INTRODUCTION

Proteus species are among the commonly implicated pathogens in hospital as well as community acquired infections. This pathogen has a diverse mode of transmission, and hence can cause infection in different anatomical sites of the body. Some of the incriminating sources of transmission are soil, contaminated water, food, equipments, intravenous solutions, the hands of patients and healthcare personne. The genus Proteus, which was described for the first time by Hauser in 1885, belongs to the Enterobacteriaceae family. In this family it is placed in the tribe Proteeae, together with the genera Morganella and Providencia. These bacteria are gram negative rod measuring 0.6 to 6.0 µm in length and 0.3 to 1.0 µm in width, motile by peritrichous flagella, facultative anaerobic non spore forming, non-capsulated, most isolates have fimbriae. Proteus species are distinguishable from most other genera by their ability to swarm across agar surfaces of solid media.

Epidemiology

Members of the genus Proteus are widely distributed in the natural environment, including polluted water, soil, and manure. Due to their proteolytic activity, the ability to hydrolyze urea to ammonia and carbon dioxide, as well as the oxidative deamination of amino acids, these bacteria are involved in the decomposing of the organic matter of the animal origin. They are also present in the

ABSTRACT

Infectious diseases are one of the major problems in developing as well as developed countries. Plants produce a diverse range of bioactive molecules, making them rich source of different types of medicines. Most of the drugs today are obtained from natural sources or semi synthetic derivatives of natural products used in the traditional systems of medicine. Thus, it is a logical approach in drug discovery to screen traditional natural products. Approximately 20% of the plants found in the world have been submitted to pharmaceutical or biological test and a sustainable number of new antibiotics introduced in the market are obtained from natural or semi synthetic resources. Medicinal plants are finding their way into pharmaceuticals, cosmetics, and neutraceuticals. In pharmaceutical field medicinal plants are mostly used for the wide range of substances present in plants which have been used to treat chronic as well as infectious diseases. Long before mankind discovered the existence of microbes, the idea that certain plants had healing potential, indeed, that they contained what we would currently characterize as antimicrobial principles, was well accepted. Since antiquity, man has used plants to treat common infectious diseases and some of these traditional medicines are still included as part of the habitual treatment of various maladies. The drugs already in use to treat infectious disease are of concern because drug safety remains an enormous global issue. Most of the synthetic drugs cause side effects and also most of the microbes developed resistant against the synthetic drugs. To alleviate this problem, antimicrobial compounds from potential plants should be explored. These drugs from plants are less toxic, side effects are scanty and also cost effective. They are effective in the treatment of infectious diseases while simultaneously mitigating many of the side effects that are often associated with synthetic antimicrobials. Plants are rich source of antibacterial agents because they produce wide array of bioactive molecules, most of which probably evolved as chemical defense against predation or infection. A major part of the total population in developing countries still uses traditional folk medicine obtained from plant resources with an estimation of WHO that as many as 80% of world population living in rural areas rely on herbal traditional medicines as their primary health care, the study on properties and uses of medicinal plants are getting growing interests. In recent years, this interest to evaluate plants possessing antibacterial activity for various diseases is growing. The present antibacterial review of the plant extracts demonstrates that folk medicine can be as effective as modern medicine to combat pathogenic microorganisms. The millenarian use of these plants in folk medicine suggests that they represent an economic and safe alternative to treat infectious diseases.

Keyword: Antibacterial activity, Traditional medicinal plants, Proteus, Virulence factors.

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human gastrointestinal tract of humans and animals\textsuperscript{6}. \textit{P. mirabilis} was most frequently isolated from dogs, cows and birds\textsuperscript{7}. It is by far the most common species identified in clinical specimens. The most common infections caused by \textit{Proteus} spp. are urinary tract infections (UTIs). \textit{Proteus} spp. can be found to colonize the vaginal introitus prior to onset of bacteruria. Therefore, like \textit{Escherichia coli}, \textit{Proteus} spp. causes urinary tract infections by ascending from the rectum to the periurethra and bladder. 

