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Comparative Analytics of urine sample reported with Urinary tract infection

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Abstract

Urinary tract infection (UTI) has been reported most often in recent days. In a clinical aspect there are various reasons for this cause. Out of 100 samples tested (Clinical samples from Rashi Diagnostic Center-Bangalore NABL laboratory), under the analytical aspect several comparative analysis was done. Urine was tested within half an hour of the collection. Physical characteristics of Urine sample were studied initially. Laura M is the device used to analyses the Uro-dip. Sugar and the presence of albumin was also found. Sediment of the centrifuged sample was subjected to gram staining and direct microscopic analysis. Pus cells, epithelial cells, yeast cells and rod shaped bacteria. It was found that epithelial cells are visualized in female samples and very less or not visualized in male samples. Bilirubin content, Bile salt content and ketone bodies were analyzed and compared in each of the samples. Sample is then subjected to culturing were the T streak is done on the Mac Conkey agar and Blood agar. This will differentiate between the lactose and Non-Lactose fermenting bacteria. Each of the colony is subjected to Gram staining. Yeast cells are also reported often. Though the yeast cells are the commensals they are considered non- pathogenic. But it was found that the yeast with pseudo-hyphae are pathogenic in nature. Both Lactose and Non-Lactose fermenting bacterial colonies from Blood agar is subjected to various biochemical methods to identify the organism. The most commonly noticed non-lactose fermenting organism was Pseudomonas spp. And Lactose fermenting organisms were Escherichia coli, Enterobacteria spp and Klebsiella spp. Each Colony from the culture plate was picked and streaked on the MHA agar and Kirby Bauer method has been performed (Disc diffusion method) under the McFerland standard. Zone of inhibition of each organism towards the antibiotic in the disc was recorded.

Key words: Urine sample, Epithelial cells, Urinary Tract Infection, Commensal, Kirby Bauer method,

Introduction

Pathogen that contributes to Urinary tract infection is a serious threat to mankind that's been considered as serious illness. Most common bacterial infection is found to be UTI. UTI is the most common hospital acquires nosocomial infection (Ariathianto Y 2011).Worldwide around 150million people are diagnosed per year. Females are more prone to Urinary tract infection than males (Akinkugbe et al., 1973). This is due to shorter and wider urethra. The Female reproductive anatomy paves a way for more chances of procuring urinary tract infection(Brotman RM, Shardell MD, Gajer Pet al.2014) . Association between the vaginal microbiota, menopause status and signs of vulvovaginal atrophy (Arthur et al., 1975; Duerden et al., 1990). Even though UTI is not taken seriously as other diseases the severity of the disease is so dangerous may lead to death at times. Clinical presentation varies with patients. UTI could be symptomatic with typical signs and symptom, or asymptomatic (Vogel T, Verreault R, Gourdeau Met al 2014.). Diagnostic Criteria of Nuetropenic patients who do not have pyuria are quite different. (Stamm, 2002; Weinstein, 1997). Urinary tract infection causes infection not only in urinary bladder but also to the kidney, ureter, and urethra and urinary bladder of course. Kindey is the two beaned shaped organ that filters the blood to synthesize urine. (Al-Badr A and Al-Shaikh G, 2013) Bladder is a ballon shaped organ that stores urine., Ureters are the two tubes that carry urine from kidneys to bladder and urethra carries urine from bladder to the outside of the body. (Bjerklund Johansen, T.E.; Botto, H.; Cek, M.; Grabe, M.; Tenke, P.; Wagenlehner, F.M.E.; Naber, K.G 2011).Severity of the disease depends upon the etiologic organisms, severity of the infection and the immunogenic response. Fever , urinary urgency, dysuria, cloudy/ dark colored urine. People with no neural abnormalities, strong immune response and structural issues are likely to show less symptoms and recover soon. Risk of UTI increases with cystitis, famility history, fever, female gender, sexual activity, vaginal infection, diabetes, obesity and genetic susceptibility(Bradley MS, Beigi RH, Shepherd JP 2019).Complicated UTI occurs when the individual is immunosuppressed, renal failure, cervical issue, neurological diseases due to urinary retention, pregnancy, or usage of catheters or other drainage devices. (Schappert, 1999)., (Wagenlehner, F.M.E.; Naber, K.G 2011).

