Shigellosis and Development of Multiple Antimicrobial Resistance Mechanisms of Shigella spp.

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Shigellosis is a serious public health issue. Millions of people suffer from this deadly food and water borne disease each year. The main manifestations of affected persons are bloody diarrhea with excessive dehydration. The causative agent of this disease is the bacteria Shigella spp. which has four serogroups. Though Shigella flexneri and Shigella dysenteriae are the dominant serogroups in developing countries, reports of other serogroups, namely Shigella boydii and Shigella sonnei, in the food contaminations are available. There are seasonal variations of Shigella infection throughout the world. In Asian subcontinent, monsoon and post monsoon times are the ideal for infection. The transmission of the bacteria in human is usually caused by feco-oral route or by contaminated food and water. There are several groups of antibiotics like foscomycin, macrolide, amiglycoside, tetracycline etc. which were used before. But they are now become useless as Shigella spp. is getting resistant against those drugs. The quinolone groups of antibiotics like ciprofloxacin, ofloxacin, norfloxacin, ceftriaxone etc. are the important drugs for the cure of the disease shigellosis but prevalence of drug resistant strains of Shigella spp. against those drugs are a great concern nowadays. The occurrence of plasmid mediated quinolone resistance genes (PMQR), efflux pump proteins and effective mutations at drug binding region of gyrA etc. are the major mechanisms for the development of drug resistance.

Keywords: Drug resistance; Efflux proteins; Pathogenicity; Serogroup; Virulence factors.
Shigella serogroups differs geographically. In underdeveloped countries *Shigella dysenteriae* and *Shigella flexneri* are common and generally spread by environmental surface water sources. On the other hand, *Shigella sonnei* and *Shigella boydii* are reported mostly in industrialized countries and usually spread through food sources. Antimicrobial and oral rehydration therapy are recommended to treat this disease. World Health Organization (WHO) recommended different antibiotic such as ceftriaxone, azithromycin, ciprofloxacin, pivmecillinam, for the treatment of shigellosis but the indiscriminate use of antibiotics results in the emergence of multidrug (MDR) resistant *Shigella spp.* which makes shigellosis a global threat. Particularly resistance to quinolones and cephalosporin makes the situation more challenging. Various antimicrobial resistance mechanism in *Shigella spp.* have been described by the researcher such as extrusion of drug by activating efflux pump, decrease in cellular permeability, overexpression of drug-modifying and inactivating enzymes or target modification by mutation. Thus the recurrent changes in antimicrobial resistance pattern among the *Shigella spp.* poses the complication in recommending standard drug for effective treatment of shigellosis. The current study was done to review the emergence of antimicrobial resistance among the *Shigella spp.*

**Shigellosis as an infectious acute dysentery**

Infectious diseases are a major burden and the common cause of death worldwide. More than millions of people die each year in developing countries due to this disease among them most of are the children. Dehydration by excessive fluid and electrolyte loss in stool results in acute dysentery which is the main reason of death. In developing countries diarrheal disease is not only a major health issue but also a risk factor to the travelers who travel to these countries. Treatment and preventive measures including fluid replacement and improvement of hygiene decrease the mortality rate from about 5 million to approximately 1.5 million deaths throughout the past two decades. However, increased frequency of multi-drug resistant bacteria posed the problem more challenging. *Vibrio cholerae*, multiple serovars of *Salmonella enterica*, different serotypes of *Shigella*, *Campylobacter spp.* and enteropathogenic *Escherichia coli* strains including *Escherichia coli* (ETEC) with the enteric viruses including rotor virus are the most important organisms that are frequently associated with diarrhea. Acute watery diarrhea, dysentery and persistent diarrhea are the different types produced by those pathogens. Among the enteric pathogens, *Shigella spp.* is the most pathogenic organism that causes bacillary dysentery or shigellosis. Infection occurs by feco-oral route with the contaminated food and water. Shigellosis is manifested by fever, abdominal cramps including the passage of loose stools mixed with blood and mucous. The annual number of shigellosis was estimated to be about 170 million episodes at the end of the last century with about 1 million deaths in developing countries. Global projections suggest that there are 165 million episodes of shigellosis per year, of which 99 percent occurs in less than 5 years of age. Although the number has reduced, shigellosis still remains one of the most important endemic diseases in the world.