\textit{P. mirabilis} is by far the most common species identified in clinical specimens. \textit{P. mirabilis} is a common cause of both community-acquired and catheter-associated UTI, cystitis, pyelonephritis, prostatitis, wound infections, and burn infections, and occasionally causes respiratory tract infections, chronic suppurative otitis media, eye infections (endophthalmitis), meningitis, and meningoencephalitis\textsuperscript{8}. It is a common cause of bacteremia following catheter-associated UTI\textsuperscript{9}, and in rare cases has been reported to cause cellulitis, endocarditis, mastoiditis, empymema, and osteomyelitis\textsuperscript{10}. It has also been suggested that \textit{P. mirabilis} could have a role in the etiology of rheumatoid arthritis\textsuperscript{11}.

\textit{P. vulgaris}, previously considered biogroup 2, has been reported to cause UTIs, wound infections, burn infections, bloodstream infections, and respiratory tract infections\textsuperscript{12}. There has also been one case study of \textit{P. vulgaris} causing bacteremia and brain abscesses, with the suspected point of entry being the digestive tract\textsuperscript{13}. \textit{P. penneri}, previously biogroup 1, generally causes UTIs, wound infections, burn infections, bloodstream infections, and respiratory tract infections. There has been one case study of \textit{P. penneri} Fournier's gangrene in a child with congenital genitourinary anomalies\textsuperscript{14}. Notably, \textit{P. penneri} may be incorrectly identified as \textit{P. mirabilis} due to being indole-negative, and it cannot be clearly resolved from \textit{P. vulgaris} by 16S sequencing unless using the 16S-23S internal transcribed spacer\textsuperscript{15}. Thus, the burden of human infections caused by this organism may be underestimated.

\textit{P. myxofaciens} was originally isolated from a gypsy moth and has been isolated from UTIs in India\textsuperscript{16}. \textit{P. hauseri}, previously considered biogroup 3, has not been associated with infections in humans. \textit{Proteus} rods are opportunistic bacterial pathogens which under favorable conditions cause urinary tract infections (UTIs), commonly associated with complicated urinary tract infections. They generally affect the upper urinary tract (common site of infection), causing infections such as urolithiasis (stone formation in kidney or bladder), cystitis, and acute pyelonephritis. Rare cases of bacteremia, associated with UTIs, with \textit{Proteus} spp. have also been reported. Other infections include septicaemia and wound infections, meningitis in neonates or infants and rheumatoid arthritis\textsuperscript{17,18}. Kalra Janda et al. (2006)\textsuperscript{19} and Kalra et al. (2011)\textsuperscript{20} reviewed endocarditis due to \textit{Proteus} species, and Okimoto et al. (2010)\textsuperscript{21} reported \textit{P. mirabilis} pneumonia. Brain abscesses during \textit{P. vulgaris} bacteremia were described by Bloch et al. (2010)\textsuperscript{13}. However, it should be stressed that \textit{Proteus} bacteria cause UTIs with higher frequency. This type of infections is classified as uncomplicated or complicated. Uncomplicated infections occur in patients, who are otherwise considered healthy, whereas complicated infections usually take place in patients with a urinary catheter in place or with structural and/or functional abnormalities in the urinary tract, suffering from another illness, immunocompromised, as well as after surgical intervention in the urogenital system. It was found that \textit{Escherichia coli} is a common cause of uncomplicated infections. Complicated UTIs might be polymicrobial and are usually caused by Gram-negative bacteria \textit{Proteus} spp., \textit{Providencia stuartii}, \textit{Morganella morgani}, \textit{E. coli}, \textit{Pseudomonas aeruginosa}, \textit{Klebsiella pneumonia} as well as some Gram-positive bacteria. \textit{Proteus} species can cause hematogenous infections and ascending infections, however, the latter are more common for these microorganisms\textsuperscript{14}. An overview of key \textit{Proteus} mirabilis virulence factors that contribute to catheter colonization and blockage, infection of the bladder (cystitis) and kidneys (pyelonephritis), and to the formation of urinary stones (urolithiasis), ATFs, ambient-temperature fimbiae; GdhA, glutamate dehydrogenase; IgA, immunoglobulin A; MRK, mannose-resistant Klebsiella-like; MRP, mannose-resistant Proteus-like; PMFs, \textit{P. mirabilis} fimbiae; Ptu, Proteus toxin agglutinin; ZapA, serralysin.