Asymptomatic urinary tract infected Patients UTI are more likely to be cured with simple medication such as antibiotics (Beveridge LA, Davey PG, Philips G and McMurdo MET.2011). Continuous medication might lead to alteration of normal flora of vagina and gastrointestinal tract and multi drug resistance paves way for rick of

colonization of uropathogens(Wagenlehner, F.M.E.; Naber, K.G 2012).Infection is mild and harmless at the initial stages but if neglected would cause serious lethal clinical manifestation. (Stamm, 2002; Weinstein, 1997). Biofilm formed on the tissue is the cause of the disease. To generalize it is the gram-negative bacteria that is responsible for the infection. (Cai T, Mazzoli S, Mondaini Net al. 2014)Adverse outcome of the infe ction is severe. UTI can be categorized as upper and lower urinary tract infection. Kidneys are situated at the either side of the spinal column and are capable of purifying blood and water which in turn regulates the blood pressure and the water and mineral content in the body respectively. They also continuously filter and cleanse the blood where the waste been eliminated by the body via urine. When kidney receives blood and these blood are filtered by Nephrons and thus urine is been synthesized. Urine moves through the ureter and reaches the urinary bladder and flows out of the body via urethra. (Stamm, 2002; Weinstein, 1997) (Wagenlehner, F.M.E.; van Oostrum, E.; Tenke, P.; Tandogdu, Z.; Cek, M.; Grabe, M.; Wullt, B.; Pickard, R.; Naber, K.G.; Pilatz, A.; et al 2011)

Materials and Methods

Study population: The study population are the patients with suffering symptomatic urinary tract infection.

Hundred (100) patients who were clinically diagnosed with UTI collected from Rashi Diagnostic Center-Bangalore NABL laboratory),were involved in the study. Sample of 50 males and 50 females and aged above 20 years were considered. (Choudhury S, Das SK, Jana D and Pal DK.2014) Few were excluded from the study who were not suffering from UTI and patients who have already stared the medication course such as antibiotics. Sample was collected any time in the day throughout, mid-stream urine was collected in a sterile screw cap topped bottle. The bottle was mentioned with the Name, age, sex and a bar code unique for each patient's sample. And the sample was examined on its physical, chemical and microscopic aspect in the next half an hour of the collection time.

Table 1: Colony characteristics of Bacteria isolated.

Sl. No.	Colony morphology	Code
1	Colourless, circular, smooth colonies with entire edge	B1
2	Pale white/ translucent colonies, convex, circular colonies.	B2
3	Mucoid, pale, convex, entire edged.	B3
4	Slightly yellow colonies, entire edged, smooth surface and opaque.	B4
5	Pale circular, mucoid colonies raised and entire edged.	B5

Physical characteristics of Urine sample were studied initially. Sugar (Glucose) and the presence of albumin was also found. . Laura M is the device used to analyses the Uro-dip. Urine when centrifuged, Sediment of the centrifuged sample was subjected to gram staining

