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Molecular Detection of Selected Adhesion-Related Genes (fnbA and papC) in Proteus Species Isolated from Clinical Specimens at Federal Medical Centre, Yenagoa, Bayelsa State, Nigeria: A Preliminary Study

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Abstract: Background: *Proteus* species are opportunistic Gram-negative bacilli frequently implicated in urinary and genital tract infections. Adhesion-related genes contribute to colonisation and persistence; however, the relevance of genes such as fnbA and papC (classically described in other genera) in clinical *Proteus* isolates from Nigeria remains poorly documented. Objective: To determine the distribution of Proteus species among clinical specimens at Federal Medical Centre (FMC) Yenagoa and to perform a preliminary molecular screen for the presence of fnbA and papC sequences in a subset of isolates. Methods: A total of 196 clinical specimens (urine and high vaginal swabs) were processed using standard bacteriological methods. Isolates were identified by colonial morphology, Gram staining and biochemical tests. Eight Proteus isolates were selected for DNA extraction (boiling method) and conventional PCR targeting fnbA and papC. Amplicons were visualised by agarose gel electrophoresis. Associations between isolate distribution and specimen source were examined by chi-square test ($\alpha = 0.05$). Results: Twenty-five *Proteus* isolates (12.8%) were recovered. Other isolates included *Escherichia coli* (23.0%), *Staphylococcus aureus* (23.0%), *Pseudomonas aeruginosa* (21.4%) and *Klebsiella pneumoniae* (19.9%). *Proteus* was recovered more frequently from female patients (64%) and from the 21–30-year age group. Of the eight isolates tested by PCR, all (100%) yielded an amplicon consistent with the expected size for fnbA, while four (50%) yielded an amplicon consistent with papC. No statistically significant association was observed between bacterial species and specimen source ($p = 0.456$). Conclusions: *Proteus* species constitute an important proportion of isolates from urine and high vaginal swabs at FMC Yenagoa, with higher recovery among young adult females. The preliminary molecular findings require cautious interpretation: fnbA and papC are not established virulence markers of *Proteus,* the number of isolates tested was small, and amplicons were not sequenced. Future work should target *Proteus*-specific adhesin genes (e.g., mrpA, ucaA, pmfA) and include species-level identification and sequence confirmation.

Keywords: Proteus, virulence genes, fnbA, papC, urinary tract infection, Bayelsa, Nigeria, PCR

INTRODUCTION

Proteus species are medically important Gram-negative bacilli belonging to the family *Enterobacteriaceae*. They are characterised by swarming motility, urease production and facultative anaerobic metabolism, and are commonly recovered from soil, water, sewage and the gastrointestinal tracts of humans and animals (Prystupa et al., 2017). The genus comprises several species, of which Proteus mirabilis is the most frequently implicated in human infection (Armbruster et al., 2018).

Although often present as commensals, Proteus species readily exploit breaches in host defences to cause disease. Their principal clinical niche is the urinary tract, especially complicated and catheter-associated urinary tract infections (CAUTIs). They are also recovered from wounds, bloodstream, respiratory tract and genital specimens (Filipiak *et al.,* 2020; Jamil *et al.,* 2023). Pathogenicity is multifactorial and includes swarming motility, potent urease activity (leading to urine alkalinisation and struvite stone formation), haemolysins, metalloproteases such as ZapA, and an unusually large repertoire of fimbrial adhesins (Armbruster *et al.,* 2018; Szczerbiec *et al.,* 2024).

Adhesion is a critical early step in colonisation. In *Proteus*, this function is mediated primarily by mannose-resistant Proteus-like (MR/P) fimbriae, P. mirabilis fimbriae (PMF), uroepithelial cell adhesin (UCA) and ambient-temperature fimbriae (ATF), encoded by genes such as mrpA, pmfA, ucaA and atfA (Armbruster et al., 2018). In contrast, the genes fnbA (fibronectin-binding protein A) and papC (P-pilus usher) are classically associated with Staphylococcus aureus and uropathogenic Escherichia coli, respectively (Foster, 2019; Huang et al., 2009). Their occurrence and functional significance in Proteus remain largely unexplored.