\textbf{Virulence factors of \textit{Proteus} spp.}

\textit{Proteus} bacilli possess several virulence factors that explain their uropathogenic potential, many of which have been investigated in a murine model of UTI, where they evolved a number of morphological and biochemical features which are considered as virulence factors (Table 1, Figure 1 and Figure 2). These are fimbiae, important for adhesion, flagella, crucial for bacterial ascent to the kidneys through the ureter, as well as enzymes (urease hydrolyzing urea to CO2 and NH3; leading to the formation of struvite stones, antibody-degrading proteases, complement proteins, and tissue matrix proteins; a-keto acidgenerating amino-acid deaminases which function as iron-binding siderophores), toxins, such as hemolysins, that lyse red cells and release iron, a bacterial growth factor and endotoxin (lipopolysaccharide, LPS)\textsuperscript{6}.

\textbf{Antimicrobial susceptibility}

\textit{Proteus} spp. are generally susceptible to broad-spectrum cephalosporins, aminoglycosides, and imipenem. Otherwise, \textit{P. mirabilis} is also susceptible to trimethoprime-sulfamethoxazole, ampicillin, amoxicillin and piperclillin, \textit{P. vulgaris} and \textit{P. penneri} are also susceptible to cefoxitin, cefepime, and aztreonam. \textit{P.mirabilis} is resistant to nitrofurantoin. \textit{P.vulgaris} and \textit{P.penneri} are resistant to piperacillin, amoxicillin, ampicillin, cefoperazone, cefuroxime, and cefazolin\textsuperscript{6}. \textit{Proteus} can be naturally resistant to antibiotics, such as benzylpenicillin, oxacillin, tetracycline, and macrolides\textsuperscript{6}. \textit{Proteus} spp. can acquire resistance to ampicillin through plasmid mediated beta-lactamases, and chromosomal
beta-lactamase expression has now been reported. In the last decade there have also been numerous reports of production of extended-spectrum beta-lactamases (ESBLs) by Proteus spp. The ESBLs can confer resistance to third generation cephalosporins such as cefotaxime, ceftiraxone and cefazidime, as well as the monobactam, aztreonam. The cephamycins (cefotixin, cefetetan and cefmetazole) and the carbapenems (imipenem and meropenem) are generally not hydrolyzed by ESBLs. However, resistance to carbapenems is starting to be observed in Proteus spp. A wide variety of ESBLs have been detected in P. mirabilis, and recent reports indicate a rise in ESBL-producing P. mirabilis, for instance in Japan. CTX-M-type ESBLs have been detected in P. mirabilis isolates from Korea and Taiwan. CTX-M2 is the most common ESBL in Japan and it appears to be spreading rapidly. CTX-M-type \( \beta \)-lactamases also appear to be evolving in P. mirabilis via recombination. CTX-M has been found on the P. mirabilis chromosome as part of an integrative and conjugative element (ICE) in addition to being plasmid-encoded. TEM is another common ESBL in P. mirabilis, and the most common type of ESBL in P. mirabilis isolates from Croatia and Italy. A new TEM (TEM-187) has been reported in P. mirabilis, which has broad activity against penicillins but lower activity than TEM-1. It has been suggested that TEM-187 may represent an evolution of TEM enzymes from penicillins to ESBLs, leading to underestimation of ESBLs in P. mirabilis. Other ESBL types include: VEB-1, an integron borne ESBL that was detected in a P. mirabilis isolate from a Vietnamese patient hospitalized in France, a multidrug-resistant isolate from Greece and in Taiwan; PER-1, which was detected in a P. mirabilis isolate from Italy; VIM-1, detected in three ESBL P. mirabilis isolates from Bulgaria (128); and SHV-type \( \beta \)-lactamases, detected in P. mirabilis isolates from Bulgaria and Taiwan. Metallo-beta-lactamases (MBLs) are also being reported in recent P. mirabilis isolates. For instance, one study from France identified a P. mirabilis isolate with a metallo-beta-lactamases, and a New Delhi metallo-beta-lactamase (NDM-1) has been identified in P. mirabilis isolates from New Zealand and India. Interestingly, NDM-1 was present in a genomic island in one isolate of P. mirabilis and co-occurred with a VEB-6 ESBL and SGI-1, and it has been proposed that the presence of NDM-1 in a genomic island structure may enhance the spread of carbapenemases. Multidrug resistance in P. mirabilis is