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MULTIPLE ANTIBIOTIC RESISTANCE INDICES OF STREPTOCOCCUS SUIS ISOLATED FROM PIGS AND ITS ENVIRONS

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Abstract

Streptococcus suis; a dominant specie found in pigs and environs, has been receiving drastic attention not only in causing human infections, but also for its involvement in antibiotic resistance, of which 80% of this resistant genes are encoded in the plasmid. This study was undertaken to evaluate the multiple antibiotic resistance indices of *Streptococcus suis* isolated from pigs and its environs A total of 430 samples were drawn from different sources (nasal swab, pork, pig droppings, pig feeds, bioaerosol), and screened for the presence of *Streptococcus suis* using standard microbiological techniques. The isolates obtained were characterized using their morphological, biochemical and molecular characteristics. The resistant strains were detected by subjecting the isolates to antibiotic susceptibility test using disk diffusion method.The study revealed the presence of *Streptococcus suis* strain SIO (SSS10), *Streptococcus suis* strain 347(SS347), *Streptococcus suis* strain 9401240 (SS9401240) and *Streptococcus suis* strain INT-10(SSINT-10), of which the isolates were significantly ($\alpha<0.05$) seen most in nasal swab samples. Of 24.14%, 100.00%, 41. 67% and 39.23% of SSS10, SS347, SS9401240 and SSINT-10 respectively that were resistant to antibiotics, 64.29%, 100.00% and 63.64% were multiple antibiotic resistant (MAR) strains, and 61.76% of the resistant strains had MAR index greater than 0.2. The study has shown SS10, SS347, SS9401240 and SSINT-10 were encountered from the pigs and its environs, and they exhibited significant degree of multiple antibiotic resistance, of which SS347 showed the highest percentage of MAR.

Keywords

Keywords: *Streptococcus suis,*plasmid, multiple antibiotic resistance indices, antibiotic, susceptibility

INTRODUCTION

Streptococcus suis is a facultative anaerobic bacterium that belongs to Streptococcaceae family, that resembles peanut in shape. The organism is widely distributed in the environment, especially sites where pigs are reared or butchered. *S. suis* proliferates extensively in pigs, which enables it to cause debilitating diseases in the animals (Votsch *et al.*,2018). The type of diseases it causes can be described as zoonosis, which indicates that humans who rear pigs, consume pork, slaughter pigs, and veterinarians, are mostly vulnerable (Votsch *et al.*,2018). The organism gains access to pigs via oropharyngeal mucosa, and is then conveyed to the tonsils, nasal mucosa, and the lymph nodes. It worthy to note that *S. suis* is a normal flora of upper respiratory tract, genital tract, and alimentary tract in healthy pigs, though destruction of the epithelial tissue enables the organism to gain access to the bloodstream, where systemic infection occurs (Votsch *et al.*,2018).

S. suis is the major cause of bacterial infections in swine industries, which had led to huge loss. Infected pigs develop respiratory tract infection and bacteremia, while infected humans suffer systemic infections, where several organs are damaged, producing inflammation, though its clinical manifestation appears in form of meningitis and skin infections. Diseases caused by *S. suis* are endemic in countries where pig rearing is common such as southeast Asia, and some countries in Africa (Votsch *et al.*,2018).The organism has cell wall antigens that resemble those found in enterococci, such as *Enterococcus faecalis, E. faecium,* and *E. durans,* and other Group D streptococci, as classified by Lancefield (Votsch *et al.*,2018). All strains of *S. suis* are alpha-hemolytic on sheep blood agar, but unlike enterococci, they do not grow in broth medium that contains 6.5% NaCl (Votsch *et al.*,2018).

It had been revealed that *S. suis* plays a vital role in multiple antibiotic resistance. Several antibiotics had been optimized for tackling infections caused by *S. suis,* such as tetracycline, tylosin, and sulfonamide, and it had also been shown that the antibiotics are no longer effective against the organism (Bojarska *et al*., 2016). This multiple antibiotic resistance could be attributed to acquisition of resistance genes or development of resistant species, due to improper intake or excessive utilization of antibiotics as described by Bojarska *et al*. (2016). Also, the ability of the

organism to form biofilm contributes immensely to antibiotic resistance, because, the polysaccharide and proteins that are found in biofilm prevent antibiotics from penetrating the cells (Bojarska *et al*., 2016).

