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Antibiotic Sensitivity Pattern of Diverse Soil and Air Flora of Federal University of Technology campus, Akure, Nigeria

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Authors' contributions

This work was carried out in collaboration among all authors. Author OAK designed the study, author ATN performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors OAK and ATN managed the analyses of the study. Author ATN managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Aim: This study was conducted to comparatively investigate the soil and air microflora of selected locations within the Federal University of Akure (FUTA), Ondo State, Nigeria.
Study design: Experimental design
Place and Duration of Study: The study was conducted at The Federal University Technology, Akure (FUTA), Ondo State, Nigeria comprising; School of Sciences, School of Agricultural and Agricultural Technology, School of Engineering and Engineering Technology, School of Health and Health Technology, Microbiology department, FUTA Health Centre, postgraduate hostel, female hostels (main Jibowu and Jibowu annex 1) and the male hostels (Akindeko and Abiola hall of residence) between June and July, 2019.
Methodology: Isolation of bacteria and fungi from soil samples and air was conducted using specified techniques. Antibiotic susceptibility test was conducted via agar disc diffusion technique. Plasmid analysis and curing was conducted via standard protocols.
Results: *Pseudomonas aeruginosa, Klebsiella pneumoniae*, *Escherichia coli*, *Proteus mirabilis*, *Bacillus cereus*, *B. subtilis, Staphylococcus aureus*, *S. saprophyticus* were isolated as soil and air microflora while *Candida albicans, Aspergillus fumigatus,* with *Fusarium oxysporium* were isolated

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from soil as *A. flavus, A. niger*, *Penicillium chrysogenum* was implicated in air. *Bacillus cereus and B. subtilis* showed utmost resistance to ceftazidime, cefuroxime, cloxacillin, augmentin, ceftriaxone, whereas *Enterobacter aerogenes* and *Proteus vulgaris* were susceptible to gentamycin at 17.66±1.52 mm and 16.00±2.00 mm respectively. *Staphylococcus aureus* was sensitive to gentamycin and ofloxacin at 17.30±0.57 mm and 18.66±0.57 mm. The multidrug resistant (MDR) bacterial strains were positive for plasmid DNA with 10 kilobase pairs, but were sensitive to all the antibiotics after curing indicating plasmid-borne resistance.

Conclusion: Findings from this study inferred possible health consequences of MDR soil and air microflora as potential threat to human health which necessitates proper sanitary practices across different sampling areas adopted for this study to reduce potential incidence of bacterial and mycotic infections.

Keywords: Microflora; bacteria; fungi; plasmid; resistance.

1. INTRODUCTION

Microorganisms are very tiny forms of life that can in some cases live as singular cells, albeit most additionally form colonies of cells. A microscope is generally needed to view single cells of these organisms [1]. Many more microorganisms exist in loam, where food sources are ample, than in topsoil. They are particularly plentiful in the areas promptly close to plant root, where sloughed-off cells and synthetic substances delivered by roots provide prepared food sources [1]. These organic entities are essential decomposers of natural matter, however they do different things, for example, provide nitrogen via fixation to help developing plants, detoxify innocuous synthetic compounds (toxins), and synthesize products responsible plant growth. Soil microbes have had another immediate significance for people; they are the wellspring of most antibiotic prescriptions used to manage bacterial diseases [1].

Soil is an oligotrophic mode of nutrition for the growth of fungi, more often than not, fungi are either dormant, or they metabolize and grow very slowly exploiting an array of unrefined molecules [2]. Impacts of soil on microbial action are; temperature, moisture, air circulation and soil natural matter. Soil microbes when upset by the wind blow, freed into the air and stay suspended there for an extensive stretch of time, human-related routines like burrowing or plaguing the soil may also release soil-borne microbes in the air [3]. The typical profile of indoor microbial aerosols probably has little meaning to healthy people. Nonetheless, unsafe microbial aerosols can infiltrate buildings or be generated; in either case, regardless, they can have critical antagonistic consequences for human wellbeing [4].

To develop, a few microbes require oxygen while different microscopic organisms and most achaea utilize elective electron acceptors including nitrate and sulfate (for instance, they breathe nitrate and sulfate). For these anaerobic microorganisms, oxygen might be harmful. By their actual nature, antibiotics should display specific toxicity because they are produced by one microorganism and wield varying levels of toxicity against others [5]. Plasmids are extra chromosomal and self-replicating elements in bacteria cell wall [6]. Plasmids are pieces of usually circular, self-replicating DNA which can code for an array of diverse functional gene groups [7]. Plasmid is a key dynamic that has led to the rise and global propagation of multidrug-resistant (MDR) bacteria [8,9].

Hence, the comparative investigation of the soil and air microflora of selected locations within the Federal University of Akure (FUTA) vicinity and the antimicrobial susceptibility profile of implicated bacteria was ascertained to identify soil and air microflora/mycoflora hazard evaluation on public health for human health protection.

2. MATERIALS AND METHODS

2.1 Description of Study Area

The study was conducted at The Federal University Technology, Akure (FUTA), Ondo State, Nigeria. Samples were collected from various faculties including: School of Sciences, School of Agricultural and Agricultural Technology, School of Engineering and Engineering Technology, School of Health and Health Technology, Microbiology department, FUTA Health Centre, postgraduate hostel, female hostels (main Jibowu and Jibowu annex 1) and the male hostels (Akindeko and Abiola hall of residence).

2.2 Collection and Culturing of Soil Samples

The soil samples were collected using soil auger at the depth of 10-15 cm where most of the microbial activity is concentrated. A total of 22 soil samples were collected at the rhizosphere sections of soil from the specified areas. All the samples collected were analyzed in the laboratory within 2 hours of collection for two months.