**Overview of Shigella spp.**

Kyoshi Shiga in 1896 first isolated the *Shigella dysenteriae* at the Kitasato institute, Japan. He isolated a Gram negative bacillus from stool sample which showed positive agglutination reaction against sera of patient recovering from acute dysentery. Primarily he proposed the name of this organism as *Bacillus dysentericus* in 1897, later he changed it to *Bacillus dysenteriae* in 1898. During his research he described the production of toxic factor by the organism that now known as Shiga toxin. Few years later German microbiologist Kurse (1900) isolated two similar organisms from patients’ stool samples but they were serologically different from *Bacillary dysenteriae*. Over the two decades additional three groups of related organisms were identified and taxonomically placed in the Shigella and named as *Shigella dysenteriae*, *Shigella flexneri*, *Shigella boydii* and *Shigella sonnei* to honor the Shiga, Flexner, Boyd and Sonne. The genus *Shigella* was first termed in the 1930 edition of *Bargey’s Manual of Determinative Bacteriology*. *Shigella* belongs to *Enterobacteriaceae* which are small, nocapsulated, non-motile, non sporulating facultative anaerobic Gram negative bacilli. Genus *Shigella* has four major groups with several serotypes. They are - *Shigella dysenteriae* (13
serotype), *Shigella flexneri* (15 serotypes), *Shigella boydii* (18 serotypes), *Shigella sonnei* (One serotype)\(^{16}\).

*Shigella* can also be grouped into different serogroups including A, B, C and D depending on the basis of common specific polysaccharide antigens present on the cell surface. Whole genome sequence of *E. coli* and all four *Shigella spp*. revealed that they share a common DNA backbone of approximately 3.9 Mb, interrupted by *E. coli* specific and *Shigella* specific sequences. *S. dysenteriae* and *S. flexneri* are the most common serotypes found in developing countries. *S. dysenteriae* type 1 usually cause epidemic and pandemic bacillary dysentery with severe form of disease and produce potential lethal complications due to the production of Shiga toxin. In Latin America, Asia and Europe *S. dysenteriae* type 1 causes epidemic dysentery in 1960. Asian countries such as Bangladesh (1972-78, 2003), Sri Lanka (1976), Maldives (1982), Nepal (1984-85) and Bhutan (1984-85) reports the dysentery epidemic. In India epidemics due to *Shigella* infections were reported from different parts of the country including eastern India (1984), Andaman and Nicobar Island (1986), Chandigarh (2003), Vellore (1972-73, 1997-2001), West Bengal (2002-03) in different times\(^{7}\). Frequent and occasional *Shigella* infections were reported during summer and winter from Israel\(^{17}\). Emergence of multidrug-resistance is the major problem in developing countries. In India especially in Kolkata *S. dysenteriae* type 1 became resistant to common antibiotics which results in high restriction in treatment\(^{18}\). Occasionally *S. dysenteriae* type 2 infections were reported and sometimes exceeded type 1 in the frequency of isolation. Other serotypes were encountered rarely among the diarrheal patient’s sample.

In developing countries mostly *S. flexneri* causes endemic. The serotypes 1b, 2a, 3a, 4a, and 6 were encountered in industrialized countries\(^{19}\). Several uncommon serotypes and sub-serotypes of *S. flexneri* were also isolated from different countries like Bangladesh, Egypt and Russia\(^{20,21}\). Outbreak of *S. flexneri* 2a in India as well as in Taiwan and United State were also reported\(^{22,23}\).

Outbreak due to *S. sonnei* is very rare in developing countries. There is no report of *S. sonnei* outbreak from India. Although it cause sequential outbreak but the mixture of genes with different origin found on *S. sonnei* plasmid due to the insertion of elements and number of other open reading frame. *Shigella enterotoxin 2* prevalent in *S. sonnei* and a virulence gene sat has also been reported in this serotype\(^{24}\).