Several researchers had worked on diseases caused by *S. suis* and its resistance to antibiotics such as Votsch *et al.* (2018) and Bojarska *et al.* (2016), but little information had been documented on the multiple antibiotic resistance indices of *Streptococcus suis* isolated from pigs and its environs. Hence, this work is aimed at evaluating the multiple antibiotic resistance indices of *Streptococcus suis* isolated from pigs and its environs. The information obtained from this work would accelerate the control of infectious diseases.

MATERIALS AND METHODS

Study Area: The study was carried out in Ihiala L.G.A Anambra State. Ihiala is situated at Latitude 5.85^{o}N and Longitude 6.86^{o}E, with an elevation of 144m above the sea level. It is located 48Km North of Owerri and 40Km south of Onitsha. It covers an area of 304SqKm and is bounded by Ogbaru (in Ogbaru L.G.A, Anambra State) on the West, Ozubulu (in Ekwusigo L.G.A, Anambra State), Ukpor and Osumenyi (in Nnewi South L.G.A Anambra State) in the North and in the South by Egbuoma, Ohakpu, Ozara and Oguta in Egbema/Oguta L.G.A of Imo State. Ihiala has tropical climate (rainy and dry seasons) with double maximal rainfall. The rainy season is between April and October, and the dry season is between November and March. The annual rainfall ranges from 1800mm to 2000mm. The major anthropological activities are farming/agriculture and trading, of which pig farming is one of the major farming practices. In this study, samples were collected from the major towns in Ihiala L.G.A. which included Amorka, Azia, Lilu, Okija, Mbosi, Isseke, Orsumoghu, Ubuluisiuzor and Uli.

Sample Collection

A total of 430 samples which comprises of 120 nasal swab samples, 60 pork samples, 120 pig droppings, 90 pigs feed samples, and 40 bio aerosol samples were used for this study.

Pork samples: Ready to eat samples was aseptically collected using sterile stainless spoon (Hamada) into a sterile aluminum foil from different selling locations in different towns in Ihiala L.G.A (Wang *et al.,* 2012)

Nasal swab samples: The pig's nasal septum and the environs were cleaned with cotton wool soaked in 70% ethanol. The swab stick soaked in normal saline was aseptically inserted into the nasal cavity of the pig. The swab was turned both clockwise and anticlockwise direction for effective collection. This was carefully withdrawn and inserted into the pack containing the sterile

nutrient broth in order to enrich the organisms in the samples. This was repeated for every pig (Espinosa-Gongura *et al.,* 2016)

Pig dropping samples: These were aseptically collected 2.0m away from each dropping in a particular Pigsty using sterile stainless spoon (Hamada) and polythene bag. Then, the collected samples in a particular pigsty were carefully and aseptically mixed together as a representative sample for analysis. This was repeated at different locations (Marti *et al.,* 2009).

Pig feed samples: These were randomly collected from the top, middle and bottom of the bag at a particular site using sterile stainless spoon (Hamada) and polythene bag. The collected samples were carefully and aseptically pooled together as a representative sample for analysis. This was repeated at different sampling locations (Kookier *et al.,* 2012; Wang *et al,* 2012)

Bio aerosol samples: This was carried out using sedimentation method. Sterile disposable Petri dishes (90mm X 15mm) containing 20ml of sterile solidified blood agar medium were carefully and aseptically exposed at different elevations (floor, tables and cabinets) and positions in the pigsty for 30 minutes and the plates were covered for microbial enumeration. The same procedure was repeated for every sampling location (Tshokey *et al.,* 2016; Haas *et al.,* 2017).

Transportation of the Samples: The representative samples were placed into a cooler containing ice block wrapped in a sterile polythene bag and was used for the sample transportation. The temperature of the cooler was checked and adjusted to 28^{o}C-30^{o}C by reducing the quantity of the ice inside the cooler in order to reduce or prevent microbial shock. The samples were carefully and aseptically arranged inside the cooler without direct contact with the ice bag. The cooler was then covered and the drain plug was securely taped with packing tape to prevent accidental opening of the cooler. The cooler was then safely carried to the Laboratory for analysis within 2hr of sample collection. The same procedure was repeated for other collection times (Wolking and Daris, 2013).