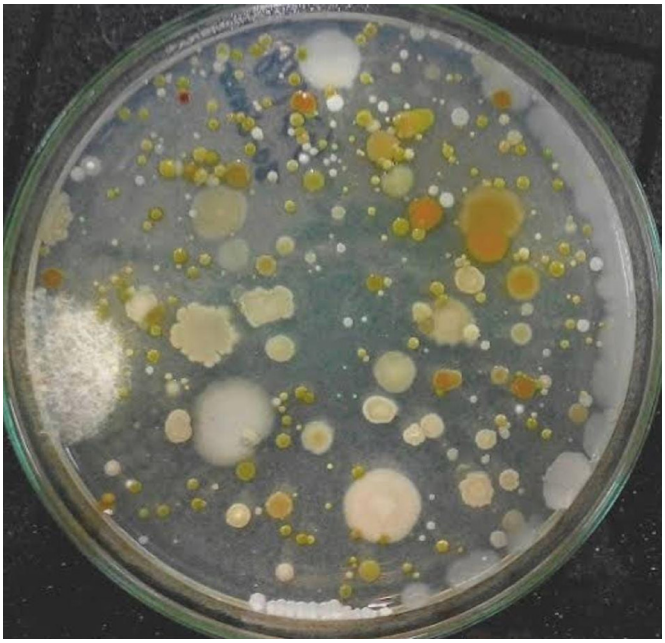
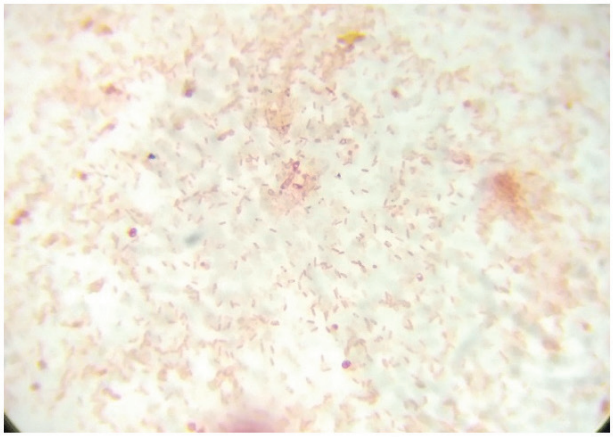
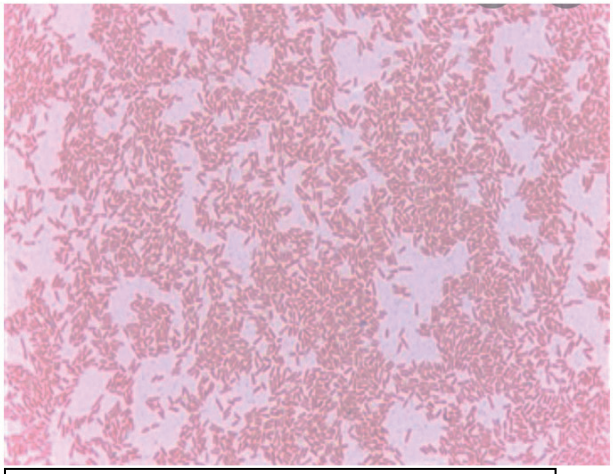


Figure 1: Crowd plate technique of Urine Sample(Pour plate Method)

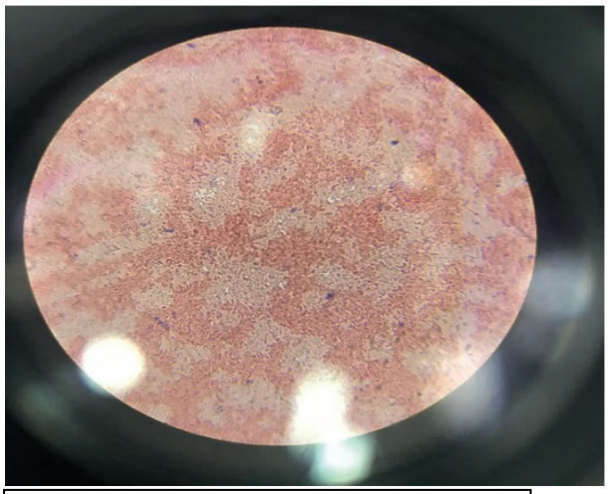
and direct microscopic analysis. Centrifugation is done at 5000 rpm for 5 min. The deposits were examined using both x10 and x40 objectives. (Al-Badr A and Al-Shaikh G2013) Samples with 10 white blood cells/mm 3 were