*S. boydii* is mainly reported from Indian subcontinent and which is least prevalent in developing countries\(^{25}\). *S. boydii* is mainly spread throughout the World by travelers. It is the second dominant serogroups in India followed by *S. flexneri*. New serovar of *S. boydii* has been reported from Bangladesh in 2005\(^{26}\).

Across the world the incidence of *Shigella* spp. depend upon the seasonal pattern. During summer or early autumn *Shigella* infection were most common in US and Europe. Kagalwalla et.al in 1992 reported the most of the *Shigella* serotypes were isolated during April-May in Saudi Arabia. Increase incidence of *Shigella* was reported form Bangladesh during post-monsoon season of August-November and pre-monsoon from the month of April - May of each year. In India specially in Kolkata *Shigella* infection was prevalent throughout the year with high isolation rate during the summer and early monsoon months\(^{8,27,28}\). *Shigella* spp. were detected more in June to July, i.e. during rainy season in Laos and Guatemala. In Hungary July to September was the peak period for the isolation of *S. flexneri* and *S. sonnei*\(^{29}\).

### Transmission and epidemiology

*Shigellosis* is endemic throughout the world, although one century is past after K. Shiga’s remarkable discovery but still it remains a global health problem. World Health Organization (WHO) estimated that 164.7 million cases of shigellosis occurred per year of which 1.1 million cases result in death in developing countries due to the poor hygiene, limited access of clean water and malnutrition. *Shigella* required only 10 -100 organisms to cause infection\(^{30}\). It is transmitted by feco-oral route or by the contaminated food and water\(^{30,31}\). Transmission by house flies has also been documented\(^{32}\). Outbreaks due do the *Shigella* spp. have been reported from different parts of the world as well as from India. In 2007 an outbreak due to the *S. flexneri* in West Bengal has been reported which affect more than 461 people\(^{33}\). Another foodborne outbreak of *S. sonnei* infection was reported from
Pakapole village, South 24 Parganas, India which affect more than 25 people in 20184. In Iran an outbreak due to the S. flexneri 2a affect more than 700 prisoners in 200735,36,37. Similarly in US an outbreak of shigellosis in 2006 was associated with the tomatoes23. MDR Shigella spp. outbreak has been reported from the Children Welfare Institute, China in 20154.

**Antibiotic resistance profile of Shigella spp.**

There are number of antibiotics recommended by WHO for the treatment of shigellosis which reduce the number of deaths per year but the extensive use of them led to an increase in isolation of multidrug-resistant Shigella spp. in several countries 7,11,19,38,39,40. Still shigellosis remains one of the most important endemic diseases in the world. In recent day’s treatment with ciprofloxacin [a ßuoroquinolone (FQ)] or one of the three second-line antibiotics, pivmecillinam, azithromycin and ceftriaxone (a third-generation cephalosporin), have been recommended. However reports are available of FQ-resistant Shigella isolates from India and other Asian countries which become a serious concern to treat shigellosis41,42,43. Antibiotic resistance genes may be located in plasmid, chromosome and mobile genetic elements like integrons and transposons of the bacteria (Table 1).Mutation in the drug target or genes associated with efflux system also cause the drug resistance (Table 2).

Centre for Disease Control and prevention (CDC) (https://wwwn.cdc.gov/narmsnow/) reports that year wise antibiotic resistant pattern among the isolated Shigella spp. is a serious threat (Fig.3). There are various mechanisms which result in resistance to antibiotics to the Shigella spp. including extrusion of drugs by activating efflux pump, decrease in cellular permeability, modifications of target sites by mutations and over expression of enzymes which modify or inactivate the drugs44,45. The possible mechanisms are listed below-