2.2.1 Enumeration of bacteria and fungi from soil samples

Nine (9 ml) of distilled water was extrapolated into test tubes using a sterile pipette, each were plugged with cotton wool wrapped in aluminium foil paper and sterilized at a standard duration of 15 mins in an autoclave. About 1 gram each of the soil samples were weighed using digital weighing balance (JA303P Pec Medical, USA) and the respective soil samples were added to test tubes taken as stocks and shaken well by placing on a vortex mixer for five minutes. The test tubes containing 9ml of sterile distilled water by using sterile pipette and followed by serial dilutions of up to 10^{-5}. From the test tubes, 1 ml of the required dilutions was transferred into petri-plates and 20 ml of already sterilized nutrient agar (NA) (Hi-Media, India) and potato dextrose agar (PDA) plates (Hi-Media, India) was poured into the petri-plates aseptically. NA petri-plates were incubated for duration of 24 hrs at a temperature of 37 ºC after rocking the plates clock-wisely and anti-clock-wisely as demonstrated by Tang and Wan, [10]; 25±2 ºC for fungi before solidification of the media. Plates were incubated in an inverted position as illustrated by Verde et al. [11].

2.3 Agar Petri-Plate Exposure to Air

The exposed air culture technique was adopted for estimating the air microflora of the sampling areas. Nutrient agar plate, mannitol salt agar plate, McConkey agar plate (Hi-media, India) were rendered in air at 1.5 metres above the ground for a duration of 10-15 minutes. Exposed plates were incubated at 37 ^{0} C for 18-24 hours as described by Syed and Sarangi, [12].

2.3.1 Enumeration of bacteria and fungi from air

Already poured and solidified Nutrient agar (NA) (Hi-Media, India) and potato dextrose agar (PDA) (Hi-Media, India) plates were exposed for 5-10 minutes using standard world health organization [13] guidelines and later incubated at 37 ºC (for bacteria) and 25±2ºC for fungi.

2.4 Identification and Characterization of Bacterial Isolates

Colonies were selected randomly and were characterized using staining and biochemical tests such as gram stain, spore stain, motility, and catalase, coagulase, indole, urease sugar fermentation tests [14]. Bacterial isolates were identified with reference to Cowan and Steel's Manual for the Identification of Medical bacteria Bergey's manual of determinative Bacteriology [14]. The bacterial isolates identification was based on cultural characteristics and biochemical tests descriptions coupled with selective media like mannitol salt agar (MSA) (Hi-Media, India), blood agar, MacConkey agar (MAC) (Hi-Media, India) to further confirm the isolates.

2.5 Identification and Characterization of Fungal Isolates

Distinct colonies were picked with a sterile inoculating needle from the pure culture isolated. It was stained with lactophenol cotton blue on a grease free glass slide and cover slip was placed on it and viewed under the microscope for the identification and characterization at X40 magnification [15].

2.6 Standardization of Bacterial Inoculum

A loop full of test bacterial isolates were inoculated on nutrient broth and incubated for 24 hours. 0.2 ml from the 24 hours' broth culture of the bacteria was dispensed into 20 ml sterile nutrient broth and incubated for 3 to 5 hours to standardize the culture to 0.5 McFarland standards (10^6 CFU/ml) before use. One percent (1%) of solution of sulphuric acid (H_2SO_4) was prepared by adding 1ml of concentrated sulphuric acid to 99 ml of distilled water. Also, 1% solution of barium ($BaCl_2$) chloride was prepared by dissolving 0.5 g of dehydrated barium chloride ($BaCl_2H_2O$) in 50ml of distilled water. About 0.6 ml of barium chloride solution was added to 99.4 ml of sulphuric acid solution and it was then mixed together. The solution was transferred into capped tube of the same type used for both the control and the test inoculums. The solution was kept at room 4 ºC until it was ready for use [16]. The bacterial suspension turbidity was made sure to be equivalent to the turbidity of McFarland standard by comparing the turbidity.

2.6.1 Antibiotic sensitivity test

This test was carried out to determine the resistance and susceptibility of the isolated bacteria to antibiotics. Standardized bacteria suspension were swabbed homogeneously across Mueller-hilton agar (MHA) (Hi-Media, India) plates via sterile swab sticks and then wafers containing antibiotic profile comprising ceftazidine (CAZ) 30µg, gentamycin (GEN) 10µg, cefixime (CXM) 5µg, augmentin (AUG) 30µg, cefuroxime (CRX) 30µg, gentamicin (GEN) 10µg, ofloxacin (OFL) 5 µg, ceftazidine (CAZ) 30µg (Oxoid, Basingstokes, UK) were placed on the agar plate. The MHA plates were incubated, and then observed after 18-24 hours incubation period at 37^{o}C [17].

2.7 Plasmid Profiling of Multi-Drug Resistant Bacteria Isolates

A gram of agarose was measured and mixed with 100 mL 1xTAE in a microwavable flask (GC America, FRP Flask, US) and set in the microwave (Toshiba EM925A5A, Tokyo, Japan) for 1-3 minutes for 1-3 minutes until the agarose is totally disintegrated with overheating avoided to allow for intact buffer with final percentage of agarose in the gel not affected. Following 3 minutes, the arrangement was taken out from the microwave and permitted to chill off to around 50 °C. At that point 10µL EZ vision DNA stain was added, the EZ vision ties to the DNA and allows for visualization of the bacterial plasmid DNA under Ultraviolet light [18].

2.7.1 Plasmid curing of multi-drug resistant bacteria isolates

Plasmid curing was achieved by inoculating 100 ml of culture grown in Luria Bertoni (LB) broth containing 10% of Sodium Dodecyl Sulfate (SDS) (817034), Merck, Darmstadt, Germany) as preferred mutagenic agent. After inoculation, the cultures were incubated at 37 °C for 24 hours with constant shaking. After 24hrs of incubation, the above procedure was used for the plasmid purification [19].

