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ORIGINAL ARTICLE

Identification and Susceptibility Testing of Non-Lactose Fermenting Gram-negative Bacilli in Urinary Tract Infection

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ABSTRACT

Background: *Urinary tract infections are one of the most common bacterial infections in humans both in community and hospital settings. The etiology of UTIs and the antimicrobial susceptibility of urinary pathogens have been changing over the years.* ***Objectives:*** *This work aimed to compare the accuracies of API 20E, Vitek1 system with GNI card with conventional reference biochemical tests for the identification of non-lactose fermenting Gram-negative bacilli in patients with urinary tract infection.* ***Methodology:*** *This study was conducted on 320 patients attending outpatient urology clinic. Physical, chemical, and microscopic examinations were done first to urine samples. Then, urine samples with pus cells <10 per high power field (HPF) or with bacterial cells or yeast were chosen for culture. These samples were 142 out 320 urine samples. These urine samples were isolated on nutrient, blood & MacConkey's agar media.* ***Results:*** *Standard bacteriological identification was done for all isolates (187 isolates) by colony morphology and microscopic examination. Only non-lactose fermenting Gram-negative bacilli (60 isolates) were further examined. Other growths were excluded. Motility test, biochemical reactions by conventional methods, API 20E, and vitek1 system with GNI card were done on non-lactose fermenting Gram-negative bacilli. Antibiotic susceptibility test by reference broth microdilution MIC procedure and Vitek1 system with GNI-108 card were done on non-lactose fermenting Gram-negative bacilli. One hundred thirty-five strains isolated from 94 hospitalized catheterized patients and fifty-two strains isolated from 48 outpatients sixty isolates (32.1%) were non-lactose fermenting Gram-negative bacilli. Out of them (thirty-one (16.5%) Pseudomonas aeruginosa, twenty (10.7%) Proteus mirabilis, six (3.2%) Proteus vulgaris, and three (1.6%) Providencia stuartii). After completion of supplemental tests, there was no difference between API 20E and vitek1 system in their ability to correctly identify Proteus mirabilis, Proteus vulgaris, and Providencia stuartii to the species level with there was difference between identifying isolates from Pseudomonas aeruginosa with vitek1 system.* ***Conclusion:*** *API 20E needs more time than vitek1 for identification of Proteus mirabilis, Proteus vulgaris, Providencia stuartii, and Pseudomonas aeruginosa, the most effective antibiotic against Pseudomonas aeruginosa isolates was ticarcillin/clavulant (77.4%), for Proteus mirabilis isolates were aztreonam and imipenem (each with 100%), for Proteus vulgaris isolates was imipenem (100%), and for Providencia stuartii isolates were amikacin, aztreonam, ciprofloxacin, imipenem, and TMP/SMX (100%).*

INTRODUCTION

Urinary tract infection (UTI) remains the most common reason for outpatients to seek medical care and for inpatients to develop nosocomial infection. Nosocomial UTIs account for up to 40% of all hospital-acquired infections. The associated morbidity and mortality are the major drain on hospital resources[1]. The etiology of UTIs and the antimicrobial susceptibility of urinary pathogens have been changing over the years. There has been a growing rate of resistance among common urinary tract pathogens.[2] Bacterial identification and susceptibility testing system, both manual and automated, are in widespread use today in clinical microbiology laboratories. The automated systems offer decreased turnaround and hands-on time compared with those offered by conventional tube biochemical identification schemes[3].

One of the most widely used systems for identification in hospital laboratories is API 20E system. Which designed for identification of the *Enterobacteriaceae*, has been extended to include the identification of NFBs as well. To maximize the use of the API 20E for nonfermenters. Six additional tests are added to generate a nine-digit profile number in the original one. Although the API 20E system identifies

Pseudomonas aeruginosa (*P. aeruginosa*), *Stenotrophomonas maltophilia (S.maltophilia)*, and *acinetobacter* species with up to 99% accuracy, particularly after 48 hours of incubation, the performance with other less common nonfermenters was often less acceptable[4].