Sample Preparation: The representative samples were prepared using the routine laboratory technique. The pork sample was grounded using sterile blender (SF-400C). Then 1.0 g each of the grounded sample pig droppings and pig feeds were aseptically weighed into a 10 mL test tube (Pyrex) each respectively, 3 mL of normal saline was aseptically added into each test tube and these were shake thoroughly and then made up to 10.0 mL using the normal saline for each test tube.

Isolation of Test Organisms from the Samples: The prepared and diluted samples (pork, pig droppings and pig feeds) were aseptically grown in blood agar (BIOTECH) which was made making use of the manufacturer's instruction and the procedures described in Cheesbrough (2006) and Frank and Robert (2015). The nasal samples were aseptically streaked in sterile poured blood agar plates (90 mm×15 mm) as described by Frank and Robert (2015). The same blood agar was used for the collection of air microbes using sedimentation techniques as described by Tshokey *et al.* (2016) and Hass *et al*. (2017). The cultured plates were carefully placed inside the bacteriological incubator (STXB128) in inverted position, and incubated at 35 ± 2^{0}C for 24 h.

Purification of the Isolates : The plates that showed discrete colonies were selected after 24 h, and aseptically streaked each colony on sterile plates (90 mm×15 mm) containing nutrient agar (BIOTECH) prepared according to the manufacturer's description. The streaked plates were placed in a bacteriological incubator in inverted positions and incubated at 35 ± 2^0C for 24 h as described in Cheesbrough (2006) and Goldman and Green (2009).

Characterization of the Pure Isolates: The pure isolates were characterized using the morphological, biochemical and molecular characteristics as described by Iheukwumere *et al.* (2018).

Determination of Prevalence of the Isolates in the Studied Samples: The occurrences of different strains of *Streptococcus* species that were encountered in nasal swab, pork, pig feeds, pig droppings and bio aerosol samples were counted and recorded according to the method of Iheukwumere *et al.* (2018).

Preparation of Test Isolate: The test isolates were prepared using the method described by Iheukwumere *et al.* (2017). The isolates were aseptically subcultured into a broth culture and incubated at $35+ 2^0$C for 24 h. The broth culture of each isolate was centrifuged using an electric centrifuge. The sediment from each culture was diluted to a turbidity that matched 0.5 McFarland standard that was prepared by mixing 0.6 mL of 1% $BaCl_2$ $2H_2O$ and 99.4 mL of 1% Conc. H_2SO_4. The prepared isolates were standardized by comparing the absorbance with that of 0.5 Macfarland standards at 640 nm using UV/visible spectrophotometer (UV1200).

***In vitro* Activity of Conventional Antibiotics against the Isolates Using Disc Diffusion Method:** The susceptibility of the isolates to the conventional antibiotics was done by using disc diffusion method on Mueller Hinton agar. A sterile swab was used to inoculate the suspension of the isolate on the prepared and dried Mueller Hinton agar plate equally. It was then left to stay for 5 minutes. A sterile forceps was used to place the commercially prepared antibacterial discs on the inoculated plates. Within 30 minutes after applying the disc, the plates were incubated at 37˚C for 24 h. Meter rule was used underside of the plates to determine the diameter zones of inhibition in millimeter (Iheukwumere *et al.,* 2018).

Data Analysis: The data obtained in this study were presented in tables and figures. Their percentages were also calculated. The sample means and standard deviations of some of the analytical data were also calculated. Chi square(x^2) was used to determine the significance of the sample sources, susceptibility patterns and degree of resistance of the isolates at 95% confidence level. The significance of the prevalence of the isolates in the studied samples were determined at 95% using one way analysis of variance (ANOVA). Pairwise comparison was analyzed using student "t" test (Iheukwumere *et al.,* 2018) .