also becoming more common. SGI-1 (Salmonella genomic island 1), an integrative mobilizable element of multidrug-resistant Salmonella typhimurium, has recently been detected in a surprisingly high percentage of P. mirabilis clinical isolates from France and indicates that P. mirabilis is a bacterial species of concern involved in dissemination of this multidrug-resistant element. SGI-1 confers resistance to a wide variety of older drugs that are no longer commonly used to treat human infection, but the multidrug-resistant regions of SGI-1 from P. mirabilis isolates had complex mosaic structures and rearrangements capable of facilitating acquisition and/or movement of antibiotic resistance genes that jeopardizes use of third-generation cephalosporins and quinolones. An ESBL-producing P. mirabilis isolate has also been identified with both TEM and CTX-M. Interestingly, ESBL production was found to be a risk factor for ciprofloxacin-resistant bacteremia due to P. mirabilis, and recent treatment with quinolone antibiotics was a risk factor for carriage of ESBL-producing P. mirabilis. A recent study from Tunisia also identified a high prevalence of plasmid-mediated quinolone resistance determinants among ESBL-producing P. mirabilis isolates. Importantly, ESBL and non-ESBL producing isolates of P. mirabilis are frequently susceptible to beta-lactam/beta-lactamase inhibitor combinations. However, there have been some reports of inhibitor resistant TEM mutants (IRT) occurring in P. mirabilis. These beta-lactamases are not inhibited by clavulanic acid, sulbactam and tazobactam. It should be noted that these beta-lactamases do not have extended-spectrum activity (that is, they do not hydrolyze third generation cephalosporins). Another mechanism of beta-lactamase inhibitor resistance in P. mirabilis isolates is presence of plasmid-mediated AmpC beta-lactamases. AmpC type beta-lactamases (also termed group 1 or class C beta-lactamases) can either be chromosomally encoded or plasmid encoded in P. mirabilis. AmpC has also been found on the chromosome as part of integrative and conjugative elements (ICE). Strains with plasmid-mediated AmpC beta-lactamases are consistently resistant to aminopenicillins (ampicillin or amoxicillin), carboxypenicillins (carbenicillin or ticarcillin) and ureidopenicillins (piperacillin). These enzymes are also resistant to third generation cephalosporins and the 7-alpha-methoxy group (cefoxitin, cefotetan, cefmetazole, moxalactam). AmpC beta-lactamases generally do not effectively hydrolyze cefepime or the carbapenems. One type of AmpC beta-lactamase is CMY, and clonal spread of CMY-producing P. mirabilis has been reported in Europe. CMY is also the predominant AmpC in Taiwan, and AmpC has been reported in P. mirabilis isolates from Korea and Spain. Carbapenemases are generally active against P. mirabilis. Meropenem is more potent than imipenem against P. mirabilis. Carbapenemases have been found in P. mirabilis, albeit rarely. A recent report has documented the presence of the class D carbapenemase, OXA-23, in P. mirabilis. Proteus vulgaris produces a chromosomally encoded beta-lactamase, referred to as the cefuroxime-hydrolyzing beta-lactamase (cefoxoximase or CmuA), which hydrolyzes cephalosporins. The enzyme can be induced by ampicillin, amoxicillin and first generation cephalosporins, weakly induced by carboxypenicillins, ureidopenicillins, cefotaxime and ceftriaxone, and inhibited by clavulanate. Strains of P. vulgaris that have a mutation in the regulatory genes of this beta-lactamase produce high levels of the enzyme and are resistant to penicillins, cefuroxime, ceftriaxone and cefotaxime.
However, these isolates will generally be susceptible to ceftazidime, aztreonam, cephymycins, carbapenems and beta-lactam/beta-lactamase inhibitor combinations. Eratopenem and meropenem are substantially more active than imipenem\(^78\). Quinolones and aminoglycosides are usually active against \textit{P. vulgaris} strains, though \textit{qnr} genes for quinolone resistance have been detected in recent isolates\(^79\). Tigecycline has lesser activity against \textit{P. vulgaris} than against other \textit{Enterobacteriaceae} (for example, MIC\(_{50}\) 4 \(\mu\)g/mL against \textit{P. vulgaris} but 0.25 \(\mu\)g/mL against \textit{E. coli})\(^90\).