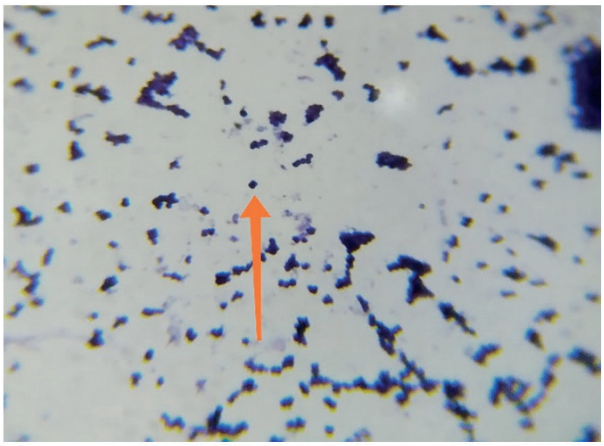
A. B1 Gram negative rods



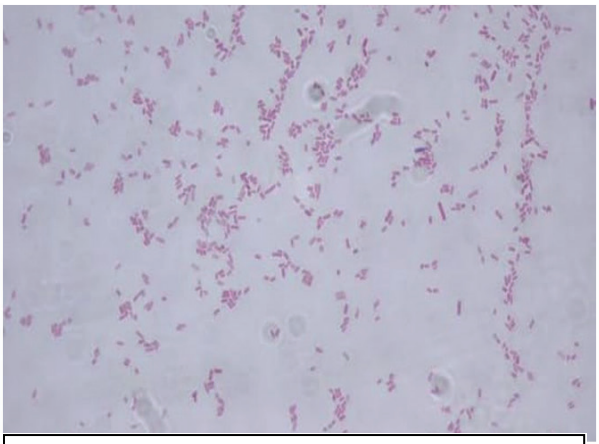
B. B2 Gram negative rods in chains



C. B3 Gram negative cocci in clusters



D. B4 Gram positive cocci



E. B5. Gram negative rods

FIG 3.1 INDOLE TEST

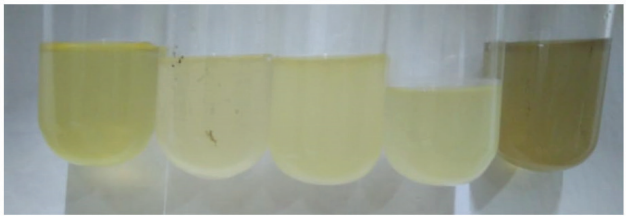


FIG 3.2 METHYL RED

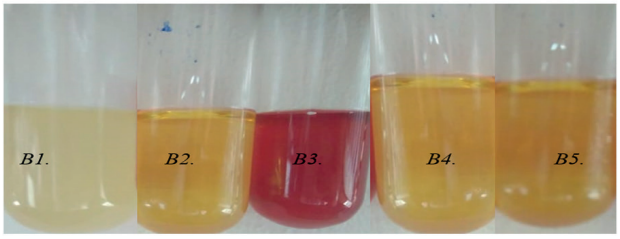


FIG 3.3 . VOGES

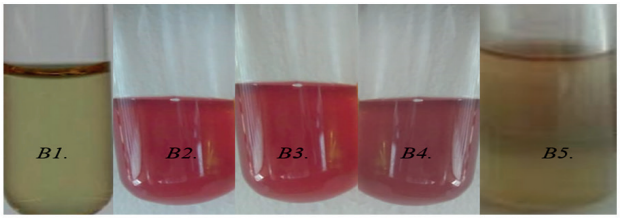
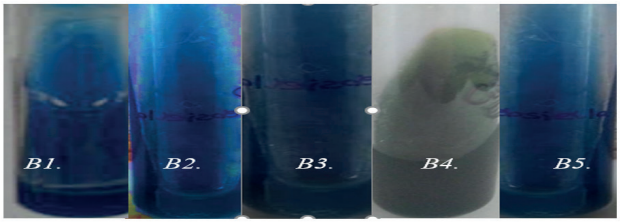
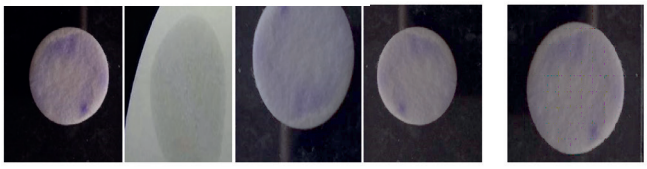