2.7.2 Post curing sensitivity testing

The plasmid cured isolates were tested against those antibiotics to which they were formerly resistant to. Post-curing sensitivity tests were conducted on the isolates using Kirby Bauer's agar disc diffusion technique as designated by Clinical Laboratory Standard Institute [20] using 24 hours old bacteria broth culture. Mueller-hinton agar (MHA) (Hi-Media, India) plates were prepared according to manufacturer's specification. The isolates were sub-cultured onto freshly prepared nutrient agar plates and incubated at 37 °C for 24 hours. One (1ml) suspension of each bacterial isolates, equivalent to McFarland standards was aseptically seeded into MHA plate respectively using sterile swab stick. The antibiotic discs comprising ceftazidime (CAZ) 30µg, gentamycin (GEN) 10µg, cefixime (CXM) 5µg, augmentin (AUG) 30µg, cefuroxime (CRX) 30µg, cloxacillin (CXC) 30µg, ofloxacin (OFL) 5µg and erythromycin (ERY) 10µg were aseptically placed on the surface of the solidified MHA (Hi-Media, India) and allowed for 30 minutes to pre-diffuse. The set up was done in triplicates for each isolate, with a purity plate containing no antibiotic disc. These were incubated for 18-24 hours at 37 °C after which the diameters of zone of inhibition were measured using a vernier caliper (Mitutoyo 530-119) (Cranbury, New Jersey, United States) and zones were compared with standard antibiotics chart as depicted by Bauer et al. [21].

2.8 Statistical Analysis

Data obtained were subjected to Analysis of Variance and Mean was compared using Duncan's New Range Test with the Statistical Package for the Social Science 20.0 (SPSS) at (p < 0.05) level of significance.

3. RESULTS AND DISCUSSION

The comparative investigation of the soil and air microflora of selected locations within the Federal University of Technology Akure (FUTA) vicinity and their antimicrobial susceptibility profile was assessed in this study. Bacteria strains enumerated include four Gram negative bacteria; *Enterobacter aerogenes*, *Proteus vulgaris, Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Two Gram positive rods; *Bacillus cereus* and *Bacillus subtilis*. Two Gram positive cocci; *Staphylococcus aureus* and *Staphylococcus epidermidis* as shown in Table 1 and 2 [14].

The presence of bacteria strains from soil samples implicated in this study are chiefly heterotrophic bacteria which could be attributed to the tolerance of these microbes to wide variations of organic matter in the soil [2].

The outcome obtained in this study likewise showed that Gram positive cocci; *Staphylococcus aureus* and *Staphylococcus epidermidis* and Gram positive rods;

Bacillus subtilis isolated from dissimilar origins where air examination was conducted in this study. This perception from this study bears semblance to the work of Tang and Wan, [10] as they also isolated Gram positive cocci and Gram positive rods from air sampling. Seasonal changes could have been attributable for disparity in the occurrence of microbial strains in soil specimens and outdoor air in relation to other previous findings as juxtaposed by Syed and Sarangi, [12].

Identified fungal isolates obtained from the different soil sampling areas by macro-morphological and micro-morphological characteristics respectively are represented in Table 3. *Fusarium oxysporium, Rhizopus oryzae, Aspergillus fumigatus*, *Aspergillus niger*, and *Candida albicans* were identified from the soil samples collected across sampling areas. *Chaetomium globosum, Aspergillus niger, Aspergillus flavus, Fusarium oxysporum, Saccharomyces cerevisiae* and *Penicillium chrysogenum* were obtained from agar plates exposed to the air across the different sampling areas as illustrated in Table 4.

The fungal strains enumerated from soil in this study demonstrate the profusion and circulation of the fungal consortia in the soil specimens and outdoor air of the study sites designated that the broad state of the soil supported the survival of the soil and air mycoflora. Soil microbes feed on the bodies of dead plants and animals. The Fungal consortia in particular, digest the intricate organic compounds that makeup living matter and condense them to simpler compounds that plants can use for food. *Penicillium* spp*, A, flavus, A. niger* and *Rhizopus* spp that have been isolated during the course of this study most especially from air examination in FUTA health centre, this translates to respiratory risks as prospective source of toxins and allergens as the fungal isolates therefore poses public health risks. This observation is supported by Verde et al*.* [11]. *Aspergillus niger* and *A. fumigatus* were also isolated from air sampling conducted around the vicinity of the clinical scenery in which spores of fungal isolates which when respired at elevated levels has the capacity to cause aspergillosis thereby posing the risk of hospital-related infections. This result is analogous with the work of Sudharsanam et al*.* [22] who detected majorly *Aspergillus niger* and *A. fumigatus* as mycoflora of hospital wards in his work on the characteristics of bio-aerosols from hospital ward in a tropical setting.

Table 1. Biochemical characterization of bacteria isolates

GR	CA	UR	IN	SP	CO	CT	MO	S	H_2S	Suspected Organisms
G + Rod	+	+	-	SP	-	+	NM	+	-	*Bacillus cereus*
G – Rod	+	+	-	NS	-	+	+	+	-	*Enterobacter aerogenes*
G – Rod	+	+	-	NS	-	+	+	+	+	*Proteus vulgaris*
G – Rod	+	+	-	NS	-	+	NM	+	-	*Klebsiella pneumoniae*
G + Cocci	+	+	-	NS	-	+	NM	+	-	*Staphylococcus aureus*
G – Rod	+	+	-	NS	-	+	+	+	-	*Pseudomonas aeruginosa*
G + Rod	-	+	-	SP	-	-	NM	+	-	*Bacillus subtilis*
G + Cocci	+	+	-	NS	-	+	NM	+	-	*Staphylococcus epidermidis*

Keys: GR= Gram staining, CA= Catalase test, UR= Urease test, IN= Indole test, NS= Non spore forming, NM= Non-motile, SP= Spore staining, CO= Coagulase test, CT= Citrate, MO= Motility test, S= Starch hydrolysis, H_2S= Hydrogen sulphide test, + = Present, - = Absent