The vitek system is an automated method for performing same-day identification and antimicrobial susceptibility tests on nonfastidious bacteria. As regards identification, Vitek system determines colorimetric and turbidimetric changes each hour and compared each reading with the initial base reading. The percent change for each well was calculated to determine a positive or negative reaction. Final results were available in 4 to 13h for isolates of the family *Enterobacteriaceae* and in 6 to 18h for nonenteric Gram-negative bacilli (GNB) [5].

This work aimed to compare the accuracies of API 20E and Vitek1 system with GNI card with conventional reference biochemical tests for the identification of non-lactose fermenting Gram-negative bacilli in patients with urinary tract infections. And also to evaluate the accuracy of vitek1 system with GNS-108 card with a reference broth micro dilution MIC procedure for the antibiotic susceptibility testing of non-lactose fermenting Gram-negative bacilli in patients with urinary tract infections.

METHODOLOGY

This study was conducted on 320 patients either attending urology outpatient clinics or admitted to different wards and departments in Zagazig University Hospitals. Patients included 214 males (their ages range from 4 years to 70 years) and 106 females (their ages range from 6 years to 65 years). All the patients were complaining from symptoms of urinary tract infection such as frequency, painful micturition, haematuria, or urgency.

Urine samples were collected from non-catheterized and catheterized patients. Samples are transported to microbiology laboratory and examined and cultured as soon as possible. Physical and chemical examinations ware done by combur-9 test .

Microscopic examination to all samples and samples with pus >10 per high power field were cultured on nutrient agar, blood agar and MacConkey's agar media (oxid)using sterile wire loop. All plates are incubated aerobically at 37°c for 24 hours .

On the second day, bacteria were identified by colony morphology, microscopic examination and motility test. Conventional biochemical reactions [6], and Biochemical reactions were done using API 20E Strips to all isolates [7]. Identification was obtained with the numerical profile.

Biochemical reactions were done to all isolates on Vitek1 apparatus (the Vitek JR (junior). (bio Merieux Vitek, Inc, Paris, France).

Principle of Vitek1

The colonies are inoculated within a liquid medium and the organism will grow only if it is capable of utilizing each substrate. The biochemical test results are matched to the reaction file (data base). The reaction file is a matrix of percent probabilities of positive tests for each biochemical test and each organism identified by the card. Organism identifications are made by converting the results of the biochemical test into positive or negative test probabilities for each taxon listed in the reaction file.

Antimicrobial susceptibility testing :

Antimicrobial susceptibility testing were done using broth micro dilution methods and by Vitek1 system using different antibiotics.

Statistical analysis:

All data coded, entered and checked to SPSS (statistical Package for Social Science).

Data analysis:

- **MIC_{50}** and **Mic_{90}** : MICs at which 50% and 90% of the tested isolates were inhibited were determined for each antibiotic.
- **Discrepancy:**
  - **Very major errors:** They were considered when and organism was defined as resistant by the reference method but was categorized as susceptible with the Vitek1 system.
  - **Major errors:** They were considered when an organism was defined as susceptible by the reference method but was categorized as resistant with the Viek1 system.
  - **Minor errors:** They were considered when an organism found to be susceptible or resistant either by the reference broth microdilution or with Vitek1 system but intermediate by the other method.
  - **Complete Agreement (CA):** Very major, major, and minor discrepancies were considered as errors.
  - **Essential Agreement (EA):** Only very major and major discrepancies were considered as errors.

RESULTS

Table 1: Distribution of isolated organisms from hospitalized catheterized patients and outpatients with UTI.

Isolated organisms	Isolates from hospitalized catheterized patients (135)		Isolates from outpatients (52)		Total	%	OR (95%CI)	X^2
	No	%	No	%				
Lactose fermenting GNB	60	44.4	30	57.7	90	48.1	0.59 (0.29-1.18)	2.64
Lactose non-fermenting GNB:	49	36.3	11	21.1	60	32.1	2.12 (1.0-4.84)	3.95
Proteus mirabilis	15	11.1	5	9.6	20	10.7	1.17 (0.37-3.94)	0.09
Proteus vulgaris	5	3.7	1	1.9	6	3.2	1.96 (0.21-45.5)	Fisher exact =1.0
Providencia stuartii	3	2.2	0	0.0	3	1.6	Undefined	Fisher exact =0.56
Pseudomonas aeruginosa	26	19.3	5	9.6	31	16.5	2.24 (0.76-7.12)	2.52
Staphylococci	10	7.4	5	9.6	15	8	0.75 (022-2.68)	Fisher exact = 1.0
Candida	16	11.9	6	11.5	22	11.8	1.03 (0.35-3.16)	0.0