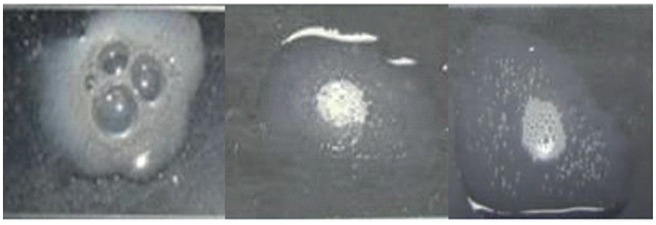
FIG 3.4 . CITRATE UTILIZATION

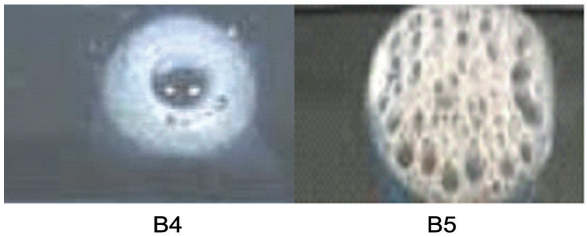


(FIG 3.5)OXIDASE TEST



(FIG 3.6)CATALASE TEST





regarded as pyuric (Smith et al., 2003). A volume of the urine samples were applied to a glass microscope slide, observed directly with the cover slip or allowed to air dry, stained with gram stain, and examined microscopically. (Chu CM and Lowder JL. 2018)Pus cells, epithelial cells, yeast cells and rod shaped bacteria. It was found that epithelial cells are visualized in female samples and very less or not visualized in male samples. Bilirubin content,

Bile salt content and ketone bodies were analyzed and compared in each of the samples. (Wagenlehner, F.M.E.; Naber, K.G 2011) Sample is then subjected to culturing were the T streak is done on the Mac Conkey agar and Blood agar. (Fig1) (Fig 2)(Table 1) Plastic calibrated loop was used for the semi – quantitative method which has a 4.0mm diameter to deliver 0.01ml. Loop full of well mixed urine sample was inoculated into the MacConkey agar. All plates were then incubated at 37^{o}C aerobically for 24 hours. This will differentiate between the lactose and Non-Lactose fermenting bacteria. Each of the colony is subjected to Gram staining. Yeast cells are also reported often. Though the yeast cells are the commensals they are considered non- pathogenic. But it was found that the yeast with pseudo-hyphae are pathogenic in nature. Both Lactose and Non-Lactose fermenting bacterial colonies from agar is subjected to various biochemical methods to identify the organism. Number of bacterial colonies (Fig 2) MICROSCOPIC VIEW OF ISOLATED ORGANISMS AFTER GRAM'S STAINING

were counted and multiplied by 100 in order to given an estimate the number of bacteria present per milliliter of urine. Each Colony from the culture plate was picked and streaked on the MHA agar and Kirby Bauer method has been performed (Disc diffusion method) under the Mc Ferland standard.). Antibiotic susceptibility testing was done were method used with standardization of the inoculum size was agar diffusion method (Baur et al. 1996). Interpretation of results was done using the zone sizes. Zones of inhibition of 18 mm was considered sensitive, 13-17 mm intermediate. Zone of inhibition of each organism towards the set of antibiotics used in the disc was recorded. (Wagenlehner, F.M.E.; Hoyme, U.; Kaase, M.; Fünfstück, R.; Naber, K.G.; Schmiemann, 2011)

Results and Discussion

100 specimens examined in this study, where all the sample showed common casual organism, the combination and concentration of the organisms tend to cause the disease serve. The microscopic examination of the centrifuged urine sample revealed that almost all the sample showed significant pyuria that pus cells quite numerous (6-8) and considered 8/hpf (high per filed) (Grabe, M.; Bjerklund-Johansen, T.E.; Bartoletti, R.; Çek, M.; Naber, K.G.; Pickard, R.S.; Tenke, P.; Wagenlehner, F.; Wullt, P. 2014).The result also proves that the patients aged above 35showed more severity of infection. The older the individual is, the more likely they are prone to UTI. Where the patients around 20-27years old they tend to recover soon even if they are infected. Again comparatively, there were more cases in females than males. Of the 100 isolates obtained,occurance of gram negative bacteria were more than gram positive bacteria. Gram negative bacteria includes *Escherichia coli 31* % ,*Pseudomonas aeruginosa*(30.78%), Xanthomonas spp 10% and *Klebsiella aerogenes*(19%). (Fig4 and Fig 5) Enumeration of Gram positive bacteria was found to be 9.22% only of the isolates (Cortes-Penfield NW, Trautner BW and Jump RLP. 2017)They include *Staphylococcus spp*. It was also found that the rate of isolates of E. coli and P. aeruginosa were higher in isolates exclusively from females. (Wagenlehner, F.M.E.; Hoyme, U.; Kaase, M.; Fünfstück, R.; Naber, K.G.; Schmiemann, 2011). The antibiotic sensitivity pattern of the organisms isolated against common anti-microbial agents is shown in results indicated that quinolones, Aztreonam 30,cefepime were the most potent of all the antibiotics. Nitrofurantoin, Ampicillin, Ofloxacin and Cotrimoxazole were poorly effective. (Bleidorn, J.; Gagyor, I.; Kochen, M.M.; Wegscheider, K.; Hummers-Pradier, E.2014) (Colgan R, Williams M.2011)