Table 2. Sugar fermentation test(s) for bacteria isolates from soil and air

Glu	Suc	Fru	Lac	Gal	Mal	Suspected Organism
+	-	-	-	-	-	*Bacillus cereus*
+	+	+	+	+	+	*Enterobacter aerogenes*
+	-	+	-	+	-	*Proteus mirabilis*
+	-	-	-	+	+	*Klebsiella pneumoniae*
+	-	-	-	+	-	*Staphylococcus aureus*
-	+	-	+	+	-	*Pseudomonas aeruginosa*
+	-	-	-	+	-	*Staphylococcus epidermidis*
+	-	-	-	-	-	*Bacillus subtilis*

Keys: GLU=Glucose, SUC= Sucrose, FRU= Fructose, LAC=Lactose, GAL= Galactose, MAL= Maltose. + = Present; - = Absent

Table 3. Macro-morphological and micro-morphological characteristics of fungi enumerated from soil samples

Isolate code	Macroscopy Characteristics	Microscopy Characteristics	Size	Suspected Organism
1	Yellowish pink creamy colonies	Cylindrical to ovoid conidia, curved septate conidiophores	Large	*Fusarium oxysporum*
2	Whitish cream lobate colonies with no true mycelium	Colonies of loose budding cells with hyaline pattern and globose round edges	Small	*Candida albicans*
3	Black and powdery like	Conidiophores smooth-walled and septate filamentous	Medium	*Aspergillus niger*
4	Fussy white fluffy mycelium with dark green downy pattern	Globose rough edged, septate filamentous conidia		*Aspergillus fumigatus*
5	Fastidious white wooly mycelium with aerial brownish projections	Smooth stolons with strewn Sporangiophores attached to globose sporangia	Medium	*Rhizopus orzyae*

Table 4. Macroscopy and microscopy characteristics of fungi isolated from air

Sample Codes	Macroscopy characteristics	Microscopy characteristics	Size	Suspected organism
1	Black and powdery-like	Conidiophores smooth-walled and septate filamentous conidia	Medium	*Aspergillus niger*
2	Fastidious grayish white mycelium with yellowish green centers and pinkish drabs	Long loutish conidiophores with radiate septate filamentous conidial heads		*Aspergillus flavus*
3	Dark globose ascomata with black hyphal appendages attached to unbranched septate	Dark globose appearance with black hyphal ascomata attached to septate unbranched hyphae	Large	*Chaetomium globosum*
4	Cream milky	Oval nascent cells	Small	*Saccharomyces cerevisiae*
5	Yellowish pink creamy colonies	Cylindrical to ovoid conidia with curved septate conidiophores		*Fusarium oxysporum*
6	Brown and cottony-like	Long upright conidiophores with round-shaped conidia	Medium	*Penicillium chrysogenum*

Table 5. Antibiotics sensitivity pattern for soil and air bacterial isolates (mm)

CAZ S = ≥21 I =18-20 R = ≤17	CRX S = ≥23 I =20-22 R = ≤19	GEN S = ≥15 I =13-14 R = ≤12	CTR S = ≥23 I =20-22 R = ≤19	ERY S = ≥23 I =14-22 R = ≤13	CXC S = ≥15 I = 12-13 R = ≤14	OFL S = ≥16 I =13-15 R = ≤12	AUG S = ≥18 I =14-17 R = ≤13	Bacterial organisms
6.10±2.02^{a}	6.10±2.02^{a}	6.10±2.02^{a}	6.10±2.02^{a}	11.33±1.52^{b}	6.10±2.02^{a}	17.00±2.00^{c}	6.10±2.02^{a}	*Bacillus cereus*
6.10±2.02^{a}	6.10±2.02^{a}	17.66±1.52^{b}	6.10±2.02^{a}	16.33±2.08^{b}	6.10±2.02^{a}	16.66±2.08^{b}	6.10±2.02^{a}	*Enterobacter aerogenes*
6.10±2.02^{a}	6.10±2.02^{a}	16.00±2.00^{b}	6.10±2.02^{a}	15.33±2.08^{b}	6.10±2.02^{a}	17.00±0.00^{b}	6.10±2.02^{a}	*Proteus vulgaris*
6.10±2.02^{a}	6.10±2.02^{a}	18.00±1.73^{c}	6.10±2.02^{a}	17.33±1.52^{bc}	6.10±2.02^{a}	16.33±00.57^{b}	6.10±2.02^{a}	*Klebsiella pneumoniae*
6.10±2.02^{a}	6.10±2.02^{a}	17.00±1.00^{c}	6.10±2.02^{a}	6.10±2.02^{a}	6.10±2.02^{a}	14.00±00.00^{b}	6.10±2.02^{a}	*Pseudomonas aeruginosa*
6.10±2.02^{a}	6.10±2.02^{a}	17.30±00.57^{b}	6.10±2.02^{a}	6.10±2.02^{a}	6.10±2.02^{a}	18.66±00.57^{c}	6.10±2.02^{a}	*Staphylococcus aureus*
6.10±2.02^{a}	6.10±2.02^{a}	6.10±2.02^{a}	6.10±2.02^{a}	17.33±00.57^{c}	6.10±2.02^{a}	15.66±00.57^{b}	6.10±2.02^{a}	*Staphylococcus epidermidis*
6.10±2.02^{a}	6.10±2.02^{a}	18.00±1.52^{c}	6.10±2.02^{a}	13.33±2.52^{b}	6.10±2.02^{a}	18.00±2.02^{c}	6.10±2.02^{a}	*Bacillus subtilis*

Data are presented as Mean ± S.D (n=3). Figures with the similar superscript letter(s) along the equivalent row are not significantly diverse (p<0.05). Keys: CAZ= Ceftazidime, CRX= Cefuroxime, GEN = Gentamycin, CTR = Ceftriaxone, CXC = Cloxacillin, OFL= Ofloxacin, AUG= Augmentin, ERY = Erythromycin

Table 6. Antibiotics sensitivity pattern of multidrug resistant bacterial isolates after plasmid curing