**Function of outer membrane permeability**

Cell wall of microorganisms is served as first barrier for penetration of antimicrobial drug into the cell. Some modification or changes in the membrane result in porin loss which increase the minimum inhibitory concentration (MIC) to the antibiotics46. Most of the antibiotics which are used to treat Shigella infections should be able to penetrate through cell membrane to reach intercellular accumulation and target site. Quinolone group of antibiotics such as nalidixic acid, ofloxacin, ciprofloxacin interfere with DNA gyrase and topoisomerase IV to inhibit DNA replication. Aminoglycoside antibiotics including streptomycin and spectinomycin bind with ribosomal subunits and inhibit protein synthesis.ß-lactam antibiotics such as cephalosporin and penicillin target the penicillin binding protein and inhibit the cell wall biosynthesis. Mutations or absence of a ~39 kDa porin in the membrane of Gram negative bacteria as for example Shigella spp. slow down the penetration of ß-lactam (Aztreonam and Dianionic moxalactam) and hydrophilic antibiotics such as penicillin and piperacillin44,46. Three mutant strain of S. dysenteriae isolated in India showed resistance to imipenem and the study reported that the resistance towards the imipenem is associated with the permeability of outer membrane proteins. It is also reported that the resistance to colicin E2 among the S. flexneri strains associate with LPSs of the outer membrane47.

**Role of efflux system**

Activation of efflux pump plays an important role in antibiotic resistance phenotype of Shigella spp. to expel the toxic compounds from the cells. Efflux system can be grouped into five families such as- the major facilitator super family, small multidrug resistance family, resistance-nodulation-division family, multidrug extrusion family and ATP binding cassette family48. In Shigella spp. a triplet complex namely AcrAB-Tol C, belonging to resistance-nodulation-division family, multidrug extrusion family and ATP binding cassette family49. In Shigella spp. a triplet complex namely AcrAB-Tol C, belonging to resistance-nodulation-division family, multidrug extrusion family and ATP binding cassette family48. In Shigella spp. a triplet complex namely AcrAB-Tol C, belonging to resistance-nodulation-division family, multidrug extrusion family and ATP binding cassette family48. In Shigella spp. a triplet complex namely AcrAB-Tol C, belonging to resistance-nodulation-division family, multidrug extrusion family and ATP binding cassette family48.
| Antimicrobial Resistance Class | Antimicrobial Resistance Mechanism | Genes Mediating Antimicrobial Resistance | Origin | Geographic Origin | References |
|--------------------------------|-----------------------------------|----------------------------------------|--------|-------------------|-----------|
| **β-Lactams**                 | Class A β-lactamases               | blaSHV 2,11,12, blaPER-2, blaTEM-1,1b,15,17, blaTEM-19,20,52, blaCTX-M-1-123 | P,C    | India, Argentina, Argentina, Lebanon, China, South Korea, China, Turkey | 80-82, 80, 83-85, 82,86-89 |
| **Class B β-lactamases**      | blaIMP-like                        |                                        | P      | India, France     | 52        |
| **Class C β-lactamases**      | blaCMY-2,59, blaDHA-1              |                                        | C, P   | China, Mexico, India, China, India, Israel | 53, 86 |
| **Class D β-lactamases**      | blaosa-1,2,5,30                    |                                        | I, P   | Mozambique, Chile, China, India, US, Egypt, Djibouti, Spain, Greece, Denmark, Peru, Iran | 87,91 |
| Quinolones                    | Plasmid-borne resistance           | qnrA, qnrB,4,19, qnrC, qnrS,I, aac-(60)-Ib-cr | P      | Iran, India, Switzerland, India, Pakistan, India | 54, 60,92, 93, 69, 92 |
| Fosfomycin                    | Efflux pump                        | qepA                                   | P      | China             | 60        |
|                               | Fosfomycin resistance enzymes      | fosA3                                  | P      | China             | 64        |
| Aminoglycosides:              |                                   | strA,B                                 | MGE    | India, Australia, Chile, Pakistan, South Korea | 67 |
| streptomycin                  | Adenyltransferase                 | aadA1,2,5                              | I, P   | Senegal, Bhutan, India, Taiwan | 65,90,94 |
| Tetracycline                  | Efflux pumps                       | tetA,B,G                               | C, P   | Mozambique, Taiwan, Iran, Spain, South Korea | 9,94,95 |
| Trimethoprim                  | Dihydrofolate                      | dfrA1,5,7,8,12,13                      | I, P   | Spain, Taiwan, Senegal | 9,90,91,94,7 |
reductases dfrA14,15,16,17 Mozambique, India, China, Iran, South Korea, Peru, France, Chile, Australia, China, India, Taiwan, Mozambique, India, Pakistan, Taiwan, China, Vietnam, Palestine, Switzerland, Vietnam