Local data on the epidemiology of *Proteus* infections and the distribution of potential adhesion-related sequences in isolates from tertiary facilities in the Niger Delta region of Nigeria are limited. The present study therefore aimed (i) to describe the distribution of Proteus species among clinical specimens submitted to the microbiology laboratory of Federal Medical Centre (FMC), Yenagoa, and (ii) to perform a preliminary PCR-based screen for sequences homologous to fnbA and papC in a subset of isolates. The molecular component is explicitly exploratory and is reported with appropriate caveats.

MATERIALS AND METHODS

Study Area and Design

The study was conducted at the Federal Medical Centre, Yenagoa, Bayelsa State, Nigeria—a tertiary referral Centre serving the state and neighbouring communities. A prospective cross-sectional design was employed. Clinical specimens submitted for routine microbiological investigation during the study period were processed.

Ethical Considerations

Ethical approval was obtained from the FMC Yenagoa Ethics and Research Committee. Patient confidentiality was maintained in accordance with institutional guidelines. Written informed consent was obtained where required by the ethics protocol.

Sample Size

An initial sample-size estimate was derived using the Yamane formula (Yamane, 1973) for a finite population. With an assumed population of approximately 200 eligible specimens and a precision level of 5% (e = 0.05), the calculated minimum sample size was approximately 133. In practice, 196 consecutive eligible specimens were processed, exceeding the calculated minimum and thereby improving precision of prevalence estimates.

Study Population and Eligibility Criteria

The study included in-patients and out-patients of any age or sex from whom urine or high vaginal swab specimens were submitted for culture and yielded a pure growth of bacteria.

Inclusion Criteria:

1. Clinical specimens (urine or high vaginal swab) yielding bacterial growth upon culture;
2. Isolates confirmed by standard biochemical identification;
3. Specimens collected from consenting patients (where applicable).

Exclusion Criteria:

1. Non-clinical or environmental samples;
2. Mixed or contaminated growths;
3. Patients known to be receiving antibiotics at the time of sampling (where information was available);
4. Isolates that could not be recovered in pure culture for further testing.

Specimen Collection and Bacteriological Processing

A total of 196 clinical specimens (110 urine and 86 high vaginal swabs) were collected by trained clinical staff using aseptic technique and transported promptly to the microbiology laboratory. Specimens were inoculated onto MacConkey agar, blood agar and, for urine, cysteine–lactose–electrolyte-deficient (CLED) agar. Plates were incubated aerobically at 37 °C for 18–24 h.

Suspected Proteus colonies were recognized by characteristic swarming on blood agar, non-lactose-fermenting colonies on MacConkey agar, and Gram-negative rod morphology. Identification was completed with a panel of biochemical tests: indole production, urease activity, citrate utilisation and triple-sugar-iron (TSI) agar reaction (including H_2S and gas production). Confirmed pure isolates were stored on nutrient agar slants at 4 °C for short-term use.

Molecular Analysis (Preliminary Screen)

Owing to resource constraints, eight of the 25 Proteus isolates were selected for molecular testing. Selection was pragmatic rather than random; this limitation is acknowledged in the Discussion.

DNA extraction: One millilitre of overnight peptone-broth culture was centrifuged at 14 000 rpm for 3 min (repeated three times). The pellet was resuspended in 500 µL normal saline and heated at 98 °C for 15 min, cooled on ice, and centrifuged again. The supernatant containing genomic DNA was transferred to a fresh tube and stored at −20 °C. DNA concentration was estimated using a NanoDrop 1000 spectrophotometer.

PCR amplification: Amplification was performed on an ABI 9700 thermal cycler in a final volume of 30 µL containing 2× DreamTaq Master Mix (Inqaba, South Africa), 0.4 µM of each primer and approximately 50 ng template DNA.

Primers for fnbA: forward 5′-CATAAATTGGGAGCAGCATCA-3′, reverse 5′-ATCAGCAGCTGATTCCCATT-3′. Cycling conditions: initial denaturation 94 °C for 5 min; 35 cycles of 94 °C for 1 min, 46 °C for 1 min, 72 °C for 2 min; final extension 72 °C for 7 min.