(Figure 4)Pseudomonas aeruginosa strain AQ_BF36 (Accession number: KY857862.1)

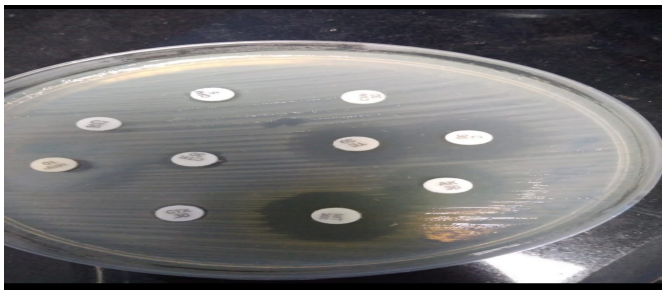
(Figure 5)Xanthomonas campestris pv. vesicatoria strain 8004 (Accession number-NC007508.1)

IDENTIFICATION OF MICRO ORGANISMS BY 16s rRNA SEQUENCING

The use of 16S rRNA gene sequencing used for the study of bacterial phylogeny and taxonomy has been by far the most common housekeeping genetic marker used for a number of reasons. These reasons include its presence in almost all bacteria, often existing as a multigene family, or operons; the function of the 16S rRNA gene over time has not changed, suggesting that random sequence changes are a more accurate measure of time(evolution); and the 16S rRNA gene(1500 bp) is large enough for informatics purposes.(Fig4 and Fig 5)

Antibiotic sensitivity of Xanthomonas campestris organism.

The organism is grown against common anti-microbial agents (antibiotics) to find out the antibiotic sensitivity pattern. Results indicated that Oflaoxacin, Chloramphenicol, Amakacin, Azithromycin, 30, Gatiflaxacin were the most potent of all the antibiotics. Cloxacellin, Ampicillin, Vancomycin and Cotrimoxazole were poorly effective. (Figure 6)



(Figure 6) Antibiotic sensitivity of Xanthomonas campestris organism.

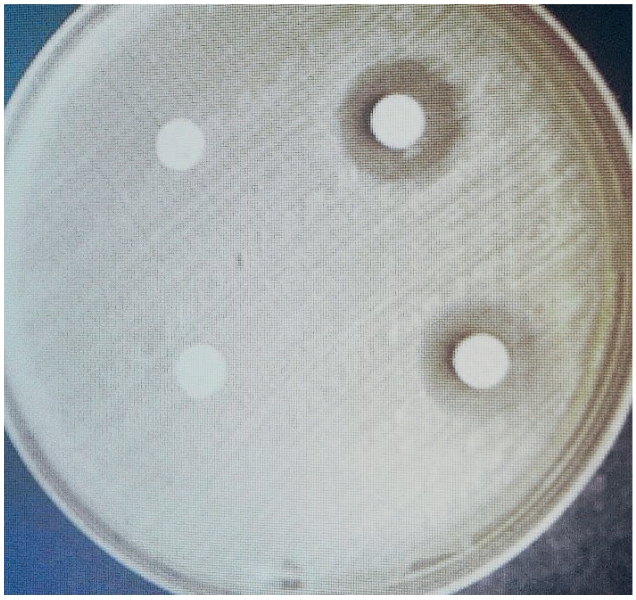
Antibiotic sensitivity of Pseudomonas aeruginosa strain AQ_BF36

The organism is grown against common anti-microbial agents (antibiotics) to find out the antibiotic sensitivity pattern. Results indicated that Ciprofloxcin, Augmentin, Gentamicin and Tetracycline were the most potent of all the antibiotics. Linomycin, Vancomycin, Streptomycin, trimethoprim and Penicillin were poorly effective. (Figure 7)

(

Figure 7) Antibiotic sensitivity of Pseudomonas aeruginosa strain AQ_BF36 Antibiotic sensitivity of Klebsiella spp.