CAZ S = ≥21 I =18-20 R = ≤17	CRX S = ≥23 I =20-22 R = ≤19	GEN S = ≥15 I =13-14 R = ≤12	CTR S = ≥23 I =20-22 R = ≤19	ERY S = ≥23 I =14-22 R = ≤13	CXC S = ≥15 I = 12-13 R = ≤14	OFL S = ≥16 I =13-15 R = ≤12	AUG S = ≥18 I =14-17 R = ≤13	Bacterial organisms
20.00±1.15^{a}	18.33±0.33^{a}	19.66±0.88^{a}	19.33±0.66^{a}	19.33±0.88^{a}	20.00±0.57^{a}	20.00±0.57^{a}	19.33±0.66^{a}	*Pseudomonas aeruginosa* (AB)
20.00±0.57^{a}	20.00±0.00^{a}	20.33±0.66a	19.33±0.66^{a}	20.66±0.57^{a}	20.33±0.33^{a}	20.66±0.88^{a}	19.33±0.33^{a}	*Staphylococcus epidermidis* (JB)

Data are presented as Mean ± S.D (n=3). Values with the identical superscript letter(s) alongside the same row are not significantly diverse (p<0.05); Keys: CAZ= Ceftazidime, CRX= Cefuroxime, GEN = Gentamycin, CTR = Ceftriaxone, CXC Cloxacillin, OFL= Ofloxacin, AUG= Augmentin, ERY = Erythromycin

Plate 1. Pure *Candida* sp. on potato dextrose agar from soil samples

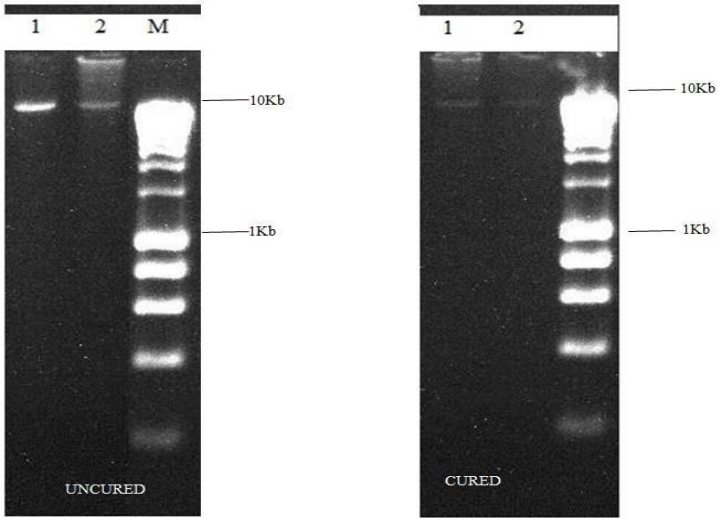

Fig. 1. Plasmid profiling and curing of bacterial isolates; (Lane 1 =AB, Lane 2= JB); AB= *Pseudomonas aeruginosa* (Soil); JB= *Staphylococcus aureus* (Air)

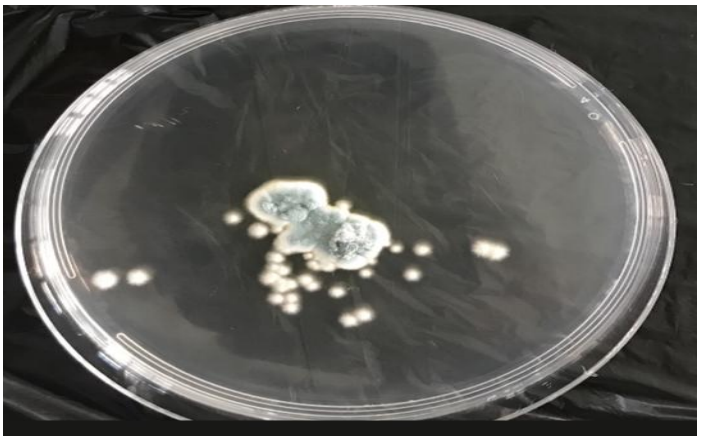

Plate 2. Pure *Penicillium* sp; on Potato dextrose agar from outdoor air

Assortments of fungi strains of mycotic importance occurred across different sample points in the university campus, but the findings of this study also generally suggests the high occurrence rates of fungal strains that pose greater public health risks in the non-residential areas of the study site. This may be due to the high incursion of persons into these sampling areas as reported by Kumari et al. [23]; Aina et al. [24]; Panaiyadiyan and Chellaia, [25]; Dalal, [26].The fungal strains of overriding occurrence in the sampling points (*Aspergillus* spp) have been implicated to cause wide range of systemic mycoses when their vegetative spores are inhaled accidentally as particularly described by Vivienne et al. [27]. The reason for this is that proper sanitary practices were not inculcated by different persons across these areas as waste food items and other refuse materials are not properly disposed, thus aiding the intermittent spread of fungal spores of mycotic importance obtained across the sampling points. Additionally, these awful sanitary practices across densely populated Nigerian university campus centers were also observed in the findings of Aina et al. [24]; Latha et al. [28]; Ogunwonyi et al. [29]; Sa'adatu et al. [30]; Vivienne et al. [27]. Appropriate hygienic practices are however recommended across different sampling areas adopted for this study to reduce possible occurrence of mycotic infections.