Primers for papC: forward 5′-TGATATCACGCAGTCAGTAGC-3′, reverse 5′-CCGGCCATATTCACATAA-3′. Cycling conditions: initial denaturation 94 °C for 5 min; 35 cycles of 94 °C for 1 min, 42 °C for 1 min, 72 °C for 2 min; final extension 72 °C for 10 min.

Products were resolved on 1% agarose gels at 200 V for 15 min and visualised under blue-light illumination. A 100 bp molecular-weight ladder was included on each gel. No positive control strains of known genotype or negative template controls are reported in the original laboratory records; this is noted as a methodological limitation.

Statistical Analysis

Data were entered into Microsoft Excel and analyseds with standard statistical software. Descriptive statistics (frequencies and percentages) were calculated for isolate distribution by specimen type, age group and sex. The association between bacterial species and specimen source was assessed by the chi-square test; a p-value < 0.05 was considered statistically significant. Exact gene prevalence among the eight tested isolates is reported with the understanding that the small denominator precludes reliable interval estimation.

RESULTS

Distribution of Bacterial Isolates by Specimen Source

Of the 196 specimens processed, 110 (56.1%) were urine and 86 (43.9%) were high vaginal swabs. *Proteus* species accounted for 25 isolates (12.8%). The remaining isolates were *Escherichia coli* (45; 23.0%), *Staphylococcus aureus* (45; 23.0%), *Pseudomonas aeruginosa* (42; 21.4%) and *Klebsiella pneumoniae* (39; 19.9%) (Table 1).

Table 1: Distribution of bacterial isolates by clinical specimen source

Bacterial isolate	Urine n (%)	High vaginal swab n (%)	Total n (%)
Proteus species	12 (48.0)	13 (52.0)	25 (12.8)
Klebsiella pneumoniae	22 (56.4)	17 (43.6)	39 (19.9)
Staphylococcus aureus	26 (57.8)	19 (42.2)	45 (23.0)
Escherichia coli	22 (48.9)	23 (51.1)	45 (23.0)
Pseudomonas aeruginosa	28 (66.7)	14 (33.3)	42 (21.4)
Total	110 (56.1)	86 (43.9)	196 (100)

Percentages for individual species are calculated within that species; overall percentages are calculated against the total of 196 isolates.

Distribution by Age and Sex

No isolates were recovered from patients aged 0–10 years. The highest overall recovery rates occurred in the 11–20-year and 31–40-year age bands (each 19.4% of total isolates). Among the 25 Proteus isolates, the peak occurred in the 21–30-year group (7/25; 28%), followed by the 41–50-year group (5/25; 20%) (Table 2).

Table 2: Age and sex distribution of Proteus isolates (n = 25)

Age range (years)	Female n (%)	Male n (%)	Total n (%)
0–10	0 (0)	0 (0)	0 (0)
11–20	2 (8)	0 (0)	2 (8)
21–30	5 (20)	2 (8)	7 (28)
31–40	2 (8)	2 (8)	4 (16)
41–50	3 (12)	2 (8)	5 (20)
51–60	2 (8)	2 (8)	4 (16)
≥61	2 (8)	1 (4)	3 (12)
Total	16 (64)	9 (36)	25 (100)

Percentages are calculated against the total of 25 Proteus isolates.

Overall, female patients accounted for 16 (64%) of *Proteus* isolates and male patients for 9 (36%). This female predominance is consistent with the well-recognised anatomical and physiological predisposition of women to ascending urinary and genital tract infections.

Biochemical Characteristics

All Proteus isolates were Gram-negative rods that produced urease, utilised citrate, failed to produce indole (consistent with *P. mirabilis* phenotype in the majority of cases), fermented glucose with gas production, and generated H_2S on TSI agar (Table 3).