This table shows there is significant difference between non-lactose fermenting GNB isolated from the hospitalized catheterized patients and outpatients. The non-lactose fermenting GNB have an increased risk of UTI from the hospitalized catheterized patients than outpatients (OR=2.12)

Table 2: Distribution of non-lactose fermenting organisms

Non-lactose Fermenting organisms	Isolates from hospitalized catheterized patients		Isolates form outpatients		OR (95%CI)	P value
	No	%	No	%		
Proteus mirabilis	15	30.6	5	45.5	0.50 (0.11-22.8)	0.31
Proteus vulgaris	5	10.2	1	9.1	1.14 (0.1-28.6)	1.0
Providencia stuartii	3	6.1	0	0.0	Undefined	1.0
Pseudomonas aeruginosa	26	53.1	5	45.5	1.36 (0.31-6.06)	0.64

This table shows no significant difference between different non-lactose fermenting GNB isolates from hospitalized catheterized patients and outpatients. There is increased risk of UTI by *Proteus vulgaris* and *Pseudomonas aeruginosa* in hospitalized catheterized patients than outpatients (OR=1.14-1.36).

Table 3: Distribution of non-lactose fermenting organisms causing UTI in relation to each other.

Non-lactose fermenting organisms	No	%
Proteus mirabilis	20	33.3
Proteus vulgaris	6	10
Providencia stuartii	3	5
Pseudomonas aeruginosa	31	51.7

This table shows that *Pseudomonas aeruginosa* was the highest organism (51.7%) isolated and *Providencia stuartii* was the least organism isolated (5%).

Table 4: Identification of non-lactose gram negative bacilli causing UTI by conventional methods, API 20E, and Vitek 1

Organisms	Conventional BR as reference method	Number of isolates									
		Identified as						With no identification		Needing supplemental testing	
		Correct species		Correct genus only		Incorrect genus or species					
		API	Vitek	API	Vitek	API	Vitek	API	Vitek	API	Vitek
Proteuns mirabilis	20	20	20	0	0	0	0	0	0	0	0
Proteus vulgaris	6	6	6	0	0	0	0	0	0	0	0
Pseudomonas aeruginosa	31	31	31	0	0	0	0	0	2	29	0
Providencia stuartii	3	3	3	0	0	0	0	0	0	0	0

This table shows after the completion of supplemental testing, there was no difference between API 20E and Vitek 1 system in their ability to correctly identify *Proteus mirabilis*, *Proteus vulgaris*, and *Providencia stuartii* to the species level while there was difference between API 20E and Vitek1 system, with API 20E correctly identifying to the species level more isolated from *Pseudomonas aeruginosa* than Vitek 1 system.

Table 5: Incubation times in hours required for API 20E and Vitek1 Results to be correct to genus and species for all organisms tested.

Organisms	API 20E X±SD	Vitek 1 X±SD	Pt	P
Proteus mirabilis	20.8±1.66	67. ±2.53	25.1	<0.001
Proteus vulgaris	21.3±2.5	9.5±0.88	14.7	0.001
Pseudomonas aeruginosa	48.2±4.7	6.8±.27	38.9	0.001
Providencia stuartii	21±3	6±1	7.2	0.001

This table shows that there is a high significant difference between API 20E and Vitek 1 in the time needed for identification of *Proteus mirabilis*, *Proteus vulgaris*, *Providencia stuartii*, and *Pseudomonas aeruginosa* with API 20E needed more time than Vitek1 for their identification (p value <0.001).

