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Content Details:

Addae Ruth (Author) *Jamesbert Hospital*	**Psychiatric and Mental Health Nursing in Africa - A Case Study in Ghana.**

Introduction:

This study delves into the landscape of psychiatric and mental health nursing in Africa, with a specific focus on Ghana. Mental health remains a critical aspect of public health, and understanding the challenges and opportunities within the context of African nations is essential. The cultural, social, and economic nuances in Ghana provide a unique backdrop to explore the role of psychiatric and mental health nursing in promoting holistic well-being.

Method:

A comprehensive research approach is employed, combining qualitative and quantitative methods. Qualitative data is gathered through in-depth interviews with psychiatric nurses, mental health professionals, and service users. Additionally, quantitative data is collected through surveys and the analysis of healthcare records. The mixed-method design allows for a nuanced understanding of the complexities surrounding psychiatric and mental health nursing in the Ghanaian context.

Results:

Preliminary findings indicate a growing awareness of mental health issues in Ghana, coupled with challenges such as stigma, limited resources, and the need for culturally competent care. Psychiatric and mental health nurses play a crucial role in addressing these challenges, contributing to the development of community-based interventions and promoting mental health literacy. The study further reveals the impact of cultural factors on help-seeking behavior and the provision of mental health services.

Conclusion:

The case study in Ghana underscores the importance of tailoring psychiatric and mental health nursing practices to the cultural and contextual specifics of the African continent. Integration of community-based approaches, destigmatization efforts, and capacity-building for healthcare professionals emerge as key strategies. By understanding the unique challenges in Ghana, mental health policymakers and practitioners in Africa can formulate more effective and culturally sensitive interventions.

Keywords: Psychiatric Nursing, Mental Health Nursing, Africa, Ghana, Case Study, Cultural Competence, Stigma, Community-Based Interventions, Mental Health Literacy, Healthcare Resources, Holistic Well-being.

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Vincent Opoku (Author) *Sunyani Regional Hospital*	**Evidence-Based Nursing - A nursing informatic approach - a case study of Ghana and Sub-Saharan Africa.**

Abstract:

This paper explores the implementation of evidence-based nursing practices in Ghana and Sub-Saharan Africa through a nursing informatics approach. The study investigates the utilization of information and communication technologies (ICTs) in promoting evidence-based nursing, with a focus on enhancing healthcare outcomes and advancing the nursing profession. The case study analyzes the current state of evidence-based nursing in the region, identifies challenges, and proposes strategies to leverage nursing informatics for improved patient care. The findings aim to contribute to the global discourse on healthcare technology adoption and its impact on nursing practices, particularly in resource-constrained settings.

Introduction:

Evidence-based nursing (EBN) is fundamental to delivering high-quality healthcare and enhancing patient outcomes. In Sub-Saharan Africa, including Ghana, the integration of evidence-based practices into nursing is of paramount importance to address the unique healthcare challenges in the region. This paper explores the role of nursing informatics in facilitating evidence-based nursing in Ghana and Sub-Saharan Africa, aiming to bridge the gap between traditional nursing practices and modern healthcare demands.

Method:

The study employs a mixed-methods approach, combining qualitative and quantitative research methodologies. Surveys, interviews, and focus group discussions are conducted among healthcare professionals, nurses, and administrators in Ghana and selected Sub-Saharan African countries. The quantitative data gathered include the current adoption rates of information and communication technologies (ICTs) in nursing practices, while qualitative data focus on identifying barriers and facilitators to evidence-based nursing. The study also assesses the availability and utilization of electronic health records (EHRs), clinical decision support systems, and other informatics tools in the nursing profession.

Results:

Preliminary findings indicate that while there is a growing awareness of evidence-based nursing principles, the adoption of nursing informatics tools remains uneven across the region. Limited access to technology infrastructure, insufficient training, and resource constraints are identified as key barriers to the effective implementation of evidence-based practices. However, positive correlations between the use of nursing informatics and improved patient outcomes are observed in facilities where such technologies are successfully integrated.

Conclusion:

The study underscores the critical need for a strategic and concerted effort to integrate nursing informatics into the healthcare systems of Ghana and Sub-Saharan Africa. To promote evidence-based nursing, targeted interventions are recommended, including capacity-building programs, infrastructure development, and policy initiatives. The successful integration of nursing informatics has the potential to elevate the standard of healthcare delivery, empower nursing professionals, and ultimately improve patient outcomes in the region. This paper contributes valuable insights to the global discourse on leveraging technology to advance nursing practices, particularly in resource-constrained settings.

Keywords: Evidence-Based Nursing, Nursing Informatics, Healthcare Technology, Sub-Saharan Africa, Ghana, Information and Communication Technologies (ICTs), Patient Care, Nursing Practices.

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Wendy Adjoa Yakah (Author) *Tamale Teaching Hospital*	**Navigating the Hurdles: a Case Study on Paediatric Nursing Challenges and Approaches in Ghana.**

Background:

The fundamental purpose of the study orbits around unraveling the multifaceted challenges and developing proficient strategies pertinent to pediatric nursing in a developing nation, with a specific lens focused on Ghana. The vitality of proficient pediatric care is irrefutable, especially in developing nations where healthcare resources may be scarce or unequally distributed. Thus, an examination into the actualities and potential avenues for enhancement within this nursing subset becomes pivotal. The analysis further aims to illuminate the variances between theoretical knowledge and on-ground practicalities, thereby paving a pathway toward not only understanding the hurdles encountered by pediatric nurses but also propelling policy and procedural changes that can substantially ameliorate child healthcare in Ghana.

Methods:

A mixed-method research approach was adopted, coupling both qualitative and quantitative data to gain a holistic view of the current pediatric nursing landscape in Ghana. Structured interviews and questionnaires were administered to pediatric nurses across diverse health facilities, including hospitals and clinics in both urban and rural areas of the country. Additionally, case observations, government reports, and other available data on healthcare delivery, resources, and outcomes were analyzed. Ethical considerations were meticulously adhered to, ensuring that all participants provided informed consent and that their data was anonymized to protect their identities. The qualitative data were analyzed using thematic analysis, while quantitative data were subjected to statistical analysis using SPSS software.

Results:

The study elucidates a conglomerate of challenges faced by pediatric nurses in Ghana. The major hurdles emerged as insufficient resources, inadequate training and continuous education opportunities, high patient-to-nurse ratios, and the prevalent lack of specialized pediatric care in rural regions. A significant disparity in healthcare quality and resource availability between urban and rural areas was also highlighted. While urban centers boasted relatively better pediatric care owing to better resources and training, rural areas languished with palpably scarce resources and an acute deficiency of specialized practitioners. Pediatric nurses consistently highlighted the emotional and psychological strain engendered by the gap between the demand for pediatric care

and the available resources and support. Nurses in rural areas, in particular, articulated the need for more robust support structures, both in terms of tangible resources and training, to ensure the efficacy and psychological wellbeing of healthcare practitioners.

Conclusion:

The study underscores the pressing need to fortify pediatric nursing in Ghana through strategic interventions aimed at bridging the resource, training, and psychological support gaps identified. Particularly, an emphasis on equitable resource allocation, bolstering of training initiatives, and fortifying psychological support mechanisms for nursing staff are indispensable. Policymakers and stakeholders must engage in a collaborative and concerted effort to enhance the infrastructural, educational, and emotional support framework within which pediatric nurses operate. Furthermore, specific attention ought to be directed towards rural healthcare, ensuring that children in these areas are not disenfranchised by virtue of their geographical location. The implementation of mobile health units and telemedicine could be potent strategies in ameliorating healthcare delivery in remote areas, ensuring that quality pediatric care permeates throughout the nation.

Keywords: Pediatric Nursing, Healthcare Disparities, Developing Country Ghana, Resource Allocation, Rural Healthcare, Training and Development, Child Health Outcomes

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Alhage Drammeh (Author) *Ministry of health The Gambia*	**Causes of Jaundice and Skin Rashes among Children in Selected Rural Communities in The Gambia, West Africa.**

Abstract

The research is on the occurrence of certain diseases among children in rural and far flung parts of the Gambia, and the extent to which they are caused by lack of access to clean water.

The paper explains the purpose of the research, which is majorly to improve the health condition of children more especially those living in the rural communities.

The paper also gives a brief overview of the socio-economic situation of The Gambia, emphasizing its status as a Least Developed Country (LDC), and majority of its population living below the poverty line, with women and children hardest hit.

The research used as case studies, two rural communities in the Gambia -Basse Dampha Kunda Village and Foni Besse. Data was collected through oral interviews and medical tests conducted among people in both villages, with emphasis on children. The demographic detail of those tested is tabulated for a clearer understanding.

The results were compared, revealing that skin rashes, hepatitis and certain other diseases are more prevalent in communities lacking access to safe drinking water. These results were also presented in a tabular form.

The study established how some policy failures and neglect on the part of the Government of The Gambia is imperiling the health of many rural dwellers in the country, the most glaring being that the research team was unable to test water samples collected from the two communities, as there are no laboratory reagents for testing water anywhere in The Gambia.