\textit{P. penneri}: Like \textit{P. vulgaris}, \textit{P. penneri} is naturally resistant to ampicillin, narrow-spectrum cephalosporins and cefuroxime, by virtue of production of a similar beta-lactamase\(^81\). \textit{P. penneri} is considered to be a nosocomial pathogen with an underestimated potential to cause disease, and a recent case report identified a multidrug-resistant ESBL-producing \textit{P. penneri} isolate\(^82\).

\textit{P. mxyofaciens}: One report of \textit{P. mxyofaciens} from UTIs in India discussed antibiotic susceptibility, and found this species to be susceptible to imipenem, ciprofloxacin, amikacin, gentamicin, trimethoprim-sulfamethoxazole, aztreonam, ofloxacin and piperacillin and resistant to methicillin and nalidixic acid\(^16\).

**Resveratrol**

Resveratrol is (3,5,4'-trihydroxy-trans-stilbene) is a stilbenoid, a type of natural phenol, and a phytoalexin produced naturally by several plants especially the roots of the Japanese Knotweed (Polygonum cuspidatum), from which it is extracted commercially when under attack by pathogens such as bacteria or fungi\(^26\). Phytoalexins are low molecular weight compounds which have been shown to possess biological activity against a wide range of plant and human pathogens. Resveratrol is found in the skin of red grapes and in other fruits. It also has been produced by chemical synthesis and by biotechnological synthesis (metabolic engineered microorganisms). It has a wide range of biological activities and consequently it has many different targets and mechanisms of action. Resveratrol can prevent or slow the progression of several diseases, including cardiovascular disease, carcinogenic disease and neurodegenerative disease. It also prevents many aging processes and increases longevity. Moreover, resveratrol has anti-inflammatory, antioxidant and antimicrobial properties\(^83\). Recent studies have indicated that resveratrol has growth-inhibitory effects on some bacterial pathogens\(^84\). In the course of studying the effect of resveratrol on human pathogens, Wang \textit{et al.} (2006)\(^26\) found that resveratrol could inhibit swarming and virulence factor expression in \textit{P. mirabilis}.

**p-nitrophenylglycolyl-PNPCG**
P-nitrophenylglycolyl or 1-(4-Nitrophenyl-\(\beta\)-Dglucuronidac) (PNPG) is a chromogenic \(\beta\)-glucuronidase substrate\(^85\). The anti-swarming agent PNPG has long been used to aid the isolation of small numbers of many different pathogenic bacteria from specimens contaminated with swarming strains of \textit{Proteus} spp. In addition, PNPG has little effect on the results of a variety of identification tests performed directly on colonies from media containing PNPG\(^86\). It is relatively cheap, nontoxic and doesn’t affect red blood cells; even fastidious pathogens will grow well and with characteristic colony morphology in its presence. Its heat stability and long ‘shelf-life’ make it convenient to use in the preparation of media\(^87\).

