^S -CIP ^{DS}	36	0.064-0.5	0.1537	3-16	7.194	Ser 83 Tyr (N=2)	Ser464 Phe (N=31) Ser 464 Tyr (N=2) Ser 464 Thr (N=1)	—
<i>S.ParatyphiA</i> (N=44)									
1..	NAL ^S CIP ^S	3	0.064-0.094	0.064	3	3	—	—	—
2..	NAL ^R CIP ^{DS}	40	0.125-1.5	0.533	256	256	Ser 83 Phe(N=28) Ser 83 Tyr (N=12)	—	—
3.	NAL ^R CIP ^R	1	>32	32	256	256	Ser 83 Phe Asp 87 Asn	—	Ser 80 Iso

Note:- NAL, nalidixic acid; CIP, ciprofloxacin; NAL^S = nalidixic acid susceptible (MIC≤16 µg/ml) ; NAL^R = nalidixic acid resistance (MIC≥32 µg/ml); CIP^S = ciprofloxacin susceptible (MIC ≤0.064 µg/ml) ; CIP^{DS} = decreased ciprofloxacin susceptible (MIC > 0.064 µg/ml), CIP^R = ciprofloxacin resistance (MIC≥1 µg/ml); Ser:- Serine, Thr:- Threonine, Tyr:- Tyrosine, Phe:- Phenylalanine. (—)= No mutation detected

Table 2. DHPLC peak profiles with retention time and mutation in *gyrB* gene for *S.Typhi* isolates.

S.No.	DHPLC Peak profile	Retention time (Minutes)	Mutation in <i>gyrB</i>
1.	A	4.77	No mutation (Wild type)
2.	B	4.52	Ser 464 Thr
3.	C	4.33	Ser 464 Phe
4.	D	4.2 and 4.6	Ser 464 Tyr

Note:- Ser:- Serine, Thr:- Threonine, Tyr:- Tyrosine, Phe:- Phenylalanine