-Many rural communities lack basic amenities especially clean and potable water, as well as health facilities.

The study findings also highlighted the need for healthcare providers and medical NGOs to voice the plight of rural dwellers and collaborate with government to set up health facilities in rural areas of The Gambia.

Keywords: Jaundice, skin rashes, children, hepatitis, water sanitation, hygiene, The Gambia, village, Basse.

Purpose

This research is prompted by the recognition that a healthy society, one in which access and resources are readily available, promotes economic stability and increases development necessary to advance at a rate comparable to other countries. Countries in Africa have limited resources for health care delivery making it necessary that concerted efforts are made to ensure people remain healthy. Children must be adequately taken care of to reduce maternal and neonatal deaths and other medical tragedies through preventive and promoted activities and by addressing avoidable factors that lead to death. These factors are included in many of the health care initiatives. There is a need to ensure children with debilitating diseases and illnesses are free from pain and suffering. Due to the magnitude of importance the Government and Health Care providers play together as stakeholders as advocates, promoting access to care and treatment must be a top priority.

Background

The Gambia is a member of the Commonwealth of Nations and the smallest country in mainland Africa, with a land area of 11 300 sq km. The country is located on the Western tip of West Africa. It has 80km of coastline while its terrestrial borders are surrounded by Senegal. The Gambia has a population of roughly 2.101 million people (2017 estimates). Over half of the population is mainly young people (over 60%) below 25 years (1). Economic growth in The Gambia is dominated by farming, fishing, and tourism. The country is beset by the following social challenges:

- Chronic Poverty- With a Per Capita Income of $488 USD, The Gambia is one of the poorest countries in the World and classified among the Least Developed Country (LDC).
- Over 60% of Gambian population lives in poverty, of which 63% are women who carry a disproportionate burden of poverty.
- Poor water and sanitation related deaths account for 20% of under-five (U-5) deaths. U-5 mortality rates in rural areas are estimated to be 36% higher than those in urban areas (3).
- key water sector constraints include provision of sustainable development and management of water resources to meet higher demands for domestic water supply and sanitation.

The Study Methodology

The paper is based mainly on a field study conducted in 2023 in Basse Dampha Kunda Village and Foni Besse, rural communities in the Upper River Region (URR) and West Coast Region (WCR) of The Gambia respectively. A baseline survey was used in this study because it enables the researcher not only to discover and describe, but also to explain the actual process. Basse

Dampha Kunda Village has a population of over four thousand according to the population and housing census, with 90% of the people living below the poverty line. The population is expected to grow by 10 per cent in the next five years (1).

Foni Besse Village has a population of 2500 according to population and housing census 2012 with 75% living below the poverty line, it has a population growth of 0.5% per year.The ethnic distribution represented mainly Mandinka, wolof, Manjago, and Fula. While in Basse Dampha Kunda Village; Mandinka and Fulas are the ethnic majority. The health care research team lived and interviewed mainly in the two villages with locally known, trusted, and trained research assistants (1,4)

In this study, data were collected through oral interviews and medical tests. The questions were asked in a more contingent manner. Interviews were audio-taped and transcribed verbatim.

Table 1: Demographic Details of people tested in Basse Dampha Kunda Village

Variable	Number	Percentage	
Age 50-90 25-49 10-24 5-9 0-8	 275 631 326 272 152	 16.6 38.1 19.7 16.4 9.1	 1656
Gender Male Female	 470 1186	 28.4 71.6	 1656
Ethnicity Mandinka Fula	 1586 70	 95.8 4.2	 1656
Educational English Arabic Non formal education	 110 1340 206	 6.6 80.9 12.4	 1656
Occupation Teacher Domestic farmer Non employment	 35 1352 269	 2.1 81.6 16.2	 1656

Table 2: Demographic Details of people tested in Foni Besse Village

Variable	Frequency	Percentage(%)	
Age 50-90 25-49 10-24 5-9 0-4	 250 342 437 225 73	 18.8 25.7 32.2 17.0 5.5	1327
Gender Male Female	 352 975	 26.5 73.4	
Ethnicity Jolas Mandinka Fulas Others	 1005 267 55	 75.7 20.1 4.1	
Educational level English Arabic Non formal	 975 206 146	 73.4 15.5 11.0	
Occupation Domestic farmer Teacher Student Non occupation	 860 125 600 58	 64.8 9.4 45.2 4.3	

Results And Findings

The results where compared, revealing that skin rashes, hepatist and certain other diseases are more prevalent in communities lacking safe drinking water this results were also presented in a tabular form.

Basse Dampha Kunda

People in Basse Dampha Kunda rely mostly on unimproved shallow wells, boreholes, and streams which are often contaminated. Water in some areas is high in iron and manganese. Due to inadequate access to clean water supply and poor hygiene practices, there is a high level of water

contamination during water irrigation from the boreholes, handling practices, and storage which undermines having an improved water source. Furthermore, due to the shortage of water the entire population depends on a single borehole for its irrigation system as every family here relies on agriculture for sustenance. Consequently, poor sanitation and hygiene have become a challenging issue for the community.

The socio-economic situation in Foni Besse Village is similar to Basse Dampha Kunda Village and indeed most rural communities in The Gambia. It is also an agrarian community although it relies more on rain-fed agriculture than Basse Dampha Kunda
In a random data collection procedure, 1656 people in Basse Dampha Kunda Village were screened for hypertension, jaundice, skin rashes, diabetes, asthma and traumatic stress disorder out of which 224 children aged 0-15years were screened for jaundice and skin rashes.

200 children (89.2%) had only skin rashes without jaundice. The remaining children were presented with jaundice and skin rashes while most adults were diagnosed with diabetes, asthma, and traumatic stress disorder.

A random sample was collected from 20 children for hepatitis tests. The samples tested positive for hepatitis A virus. All 20 children presented with jaundice and were negative for either hepatitis B or C. This could be due to water contamination with hepatitis A virus. Hepatitis A is an inflammation of the liver caused by the hepatitis A virus (HAV). The virus is primarily spread when an uninfected (and unvaccinated) person ingests food or water that is contaminated with the faeces of an infected person. The disease is closely associated with unsafe water or food, inadequate sanitation, poor personal hygiene, and oral-anal sex. The World Health Organization (WHO) estimates that in 2016, 7134 persons died from hepatitis A worldwide (accounting for 0.5% of the mortality due to viral hepatitis (2,4). This is a cause of concern.

Table 3: Occurrence of Skin Conditions and Jaundice among 224 Children Under 10 in Basse Dampha Kunda Village

Age of children with jaundice and skin rashes	Number	Percentage (%)	Total
10-15 5-9 0-4	4 10 9	16.6 41.6 37.5	24
child with skin rashes with no Jaundice 10-15 5-9 0-4	 75 100 25	 37.5 50.0 12.5	 200
Knowledge of their mothers on cause of jaundice and skin rashes Yes No	 0 224	 100	 224
Source of water supply for the children Borehole Well Strims	 200 20 4	 89.2 8.9 1.7	 224
Hepatitis test HepA positive Negative Hep B HepC	 9 215	 4.0 96.0	 224
Mode of transporting water Gallon Local tap	200 15 9	89.2 6.7 4.0	

Foni Besse Village

People in Foni Besse rely mainly on clean water supply, adequate irrigation system, and scanty boreholes. As a result, no cases of jaundice were found amongst children in the village.

Skin rashes account for 20% in children aged 10-15, 64% in age 5-9 and 16% below 5years respectively, this could be due to poor hygiene, allergies, and tropical weather conditions. Therefore, none of the children were further tested for hepatitis (4).
The table below highlights some significant findings as to why people of Foni suffer less from water-borne diseases compared to those at Basse Dampha kunda.

Table 4: Occurrence of Skin Conditions and other diseases among 50 Children Under 10 in Foni Besse Village

Variables	Numbers	Persentages(%)	Total
Age of children having both jaundice and skin rashes 10-15 5-9 0-4	 00 00 00	 0 0 0	 00
Age of children having skin rashes only 10-15 5-9 0-4	 10 32 8	 20 64 16	 50
Hepatitis test HepA Hep B Hep C	Negative for all 50	100	
Know causes of jaundice Yes No	 00 50	 0 100	 50
Source of water supply Borehole Well Streams Tap water	 10 5 0 35	 20 10 0 70	 50
Mode of transporting water from borehole to home Gallon local community tap	 10 40	 20 80	 50

Water samples from water sources in Basse Dampha Kunda Village and Foni Besse Village were collected by the research team for further investigation. However, no test could be conducted on the water as there are no laboratory reagents anywhere in The Gambia, not even in the facilities of the country's utility provider, the National Water and Electricity Company (NAWEC).