RESULTS

A total of 430 samples were collected from five different sources of which the nasal swab and pig dropping samples were collected more (Table 1). The study revealed that the implicated isolates were detected most from bio-aerosol samples whereas the lowest detection was seen in pig droppings. Also, a total of 103 samples were positive to the implicated isolates whereas 327 samples were negative. The study further showed that there was association between the sources of the samples collection and the occurrences of the isolates as the data obtained were statistically significant ($p<0.05$).

The present study revealed that isolates Q, R, S and Y exhibited similar growth elevation (Table 2). They were Gram positive, cocci, and non-motile. Isolates Q and S showed grey-white appearance on blood agar with smooth edge, shiny and mucoid and capsulated. Isolates S and Y showed whitish appearance on blood agar, with entire edge, glisten and non-capsulated. The isolates were arranged in diplo and short chains except isolate S that was only arranged in short chains. The study (Table 3) showed that the isolates exhibited alpha (α) haemolysis on blood agar. They were negative to catalase, indole, voges prokauer (VP) and oxidase. They were not able to utilise hiparate, sorbitol, ribose neither did they grow on 6.5% NaCl. They utilized esculin, lactose, glucose, trehalose, sacharose and starch. Isolate Q, R and Y utilized inulin whereas isolate S showed slight utilization. Isolates Q and Y exhibited similar characteristics in utilization of salicin (slight) whereas the characteristics of isolate S was not able to utilize salicin. Isolates S and Y utilized arabinose whereas isolates Q and R showed slight utilization to arabinose. The concentrations and respective absorbance of nucleic acids extracted from the bacterial isolates at varying wavelength are shown in Table 4. The absorbance ratio ($^{260}/_{280}$) of the nucleic acids confirmed with their identities as deoxyribonucleic acid (DNA) as it ranges from $1.80 \leq x \leq 1.90$. The molecular identities of the isolates are shown in table 5. The identities were above the stipulated percentage (95%), and these revealed the identities of isolates Q, R, S and Y as *Streptococcus suis* strain S10 (SSS10), *Streptococcus suis* strain 347 (SS347),*Streptococcus suis* strain 9401240 (9401240), and *Streptococcus suis*strain INT-10 (SSINT-10).

The study showed that a total of 103 isolates were seen in the studied samples, of which nasal swab harboured most the isolates whereas the least occurrence was seen in pig feeds. The study further showed that there was association between the sources of the sample collection and the occurrences of the isolates as the data gotten from the data were statistically significance ($p<0.05$). It was also observed that 4 strains of *Streptococcus suis* (SSS10, SS347, SS9401240, and SSINT-10) were implicated in the study and SSS10 was most significantly ($p<0.05$) detected in the studied samples. SS347 was not detected in pork, pig droppings and pig feeds. SS9401240 was detected in pig feeds, SSS10 and SSINT-10were detected in all the studied samples and nasal swab samples harboured all the identified bacterial isolates (Table 6).

The study showed that 66.02% of the total isolates were susceptible to conventional antibiotics whereas 33.68% were resistance. The study also revealed that 100% of SS347 were resistant followed by SS9401240, SSINT-10 and SSS10 showed resistance to conventional antibiotic. The

data obtained from this study showed a statistical significance difference ($P<0.05$) between the strain of bacterial isolates and susceptibility patterns to conventional antibiotics.

The present study showed that 32.35% of the resistance bacterial isolates (SAR) whereas 67.65% exhibited multiple antibiotic resistance (MAR). It was observed that 100% of SS347 exhibited MAR. The study further showed that there was an association between the strains of the organism and the degree of resistance exhibited against conventional antibiotics as the data gotten from the study were statistically significant ($P<0.05$).

The study showed that the isolates exhibited varying MAR indices ranging from 0.1 to 0.7 as shown in Table 9. The isolates exhibited MAR indices of 0.1 to 0.7 except SS347 which exhibited MAR index of 0.3, 0.6, and 0.7**.** SSS10, SS347 and SSINT-10 exhibited the MAR index of 0.7 where the maximum degree of resistance was attained in this in this study. Therefore, the four isolates exhibited high MAR index as their Mar index exceeded 0.2.