Table 6: EA, CA and discrepancies between Vitek 1 and references microdiluation method for 31 *Pseudomonas aeruginosa* isolates

Antibiotic	*No (5) of strains with*									
	EA		CA		Minor		Major		Very major	
	No	%	No	%	No	%	No	%	No	%
Amikacin	29	93.55	24	77.4	5	16.1	2	6.5	0	0.0
Ampicillin	30	96.8	28	90.3	2	6.5	0	0.0	1	3.2
Aztreonam	27	88.4	23	74.1	4	12.9	1	3.2	3	9.7
Cefazolin	30	96.8	29	93.5	1	3.2	0	0.0	1	3.2
Cefotaxime	31	100	24	76.7	7	22.6	0	0.0	0	0.0
Cefoxitin	31	100	29	93.5	2	6.5	0	0.0	0	0.0
Ceftazidime	29	93.5	22	70.5	7	22.6	0	0.0	2	6.5
Ceftazidime	31	100	30	96.8	1	3.2	0	0.0	0	0.0
Ciprofloxacin	28	90.3	24	77.4	4	12.9	3	9.7	0	0.0
Gentamicin	27	88.4	25	80.6	2	6.5	3	9.7	1	3.2
Imipenem	29	93.5	24	78.2	5	16.1	2	6.5	0	0.0
Nitrofurntoin	29	93.5	28	90.3	1	3.2	0	0.0	2	6.5
Piperacillin	26	83.9	25	80.6	1	3.2	0	0.0	5	16.1
Ticarcillin/Clavulante	30	96.8	28	90.3	2	6.5	0	0.0	1	3.2
Tobramycin	29	93.5	27	88.4	2	6.5	2	6.5	0	0.0
TMP/SMX	31	100	26	83.6	5	16.1	0	0.0	0	0.0
Overall correlation	27	94.3	26	83.9	3	10.3	1	3.2	1	3.2

This table shows that EA for Vitek 1 for All antibiotics with *Pseudomonas aeruginosa* was 94.3% CA was 83.9%, ME was 10.3% ME was 3.2% and VME was 3.2%.

Table 7: EA, CA and discrepancies between Vitek 1 and references microdiluation method for 20 *Proteus mirabilis* isolates

Antibiotic	No (%) of strains with									
	EA		CA		Minor		Major		Very major	
	No	%	No	%	No	%	No	%	No	%
Amikacin	20	100	16	80	4	20	0	0.0	0	0.0
Ampicillin	19	95.0	18	90	1	5	1	5	0	0.0
Aztreonam	20	100	15	75	5	15	0	0.0	0	0.0
Cefazolin	19	95	15	75	4	20	1	5	0	0.0
Cefotaxime	19	95	18	90	1	5	0	0.0	1	5
Cefoxitin	19	95	16	80	3	15	0	0.0	1	5
Ceftazidime	19	95	14	70	5	25	0	0.0	1	5
Ceftazidime	17	85	16	80	1	5	2	10	1	5
Ciprofloxacin	19	95	19	95	0	0	1	5	0	0.0
Gentamicin	20	100	18	90	2	10	0	0.0	0	0.0
Imipenem	17	85	16	80	1	00.0	3	15	0	0.0
Nitrofurntoin	19	95	18	90	1	5	0	0.0	1	5
Piperacillin	20	100	20	100	0	0.0	0	0.0	0	0.0
Ticarcillin/Clavulante	19	95	19	95	0	0.0	0	0.0	1	5
Tobramycin	20	100	17	85	3	15	0	0.0	0	0.0
TMP/SMX	19	95	15	75	4	20	1	5	0	0.0
Overall correlation	19	95	17	85	2	10	1	5	0	0.0

This table shows that EA for Vitek 1 for all antibiotics with Proteu mirabilis was 95% CA was 85%, mE was 10% ME was 5% and there was no VME.

Table 8: EA, CA and discrepancies between Vitek1 and reference microdiluation method for 6 *Proteus vulgaris* isolates.