These findings have also indicated some major issues that are worth the healthcare workers' consideration:

Official policy failures are imperiling lives especially in rural, remote communities in The Gambia as the government has failed to live up to its responsibility of providing necessities or amenities for most of the population especially those in rural areas. For example:

- The community of Basse Dampha Kunda has not been provided with clean water by the government.
- There is no single health facility in the community.
- There is no provision for mobile clinics to visit rural communities like Basse Dampha kunda and conduct medical checks and provide treatment for the population.
- There is no emergency transportation available to evacuate patients to hospitals in the nearest town or city.
- There are no government sanitary or health inspectors to advise the people on safe practices that would preserve their streams and other sources of water supply from contamination or pollution.
- There are no agricultural extension workers or environmental officers to advise the people on the use of fertilizers, chemicals, or pesticides. Education around how some of these substances can contaminate sources of water supply if wrongfully or indiscriminately applied is not available.

One of the direct results of the neglect of rural communities is increased rural-urban migration. The Gambia has a high population growth rate, and over the last few decades the country has witnessed an upsurge in rural-urban migration, with many people moving from the hinterland to urban areas such as the Greater Banjul Area and other regional and provincial towns. This has resulted in increased unemployment and pressure on available amenities including health facilities.

In summary, issues as indicated in the findings, have significant implications for healthcare providers. Intentionally or unintentionally healthcare providers are positioned to be agents of social justice. As a profession that upholds social justice, healthcare provide rs also need to be socially and politically conscious. They must at a minimum attempt to engage the political leaders

and draw their attention to the unfortunate neglect happening in rural communities. Hence the formation of the Ocean Health Foundation.

Conclusion

In general, there were differences Between the two villages with respect to accessing a water supply. The lack of clean water in many rural communities in The Gambia is a cause for concern, as it leads to the spread of skin rashes and other diseases endangering the life of rural inhabitants, especially children.

Recommendation

Experts have suggested to address this challenge, the government should prioritize the following: (i) implementation of the National Water Policy; (ii) strengthening of the human and infrastructure capacities of sector institutions to perform their mandates; and (iii) to empower communities to participate effectively in water management. These priorities make up the current water sector reforms of The Gambia. The Ocean Health Foundation involvement currently seeks to collaborate with the government and other related organizations and agencies to address these problems. The Foundation realizes the seriousness of the situation and remains cognizant in its efforts to work towards a solution based approach, keeping the safety and wellbeing of the citizens the first priority and abstain from any endeavors that can be used as a political ploy.

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Juliet Kwakyewaa Ofori (Author) *Ho Teaching Hospital*	**Mental Health and Wellbeing - a pediatrician's approach - a case study of Ghana.**

Abstract:

This paper delves into the critical intersection of mental health and wellbeing from a paediatrician's perspective, with a specific focus on a case study conducted in Ghana. Recognizing the global importance of addressing mental health in children, this study aims to shed light on the challenges faced in a developing country context and explore effective approaches for promoting mental health and wellbeing among the pediatric population in Ghana. The paper provides insights into the background and context of mental health in children, outlines the methods employed for the case study, presents the results obtained, and concludes with recommendations for enhancing mental health outcomes in pediatric care settings.

Background and Aims:

Children's mental health is a vital aspect of overall wellbeing, and addressing it requires a comprehensive understanding of contextual factors, especially in developing nations like Ghana. The paper begins by examining the existing literature on pediatric mental health, highlighting the unique challenges faced in resource-constrained environments. The aims include identifying the prevalent mental health issues in Ghanaian children, understanding the cultural and societal influences, and proposing effective strategies for pediatricians to enhance mental health outcomes.

Methods:

A case study approach was employed to delve into the intricacies of pediatric mental health in Ghana. A multidisciplinary team, including paediatricians, psychologists, and social workers, collaborated to collect qualitative and quantitative data. The study utilized surveys, interviews, and observations to assess the mental health status of children in different age groups. Additionally, community engagement activities and focus group discussions were conducted to grasp the cultural nuances affecting mental health.

Results:

The results section provides a comprehensive analysis of the gathered data. It outlines the prevalent mental health issues among Ghanaian children, such as anxiety, depression, and trauma, and elucidates the contributing factors. Additionally, the paper explores the existing support systems and interventions, highlighting both successes and challenges. The results also shed light on the cultural perceptions of mental health in Ghana and their impact on seeking and receiving care.

Conclusion:

Drawing from the findings, the conclusion section synthesizes key takeaways and proposes recommendations for paediatricians and policymakers. It emphasizes the importance of a holistic approach to pediatric mental health, considering cultural, social, and economic factors. The conclusion also advocates for community-based interventions, increased awareness, and policy reforms to create a supportive environment for children's mental health in Ghana.

Keywords: Pediatric Mental Health, Wellbeing, Developing Countries, Ghana, Case Study, Cultural Influences, Intervention Strategies, Community Engagement, Paediatrician's Approach, Global Health.

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Yaw Arkoh-Badu Essuman (Author)

Korle Bu Teaching Hospital, Ministry of Health, Government of Ghana

Christian Obirikorang, PhD (Co-Author)
Kwame Nkrumah University of Science and Technology (KNUST)

Association of rs5186 and rs11091046 variations of the angiotensin II receptor gene with essential hypertension; a case-control study in a Ghanaian population.

Abstract

Introduction:

Genetic variation of Angiotensin II Receptor type I (AGTR1) and type II (AGTR2) genes have been found in individuals with essential hypertension (EH). There is a paucity of data on genetic factors contributing to EH in the Ghanaian population. The present study investigated the presence of genetic variants of AGTR1 (rs5186) and AGRT2 (rs11091046) genes and their association with EH.

Methods:

We analyzed the rs5186 and rs11091046 variations in 100 patients with clinically diagnosed EH and 100 healthy controls. Questionnaires were used to acquire information on participants' sociodemographic hemodynamic and anthropometric parameters. Logistic regression models were used to assess the associations between genetic variations and EH

Results:

The cases had higher minor allele frequencies of rs5186 (25% vs. 6%, p <0.001) and rs11091046 (62.1% vs 41.5%, p = 0.004) than controls. The recessive genotype of rs11091046 was found in 61% of patients and 13% of controls. Control and EH participants had significantly different mean body mass index and systolic and diastolic blood pressures among the different genotypes (p < 0.05). In an adjusted regression analysis, only rs11091046 was significantly associated with EH [aOR= 9.57 (95%CI: 3.77-24.30)].

Conclusion:

The study highlights that genotypes and alleles of rs5816 and rs11091046 exist among essential hypertensives in the Ghanaian population and variants of the rs11091046 gene are determinants of predisposing individuals to EH.

Keywords: Angiotensin II, Angiotensin Receptor, Essential hypertension,allelic variation, rs5186 and rs11091046

Introduction

Essential hypertension (EH) is a significant global health threat with insufficient treatment options and poor prognosis [1, 2]. It is an asymptomatic disease characterized by increased blood volume and vascular resistance or continuous vasoconstriction, resulting in elevated blood pressure [3]. It is the most common modifiable risk for morbidity and the leading underlying cause of mortality globally [4].

Review and meta-analysis studies have indicated that the prevalence of hypertension in Ghana is high and persisted for decades. More than one out of every four adults has hypertension [5]. Despite the fact that the Ghanaian government has established national strategic papers on noncommunicable illnesses and nutrition to minimize the country's hypertension burden, hypertension is becoming more common at an alarming rate [6]. The complicated and asymptomatic nature of hypertension makes diagnosis and prediction of who will get the disease difficult, emphasizing the importance of identifying underlying variables.

Hypertension triggers are multifaceted, combining genetic and environmental variables that interact to raise blood pressure [7-9]. Genome-wide association studies (GWAS) have over the years discovered a variety of modest genetic variances, and these variances among populations may account for hereditary vulnerability to EH [4]. There is a consensus that some of the disparities in hypertension prevalence and control in Sub-Saharan Africa may be explained by genetic diversity [10].

Single nucleotide variations (SNVs) account for more than 90% of genetic mutations among individuals and evidence from the literature shows that genetic variations are significant risk factors for hypertension [11-13]. Previous studies have demonstrated the genetic pre-disposibility of renin-angiotensin-aldosterone system (RAAS) components in complex diseases such as EH, CVDs, and progressive renal failure [14, 15]. Several SNVs of RAAS have been shown to be associated with hypertension including the angiotensinogen (AGT)-TI47M gene, and AGT-M235T; angiotensin-converting enzyme (ACE) I/D; angiotensin receptors (AGTRs) and aldosterone synthase C-344T [16]; [17]. One of the most important contemporary discussions in the etiology of EH has focused on the involvement of Angiotensin II (Ang II). Ang II is the main active peptide of the renin-angiotensin system (RAS) and its action is made possible by two available receptors, angiotensin II receptor type 1 (AGTR1; rsID: rs5186) and angiotensin II receptor type 2 (AGTR2; rsID:rs11091046) [18]. Ang II can bind to both the AGTR1 and AGTR2 [19].

Several studies have shown that the presence of SNVs rs5186 gene and rs11091046 gene are linked to EH in other populations [20, 21], however, the association between variations in the rs5186 and rs11091046 genes and EH in the Ghanaian population has not been explored. This emphasizes the importance of determining whether these SNPs are present and linked to EH in our population. Therefore, we investigated the allele prevalence risk of the rs5186 and rs11091046 variation in EH patients and normotensive controls.