Phenicols Chloramphenicol catA-like P Taiwan, Mozambique, India 90

Acetyltransferase genes catP P Pakistan 69

Efflux pumps cmlA1 I, P Taiwan 94

Colistin Plasmid-borne resistance mcr-1 P China, Vietnam 73

Macrolide Enzymatic inactivation mphA P Palestine, Switzerland 60

rRNA methylase ermB P Vietnam

Abbreviation: P, plasmid; C, chromosome; I, integrin; —, unknown; MGE, mobile genetic element.

responsible for selective hydrolysis of ceftriaxone, cefotaxime and ceftazidime51. Till now several reports from different parts of the world like Canada, Turkey, Israel, Argentina, China and India showed that Shigella spp. harbor different ESBL encoding genes (Table 1).

**Class B β-Lactamase**

Class B β-lactamase can hydrolyze carbapenem and other α-lactam. A study reported that, a metallo-α-lactamase (MET 1) encoded by a plasmid mediated gene IMP-3 in S. flexneri conferred resistance against sulfonamide and kanamycin. S. sonnei and S. flexneri isolated from Andaman and Nicobar Island in India showed the presence of bla<sub>VIM</sub> and bla<sub>IMP</sub>, which conferred the resistance to carbapenem52.

**Class C β-Lactamase**

Ceftriaxone and cephalosporin has been recommended to treat the MDR Shigella spp. However Shigella spp. resistant to those antibiotics has also been reported. Class C β-Lactamase, known as AmpC-type enzymes are encoded by both chromosomal and plasmid genes. CMY-2, a plasmid encoded AmpC β-lactamase firstly identified in S. sonnei isolates which was obtained from a dysentery outbreak in Taiwan and there after CMY-2 have been reported in several countries like China, Iran, Costa Rica and India53-55. Different AmpC genes are listed in table1.

**Class D β-Lactamase**

Resistance to cloxacillin, ampicillin, cephalothin, oxacillin mainly mediated by class D β-lactamase or OXA-type β-lactamase56. OXA-type β-lactamase encoding gene bla<sub>OXA</sub> have been identified in integrons and plasmids in different Gram negative bacteria including Shigella spp. especially in S. flexneri57. bla<sub>OXA-1</sub> and bla<sub>OXA-30</sub> are differed from each other by having a single mutation at codon 131, containing Tn2603 and Tn1409 transposons respectively.

**Quinolones and fluroquinolones resistance**

**Resistance to fluroquinolones due to chromosomal target site mutations**

Quinolones are used to treat shigellosis for a very long time across the world58. This group of antibiotics mainly consists of ciprofloxacin, norfloxacin, ofloxacin, levofloxacin, nalidixic acid etc. There are various genes present into the chromosomes as well as plasmids of the bacteria Shigella which confer resistance against these
Table 2. Frequency of amino-acid and nucleotide changes in the quinolone resistance determining regions of Shigella isolates in different parts of the world