**Fatty acids**

The antibacterial activity of long-chain unsaturated fatty acids have been well known for many years. Fatty acids function as the key ingredients of antimicrobial food additives which inhibit the growth of unwanted microorganisms. Linoleic and oleic acids are antibacterial components in the herbs (\textit{Helichrysum pedunculatum} and \textit{Schotia brachypetala}). Besides normal fatty acids, fatty acid derivatives showing potent antimicrobial activities exist in nature. These are mainly found in microorganisms, algae, or plants, which may mediate chemical defense against microorganisms. Additionally, long-chain unsaturated fatty acids are bactericidal to important pathogenic microorganisms, including Methicillin-resistant \textit{Staphylococcus aureus}, \textit{Helicobacter pylori} and \textit{Mycobacteria}. These antibacterial actions of fatty acids are usually attributed to long-chain unsaturated fatty acids including oleic acid, linoleic acid, and linolenic acid, while long-chain saturated fatty acids, including palmitic acid and stearic acid, are less active. However, their primary molecular target still remains unknown. Fatty acids are one of the most ubiquitous components of bacterial cell membranes. Interestingly, it has been shown that exogenously added fatty acids modulate various bacterial activities, including motility, virulence, cell growth, and differentiation. Swarming growth is also influenced by fatty acids. Oleic acid stimulates, whereas lauric and myristic acids inhibit this phenomenon, respectively. Straight-chain saturated fatty acids (SCFAs) repress swarming motility and hemolysin production in \textit{Proteus mirabilis} and \textit{Serratia marcescens}\(^87\).

**Urea**

Urea or carbamide is an organic compound with the chemical formula CO\((\text{NH}_2)\)_2\(^98\). It serves an important role in the metabolism of nitrogen-containing compounds by animals and is the main nitrogen-containing substance in the urine of mammals. It is a colorless, odorless solid, highly soluble in water and practically non-toxic (LD\(_{50}\) is 15 g/kg for rat), it is neither acid nor alkaline. Urea has experimentally been demonstrated to possess anti-swarming properties and recommended for routine laboratory usage\(^90\). It is commonly used in culture media designed for the identification of pathogens of UTIs including \textit{Proteus} spp. However, reports have been silent on \textit{Proteus} swarming prevention possibilities. Urea is primarily used in selective and composite media to identify urease producing microorganisms. In recent times, the possibilities of exploiting the anti-swarming property of urea to aid isolation and identification of single colonies on solid media are been confirmed\(^90\).

**Ethanol**

Ethanol also called ethyl alcohol, pure alcohol, grain alcohol, is a volatile, flammable, colorless liquid with the structural formula CH\(_3\)CH\(_2\)OH, often abbreviated as...
Table 1: Biochemical characteristics common to the genera *Proteus*, *Morganella* and *Providencia*.

<table>
<thead>
<tr>
<th>Biochemical test</th>
<th>Proteus</th>
<th>Morganella</th>
<th>Providencia</th>
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<tbody>
<tr>
<td>Arginine dihydrolyase</td>
<td>–</td>
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<td>–</td>
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<td>Lysine decarboxylase</td>
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<tr>
<td>Ornithine deaminase</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Phenylalanine deaminase</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Growth on KCN</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>d-Glucose from acid</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Acid from melibiose</td>
<td>–</td>
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<td>–</td>
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<tr>
<td>Nitrate from nitrate</td>
<td>+</td>
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<td>+</td>
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<tr>
<td>Oxidase production</td>
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<td>ONPG production</td>
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<td>Pectate utilization</td>
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<tr>
<td>Tartrate utilization</td>
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Symbols and Abbreviations: +, present; –, absent; KCN, potassium cyanide; and ONPG, o-nitrophenyl-β-d-galactopyranoside.

C$_2$H$_7$OH or C$_2$H$_5$O. It has bactericidal activity and is used often as a topical disinfectant$^{92,93}$. Ethanol at 90% added to the medium at a 5% concentration is also a very effective anti-swarm agent. It allows an easier isolation of gram-positive cocci and members of the families *Enterobacteriaceae* and *Pseudomonaceae*. However, when ethanol is used in blood agar medium, hemolytic reactions cannot be reliably determined. In some cases, the addition of chemical agents such as ethanol can interfere with the growth of other bacteria$^{94,95}$.  