Material and methods

Study Design Population

The study is a case-control one that constitutes a total of 200 participants that were selected at random. This study was carried out at the Diabetes/Hypertension Clinic at New Crystal Hospital-Ashaiman from May 2019 to October 2020. New Crystal Hospital is a 100-bed hospital located in the commercial heart of Ashaiman municipality of the Greater Accra region of Ghana with several branches in and around Tema and its environs. Participants were stratified into two groups; 100 patients clinically diagnosed with EH and 100 healthy controls Participants with comorbidities such as diabetes, kidney and heart disease, and secondary hypertension were all excluded from the study.

Ethical Approval

Ethical clearance was sort from the Committee on Human Publications and Research Ethics (CHPRE) at KNUST (reference: CHRPE/AP/404/19). Permission was given by the New Crystal Hospital before the commencement of the study (reference: NCH/ADM/19/016). Informed consent was also sought from the participants before the start of the study and participants had the option to opt out of the study without cohesion at any point of the study.

Demography and anthropometric measurement

Questionnaires were administered to participants to acquire information on their socio-demographics, medical conditions, and lifestyle patterns that could influence hypertension status like smoking habits, medications, etc. Participants' anthropometric measurements that included weight and height were also taken and their body mass index (BMI) (kg/m^2) was calculated. EH was also determined through accessing patient records as individuals having systolic blood pressure ≥ 140mmHg and/or diastolic blood pressure ≥90mmHg with no secondary cause according to American College of Cardiology/ American Heart Association Guidelines for Detection of High Blood Pressure– 2017 [22].

Sample Collection and analysis

A 5ml of peripheral venous blood was collected from the subjects into K_2EDTA test tube and SST. Fasting blood sugar (FBS) was determined with the Life check glucometer; Lipid profile (Cholesterol, Triglyceride, Direct HDL Cholesterol, LDL Cholesterol, VLDL, Coronary Risk), and Renal function test (Blood Urea, Serum Creatinine level, and Electrolytes) were analyzed with the Vitros 5600 automatic chemistry analyzer (Ortho Clinical Diagnostics, New York, USA). Samples were stored at 4°C for blood chemistry analyses and DNA extraction for downstream amplification using tetra-primer amplification refractory mutation system polymerase chain reaction (ARMS-PCR) [23].

Biochemistry analysis

Samples were analyzed with the Vitros 350 serum chemistry analyzer (Ortho clinical diagnostics, 2013, New York, USA). The serum samples were analyzed for urea, creatinine, fasting blood sugar, total cholesterol, LDL-cholesterol, HDL-cholesterol, and Triglycerides. Dyslipidemia was defined when the participants had either total cholesterol ≥ 200 or triglycerides 150mg/dL (1.7mmol/L) or HDL < 40mg/dL (1.03mol/L) in males and < 50mg/dL (1.29mmol/L) in females. Fasting blood glucose levels of ≥ 7mmol/L were also considered hyperglycemia [24].

Genomic DNA Extraction

Genomic DNA was extracted using the modified non-enzymatic salting-out method from extracting DNA from nucleated cells [25]. After the procedure, agarose gel electrophoresis was used for DNA quantification. The genomic DNA was kept at -20^{0}C for the downstream genotyping procedure.

Variation Analysis

The rs5186 and rs11091046 gene variations were genotyped by using the modified tetra-primer ARMS PCR method after the primers were designed and manufactured. From the NCBI GenBank sequence of human ATR1 rs5186 and ATR2 rs11091046 gene (accession numbers: NC_00000.12 (148697903..148743003) and NC_000023.11 (116170744..116174974), two special sets of primers for the T-ARMS PCR were designed by using the web-based software accessible from the website (http://sci.ui.ac.ir/*rahgozar).

The primers and their specific information used for the T-ARMS PCR for the detection of rs5186 and rs11091046 are provided below.

Rs5186

Forward Inner Primer (Allele 'a'):
5'-3': CTGCAGCACTTCACTACCAAATGAACA Tm= 63.8

Reverse Inner Primer (Allele 'c'):
5'-3': CTCCTTCAATTCTGAAAAGTAGCTGAG Tm= 59.8

Forward Outer Primer:
5'-3': TTTTTATGGCTTTCTGGGGAAGAA Tm= 58.8

Reverse Outer Primer:
5'-3': TGGAAACTGGACAGAACAATCTGAAA Tm= 60.9

Product for allele 'a' Size: 354 Product Tm: 78.5 Annealing Temperature: 58.3
Product for allele 'c' Size: 293 Product Tm: 79.4 Annealing Temperature: 58.3
Product size of two outer primers: 594

Rs11091046

Forward Inner Primer (Allele 'a'):
5'-3': TAGGCATATGCTTCTTTAAAGAA Tm= 56

Reverse Inner Primer (Allele 'c'):
5'-3': TGCAAGAGGAATATAATTTATAACG Tm= 55.5

Forward Outer Primer:
5'-3': GATTTCCTCTTGAACCAAAA Tm= 54

Reverse Outer Primer:
5'-3': AGAAACCTTTAAACAATCATTAAGAT Tm= 55.8

Product for allele 'a' Size: 274 Product Tm: 76.9 Annealing Temperature: 55.6
Product for allele 'c' Size: 173 Product Tm: 77.6 Annealing Temperature: 55.6
Product size of two outer primers: 400

Genotyping of rs5186 and rs11091046

Each 25 µL reaction mixture contained 1X of OneTaq® 2X Master Mix (New England Biolabs), 0.2µM each of inner and outer primers, and 50-100 ng of DNA sample. Incubation of the 25µL reaction mixture was completed at 94ºC for 5 minutes, followed by 30 cycles of 30-sec denaturation (94ºC), and 1 min annealing (58.3ºC), 30-sec extension (72ºC), an additional 10-minute extension at 72ºC at the end of the 30 cycles. The final product was visualized with 2% (w/v) of agarose gel electrophoresis alongside a 100 bp marker with Ethidium bromide stain (Sigma-Aldrich, St. Louis, USA) and UV transillumination was used for analysis. The rs11091046 also yielded 274bp for the A allele and 173bp for the C allele. The product of the two outer primers yielded 400bp

Data Analysis

The data on participants' demographic characteristics, clinical, laboratory results as well as genotyping results were entered into Excel and coded in Statistical Software for Social Sciences (SPSS, version 23, California) and continuous variables were compared using t-test and discontinuous variables with Chi-squared test. Results were represented as tables and figures. To see if there was a link between EH and each SNV, we used logistic regression models with each SNV as a predictor variable, with values equal to the number of copies of the minor allele in an additive model, presence of at least one copy of the minor allele in a dominant model, and presence of two copies of the minor allele in a recessive model. Variables such as sex, family history of hypertension (first-degree relative), exercise history, smoking history, alcohol

consumption history, and age were controlled for in the adjusted model. A p-value <0.05 was considered statistically significant.

Results

Socio-demographics of study participants

Table 1 shows the socio-demographic characteristics between the cases and the control group. The study included a total of 100 EH patients (21 males, 79 females) and 100 normotensive controls (38 males, 62 females). The mean age of the cases was significantly higher than the controls ($p < 0.001$). The proportion of females in the case group was significantly higher than the controls ($p < 0.001$). BP and DBP readings were considerably higher in hypertensives compared to controls ($p > 0.05$). Furthermore, hypertensives had significantly higher total cholesterol, HDL-C, LDL-C, urea, and creatinine levels than controls ($p > 0.05$). Hypertensives had slightly higher triglyceride levels than normal persons ($p = 0.370$), but the difference was not significant. Na, K, Cl, VLDL, and CR were among the blood biochemical analytes that did not differ substantially between hypertensives and controls ($p>0.05$). In hypertensive patients, obesity, hyperglycaemia, and uncontrolled blood pressure were all increased when compared to controls.