Out of the eight antibiotics tested for antimicrobial susceptibility activity, it was observed that *Pseudomonas aeruginosa, Klebsiella pneumoniae*, *Bacillus cereus and Bacillus subtilis* showed utmost resistance to multiple antibiotics comprising ceftazidime, cefuroxime, cloxacillin, augmentin, ceftriaxone, whereas *Enterobacter aerogenes* and *Proteus vulgaris* were susceptible to gentamycin at 17.66±1.52 mm and 16.00±2.00 mm respectively. *Staphylococcus aureus* was sensitive to gentamycin and ofloxacin at 17.30±0.57 mm and 18.66±0.57 mm as illustrated in Table 4 and interpreted via Clinical and Laboratory Standard Institute (CLSI) standard in Table 5. The cause of increasing resistant among the resistant bacteria in our study might be due to the advancement of multidrug resistant and antibiotic extrusion on antimicrobial agents such as the ones employed in this study. The plasmid bands of two of the multidrug resistant bacterial strains showed visible plasmid bands as shown in Fig. 1. The result from Table 5 shows that *Pseudomonas aeruginosa* and *Staphylococcus aureus* were sensitive to the corresponding antibiotics that they were initially resistant to before curing. This suggests that the initial resistance of *P. aeruginosa* and *S. aureus* to the ceftazidime, cefuroxime, ceftriaxone, cloxacillin, augmentin, and erythromycin were plasmid-mediated as they all showed susceptibility after post curing as illustrated in Table 6. *Pseudomonas aeruginosa* (soil) and *Staphylococcus aureus* (outdoor air) showed positive amplication of single plasmid gene bands with sizes greater than ten kilobase pairs (>10 kbp) at the uncured electrophoretic bands.The electrophoretic plasmid bands of these two MDR bacterial strains showed cured plasmids after plasmid curing analysis as displayed in Fig. 1. This is an indication that the origin of plasmid-mediated resistance in bacterial strains from soil specimens and outdoor air could owed to the mixing of both MDR and non-MDR strains of bacteria enumerated in this study, this could result in genetic recombination of plasmids between bacteria or stimulation of multidrug resistance by proteins secreted by MDR bacteria as stated by Prakasam et al. [31].

4. CONCLUSION

The findings of this study have exposed a satisfactory comparative overview of the soil and air microflora of selected densely populated areas of the Federal University of Technology, Akure. This study juxtaposed the diversity of different bacterial and fungal consortia with emphasis on the activities predominant at different sampling areas in this study. Possible health consequences of MDR soil and air flora as potential threat to human health which necessitates proper sanitary practices across different sampling areas adopted for this study to reduce potential incidence of bacterial and mycotic infections.

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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APPENDIX

Descriptives

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
ANTIBIOTICS	24	1.0000	8.0000	4.500000E0	2.3405685
S1	24	.00	19.00	5.5417	7.52953
S2	24	.00	19.00	6.1250	8.14709
S3	24	.00	19.00	6.3333	8.41668
S4	24	.00	18.00	6.0417	8.02431
S5	24	.00	19.00	6.4583	8.55661
S6	24	.00	18.00	4.0833	7.24669
S7	24	.00	18.00	4.3333	7.67643
S8	24	.00	18.00	3.8750	6.90502
S9	24	.00	19.00	4.5000	7.97278
S10	24	.00	19.00	4.3333	7.69340
S11	24	.00	18.00	4.3750	7.75053
S12	24	.00	19.00	4.4583	7.89595
S13	24	.00	18.00	6.2917	8.31698
S14	24	.00	19.00	4.4583	7.90695
S15	24	.00	19.00	6.4583	8.56677
S16	24	.00	18.00	6.0000	7.95640
S17	24	.00	18.00	4.1667	7.38192
S18	24	.00	18.00	4.3333	7.67643
S19	24	.00	18.00	5.8750	7.80364
S20	24	.00	18.00	4.3333	7.67643
S21	24	.00	18.00	4.0000	7.10786
Valid N (listwise)	24				

Oneway s1 s2 s3 s4 s5 s6 s7 s8 s9 s10 s11 s12 s13 s14 s15 s16 s17 s18 s19 s20 s21 by antibiotics; /statistics descriptives ho mogeneity;/missing analysis; /posthoc=duncan alpha(0.05)

Descriptives

		N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
						Lower Bound	Upper Bound		
S1	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	16.0000	2.00000	1.15470	11.0317	20.9683	14.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	11.3333	1.52753	.88192	7.5388	15.1279	10.00	13.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	17.0000	2.00000	1.15470	12.0317	21.9683	15.00	19.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	5.5417	7.52953	1.53696	2.3622	8.7211	.00	19.00
S2	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	16.3333	2.51661	1.45297	10.0817	22.5849	14.00	19.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	16.3333	2.08167	1.20185	11.1622	21.5045	14.00	18.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	16.3333	1.52753	.88192	12.5388	20.1279	15.00	18.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.1250	8.14709	1.66302	2.6848	9.5652	.00	19.00
S3	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.6667	1.52753	.88192	13.8721	21.4612	16.00	19.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	16.3333	2.08167	1.20185	11.1622	21.5045	14.00	18.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	16.6667	2.08167	1.20185	11.4955	21.8378	15.00	19.00

Descriptives

		N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
						Lower Bound	Upper Bound		
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.3333	8.41668	1.71805	2.7793	9.8874	.00	19.00
S4	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	16.0000	2.00000	1.15470	11.0317	20.9683	14.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	15.3333	2.08167	1.20185	10.1622	20.5045	13.00	17.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	17.0000	.00000	.00000	17.0000	17.0000	17.00	17.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.0417	8.02431	1.63795	2.6533	9.4300	.00	18.00
S5	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	18.0000	1.73205	1.00000	13.6973	22.3027	16.00	19.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	17.3333	1.52753	.88192	13.5388	21.1279	16.00	19.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	16.3333	.57735	.33333	14.8991	17.7676	16.00	17.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.4583	8.55661	1.74661	2.8452	10.0715	.00	19.00
S6	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.3333	.57735	.33333	15.8991	18.7676	17.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	15.3333	.57735	.33333	13.8991	16.7676	15.00	16.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.0833	7.24669	1.47922	1.0233	7.1433	.00	18.00
S7	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	16.6667	.57735	.33333	15.2324	18.1009	16.00	17.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	18.0000	.00000	.00000	18.0000	18.0000	18.00	18.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.3333	7.67643	1.56694	1.0919	7.5748	.00	18.00
S8	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.0000	1.00000	.57735	14.5159	19.4841	16.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	14.0000	.00000	.00000	14.0000	14.0000	14.00	14.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	3.8750	6.90502	1.40948	.9593	6.7907	.00	18.00
S9	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.3333	.57735	.33333	15.8991	18.7676	17.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	18.6667	.57735	.33333	17.2324	20.1009	18.00	19.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.5000	7.97278	1.62744	1.1334	7.8666	.00	19.00
S10	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00