*Sodium Azide*  
Sodium azide is the inorganic compound with the formula NaN$_3$. It is used for the preparation of other azide compounds. It is an ionic substance, is highly soluble in water, and is very acutely toxic$^{96}$. It is a potent bacteriostatic that is frequently used to protect a diverse array of stock solutions (e.g., antibodies) and samples (e.g., milk, fecal specimens) from prokaryotic contaminants. NaN$_3$ binds to heme-iron (cytochrome oxidase, catalase) leading to chemical asphyxiation of affected cells. However, the bacteriostatic effects of NaN$_3$ appear to be limited to Gram-negative *Bacteria*, whereas Gram-positive *Bacteria* are largely resistant to the compound$^{97}$. The addition of sodium azide to blood agar media was reported to abolish the swarming of *Proteus* without affecting the isolation of clinically important *Staphylococci* and *Streptococci*, but blood agar media containing azide are not widely used in the clinical laboratory because azide turns out to be a poor anti-swarm agent and, it shows growth inhibition of certain *Streptococci*$^{98}$.  

*Antimicrobial activity*  
Plant based antimicrobials represent a vast untapped source. The use of plant extract for medicinal treatment has become popular when people realized that the effective life span of antibiotic is limited and over prescription and misuse of traditional antibiotics are causing microbial resistance$^{99}$. Traditionally used medicinal plants produce a variety of compounds of known therapeutic properties$^{99}$. In recent years, antimicrobial properties of medicinal plants are being increasingly reported from different parts of the world$^{100}$. At present, nearly 30% or more of the modern pharmacological drugs are derived directly or indirectly from plants and their extracts dominate in homeopathic or ayurvedic medicines$^{101-115}$. Considering the vast potentiality of plants as sources for antimicrobial drugs, this study aimed to detect the antibacterial activities of some natural plant extracts and investigate the effect of some commercial antibiotics against multi-drug resistant human clinical bacterial isolates.  

Traditional medicinal plants used  
The medicinal properties of those plants were studied by several workers in Tamilnadu. It is very important to document the information about the medicinal plants from traditional healers to protect the knowledge of plant usage, because the younger generation is not interested to carry on the traditional knowledge. Many medicinal plants are given, which are used by traditional healers for their antimicrobial properties. Hereby, the mentioned plants are taken from references which are already included in ethnobotanical surveys$^{104}$. This paper reviews specifically about the plants having antimicrobial properties. The increasing interest on traditional ethnomedicine may lead to discovery of novel therapeutic agent. Since, plant contains potential antimicrobial components that may be useful for evolution of pharmaceutical for the therapy of ailments. Plants with possible antimicrobial activity should be tested against some microbes to confirm the activity. Researchers are increasingly turning their attention to folk medicine looking for new leads to develop better drugs against cancer, as well as viral and microbial infections. The activity of plant extracts on bacteria and fungi has been studied by a very large number of researchers in different place of the world. The specific plants to be used and the methods of application for particular ailments were passed down through oral tradition. Plants with possible antimicrobial activity should be tested against some microbes to confirm the activity.  

Bioactive compounds  
The medicinal value of plants lies in some chemical substances that produce a definite physiological action on the human body and these chemical substances are called phytochemicals. These phytochemicals were used to cure the disease in herbal and homeopathic medicines$^{117}$.  