Table 1: Demographic, anthropometric, and metabolic characteristics of study participants

Variables	NMT/Controls (n=100)	HPT/Cases (n=100)	P-values
Age	40.14 ± 14.69	61.35 ± 13.48	<0.0001
Gender			
Female	62 (62.0%)	79 (79.0%)	<0.0001
Male	38 (38.0%)	21 (21.0%)	<0.0001
Anthropometric Indices			
BMI (Kg/m2)	24.68 ± 5.66	26.57 ± 5.46	0.017
SBP (mmHg)	117.40 ± 13.07	139.17 ± 15.77	<0.0001
DBP (mmHg)	74.90 ± 8.93	84.95 ± 9.08	<0.0001
Biochemical analytes			
Total cholesterol (mmol/L)	4.68 ± 1.07	5.59 ± 1.30	<0.0001
Triglycerides (mmol/L)	1.06 ± .46	1.12 ± .45	0.370
HDL-C (mmol/L)	1.20 ± .30	1.39 ± .37	<0.0001
LDL-C (mmol/L)	3.17 ± .83	3.94 ± 1.10	<0.0001
Glucose (mmol/L)	5.63 ± 2.29	6.493 ± 3.6897	0.050
Urea (mmol/L)	4.24 ± 1.51	4.98 ± 1.46	<0.001
Creatinine (umol/L)	75.95 ± 19.48	87.55 ± 30.67	0.002
NA+	141.23 ± 2.9	140.17 ± 4.73	0.056
K+	4.24 ± .37	4.17 ± 0.37	0.162
Cl-	101.03 ± 6.49	100.11 ± 2.66	0.192
EGFR	111.55 ± 25.48	81.84 ± 23.01	<0.0001
VLDL	18.91 ± 8.19	19.99 ± 8.21	0.351

CR	4.026 ± .87	4.09 ± 0.73	0.531
BMI Status			
Underweight	8 (8.0%)	2 (2.0%)	0.100
Normal	48 (48.0%)	45 (45.0%)	0.777
Overweight	26 (26.0%)	27 (27.0%)	0.999
Obese	18 (18.0%)	26 (26.0%)	0.232
Uncontrolled BP	5 (5.0%)	40 (40.0%)	<0.0001
Hyperglycaemia	6 (6.0%)	15 (15.0%)	0.063

Variables are presented as mean ± SD and compared using a t-test and compared using Mann–Whitney test. Unless otherwise stated, all variables are presented as frequencies and compared using the Chi-square test. BMI – body mass index, SBP – systolic blood pressure, DBP – diastolic blood pressure, NA^+ - Sodium-ion, K^+ - Potassium ion Cl^- - Chloride ion, EGFR – estimated glomerular filtration rate, VLDL – very low-density lipoprotein, CR – Coronary Risk

Genotype and Allele Frequencies of rs5186 and rs11091046 Genes

Figure 2 depicts the genotype frequencies of rs5186 and rs11091046 in cases and controls. Between the cases and controls, the minor allele frequency (MAF) of rs5186 was 25% vs. 6% ($p < 0.001$). In addition, the MAF of rs11091046 was 62.1% vs 41.5% ($p = 0.004$) in cases vs controls. The AA genotype for the rs5186 gene is the most predominant in both cases (62.0%) and controls (88.0%). The rs5186 recessive genotype (CC) was not found in the controls but was found in 12% of the cases. While the AA genotype predominates in cases (61.0%), CA was the highest frequency represented in controls (57.0%). The recessive rs11091046 genotype was found in 61 percent of cases and only 13 percent of the control group.

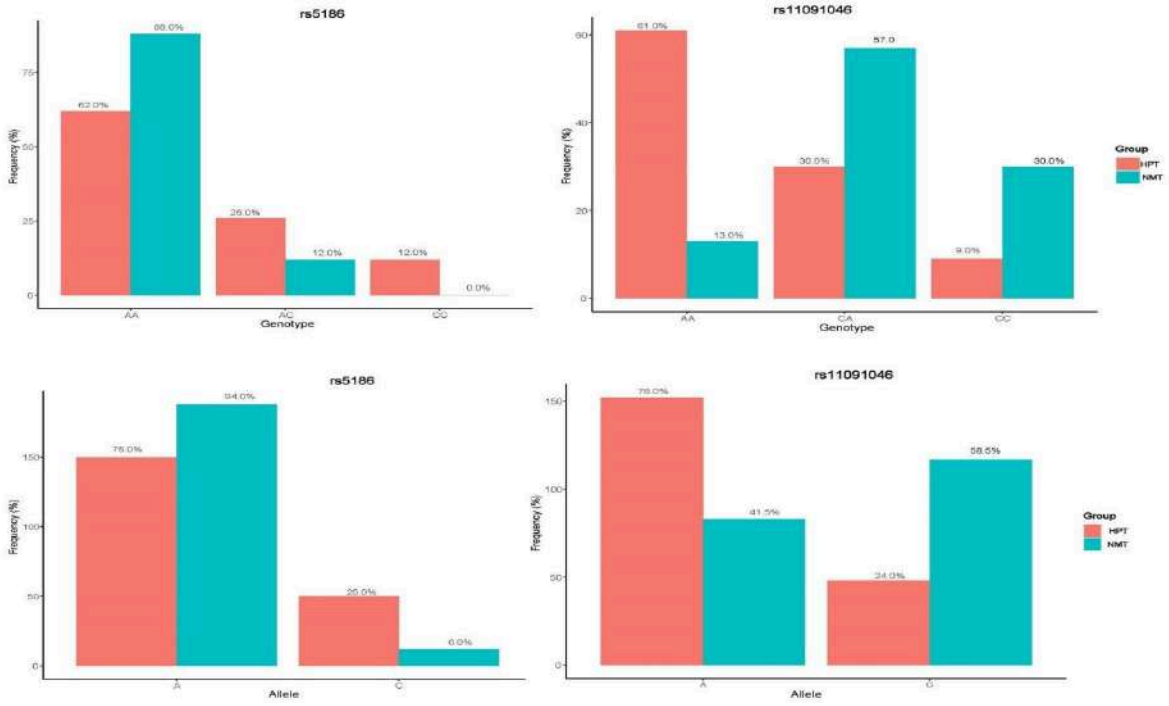

Figure 1: Distributions of genotype and allele frequencies between EH and control groups

Comparison of hemodynamic indices and BMI between case and control based on rs5186 and rs11091046 genotypes

Figure 2 shows the mean distribution of SBP, DBP, and BMI measurements among the different genotypes These parameters were predominantly found to differ significantly between healthy controls and hypertensive patients ($p<0.05$) for most of the rs5186 genotypes. Likewise, they s were also found to be significantly higher cases compared to control ($p<0.05$) for a majority of the rs11091046 genotypes.

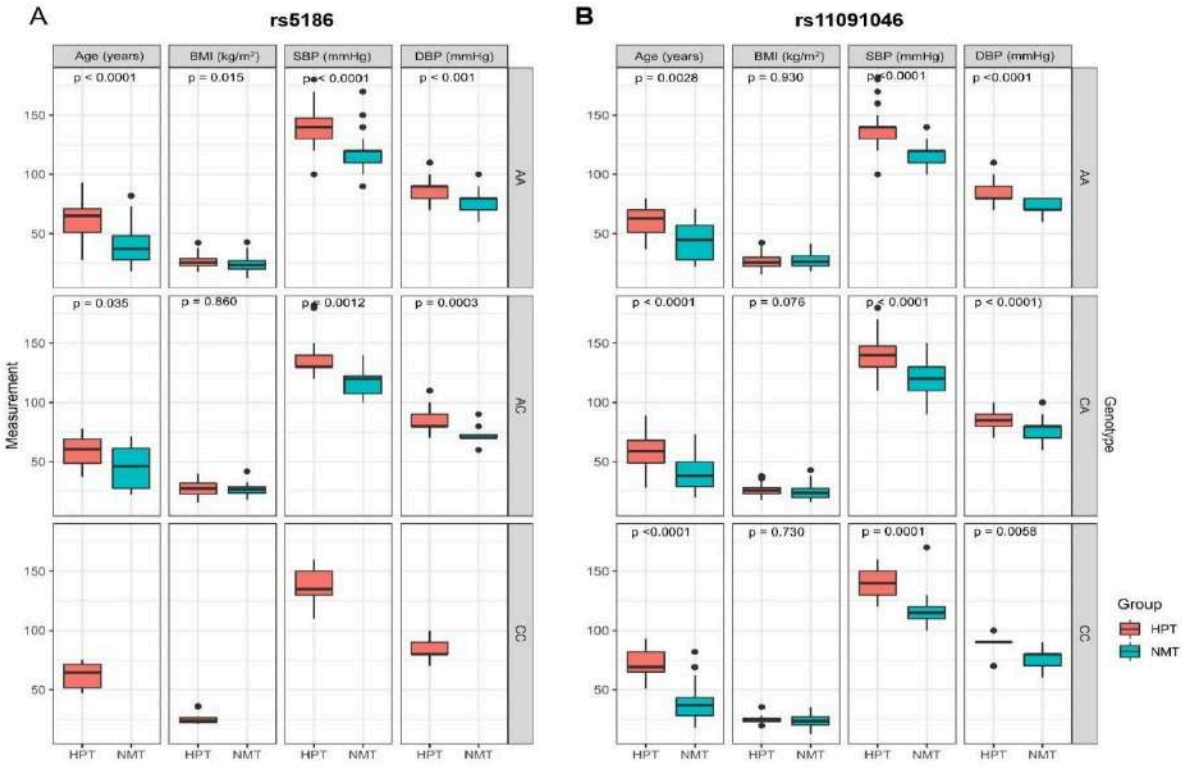

Figure 2: Comparison of hemodynamic indices and BMI between case and control based on the various genotypes

Association between rs5186 and rs11091046 variations and EH

Table 2 shows the relationship between rs5186 and rs11091046, and hypertension under different inheritance models. Both rs5186 and rs11091046 were substantially related to an elevated risk of hypertension in the crude model ($p < 0.05$). However, in the adjusted model, only rs11091046 was significantly associated with hypertension under the recessive model [aOR= 9.57 (95% CI: 3.77-24.30)], additive model 1 [aOR = 6.96 (95% CI: 2.61-18.51)] and additive model 2 [aOR = (95% CI: 14.45 (3.07-68.30)] respectively.