Table 1: Sample sources and occurrences of the isolates

Source	Total Sample	Positive (%)	Negative (%)
Nasal swab	120	38(31.67)	82(68.33)
Pork	60	17(28.33)	43(71.67)
Pig droppings	120	13(10.83)	107(89.17)
Pig feeds	90	11(12.22)	79(87.78)
Bio-aerosol	40	27(60.00)	16(40.00)
Total	430	103(23.95)	327(76.05)

Table 2: Morphological characteristics of the isolates

Parameter	Isolate Q	Isolate R	Isolate S	Isolate Y
Colour of the isolate on BA	Grey white	Whitish	Grey white	Whitish
Size (mm)	1.80	1.50	1.70	1.60
Elevation	Convex	Convex	Convex	Convex

Edge	Smooth	Entire	Smooth	Entire
Appearance of the surface	Shiny and mucoid	Glisten	Shiny and mucoid	Glisten
Gram reaction	Positive	Positive	Positive	Positive
Cell Morphology	Coccus	Coccus	Coccus	Coccus
Cell Arrangement	Diplo and short chains	Diplo and short chains	Short chains	Diplo and short chains
Capsule	Positive	Negative	Positive	Negative
Motility	Negative	Negative	Negative	Negative

BA= Blood Agar; mm = Millimetre

Table 3: Biochemical characteristics of the isolates

Parameter	**Isolate Q**	**Isolate R**	**Isolate S**	**Isolate Y**
Catalase	-	-	-	-
Indole	-	-	-	-
V.P	-	-	-	-
Oxidase	-	-	-	-
Growth on 6.5% NaCl	-	-	-	-
Esculine	+	+	+	+
Inulin	+	+	+	+
Lactose	+	+	+	+
Glucose	+	+	+	+
Trehalose	+	+	+	+
Hiparate	-	-	-	-
Salicin	+/-	+	-	+/-
Sacharose	+	+	+	+

Starch	+	+	+	+
Arabinose	+/-	+/-	+	+
Sorbitol	-	-	-	-
Ribose	-	-	-	-
Haemolysis	α	A	A	α

+= Positive; - = negative; V.P = Voges-Proskaeur; % = percentage

Table 4: Purity of nucleic acids extracted from the extracts

Isolate	Conc (ng/ul)	ABS_{260}	ABS_{280}	$^{260}/_{280}$
Q	112.40	3.0142	1.6562	1.82
R	103.50	3.1632	1.7191	1.84
S	99.70	2.4664	1.3627	1.81
Y	121.30	3.3112	1.7613	1.88

Table 5: Molecular identities of the bacterial isolates

Isolate	Maximum score	Total score	Query Cover	E-value	Identity (%)	Accession Number	Description
Q	167	8077	96	5e-37	100.00	LR738721.1	*Streptococcus suis* strain S10 (SSS10)
R	152	3036	100	2e-32	96.74	LR738724.1	*Streptococcus suis* strain 347 (SS347)
S	148	2962	95	2e-31	98.81	LR738724.1	*Streptococcus suis* strain 9401240 (SS9401240)
Y	161	8781	93	9e-35	98.89	CP041994.1	*Streptococcus suis* strain INT-01 (SSINT-01)

Table 6: Prevalence of the bacterial isolates in the studied samples

Source	SSS10 (%)	SS347 (%)	SS9401240 (%)	SSINT-10(%)	Total
Nasal Swab	19(50.00)	3(7.89)	7(18.42)	9(23.68)	38
Pork	10(58.82)	0(0.00)	1(5.88)	6(35.29)	17
Pig Droppings	8(66.67)	0(0.00)	1(8.33)	3(23.08)	12
Pig feeds	7(63.64)	0(0.00)	0(0.00)	4(36.36)	11
Bio aerosol	14(58.33)	1(4.17)	3(12.50)	6(25.00)	24
Total	58(56.31)	4(3.88)	12(11.65)	28(11.65)	103(100.00)

P_f = 0.00243; SSS10* = 0.003388, P (SS347/SSINT-10) = 0.001114;