| Target Site | Codon | Amino-Acid Changes | Nucleotide Mutation | Shigella spp. | Country of Detection | References |
|-------------|-------|---------------------|---------------------|---------------|----------------------|------------|
| **gyrA**    | 57    | Asn’!Lys            | AAT’!AAA            | *S. flexneri* | China                | 99         |
|             | 69    | Gln’!Trp            | —                   | *S. sonnei*   | India                | 93         |
|             | 80    | His’! Gly           | CAT’!GGT            | *S. dysenteriae* | Belgium | 99         |
|             | 83    | Ser’!Leu            | TCG ’!TTG           | *S. boydii*   | China, Bangladesh, India | 92         |
|             | 180   | Asp’!Met            | —                   | —             | —                    | 27         |
|             | 83    | Ser’!Leu            | —                   | —             | —                    | —          |
|             | 181   | Glu’!Lys            | —                   | —             | —                    | —          |
|             | 87    | Asp’!Asn            | —                   | —             | —                    | —          |
|             | 192   | Phe’!His            | —                   | —             | —                    | —          |
|             | 25    | Ile’!Met            | —                   | —             | —                    | —          |
|             | 39    | Glu’!Lys            | —                   | —             | —                    | —          |
| **gyrB**    | 517   | Gln’!Arg            | CAG’!CGA            | *S. flexneri* | China                | 61         |
| **parC**    | 64    | Ala’!Asp            | GCC’!GAC            | *S. flexneri* | India, China         | 93         |
|             | 64    | Ala’!Cys            | GCC’!TGC            | *S. sonnei*   | China                | 93         |
|             | 80    | Ser’!Ile            | AGC’!ATC            | *S. dysenteriae* | China, Bangladesh, India | 92         |
|             | 85    | Ala’!Ser            | GCG’!TCG            | *S. boydii*   | Switzerland          | 60         |
drugs. They can be mainly classified into plasmid mediated quinolone resistance genes (PMQR) and quinolone resistance determining regions (QRDR). Efflux pump attributor proteins also confer resistance to quinolones of the bacteria. gyrA, gyrB, parC and parE are the corresponding subunits of DNA gyrase and topoisomerase IV, which are encoded by gyrA, gyrB, parC and parE gene respectively (Table 1). Quinolones bind with QRDR region of DNA gyrase and mutation in that region causes reduced susceptibility to the quinolones. The most mutations have been found in between Ala 67 and Gln 07 in several studies\(^5^9\). A very recent study reported the mutations at the position 83 (Ser-83-Leu) and 87 (Asp-87-Asn) of gyrA in the Shigella spp. isolated from environmental water samples of in and around Kolkata have higher MIC to quinolones\(^2^7\). Some researchers reported that a single mutation in gyrA cannot decrease the susceptibility to quinolone and for that further mutation in parC and gyrA region are needed\(^6^0,^6^1\). Amino acid and nucleic acid changes in QRDR region of gyrA, gyrB, parC and parE in Shigella spp. are shown in table 2.

At parE two novel mutations at codons 408 and 458 have recently been identified among the Shigella spp. isolated in India (2011) and in China (2016)\(^2^8,^6^2\). Mutation in codon 408 is associated with resistance to nalidixic acid but not to ciprofloxacin whereas mutation at codon 458 conferred resistance to both nalidixic acid and ciprofloxacin.

**Plasmid mediated resistance**

Presence of plasmid mediated gene namely qnr (qnrA, qnrB, qnrC, qnrD, qnrS, qep, aac[6’]-lb-cr) at the plasmid-mediated quinolone resistance region (PMQR) is also one of the main reason to gain resistance to the quinolones among the Shigella spp. A study from China reported that aac(6’)-lb-cr and qepA positive showed a high level of resistance to quinolones\(^4^9\). Gene aac(6’)-lb-cr encodes an acetyltransferase which reduce the activity of quinolones. Although the mutation in the QRDRs of DNA gyrase and topoisomerase IV genes

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![Image](image-url)

**Fig. 1.** Mechanism of Shigella pathogenesis: *S. flexneri* encounters host macrophages after crossing the epithelial barrier (EC) and entry into M cells. The bacteria avoid degradation into the macrophages and enter into EC from basolateral side and move into cytoplasm. The PMN are attracted concomitantly by proinflammatory signals and EC with the activation of NK cells. As a result, the PMN disintegrates the EC lining with immense intensification of infection and tissue destruction which facilitate the invasion of more bacteria. Finally Shigella is killed through PMN mediated phagocytosis.
is the main cause of resistance to fluoroquinolones but PMQRs may expedite in selection of isolates showing higher levels of resistance through extra chromosomally encoded mechanisms and admit reduced susceptibility to fluoroquinolones.