Descriptives

		N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
						Lower Bound	Upper Bound		
	GEN	3	17.6667	.57735	.33333	16.2324	19.1009	17.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	17.0000	2.00000	1.15470	12.0317	21.9683	15.00	19.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.3333	7.69340	1.57041	1.0847	7.5820	.00	19.00
S11	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.6667	.57735	.33333	16.2324	19.1009	17.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	17.3333	1.15470	.66667	14.4649	20.2018	16.00	18.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.3750	7.75053	1.58207	1.1022	7.6478	.00	18.00
S12	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	18.0000	1.00000	.57735	15.5159	20.4841	17.00	19.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	17.6667	.57735	.33333	16.2324	19.1009	17.00	18.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.4583	7.89595	1.61175	1.1242	7.7925	.00	19.00
S13	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	17.3333	.57735	.33333	15.8991	18.7676	17.00	18.00
	GEN	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	17.3333	.57735	.33333	15.8991	18.7676	17.00	18.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	15.6667	.57735	.33333	14.2324	17.1009	15.00	16.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.2917	8.31698	1.69770	2.7797	9.8036	.00	18.00
S14	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.0000	1.00000	.57735	14.5159	19.4841	16.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	18.6667	.57735	.33333	17.2324	20.1009	18.00	19.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.4583	7.90695	1.61400	1.1195	7.7971	.00	19.00
S15	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	18.3333	.57735	.33333	16.8991	19.7676	18.00	19.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	15.3333	.57735	.33333	13.8991	16.7676	15.00	16.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	18.0000	1.00000	.57735	15.5159	20.4841	17.00	19.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.4583	8.56677	1.74868	2.8409	10.0758	.00	19.00
S16	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	15.6667	2.08167	1.20185	10.4955	20.8378	14.00	18.00
	GEN	3	15.3333	.57735	.33333	13.8991	16.7676	15.00	16.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	17.0000	1.00000	.57735	14.5159	19.4841	16.00	18.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00

Descriptives

		N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
						Lower Bound	Upper Bound		
	OFL	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	6.0000	7.95640	1.62409	2.6403	9.3597	.00	18.00
S17	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.0000	1.00000	.57735	14.5159	19.4841	16.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	16.3333	.57735	.33333	14.8991	17.7676	16.00	17.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.1667	7.38192	1.50683	1.0496	7.2838	.00	18.00
S18	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	17.6667	.57735	.33333	16.2324	19.1009	17.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	17.0000	1.00000	.57735	14.5159	19.4841	16.00	18.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.3333	7.67643	1.56694	1.0919	7.5748	.00	18.00
S19	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	14.0000	1.00000	.57735	11.5159	16.4841	13.00	15.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	17.3333	.57735	.33333	15.8991	18.7676	17.00	18.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	15.6667	.57735	.33333	14.2324	17.1009	15.00	16.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	5.8750	7.80364	1.59291	2.5798	9.1702	.00	18.00
S20	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	GEN	3	18.0000	.00000	.00000	18.0000	18.0000	18.00	18.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	16.6667	.57735	.33333	15.2324	18.1009	16.00	17.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.3333	7.67643	1.56694	1.0919	7.5748	.00	18.00
S21	CAZ	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CRX	3	17.0000	1.00000	.57735	14.5159	19.4841	16.00	18.00
	GEN	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	CTR	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	ERY	3	15.0000	1.00000	.57735	12.5159	17.4841	14.00	16.00
	CXC	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	OFL	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	AUG	3	.0000	.00000	.00000	.0000	.0000	.00	.00
	Total	24	4.0000	7.10786	1.45089	.9986	7.0014	.00	18.00

Test of Homogeneity of Variances

	Levene Statistic	df1	df2	Sig.
S1	3.274	7	16	.023
S2	5.364	7	16	.003
S3	6.980	7	16	.001
S4	5.309	7	16	.003
S5	8.720	7	16	.000
S6	13.714	7	16	.000
S7	16.000	7	16	.000

S8	4.000	7	16	.010
S9	13.714	7	16	.000
S10	3.954	7	16	.011
S11	14.171	7	16	.000
S12	4.514	7	16	.006
S13	11.429	7	16	.000
S14	4.514	7	16	.006
S15	4.519	7	16	.006
S16	6.936	7	16	.001
S17	4.514	7	16	.006
S18	4.514	7	16	.006
S19	4.519	7	16	.006
S20	16.000	7	16	.000
S21	3.429	7	16	.020

ANOVA

		Sum of Squares	df	Mean Square	F	Sig.
S1	Between Groups	1283.292	7	183.327	141.931	.000
	Within Groups	20.667	16	1.292		
	Total	1303.958	23			
S2	Between Groups	1500.625	7	214.375	131.923	.000
	Within Groups	26.000	16	1.625		
	Total	1526.625	23			
S3	Between Groups	1607.333	7	229.619	166.996	.000
	Within Groups	22.000	16	1.375		
	Total	1629.333	23			
S4	Between Groups	1464.292	7	209.185	200.817	.000
	Within Groups	16.667	16	1.042		
	Total	1480.958	23			
S5	Between Groups	1672.625	7	238.946	337.336	.000
	Within Groups	11.333	16	.708		
	Total	1683.958	23			
S6	Between Groups	1206.500	7	172.357	2.068E3	.000
	Within Groups	1.333	16	.083		
	Total	1207.833	23			
S7	Between Groups	1354.667	7	193.524	4.645E3	.000
	Within Groups	.667	16	.042		
	Total	1355.333	23			
S8	Between Groups	1094.625	7	156.375	1.251E3	.000
	Within Groups	2.000	16	.125		
	Total	1096.625	23			
S9	Between Groups	1460.667	7	208.667	2.504E3	.000
	Within Groups	1.333	16	.083		
	Total	1462.000	23			
S10	Between Groups	1352.667	7	193.238	356.747	.000
	Within Groups	8.667	16	.542		
	Total	1361.333	23			
S11	Between Groups	1378.292	7	196.899	945.114	.000
	Within Groups	3.333	16	.208		
	Total	1381.625	23			
S12	Between Groups	1431.292	7	204.470	1.227E3	.000
	Within Groups	2.667	16	.167		
	Total	1433.958	23			
S13	Between Groups	1588.958	7	226.994	1.816E3	.000
	Within Groups	2.000	16	.125		
	Total	1590.958	23			
S14	Between Groups	1435.292	7	205.042	1.230E3	.000
	Within Groups	2.667	16	.167		
	Total	1437.958	23			