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These are non-nutritive substances, have protective or disease preventive property\(^{106}\). There arises a need and therefore to screen medicinal plants for bioactive compounds as a basis for further pharmacological studies. With advances in phytochemical techniques, several active principles of many medicinal plants have been isolated and introduced as valuable drug in modern systems of medicine. The most important of these bioactive compounds are alkaloids, flavonoids, tannins and phenolic compounds\(^{107}\). These are the important raw materials for drug production\(^{118}\). Most plants contain several compounds with antimicrobial properties for protection against aggressor agents, especially microorganisms\(^{119}\). Antimicrobials of plant origin have enormous therapeutic potential and have been used since time immemorial. They have been proved effective in the treatment of infectious diseases simultaneously mitigating many of the side effects which are often associated with synthetic antibiotics\(^{2}\). Many infectious diseases have been known to be treated with herbal remedies based on ethnomedical knowledge. Natural products, either as pure compounds or as standardized plant extracts, provide unlimited opportunities for new drug leads because of the
unmatched availability of chemical diversity. Therefore, researchers are increasingly turning their attention to folk medicine, looking for new leads to develop better drugs against microbial infections. Thus, it is anticipated that phytochemicals with adequate antibacterial efficacy will be used for the treatment of bacterial infections. The antibacterial activity of ethanol extracts was determined by agar well diffusion method. The plant extracts were more active against Gram-positive bacteria than against Gram-negative bacteria among all the pathogens, all Gram-positive bacteria were inhibited by all four plant extract. All Gram-negative bacteria i.e. Pseudomonas spp, Proteus spp, Escherichia coli, Shigella dysenteriae, Klebsiella pneumonia and Salmonella typhi were showed zone of inhibition against extract of Ocimum sanctum.

In vitro microbicidal activity of the methanol extract of Origanum marjorana L. was tested against six bacteria (Bacillus subtilis, B. megaterium, Escherichia coli, Proteus vulgaris, Pseudomonas aeruginosa and Staphylococcus aureus). The methanol extract of O. marjorana can be used as an effective herbal protectant against different pathogenic bacteria.

The inhibitory activity was highly significant in the aqueous extracts of Oxalis corniculata. Most of the plant extracts showed significant antibacterial activity than bacitracin. MIC of aqueous extract of twelve plants varied between 4-50 μl. Results indicate the potential of these plants for further work on isolation and characterization of the active principle responsible for antibacterial activity and its exploitation as a herbal alternative to Oxalis Accia nilotica varied between 9-35.5 mm. Whereas corniculata was effective against all the tested bacteria in case of Lawsonia inermis it varied between 9 to except Shigella sonnei and Proteus mirabilis. Effectiveness of organic extracts of Piper nigrum fruit against pathogenic strains of Escherichia coli (MTCC 723), Staphylococcus aureus (MTSS 96), Streptococcus pyogenes (MTCC 442), Proteus mirabilis (MTCC 1429) by tube dilution method. The study revealed that 70% alcoholic hot extract had higher antibacterial activity as compared to chloroform hot and petroleum ether cold extracts. The aqueous extract was found to be antibacterial and it was studied against various Gram-positive and Gram-negative bacterial strains by using MIC, agar well diffusion method to find zone of inhibition. The MIC results of aqueous extract of Plectranthus amboinicus indicated that Proteus vulgaris, Bacillus subtilis and Staphylococcus aureus were least susceptible among the organisms tested and Escherichia coli, Klebsiella pneumonia and Pseudomonas aeruginosa are not shown any inhibition to aqueous extract of Plectranthus amboinicus.

CONCLUSION

Many medicinal plants have been found effective in the cure of bacterial diseases. Due to increasing antibiotic resistance in microorganisms and side effects of synthetic antibiotics medicinal plants are now gaining popularity in the treatment of bacterial infections. The use of traditional medicines and medicinal plants in most developing countries as therapeutic agents for the maintenance of good health has been widely observed. Furthermore, an increasing reliance on the use of medicinal plants in the industrialized societies has been traced to the extraction and development of drugs and chemotherapeutics from these plants as well as from traditionally used herbal remedies. Medicinal plants are considered as clinically effective and safer alternatives to the synthetic antibiotics. According to World Health Organization, medicinal plants would be the best source to obtain a variety of drugs. Extensive research in the area of isolation and characterization of the active principles of these plants are required so that better, safer and cost effective drugs for treating bacterial infections can be developed.

ACKNOWLEDGMENT

Authors are thankful to Department of Biology, University of Babylon, for providing facilities during preparation of this review article.

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