P (SS9401240/SSINT-10) = 0.03187, % = Percentage

Table 7: Conventional antibiotic susceptibility patterns of the isolates

Isolate	N	Susceptibility Strain (%)	Resistance Strain (%)
SSS10	58	44 (75.86)	14 (24.14)
SS347	4	0 (0.00)	4 (100.00)
SS9401240	12	7 (58.33)	5 (41.67)
SSINT-10	28	17 (60.71)	11 (39.23)
TOTAL	103	68 (66.02)	34 (33.68)

SSS10-*Streptococcus suis* strain S10, SS347-*Streptococcus suis* strain 347

SS9401240 –*Streptococcus suis* strain 9401240, SSINT-10 –*Streptococcus suis* strainINT-10

X^2(11.06) >CV (7.81); p = 0.05, N = Number of isolates, % = Percentage

Table 8: Degree of resistance exhibited by the isolates

Isolate	NR	SAR (%)	MAR (%)
SSS10	14	5 (35.71)	9 (64.29)
SS347	4	0 (0.00)	4 (100.00)
SS9401240	5	2 (40.00)	3 (60.00)

SSINT-10	11	4 (36.36)	7 (63.64)
Total	34	11 (32.35)	23 (67.65)

X^2(2.19) <CV (7.81); p> 0.05, % = Percentage, SSS10-*Streptococcus suis* strain S10

SS347-*Streptococcus suis* strain 347 ; SS9401240 –*Streptococcus suis* strain 9401240 ;

SSINT-10 –*Streptococcus suis* strainINT-10 ; NR – Number of Resistance;

SAR – Single Antibiotic Resistance strain; MAR – Multiple Antibiotic Resistance strain

Table 9: Multiple antibiotic resistance (Mar) indices of the isolates

Mar Index	SSS10 (%) n=14	SS347 (%) n=4	SS9401240 (%) n=5	SSINT-10 (%) n=11
0.1	5 (35.71)	0 (0.00)	2 (40.00)	4 (36.36)
0.2	1 (7.14)	0 (0.00)	1 (20.00)	0 (0.00)
0.3	3 (21.43)	1 (25.00)	0 (0.00)	2 (18.18)
0.4	0 (0.00)	0 (0.00)	1 (20.00)	0 (0.00)
0.5	1 (7.14)	0 (0.00)	1 (20.00)	3 (27.27)
0.6	3 (21.43)	1 (25.00)	0 (0.00)	1 (9.09)
0.7	1 (7.14)	2 (50.00)	0 (0.00)	1 (9.09)

N = Number of isolates, MAR = Multiple antibiotic resistance

SSS10-*Streptococcus suis* strain S10, SS347-*Streptococcus suis* strain 347

SS9401240 –*Streptococcus suis* strain 9401240, SSINT-10 –*Streptococcus suis* strainINT-10

DISCUSSION

The occurrences of different strains of *Streptococcus suis* in pork, pig droppings, pig feeds, nasal swab, and the pig's bio aerosol supported the findings of many researchers (Papatsiros *et al,* 2011; Gottschalk *et al,* 2013; Goyette-Desjardins *et al,* 2014; Gustarrson and Rasmussen, 2014; Looft *et al,* 2014; Takeuchi *et al,* 2017; O'Dea *et al,* 2018; Votsch *et al,* 2018; Meng *et al,* 2019; Segura *et al,* 2020). According to Segura *et al.*(2020)*Streptococcus suis* is an early colonizer of the upper respiratory tract of piglets majorly during birth canal. Takeuchi *et al.*(2017) reported the impact of

food safety campaign on *streptococcus suis* disease in humans. The highest occurrences of *Streptococcus suis* in bio aerosol agrees with the report of Burrows *et al.*(2009) who highlighted that *streptococcus suis* is a biogenic aerosol particles that are ubiquitous in the atmosphere, and due to the size, it has long atmospheric residence and can be pass through wind over long distances.The morphological, biochemical and molecular characteristics of *streptococcus suis* isolated from the studied samples corroborated with the findings of many researchers (Groves *et al,* 2015; Hatrongjit *et al,* 2016; Okura *et al,* 2016; O'Dea *et al,* 2018). Generally, the organisms were gram positive, cocci, non-motile, gray white/whitish on blood agar, α-haemolytic, catalase negative but had variation in their ability to utilize sugars which indicates varying strains. Hence, the occurrences of *Streptococcus suis* strain S10 (SSS10), *Streptococcus suis* strain 347 (SS347), *Streptococcus suis* strain 9401240 (SS9401240), *Streptococcus suis* strain INT-10 (SSINT-10) supported the findings Groves *et al.* (2015). Hatrongjit *et al.* (2016); Okura *et al.*(2016); O'Dea *et al.* (2018) who isolated different strains of *Streptococcus suis* and characterized them in their respective studies.