Table 2. Univariate and stepwise logistic regression analysis to test the association of rs5186 and rs11091046 with EH

Model	Allele	Controls (n=100)	Cases (n=100)	cOR (95% CI)	aOR (95% CI)
			rs5186		
Dominant model	wt/mt + mt/mt	12.0%	38.0%	1	1
	wt/wt	88.0%	62.0%	0.22 (0.11-0.46)**	0.38 (0.14-1.02)
Recessive	wt/mt+ wt/wt	100%	88.0%	n/c	n/c
	mt/mt	0	12.0%		
Co-dominant model	wt/m+ mt/mt	88.0%	74.0%	1	1
	wt/mt	12.0%	26.0%	2.57 (1.21-5.46)*	1.57 (0.55-4.52)
Allele Model	wt (A-allele)	88.0%	62.0%	1	1
	mt (C-allele)	12.0%	38.0%	4.50 (2.18-9.29)**	2.65 (0.99-7.11)
			rs11091046		
Dominant model	wt/mt + mt/mt	70.0%	91.0%	1	1
	wt/wt	30.0%	9.0%	0.23 (0.10-0.52)**	0.07 (0.02-0.33)**
Recessive	wt/mt+ wt/wt	87.0%	39.0%	1	1
	mt/mt	13.0%	61.0%	10.48 (5.16-21.25)**	9.57 (3.77-24.30)**
Co-dominant model	wt/mt + mt/mt	43.0%	70.0%	1	1
	wt/mt	57.0%	30.0%	0.32 (0.18-0.58)**	0.49 (0.21-1.12)
Additive model 1	wt/mt	81.0%	33.0%	1	1
	mt/mt	18.6%	67.0%	8.92 (4.23-18.77)**	6.96 (2.61-18.51)**
Additive model 2	wt/wt	69.8%	12.9%	1	1
	mt/mt	30.2%	87.1%	15.64 (6.01-40.67)**	65.10 (7.60-5557.15)**
Allele Model	wt (C-allele)	30.0%	9.0%	1	1
	mt (A-allele)	70.0%	91.0%	4.33 (1.93-9.72)**	14.45 (3.07-68.30)**

Adjusted model: sex, family history of hypertension (first-degree relative), exercise history, smoking history, alcohol consumption history, age (years). n/c- not computed; wt- wild type allele; mt- mutant type allele, aOR- adjusted odds ratio; cOR- crude odds ratio; *p-value <0.05; **p-value <0.01. Additive model was not computed for rs5186 because of zero frequencies.

Discussion

The principal drawbacks to identifying genetic causes of hypertension lie in the multiplicity of genes independently or synergistically involved in the etiologic and pathologic process, each likely imparting a minor effect, and their interaction with the environment. Despite this, two genes of the angiotensin II receptors have proven reliable in elucidating the link to the development of hypertension in several populations, albeit with differing outcomes. This study assessed the relationship between rs5186 and rs11091046 genetic variations and EH.

The study's findings revealed that the recessive genotype (CC) of rs5186 was exclusively found in EH and not in healthy controls. When comparing hypertensive patients to controls, higher frequencies of dominant and co-dominant genotypes were found. In addition, SNVs of rs11091046 showed a significant association with EH in univariate analysis, suggesting a possible relationship between the recessive genotype of rs5186 and EH; nevertheless, there the multivariate models showed no significant association. These results are in line with the findings from a pioneer study by Bonnardeaux et al. [26] who found a strong link between rs5816 gene variants and severe hypertension as well as a higher prevalence of AC and CC genotypes in hypertensive patients than

in healthy controls [26]. A similar trend of results with an increased CC genotype prevalence in hypertensive patients has been reported in case-control studies by Stankovic et al from Serbia [27], Ono et al from Japan [28], and Jiang et al from China [29] respectively. Conversely, Kooffreh et al [30] found that healthy and hypertensive patients in Nigeria had 99% wild-type genotype and 0% variant type (CC) genotype of rs5186. Other studies [31-33] similarly showed a 0% or low prevalence of the CC genotypes in hypertensive patients. The literature shows that the link between rs5186 and EH is demographic-specific. While Yako et al, found a significant association between rs6186 and hypertension in the African population in a review and meta-analysis study [34], Liu et al., 2015 found no association between rs5186 and hypertension in African Americans but did in Asians and Caucasians [35]. Later, Fajar et al., in 2019 found AT1R-rs5186 to be a significant SNP associated with the risk of EH [14]

It has been documented in the literature that the rs11091046 gene is implicated in the regulation of pressure natriuresis and hypotension in the kidney [36, 37]. Genetic variation in rs11091046 which involves the substitution of cytosine with adenine in the genome's sequence at position 3123 has been reported to be an essential risk factor for the onset of hypertension [38]. Our results reveal mean SBP, and BPD were significantly higher in cases compared to controls for the rs11091046 genotypes. Interestingly, we found that SNVs in the rs11091046 gene were independently associated with EH status in a multivariate model adjusting for cofounders. Thus, these findings raise the possibility that rs11091046 variations, as some studies have reported in other populations, may play a role in the pathophysiology of hypertension among Ghanaian hypertensives. Miyaki et al found that rs11091046 variation was a strong predictor of blood pressure response to dietary intake salt intake in a Japanese population [39]. Our results, however, do not concord with those reported by Kabadou et al [15] in a Tunisian population or those of other studies elsewhere [40, 41] that found no association between the genetic variation of rs11091046 with hypertensive status. The discrepancies between our results and those of earlier studies on the role of gene variation in rs5186 and rs11091046 in the development of hypertension may be due to differences in the genotyping technology employed, study design used, sample size, geographical areas, and demographic lifestyles.

Obesity also has a significant impact on the RAAS system's regulation. In obese patients, inadequate RAAS activation influences insulin resistance, sympathetic nervous system activation, and inefficient renal salt management all of which lead to renal dysfunction and EH [42, 43]. Increased production and release of angiotensinogen by adipose tissue in obese individuals support the involvement of RAAS activation in adipose tissue dysfunction [42]. Patients with the rs11091046 variation have higher serum total cholesterol and LDL-cholesterol than healthy controls. This finding is similar to a study by Lapierre et al, [44] who reported patients withrs5186 had higher levels of serum total cholesterol and LDL cholesterol than in their control group.

The study is not without limitations. The study is an exploratory one in a small cohort that investigated SNV in only two genes, however genetic variables that cause EH are numerous. When compared to a wider population, the effect of the changes in this study's small group may be

unpredictable. More data on these gene variations would help us establish a higher degree of findings and implementations among Ghanaians.

Conclusion

The study highlights the existence of genotypes and alleles of rs5816 and rs11091046 among essential hypertensives in the Ghanaian population. rs11091046 genetic variants were identified as a significant determinant for EH. As a result, identifying this SNP is critical for future association studies as well as for categorizing high-risk hypertension patients therapeutically. More studies in a larger population are required to confirm our findings.

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Christiana Anima (Author) *Tamale Teaching Hospital*	**Pandemic Response and Long-term impacts – A case study of Africa.**

Abstract:

This paper presents a comprehensive analysis of pandemic preparedness and response in Africa, utilizing a case study approach. The study aims to examine the background of pandemic preparedness in African nations, elucidate the strategies employed, evaluate the effectiveness of these measures during the COVID-19 pandemic, and draw conclusions to improve future preparedness and response strategies. The study reveals critical insights into the strengths and weaknesses of Africa's pandemic management, offering recommendations for enhancing its capacity to combat future public health crises.

Background:

Africa, a continent characterized by diverse cultures, socio-economic variations, and healthcare infrastructural disparities, faces unique challenges in managing pandemics. The emergence of the COVID-19 pandemic highlighted existing gaps in healthcare systems, resource allocation, and emergency response capacities across African countries. This background necessitates a thorough investigation to identify the strengths and weaknesses of pandemic preparedness and response strategies in the continent.

Aims:

- To assess the existing pandemic preparedness strategies in African nations.
- To evaluate the effectiveness of these strategies during the COVID-19 pandemic.
- To analyze the impact of socio-economic and healthcare disparities on pandemic response.
- To propose recommendations for enhancing pandemic preparedness and response in Africa.

Methods:

This study adopts a mixed-methods approach, combining qualitative and quantitative research methodologies. Data is collected from diverse sources, including government reports, academic literature, WHO publications, and interviews with public health experts. The qualitative analysis involves thematic coding of interviews and content analysis of documents, while quantitative data is subjected to statistical analysis for trends and patterns.

Results:

The analysis revealed that African nations demonstrated varied levels of pandemic preparedness, influenced by factors such as governance, healthcare infrastructure, public awareness, and international collaboration. Responses to the COVID-19 pandemic ranged from robust measures in some countries to challenges in resource allocation and implementation in others. Socio-economic disparities significantly affected the ability of certain regions to respond effectively.