**Fosfomycin resistance**

Fosfomycin inhibit cell-wall biosynthesis by inactivating the MurA enzymes. Although fosfomycin have been used to treat microbial infections for four decades but fosfomycin resistance have also been found in several enteropathogens including *Shigella spp*. Resistance to fosfomycin occurred primarily by two mechanisms: mutations in the *uhpA/T* and *glpT* genes which encode proteins responsible for two carrier dependent system associated with the uptake of fosfomycin; fosfomycin modifying enzymes containing two kinase (FomA, FomB) and three metallo enzymes (FosX, FosA and FosB). For the first time fosfomycin modifying enzymes was reported from China among the isolated strain of *S. flexneri* from patient’ samples.

![Molecular architecture of the S. flexneri Mxi-Spa T3SS](image)

**Fig. 2.** Molecular architecture of the *S. flexneri* Mxi-Spa T3SS: The T3SS comprises of four main parts. The basal body that extests the bacterial inner membrane (IM), the periplasm and the outer membrane (OM). There is cytoplasmic ring consists of proteins in the T3SS which help in the transport process and facilitate the recognition of substrates, substrate unfolding and chaperone release. The LPS which is the major bacterial surface antigen and the peptidoglycan (PGN) molecules are located respectively on the surface and in between the inner and outer membrane.
Aminoglycoside resistance

Aminoglycosides are being used to treat various bacterial infections for a long time. They are associated with different kinds of mechanisms such as enzymatic inactivation, ribosomal modifications, and active efflux pump. Out of these mechanisms, aminoglycoside modifying enzymes are the most common in clinical settings. Aminoglycoside adenyltransferase (aadA gene cassettes) is very significant in Shigella spp. which confers resistance to streptomycin and spectinomycin. Different types of aadA gene cassette have been identified in enterobacteriaeae but aadA1 and aadA2 has high prevalence among the isolated Shigella spp.. Genes strA and strB which encode aminoglycoside phosphotransferase are also well dispersed among the plasmid (IncFII and pNV-Y394) of the isolated Shigella spp.. A study from India reported that 100% and 88% of S. dysenteriae and S. flexneri harbored strA genes which confer resistance to streptomycin.

Tetracycline resistance

Roberts et al. reports five tetracycline-efflux genes-tet(A), tet(B), tet(C), tet(D) and tet(G) with one ribosomal protection protein encoded by tet(M) that have been identified among the Shigella spp. Various tet genes flanked by transposases were identified in a ~20.4 kb of genomic island encoding MDR genes. Identical MDR cassette was firstly identified in S. flexneri 2a YSH6000 strain which is referred to as Shigella resistance locus-pathogenicity island. Moreover presence of the MDR genes also reported in the E. coli plasmid pRs225 with similar arrangement which suggests that tet genes might be dispersed among the other species by horizontal gene transfer. S. dysenteriae isolated from dysentery outbreaks in different parts of India showed that tet(B) was more common (90%) than tet(A) among the isolates.

Phenicol resistance

Phenicols have been used for past few years to treat Shigella infection but the treatment is more challenging now a days due to resistance to these antibiotics. Resistance to chloramphenicol in Shigella spp. is associated with the cat genes [catA (catA1, catA2, catA3) and catB (catB2, catB3, catB7, catB8)] encoding chloramphenicol acetyltransferase, activation of efflux pump by cmlA (cmlA1, cmlA4, cmlA9) genes and/or by fluorinated and unfluorinated phenicols (flor) by major facilitator-superfamily proteins. About 96 Shigella were isolated from diarrheal patients sample in Pakistan and out of them 69 (72.9%) were resistant to chloramphenicol.