The occurrences of SSS10, SS347, SS9401240 and SSINT-10 in the studied samples agree with the findings of many researchers (Goyette-Desjardins, 2014; O'Dea *et al.,* 2018; Kerdson *et al.,* 2020; Segura *et al.,*2020). The highest occurrence of SSS10 in the studied sample could be attributed to diversity and survival rates of the isolates. The absence of SS347 in the pork, pig droppings and pig feeds could be attributed to low diversity and poor survival rate of the isolate in the samples. Mural *et al.,* (2017) and Preetha and Narayunan (2020) reputed that intrinsic factors play a vital role in determining the existence and survival of microbes in any sample.

The resistance of different strains of *Streptococcus suis* isolated from the pigs and environs against the conventional antibiotics observed in this study agreed with the findings of many researchers (Palmieri *et al,* 2011; Huang *et al.,* 2016; Hernandez-Garcia *et al.,* 2017; Libante *et al.,* 2019; Yongkiettrakul *et al.,* 2019; Segura *et al.,* 2020). Palmieri *et al.* (2011) reported that resistant to antibiotics could be attributed to massive use of antibiotics in piggery industries either for growth promotion, prophylaxis or therapy and these attributes to the emergence and spread of antibiotic resistance. They also reported resistance of *Streptococcus suis* against tetracycline, macrolides, aminoglycosides, chloramphenicol, antitolate drugs streptothricin and cadmium salts. The above findings also corroborate with the findings of Hernandez-Garcia *et al.,* (2017) and Yongkiettrakul *et al.,* (2019) who reported that the recent *S. suis* isolates have become resistant to all classes of antibiotics used in pigs. SS347 showed 100% resistance to the conventional antibiotics and this confirms the report of Hernandez-Garcia *et al.,*(2017) who pointed out that those *S.suis*isolated from non-clinical cases are more resistant than those isolated from clinical cases. Yongkiettrakul *et al.,* (2019) reported commensal sites (non-clinical sites) were the sites of transmission of *S. suis* resistance strains to other pigs.

The occurrences of more multiple antibiotic resistance (MAR) strains of *S. suis* than single antibiotic resistance (SAR) strains observed in this study corroborated with the findings of Haung *et al.,* (2016), Huang *et al.,* (2019) and Yongkietrakul *et al.,* (2019), Hernandez-Garcia *et al.,*

(2017) reported that the existence of multiple antibiotic resistance (MAR) was due to endogenous resistome such as ribosomal protection genes, gene for methylase medicated target site modification and exogenous genetic elements such as integrative and conjunctive elements, transposons, genomic islands phases and chimeric elements.

The varying MAR indices ranging from 0.1-0.7 exhibited by the studied isolates supported the report of Huang *et al.,* (2016) who considered *S. suis* as a niche for antimicrobial resistance and represents a high risk of transmission of resistance to other pathogens. Libante *et al.,* (2019) made a comprehensive research in existence identification of antimicrobial resistance genes present in *S. suis* and found out that high MAR almost occurred in the organism. The occurrences of high MAR index (> 0.2) in this study calls for urgent attention and intervention.

Conclusion: The present study has shown that *Streptococcus suis* strain S10 (SSS10), *Streptococcus suis* strain 347 (SS347), and *Streptococcus suis* strain 9401240 (SS9401240) and *Streptococcus suis* strain INT-10 (SSINT-10) were the implicated isolates in the nasal, pork, pig droppings, pig feeds and bio aerosol samples, of which SSS10 was predominant. The isolates exhibited different degrees of resistance to the conventional antibiotics of which multiple antibiotic resistant (MAR) strains were predominant.

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