Conclusion:

Africa's response to the COVID-19 pandemic underscores the need for improved pandemic preparedness strategies, with a focus on bolstering healthcare systems, enhancing international collaboration, and addressing socio-economic disparities. Key recommendations include investments in healthcare infrastructure, improved data collection and surveillance systems, capacity building, and equitable distribution of resources to ensure an efficient and coordinated response to future pandemics.

Keywords: Pandemic Preparedness, Pandemic Response, COVID-19, Africa, Healthcare Systems, Socio-economic Disparities, Public Health, International Collaboration, Emergency Response, Healthcare Infrastructure.

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Farzaneh Tayebi (Author)

Yasouj University

Abolfazl Heydari (Co-Author)

Mahnaz Farahi (Co-Author)

Hassan Sheibani (Co-Author)

Enhanced Removal of Anionic Dye Compounds from Aqueous Solutions using Beta-Cyclodextrin Polymer Crosslinked with Epichlorohydrin.

Abstract

Achieving clean water is one of the increasing needs of people, which faces alarming challenges, and new approaches are necessary to remove organic molecules such as dyes from water. In this work, β-cyclodextrin polymerized by epichlorohydrin as a crosslinking agent (β-CDP) was prepared to remove methyl orange from aqueous solutions. Fourier-transform infrared spectroscopy and Scanning Electron Microscope verified the successful preparation of β-CDP hydrogels and their morphology surface. Differential scanning calorimetry and Thermogravimetric analyses were utilized to examine their thermal properties. The swelling properties of the β-CDP hydrogel were investigated in water and simulated body media (pH: 3, 7, and 10). According to the results, β-CDP hydrogel in a neutral medium has the highest water absorption. Finally, the capability of the prepared hydrogel for methyl orange removal was investigated, and the absorbent amount and absorption time were optimized. The results showed that the maximum methyl orange absorption is obtained when 5 mg β-CDP hydrogel and a reaction time of 300 minutes. examined. The laboratory findings are more compatible with the Langmuir equation than the Freundlich isotherm diagram.

Keywords: Methyl orange removal, β-Cyclodextrin, hydrogel, Epichlorohydrin

Introduction

The rapid growth of the global industrial economy has led to the widespread use of organic dyes for dyeing in a wide range of industries, including textile, dyeing, leather, paper, food, cosmetics, and other industries. Unfortunately, wastewater-containing dyes are very stable and resistant to biodegradation due to their aromatic and complex molecular structures causing many environmental problems (Salleh, Mahmoud, Karim, & Idris, 2011). These colors are poisonous and cause cancer, genetic mutation, skin issues, etc. Therefore, achieving clean water is one of people's increasing needs, which faces alarming challenges, and new approaches are necessary to remove dye from water (Herrera, Futalan, Gapusan, & Balela, 2018). Among hazardous anionic dyes, methyl orange (MO) is commonly employed in the aforementioned industries. It has significant toxicity due to its azo group; therefore, its removal from aqueous wastes interest researchers. Physical, chemical, and biological treatments remove synthetic dyes like MO. These methods include membrane filtration (Al-Rashdi, Johnson, & Hilal, 2013), sedimentation, coagulation (Liu, Xiang, Xu, & Li, 2022), biological treatment (Paz, Carballo, Pérez, & Domínguez, 2017), absorption (Mokhtari, Ghaedi, Dashtian, Rahimi, & Purkait, 2016), ion exchange (Jia et al., 2020), electrochemical process (Wang, Liu, Ye, Lin, & Yang, 2020), photocatalytic degradation (Dai, Chen, Peng, Ke, & Yi, 2007) and ozonation (Dong, Yao, Tao, Shi, & Wei, 2023). It has been shown that the absorption process in which adsorbents are used for dye removal. This technique is effective because the adsorbent is easily separated from the polluted wastewater, has low operating costs, and produces no toxic substances (Gil, Assis, Albeniz, & Korili, 2011). Adsorbents such as graphene oxide (Soleimani, Tehrani, & Adeli, 2018), activated carbon (Gong et al., 2013), carbon nanotubes (Ai & Jiang, 2012), and nanocomposite hydrogels (Fan, Shi, Lian, Li, & Yin, 2013) have been reported to remove toxic dyes from wastewater. Hydrogels are low-cost, retrievable, and simple to use adsorbents that can absorb dye-contaminated wastewater (Hosseinzadeh & Khoshnood, 2016; Paul Guin, Bhardwaj, & Varshney, 2016). Hydrogels, three-dimensional cross-linked polymers with high molecular weight, may absorb many times their original volume of water without dissolving. Their volume increases reversibly because they absorb and store a lot of water (Zhou, Luo, Liu, Chu, & Crittenden, 2018). The temperature change (Gupta, Carrott, Ribeiro Carrott, & Suhas, 2009), pH (Annadurai, Juang, & Lee, 2002), and ion concentration (Arami, Limaee, & Mahmoodi, 2006)

play an essential role in the reversible swelling of hydrogels. Polymeric hydrogels absorb ionic dyes due to their carboxylic acid, amine, hydroxyl, and sulfonic functional groups. Various polymer adsorbents have been used to remove MO from water, some of which are mentioned. Jiang et al. (2018) selectively removed MO using glutaraldehyde cross-linked chitosan/β-CD copolymer. MO has high dye selectivity and adsorption capacity of 392 mg/g at 10 mg/50 mL (Y. Jiang et al., 2018). Vo et al. (2020) showed that the graphene oxide-chitosan composite hydrogel has a high absorption capacity for the removal of MO and can be reused several times without losing the removal capacity (Vo et al., 2022). Jiang et al. (2023) found that β-CD treated with acrylic acid effectively adsorbs methyl blue/methyl orange combination, with high removal efficiency (75-88%) in neutral to acidic environments (M. Jiang et al., 2023). A copolymer of β-CDP, cross-linked with epichlorohydrin (PECH), was developed to enhance the absorption capacity and removal effectiveness of polymer adsorbents for MO removal. β-CD, a ubiquitous torus-shaped cyclic oligosaccharide with a hydrophobic cavity, may be utilized to create a pH-sensitive cross-linked gel (Mahmood, Ahmad, Sarfraz, & Usman Minhas, 2018). The specific structure of β-CD creates an excellent capacity to form complexes with organic molecules such as dyes by providing host-guest interactions (Dodziuk, 2006). Insoluble β-CD polymers and copolymers can be prepared using epichlorohydrin (PECH), a covalent cross-linking agent (Crini & Morcellet, 2002). Cross-linking is a standard method to prepare hydrogels with different mechanical properties and improved absorption capacity. β-CDP is an antimicrobial polymer with a low molecular weight (up to 1000), which can inhibit bacteria or fungi, so it has been widely used in the preparation of plastics (Thomassin, Lenoir, Riga, Jérôme, & Detrembleur, 2007), textiles (Lim & Hudson, 2004; Qian, Xiao, Zhao, & He, 2011), water treatment (Blackburn, Harvey, Kettle, Payne, & Russell, 2006; Krajewska, 2005) etc. In this research work, poly β-CDP was prepared as polymeric hydrogels, and its ability to remove MO anionic dye was investigated. Cationic hydrogel has been synthesized from β-CDP, epichlorohydrin, with different ratios. The structure of these hydrogels was determined by analyses such as differential scanning calorimetry (DSC), thermal gravimetry (TGA), scanning electron microscopy (SEM), and Fourier transform infrared spectroscopy (FT-IR). The produced hydrogels absorbed MO, and the effects of adsorbent dosage, time, and MO concentration were examined. Langmuir and Freundlich isotherms fitted adsorption data and found the right model.

Experimental

Materials

The chemicals including β-cyclodextrin, hydrochloride, sodium hydroxide, epichlorohydrin, methyl orange, potassium sulfate, copper sulfate, sulfuric acid, potassium hydrogen phthalate, potassium dihydrogen phosphate, hydrochloric acid, and sodium bicarbonate were purchased from Sigma Aldrich company. Bidistilled water, ethanol, and acetone were used to prepare β-cyclodextrin hydrogels.

Synthesis of β-cyclodextrin hydrogel by epichlorohydrin crosslinking

Synthesised hydrogel by adding 0.5 gr β-cyclodextrin, 0.5 ml distilled water, and a little quantity of sodium borohydride to a round-bottom flask. Stirred for 5 min. Afterward, 0.45 ml of epichlorohydrin was added to the solution at 50°C for 4 minutes and mixed entirely for 3 minutes. After that, 0.51 ml of sodium bicarbonate (40% w/w) was added drop by drop at 50°C for 60 minutes until the solution turned into a colorless jelly. The approximate duration of gelation is 46 minutes. Washing the product with distilled water and ethanol multiple times purified it. After drying, the result was white powder.

Characterization of the β-CDP hydrogels:

FT-IR analysis

FT-IR spectra are a rapid and effective method for identifying and ensuring the synthesis of β-CDP hydrogel by examining the functional group. Fourier transform infrared (FT-IR) spectra were recorded using Bruker Tensor 27 FT-IR Spectrometer, and synthesized hydrogel's melting point was measured using Electrothermal IA9200 (England). KBr tablets were made hydrogel with various, and its FT-IR spectra were recorded.