Antibiotic	No (%) of strains with									
	EA		CA		Minor		Major		Very major	
	No	%	No	%	No	%	No	%	No	%
Amikacin	6	100	5	83.3	1	16.7	0	0.0	0	0.0
Ampicillin	6	100	6	100	0	0.0	0	0.0	0	0.0
Aztreonam	5	83.3	4	66.6	1	16.7	0	0.0	1	16.7
Cefazolin	5	83.3	4	66.6	1	16.7	1	16.7	0	0.0
Cefotaxime	6	100	5	83.3	1	16.7	0	0.0	0	0.0
Cefoxitin	6	100	5	83.3	1	0.0	0	0.0	0	0.0
Ceftazidime	6	100	4	66.6	2	33.3	0	0.0	0	0.0
Ceftazidime	5	83.3	5	83.3	0	0.0	0	0.0	1	16.0
Ciprofloxacin	6	100	6	100	0	0.0	0	0.0	0	0.0
Gentamicin	6	100	6	100	0	0.0	0	0.0	0	0.0
Imipenem	5	83.3	4	66.6	1	16.7	0	16.7	0	0.0
Nitrofurntoin	6	100	6	100	0	0.0	1	0.0	0	0.0
Piperacillin	6	100	4	66.6	2	33.3	0	0.0	0	0.0
Ticarcillin/Clavulante	6	100	6	100	0	0.0	0	0.0	0	0.0
Tobramycin	6	100	5	83.3	1	16.7	0	0.0	0	0.0
TMP/SMX	6	100	4	66.6	2	33.3	0	0.0	0	0.0
Overall correlation	6	100	5	83.3	1	17.6	0	0.0	0	0.0

This table shows that EA for Vitek 1 for all antibiotics with *Proteus vulgaris* was 100%, CA was 83.3% ME was 17.6, and there was no ME and VME.

Table 9: EA, CA and discrepancies between Vitek1 and reference microdiluation method for 3 *Providencia stuartii* isolates

Antibiotic	No (%) of strains with									
	EA		CA		Minor		Major		Very major	
	No	%	No	%	No	%	No	%	No	%
Amikacin	3	100	3	100	0	0.0	0	0.0	0	0.0
Ampicillin	3	100	3	100	0	0.0	0	0.0	0	0.0
Aztreonam	3	100	2	66.7	1	33.3	0	0.0	0	0.0
Cefazolin	3	100	3	100	0	0.0	0	0.0	0	0.0
Cefotaxime	3	100	2	66.7	1	33.3	0	0.0	0	0.0
Cefoxitin	2	66.7	0	0.0	2	66.7	1	33.3	0	0.0
Ceftazidime	3	100	2	66.7	1	33.3	0	0.0	0	0.0
Ceftazidime	3	100	3	100	0	0.0	0	0.0	0	0.0
Ciprofloxacin	2	66.7	2	66.7	0	0.0	1	33.3	0	0.0
Gentamicin	2	66.7	2	66.7	0	0.0	1	33.3	0	0.0
Imipenem	3	100	2	66.7	1	33.3	0	0.0	0	0.0
Nitrofurntoin	3	100	3	100	0	0.0	0	0.0	0	0.0
Piperacillin	2	100	2	66.7	0	0.0	1	33.3	0	0.0
Ticarcillin/Clavulante	3	100	2	66.7	1	33.3	0	0.0	0	0.0
Tobramycin	2	66.7	2	66.7	0	0.0	0	0.0	1	33.3
TMP/SMX	2	66.7	2	66.7	0	33.3	1	33.3	0	0.0
Overall correlation	3	100	2	66.7	1	0.0	0	0.0	0	0.0

This table shows that EA for Vitek 1 for all antibiotics with *Providencia stuartii* was 100%, CA was 66.7%, ME was 33.3%, and there was no ME and VME.

DISCUSSION

Urinary tract infection (UTI) is an old problem that continues to present new challenges due to change in the etiology of UTIs and in the antimicrobial susceptibility of urinary pathogens over the years. Factors such as the changing in patient population and extensive use and abuse of antimicrobial agents could contribute to changes in the microbial profile of urinary tract isolates [8].

In the present study, the frequency of pathogens causing UTI is listed in (Table 1). The most frequently isolated species from hospitalized catheterized patients were: lactose fermenting GNB (44.4%), *Pseudomonas aeruginosa* (19.3%), *Candida* (11,9%), and *Proteus mirabilis* (11.1%), while from outpatients were : lactose fermenting GNB (57.7%) *Candida* (11.5%), *Pseudomonas aeruginosa*, *Proteus mirabilis*, and *Staphylococci* (9.6%for each) *Proteus vulgaris* (1.9%).

Neto et al. (2003)[9] results were in agreement with our results; they found that Gram-negative bacteria caused approximately 80% of cases with hospital-acquired UTI. The most common pathogens were E. coli (26%), klebsiella sp. (15%), *P. aeruginosa* (15%) and enterococcus sp. (11%).