Colistin resistance

Colistin (polymixin E) interacts with the outer membranes of Gram negative bacteria. The gene responsible for colistin is a plasmid-mediated polymyxin resistance gene namely in mcr-1 have been identified in the Shigella spp.. Gene mcr-1...
isolated from Chaina, Vietnam and Australia. 1 integron have been recognized in S. sonnei conjugation. Gene cassette array carried by class 1 integrons may transfer to other species via plasmid. This integron associated antibiotic occurring in a cassette in both class 1 and class 2 integrons. Class 2 integrons borne on to trimethoprim and aadA, streptominycin (dfrA1) and trimethoprim resistant. Gene cassettes and 12 of them have been identified among the bacteria which confers resistance to trimethoprim have been detected among different groups of Shigella spp. Almost 42 types of dfr genes have been detected among different groups of bacteria which confers resistance to trimethoprim. The resistance mediated by efflux pumps including OmpA, OmpW, mefA and msrA. Reduced susceptibility to azithromycin among the isolated Shigella spp. have been continuously reported from different parts of the world such as Asia, North-America, Australia and US.

Sulfonamide and trimethoprim resistance

Spreading of trimethoprim-sulfonamide resistance among the Shigella spp. across the different parts of the world make this drug ineffective to treat shigellosis. This is mainly due to mutational or recombinational changes in target enzymes (dihydropteroate synthase and dihydrofolate reductase respectively). The genes responsible for encoding dihydropteroate synthase and dihydrofolate reductase are sul and dfr respectively. Almost 42 types of dfr genes have been detected among different groups of bacteria which confers resistance to trimethoprim and 12 of them have been identified among the trimethoprim resistant Shigella spp. Gene cassettes within class 1 integrons among the Shigella plasmid or chromosome often encodes resistance to trimethoprim (dfr-A), streptomycin (aadA) and ampicillin (oxa-1). Class 2 integrons borne on Tn7 have often been found in Shigella spp., and gene cassette arrays of them usually contain dfrA1, sat1 and aadA1. Resistance to trimethoprim is mainly associated with the presence of dfrA1 genes occurring in a cassette in both class 1 and class 2 integrons. This integron associated antibiotic resistance may transfer to other species via plasmid conjugation. Gene cassette array carried by class 1 integron have been recognized in S. sonnei isolated from Chaina, Vietnam and Australia. The genes responsible for sulfonamide resistance are sul1, sul2 and sul3, very common in Shigella spp. Different studies from the different parts of the world showed that number of Shigella spp. especially S. sonnei isolated from 2000 onwards have 100% resistance to the sulfonamides.

Macrolide resistance

Currently WHO recommends azithromycin as a second line treatment for shigellosis but now a days this antibiotics are becoming resistant day by day. CDC reports that approximately 3% of the all tested Shigella spp. is getting resistant to azithromycin. Possibly there are four mechanisms which mediate the resistance to these drugs including enzymatic inactivation by phosphotransferase encoded by mph gene or esterase encoded by ere determinant; target site modification by rRNA methylase encoded by erm genes; punctual mutation in rplV encoding L22 ribosomal protein, rplD encoding L4 ribosomal protein and rrlH (23 rRNA); drug resistance mediated by efflux pumps including OmpA, OmpW, mefA and msrA. Reduced susceptibility to azithromycin among the isolated Shigella spp. have been continuously reported from different parts of the world such as Asia, North-America, Australia and US.

Thus frequent shifts in antimicrobial resistance profiles of Shigella isolates caused difficulty in recommending standard drugs for effective treatment of the disease.

CONCLUSION

Shigellosis is one of the most important health concerns in countries that yet to overcome many socioeconomic challenges. There are several virulence factors and enterotoxins which confer the pathogenicity of the bacteria Shigella, the causative agent of this disease. There were several antibiotics like ampicillin, tetracycline, foscomycin, trimethoprim, sulfonamide, macrolide group which now became ineffective. Only some fluoroquinolone group of antibiotics is active to combat the disease. But indiscriminate use of antibiotics and other risk factors help to develop a number of antibiotic resistant strains of Shigella spp. into the environment. This difficult situation demands the discovery of new and better drugs. So, it is very much essential to search for the actual mechanisms of developing drug resistance into the bacterial cells. In this review, we summarized the recent advancement of knowledge regarding different drugs used to combat the disease, latest pattern of drug resistance, development of antibiotic resistance mechanisms of Shigella spp. for better understanding of the host microbe interaction and to build up new strategy to combat this disease.
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N/A

Conflicts of interest

All authors declare that they have no conflict of interest.

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