ANOVA

		Sum of Squares	df	Mean Square	F	Sig.
S15	Between Groups	1684.625	7	240.661	1.155E3	.000
	Within Groups	3.333	16	.208		
	Total	1687.958	23			
S16	Between Groups	1444.667	7	206.381	291.361	.000
	Within Groups	11.333	16	.708		
	Total	1456.000	23			
S17	Between Groups	1250.667	7	178.667	1.072E3	.000
	Within Groups	2.667	16	.167		
	Total	1253.333	23			
S18	Between Groups	1352.667	7	193.238	1.159E3	.000
	Within Groups	2.667	16	.167		
	Total	1355.333	23			
S19	Between Groups	1397.292	7	199.613	958.143	.000
	Within Groups	3.333	16	.208		
	Total	1400.625	23			
S20	Between Groups	1354.667	7	193.524	4.645E3	.000
	Within Groups	.667	16	.042		
	Total	1355.333	23			
S21	Between Groups	1158.000	7	165.429	661.714	.000
	Within Groups	4.000	16	.250		
	Total	1162.000	23			

Homogeneous Subsets

S1

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
ERY	3		11.3333	
GEN	3			16.0000
OFL	3			17.0000
Sig.		1.000	1.000	.297

Means for groups in homogeneous subsets are displayed.

S2

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
GEN	3		16.3333
ERY	3		16.3333
OFL	3		16.3333
Sig.		1.000	1.000

Means for groups in homogeneous subsets are displayed.

S3

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
ERY	3		16.3333
OFL	3		16.6667
GEN	3		17.6667
Sig.		1.000	.205

Means for groups in homogeneous subsets are displayed.

S4

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
ERY	3		15.3333
GEN	3		16.0000
OFL	3		17.0000
Sig.		1.000	.075

Means for groups in homogeneous subsets are displayed.

S5

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
OFL	3		16.3333	
ERY	3		17.3333	17.3333
GEN	3			18.0000
Sig.		1.000	.165	.346

Means for groups in homogeneous subsets are displayed.

S6

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
ERY	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
OFL	3		15.3333	
GEN	3			17.3333
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S7

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
ERY	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
GEN	3		16.6667	
OFL	3			18.0000
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S8

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
ERY	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
OFL	3		14.0000	
GEN	3			17.0000
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S9

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
ERY	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
GEN	3		17.3333	
OFL	3			18.6667
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S10

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
ERY	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
OFL	3		17.0000
GEN	3		17.6667
Sig.		1.000	.284

Means for groups in homogeneous subsets are displayed.

S11

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
ERY	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
OFL	3		17.3333
GEN	3		17.6667
Sig.		1.000	.384

Means for groups in homogeneous subsets are displayed.

S12

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
ERY	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
OFL	3		17.6667
GEN	3		18.0000
Sig.		1.000	.332

Means for groups in homogeneous subsets are displayed.

S13

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
GEN	3	.0000		
CTR	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
OFL	3		15.6667	
CRX	3			17.3333
ERY	3			17.3333
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S14

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
ERY	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
GEN	3		17.0000	
OFL	3			18.6667
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S15

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
ERY	3		15.3333	
OFL	3			18.0000
GEN	3			18.3333
Sig.		1.000	1.000	.384

Means for groups in homogeneous subsets are displayed.

S16

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CTR	3	.0000		
CXC	3	.0000		
OFL	3	.0000		
AUG	3	.0000		
GEN	3		15.3333	
CRX	3		15.6667	15.6667
ERY	3			17.0000
Sig.		1.000	.634	.070

Means for groups in homogeneous subsets are displayed.

S17

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
ERY	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
OFL	3		16.3333
GEN	3		17.0000
Sig.		1.000	.063

Means for groups in homogeneous subsets are displayed.

S18

Duncan

Antibiotics	N	Subset for alpha = 0.05	
		1	2
CAZ	3	.0000	
CRX	3	.0000	
CTR	3	.0000	
ERY	3	.0000	
CXC	3	.0000	
AUG	3	.0000	
OFL	3		17.0000
GEN	3		17.6667
Sig.		1.000	.063

Means for groups in homogeneous subsets are displayed.

S19

Duncan

Antibiotics	N	Subset for alpha = 0.05			
		1	2	3	4
CAZ	3	.0000			
CRX	3	.0000			
CTR	3	.0000			
CXC	3	.0000			
AUG	3	.0000			
GEN	3		14.0000		
OFL	3			15.6667	
ERY	3				17.3333
Sig.		1.000	1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S20

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
CRX	3	.0000		
CTR	3	.0000		
ERY	3	.0000		
CXC	3	.0000		
AUG	3	.0000		
OFL	3		16.6667	
GEN	3			18.0000
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

S21

Duncan

Antibiotics	N	Subset for alpha = 0.05		
		1	2	3
CAZ	3	.0000		
GEN	3	.0000		
CTR	3	.0000		
CXC	3	.0000		
OFL	3	.0000		
AUG	3	.0000		
ERY	3		15.0000	
CRX	3			17.0000
Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.

Peer-review history:
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