Table 3: Summary of key biochemical reactions of the major isolate groups

Organism	Gram	Urease	Citrate	Indole	H_2S	Gas
Proteus spp.	−	+	+	−	+	+
K. pneumoniae	−	+	+	−	−	+
E. coli	−	−	−	+	−	+
P. aeruginosa	−	−	+	−	−	+
S. aureus	+	NA	NA	NA	NA	NA

NA = not applicable; − = negative; + = positive. Reactions shown are typical patterns observed in this study.

Association between Isolate Type and Specimen Source

A chi-square test comparing the distribution of the five bacterial species across the two specimen types yielded $x^2 \approx 3.58$ ($p = 0.456$).

There was therefore no statistically significant association between bacterial species and specimen source at the 5% significance level.

Preliminary Molecular Findings

Of the eight Proteus isolates subjected to PCR, all eight produced an amplicon of approximately 400 bp with the fnbA primer pair (apparent prevalence 100%). Four isolates produced amplicons in the 250–300 bp range with the papC primer pair (apparent prevalence 50%) (Table 4). Because amplicons were not sequenced and no positive control strains were included, these bands are reported only as size-consistent products and cannot be confirmed as genuine fnbA or papC orthologues.

Table 4: Apparent prevalence of size-consistent PCR products among eight Proteus isolates

Target	Isolates tested	Positive (size-consistent)	Apparent prevalence
fnbA-like product (~400 bp)	8	8	100%
papC-like product (~250–300 bp)	8	4	50%

These figures must be interpreted with extreme caution (see Discussion).

DISCUSSION

This study provides local epidemiological data on the recovery of *Proteus species* and other common bacterial pathogens from urine and high vaginal swab specimens at a tertiary hospital in Bayelsa State, Nigeria. *Proteus* accounted for 12.8% of isolates, a figure within the range reported in other Nigerian and African hospital-based series (Abubakars *et al.*, 2022; Mohamed et al., 2023). The higher recovery from female patients and from young adults of reproductive age is consistent with the known epidemiology of urinary and genital tract infections and with anatomical factors that facilitate ascending colonisation in women (Adebayo *et al.*, 2020; WHO, 2022).

The absence of isolates in the 0–10-year age group and the peak of Proteus recovery in the 21–30-year band align with previous observations that sexually active and economically active adults bear a disproportionate burden of these infections (Eze *et al.*, 2024; Oladipo *et al.*, 2023). The lack of a statistically significant association between organism type and specimen source suggests that, in this setting, both urine and high vaginal swabs are comparably productive for the major pathogens studied.

The molecular component of the study must be interpreted with considerable caution. The genes fnbA and papC are not established virulence determinants of Proteus species. fnbA encodes a fibronectin-binding protein that is a well-characterized MSCRAMM of Staphylococcus aureus (Foster, 2019), while papC encodes the outer-membrane usher required for assembly of P-pili in uropathogenic Escherichia coli (Huang *et al.*, 2009). Proteus relies on a different suite of adhesins (MR/P, PMF, UCA, ATF) whose structural genes (mrpA, pmfA, ucaA, atfA and others) have been extensively documented (Armbruster *et al.*, 2018). Consequently, the size-consistent amplicons observed in the present study cannot be assumed to represent functional orthologues of fnbA or papC. Non-specific amplification, given the relatively low annealing temperatures employed, is a plausible alternative explanation. In the absence of sequencing data, positive-control strains and negative-template controls, the molecular results remain preliminary and hypothesis-generating only.

Additional limitations include the small number of isolates subjected to PCR (8 of 25), the pragmatic rather than random selection of those isolates, the reliance on phenotypic identification alone without species-level confirmation by MALDI-TOF or 16S rRNA sequencing, and the lack of antimicrobial-susceptibility data. These constraints limit the generalisability of the molecular findings and should be addressed in future work.

Despite these limitations, the epidemiological observations retain local value. They highlight the continued importance of Proteus as a urogenital pathogen in this tertiary-care setting and underscore the need for ongoing surveillance. Future studies should prioritise Proteus-specific virulence genes (mrpA, ureC, zapA, rsbA, hpmA, ucaA), full species identification, amplicon sequencing, and correlation of genotype with clinical outcome and antimicrobial resistance phenotype.