The organism is grown against common anti-microbial agents (antibiotics) to find out the antibiotic sensitivity pattern. Results indicated that Ciprofloxacin, Imipenem were the most potent of all the antibiotics. Amoxicillin and amikacin were poorly effective. (Figure 8)



(Figure 8) Antibiotic sensitivity of Klebsiella spp.

Antibiotic sensitivity of Staphylococcus spp.

The organism is grown against common anti-microbial agents (antibiotics) to find out the antibiotic sensitivity pattern. Results indicated that Penicillin, Oxacillin, Cephalothin, Trimethoprim, Tlosin were the most potent of all the antibiotics. Ampicillin was poorly effective. (Figure 9)

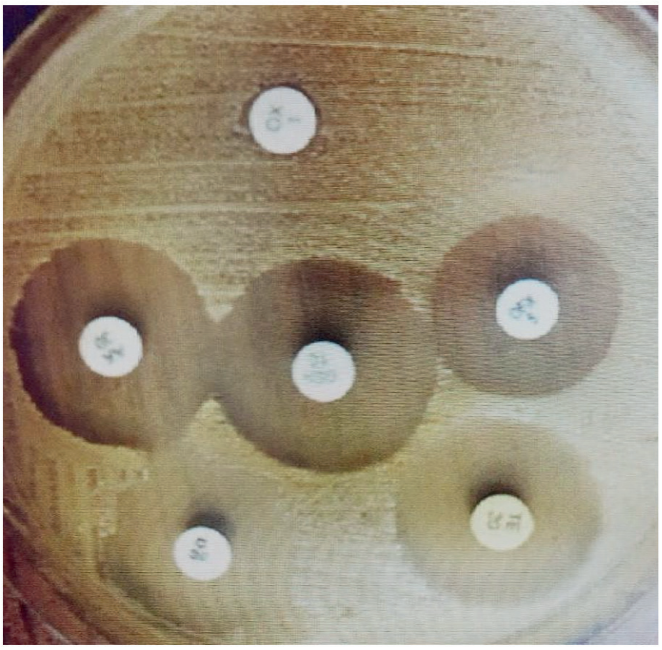
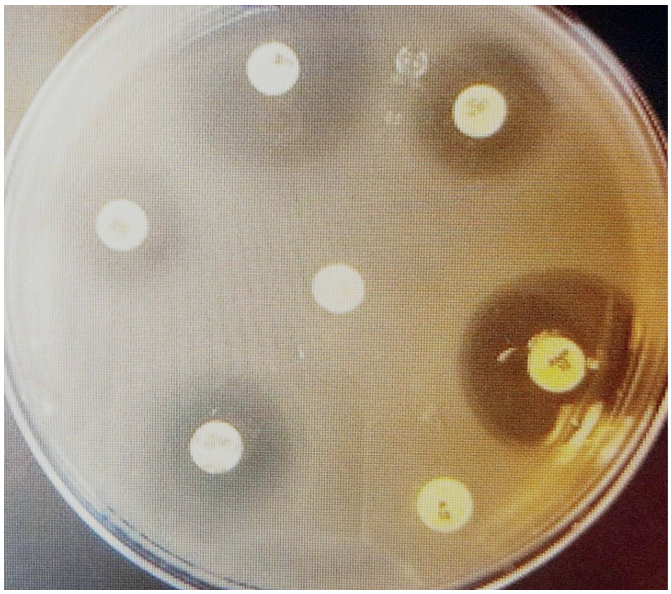


Figure 9) Antibiotic sensitivity of Staphylococcus spp.

Antibiotic sensitivity of Escherichia coli.

The organism is grown against common anti-microbial agents (antibiotics) to find out the antibiotic sensitivity pattern. Results indicated that Amikacin, Norfloxacin, Gentamicin, tobramycin were the most potent of all the antibiotics. Ceftriaxone, Cefepime, and Cefepime were poorly effective. (Figure 10)



(Figure 10) Antibiotic sensitivity of Escherichia coli.

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