In the present study, there was no significant difference between *Proteus* species isolates of hospital-acquired UTIs and community-acquired UTIs (p value >0.05) but there was 2 times risk of UTI by *Proteus* species in the hospital than in the community.

Zhonghua (1999)[10] results are the same as the results of our work; *Proteus* spp isolates were isolated 2 times more from patients with hospital-acquired UTIs (51/74, 68.9%) than from patients with community-acquired UTIs (23/74.31.1%).

Identification and therapy of GNB in hospitalized patients remain a major challenge for clinical microbiology laboratory because there are continued prominences of GNB as pathogens, development of antibiotic resistance, and the need to define the epidemiology of nosocomial infections. These needs require that laboratories provide rapid, accurate, and cost-effective identification and susceptibility of GNB[11].

Although the classical macro tube methods of bacterial identification remain useful as reference methods. They are to slow, cumbersome, and subjective for routine use in a clinical microbiology laboratory[12] .

Automated or semi automated commercial systems for bacterial identification and antibiotic susceptibility testing were introduced in clinical bacteriology laboratories more than 20 years ago. These systems have been developed to permit provision of test results in a matter o hours rather than days, as has been the case with traditional overnight procedures [13].

In the present study we compare the accuracy of API 20E and Vitek1 system with GNI card with the use of the different conventional biochemical reactions as a

reference method in the identification of non-lactose fermenting GNB isolated from those patients with UTI. After completion of supplemental testing, there was no difference between API 20E and Vitek1 system in their ability to correctly identify *Proteus mirabilis*, *Proteus vulgaris*, and *Providencia stuartii* to the species level. On the other hand, there was a difference between API 20E and Vitek1 system in identification of *Peudomonas aeruginosa* to the species level, with API 20E correctly identify more isolates than Vitek 1 system (table 4).

In the present study, API 20E needs more time than Vitek1 for the identification o *Proteus mirabilis*, *Proteus vulgaris*, *Providencia stuartii*, and Pseudomonas areuginosa (p value <0.001). The longest time for identification was with *Pseudomonas aeruginosa*. This was because *Pseudomonas aeruginosa* needs supplemental testing for its identification with API 20E (table 5).

These results coincide with the results of Eigner et al. (2003)[14] who found that API 20E correctly identified 48.3% of all isolates at 18 to 24 hours including 100% of the isolates of the family *Enterobacteriaceae* (*Proteus mirabilis*, *Proteus vulgaris* and *Providencia stuartii*) and 0% of *Pseudomonas aeruginosa* at 24 hours. After 48 hours, 6.5% of *Pseudomonas aeruginosa* was correctly identified following supplemental testing. 100% of *Pseudomonas aeruginosa* were correctly identified to the species level. On the other hand. Vitek1 system correctly identified to the species level 96% of all isolates at 10 hours, including 96.5% of the members of the *Enterobacteriaceae* and 96.7% of *Pseudomonas aeruginosa*. At 18 hours, 98.3% of the isolates were identified because one *Pseudomonas aeruginosa* did not been identified.

In our study, we evaluate Vitek 1 system with GNS-108 card, with use of broth micordilution as a reference method.

Table (6) presents the evaluation of the accuracy of Vitek1 system in testing the antimicrobial susceptibility of *Pseudomonas aeruginosa* isolated with broth microdilution method used as reference method the Essential Agreement (EA) for Vitek1 for all antibiotics with *Peudomonas aeruginosa* was 94.3% the complete agreement (CA) for Vitek1 range from 70.5% (Ceftazidime) to 96.8% (Ceftizoxime). The Vitek1 Minor errors (mE) rate was 10.3%. the mE rate was higher with cefotaxime and ceftazidime (22.6%) and lower with cefazolin, ceftizoxime, nitrofurantoin, and piperacillin (3.2%). The Vitek1 Major Errors (ME) rate was 2.6%. No ME rate with ampicillin, cefazolin, cefotaxime, cefoxith, ceftazidime, ceftizoxime, nitrofurantoin, piperacillin, ticarcillin/clavulante, and TMP/SMX. The ME was higher with ciprofloxacin and gentamicin (9.7%) and lower with cefazolin, ceftizoxime, nitrofurantoin, and piperacillin (3.2%). The The Vitek1 Very Major Errors (VME) rate was 3.2% No VME rate with amikacin, cefotaxime, cefoxitin, ceftizoxime, ciprofloxacin, imipenem, tobramycin, and TMP/SMX. The VME was higher with piperacillin (16.1%).