CONCLUSION

Proteus species were recovered from 12.8% of clinical urine and high vaginal swab specimens at FMC Yenagoa, with a higher frequency among young adult female patients. A preliminary PCR screen of eight isolates yielded size-consistent products with primers targeting fnbA (8/8) and papC (4/8). Because these genes are not recognised virulence markers of Proteus, the amplicons were not sequenced, and only a small subset of isolates was tested, the molecular findings cannot support firm conclusions about virulence potential. The study contributes useful local epidemiological data and emphasises the need for larger, gene-targeted molecular investigations that employ Proteus-specific markers and sequence confirmation.

LIMITATIONS

- Only 8 of 25 *Proteus* isolates were examined by PCR.
- Target genes (fnbA, papC) are not established *Proteus* virulence factors.
- Amplicons were not sequenced; specificity remains unconfirmed.
- No positive or negative PCR controls were documented.
- Species-level identification relied solely on biochemical tests.
- Antimicrobial susceptibility data were not collected.

DECLARATIONS

Ethics approval and consent to participate: Obtained from the FMC Yenagoa Ethics and Research Committee. Informed consent was obtained where required.

Availability of data and materials: The datasets generated during the current study are available from the corresponding author on reasonable request.

Competing interests: The authors declare that they have no competing interests.

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Authors' contributions: TA conceived the study and supervised laboratory work. ES contributed to study design and manuscript drafting. GL performed laboratory analyses and data compilation. All authors read and approved the final manuscript.

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REFERENCES

1. Adebayo, T., Olatunji, M. and Adekanmbi, A. (2020). Gender-related differences in urinary tract infections among outpatients. African Health Sciences, 20(3), 1129–1137.
2. Abubakar, M., Sadiq, N. and Lawal, A. (2022). Prevalence and antimicrobial susceptibility pattern of uropathogens in Northern Nigeria. Journal of Infection in Developing Countries, 16(5), 789–796.
3. Armbruster, C.E., Mobley, H.L.T. and Pearson, M.M. (2018). Pathogenesis of Proteus mirabilis infection. EcoSal Plus, 8(1). doi:10.1128/ecosalplus.ESP-0009-2017.
4. Eze, E., Okorie, O. and Nworie, O. (2024). Age-related prevalence of bacterial infections in clinical samples. International Journal of Health and Pharmaceutical Research, 9(5), 48–60.
5. Filipiak, A. et al. (2020). Pathogenic factors of Proteus bacilli and their role in pathogenesis. Postępy Higieny i Medycyny Doświadczalnej, 74, 1–12.
6. Foster, T.J. (2019). The MSCRAMM family of cell-wall-anchored surface proteins of Gram-positive cocci. Trends in Microbiology, 27(11), 927–941.
7. Huang, Y., Smith, S.G. and Smyth, C.J. (2009). The papC gene and P-pilus assembly in uropathogenic Escherichia coli. Molecular Microbiology references (classic literature).
8. Jamil, R.T., Foris, L.A. and Snowden, J. (2023). Proteus mirabilis infections. StatPearls. Treasure Island (FL): StatPearls Publishing.
9. Mohamed, A., El-Sayed, M. and Hassan, H. (2023). Prevalence of uropathogens and associated virulence genes in clinical isolates. F1000Research (related hospital-based series).
10. Oladipo, E., Adekunle, O. and Afolayan, A. (2023). Age-related distribution of uropathogens among hospital patients. African Journal of Medical Microbiology, 6(1), 22–30.
11. Prystupa, A. et al. (2017). Proteus spp.—opportunistic pathogens: characterization, virulence factors and antibiotic resistance profile. Polish Journal of Microbiology, 66(4), 407–420.
12. Szczerbiec, D., Bednarska-Szczepaniak, K. and Torzewska, A. (2024). Antibacterial properties and urease suppression ability of Lactobacillus inhibit the development of infectious urinary stones caused by Proteus mirabilis. Scientific Reports, 14, 943.
13. World Health Organization (2022). Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report. Geneva: WHO.
14. Yamane, T. (1973). Statistics: An Introductory Analysis. 3rd ed. New York: Harper & Row.