According to NCCLS (1996),[15] the higher very major errors observed with *P. aeruginosa* and piperacillin (16.1%) and ticarcillin/clavulanate (3.2%) may have been influenced by the fact that no intermediate MIC interpretive category has been established for these agents versus *P. aeruginosa*.

Table (7) presents the evaluation of the accuracy of Vitek1 system in testing the antimicrobial susceptibility of *Proteus mirabilis* isolates with broth microdilution method used as reference method. The Essential Agreement (EA) for Vitek1 for all antibiotics with *Proteus mirabilis* was 95%. The complete Agreement (CA) for Vitek1 Minor errors (mE)rate was 10%. The mE rate was higher with ceftazidime (25%) and lower with ampicillin, cefotaxim, ceftizoxim, and nitrofurantoin (5%). The Vitek1 Major Errors (ME) rate was 5% No ME rate with amikacin, aztreonam, gentamicin, nitrofurantoin, piperacillin, ticarcillin/clavulant, and tobramycin. The ME was higher with imipenem (15%) and lower with ampicillin, cefazolin, and ciprofloxacin (5%). The number of Vitek1 Very major Errors (VME) was 1 with cefotaxime, cefoxitin, ceftazidime, ceftizoxime, nitrofurantoin, and tricarcillin/clavulant. No VME rate with amikacin, ampicillin, aztreonam, cefazolin, ciprofloxacin, gentamicin, imipenem, piperacillin, tobramycin, and TMP/smx.

Table (8) presents the evaluation of the accuracy of Vitek1 system in testing the antimicrobial susceptibility of *Proteus vulgaris* isolates with broth microdilution method used as reference method. The Essential Agreement (EA) for Vitek1 for all antibiotics with *Proteus vulgaris* was 100%. The complete Agreement (CA) for Vitek1 range from 66.6% to 100% The Vitek1 Minor errors (mE) rate was 17.6%. the mE rate was with ceftazidime, piperacillin, and TMP/SMX (33.3%). The vitek1 Major Errors (ME)rate was 16.7% with both cefazolin and imipenem. No ME rate with the rest of antibiotics. The Vitek1 Very Major Errors (VME) rate was 3.2%. the VME rate was with aztreonam and ceftizoxime (16.7%). No VME rate with the rest of antibiotics.

Table (9) presents the evaluation of the accuracy of Vitek1 system in testing the antimicrobial susceptibility of *Providencia stuartii* isolates with broth microdilution method used as reference method. The Essential Agreement (EA) for Vitek1 for all antibiotics with was 100%. The complete Agreement (CA)for Vitek1 range from 66.7% to 100% The Vitek1 Minor errors (mE) rate was 33.3%. The mE rate was higher with cefoxitin (66.7%). The Vitek1 Major errors (ME) rate was 33.3% with cefoxitin, ciprofloxacin, gentamicin, piperacillin, and TMP/SMX No ME rate with the rest of antibiotics. The VME rate was with tobramycin (33.3%). No VME rate with the rest of antibiotics.

Rittenhouse et al. (1996) [16] stated that the Vitek GNB susceptibility cards were adopted by their laboratory for routine use. However, to compensate for some of the ME and VME observed with the AMS, the AMS results were reported resistant only with nitrofurantoin and *Proteus* species.

CONCLUSION

- API 20E system is better than Vitek1 system with GNI card in its accuracy for identification of *Pseudomonas aeruginosa*.
- Vitek1 system with GNI card is more rapid than API 20E in identification of *Proteus mirabilis*, *Proteus vulgaris*, *Providencia stuartii*, and *Pseudomonas aeruginosa* and both are equal in their accuracy of identification of *Proteus mirabilis*, *Proteus vulgaris*, and *Providencia stuartii*.
- Vitek1 system with GNS-108 card gave similar results to the broth microdilution method for most antimicrobial agents tested.

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