Thermal analysis

Differential scanning calorimetry (DSC) and Thermal gravimetric analysis (TGA) of β-CDP hydrogel were recorded to investigate the thermal stability and thermal properties of the hydrogel. The PC/PG STA 409 thermal analyzer was used to record the corresponding spectra.

Scanning Electron Microscope (SEM)

SEM images were used to examine the shape and diameters of produced hydrogel pores. Zeiss SIGMA VP-FESEM pictures were taken from their surfaces.

Swelling properties

The capability of the β-CDP hydrogel in water absorption was investigated. To calculate the amount of water absorption, 0.005 gr of the hydrogel with 0.5, 1, and 1.5% ratios of β-CDP was placed into the test tube and added 2.5 ml of distilled water. Mixture was mixed for 1 hour. Then each test tube was centrifuged for 15 minutes, and the supernatant solvent was separated. The water absorption of obtained hydrogel was determined using the equation (1):

$$S=(W_1-W_0)/W_p \times 100 \quad (1)$$

where S is the absorption percentage, W_0 (gr) is the hydrogel's starting weight, W_1 (gr) is its weight after water absorption, and W_p is its weight. To investigate the swelling properties of β-CDP hydrogel in the simulated media of the body, 5 mg of β-CDP hydrogel (1% β) were individually placed into three 50 ml flasks containing 2.5 ml of buffers with pHs of 3 (acidic), 7 (neutral) and 10 (alkaline) and stirred on the mixer for 1 hour. After 1 hour, each solution was centrifuged for 15 minutes and separated from the supernatant. The resulting hydrogel was weighed, and the amount of water absorption was calculated according to equation (3).

Removal of methyl orange

To determine the absorption rate of methyl orange by the prepared hydrogels, 0.005 gr of β-CDP (0.5, 1, and 1.5% B) hydrogels were individually placed into three 50 ml flasks and added 5 ml of methyl orange solution (100 ppm to 600 ppm) to it. The mixture was stirred for five hours to homogenize well. Each test tube was centrifuged for 15 minutes and separated the supernatant solution. The separated phase was analyzed by UV-Vis spectrophotometer. The absorption capacity of the hydrogel was estimated using equation (2):

$$q_e=(V(C_0-C_e))/W \quad (2)$$

where qe (mg/g) is equilibrium absorption, V (L) is methyl orange solution volume, C_0 (mg/L) is starting concentration, Ce (mg/L) is hydrogel absorbed concentration, and W (g) is hydrogel weight. The obtained results show that the hydrogel with a ratio of 1.5% of β-CDP has the most absorption. The methyl orange calibration diagram (30 ppm-1000 ppm) is provided in Figure 1.

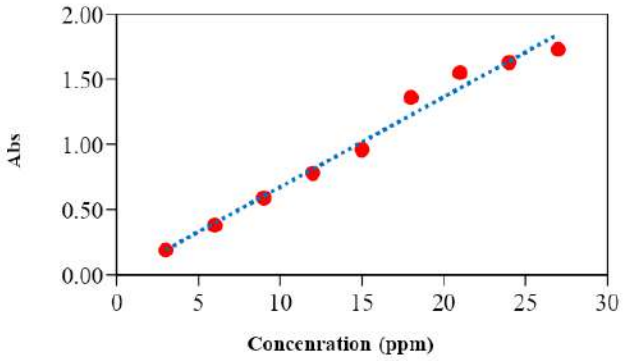

Figure 1. Calibration diagram of methyl orange.

RESULTS AND DISCUSSION

Characterization of the β-CDP hydrogels

The FT-IR spectra of β-CDP hydrogels (0.5, 1, and 1.5 % β-CDP) (Figure 2a) show a high and wide absorption peak in the 3400 cm^{-1} area, indicating OH group vibration. Stretching vibration of C-O groups has also been observed at 1030 cm^{-1}. The absorption bands at 2900 cm^{-1} are caused by aliphatic hydrogen stretching vibrations in β-CDP and epichlorohydrin monomers. The presence of the above peaks indicates the formation of β-CDP hydrogel. The SEM pictures were used to assess the shape of β-CDP hydrogel. The SEM image recorded with 20 µm magnification (Figure 2b) shows that the β-CDP is cross-linked by epichlorohydrin. Also, the images with the magnification of 10 µm (Figure 2b) show that the synthesized hydrogel has a porous surface containing holes of different sizes.

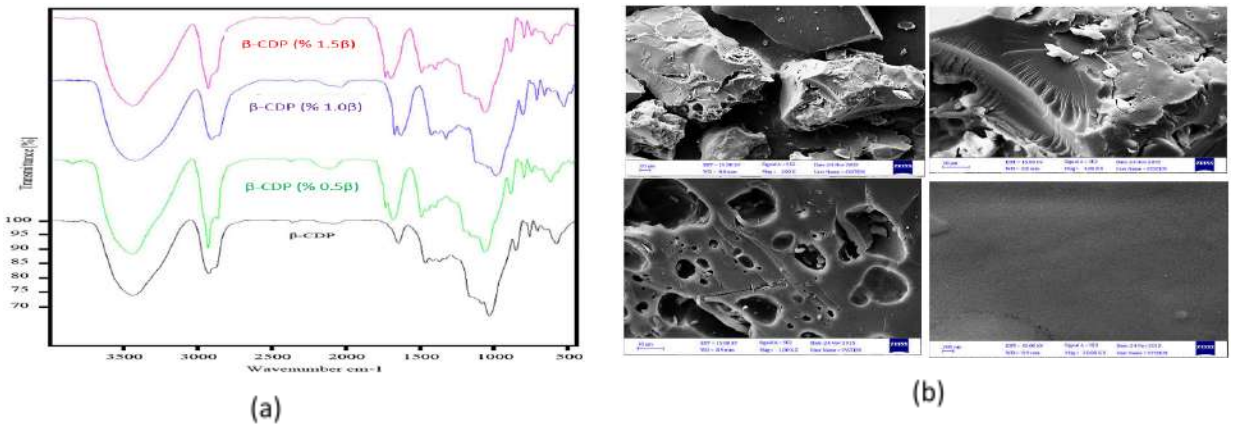

Figure 2. a) FT-IR spectra of β-CDP and β-CDP hydrogels (0.5, 1, and 1.5% β- CDP), b) SEM images of β-CDP hydrogel (1.5% β).

Differential heat flow (in DSC diagram) and its derivative (in DDSC diagram) curves for β-CDP hydrogels provided in Figures 3a and 3b were utilized to compare the thermal properties of hydrogels. The DSC spectra of β-CDP hydrogels show a peak at 250-300°C, indicating exothermic properties. The exothermic peaks are related to the decomposition of the β-CDP polymer and low changes and distinguishable intensity in β-CDP hydrogels diagrams with different ratios are observed.

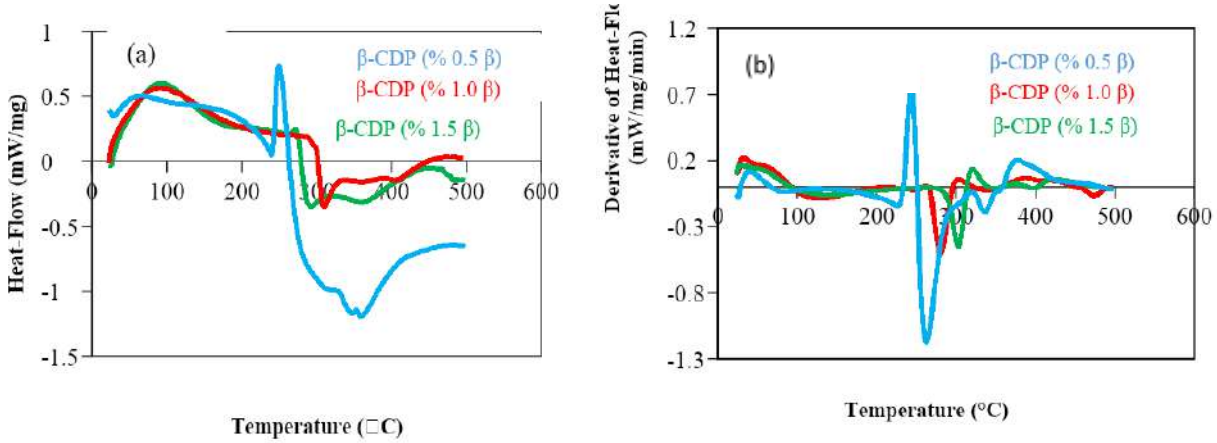

Figure 3. a) DSC and b) DDSC spectra of β-CDP hydrogels with different ratios.

According to the DSC curve of β-CDP hydrogels, the temperature peak of the β-CDP decomposition (360°C) was shifted to a lower temperature (210°C and 310°C) after mixing with excess β-CDP and exhibited a higher intensity than β-CDP polymer. Comparing these peaks with the endothermic peak in the DSC spectrum of β-DCP hydrogel shows the formation of a new compound with different characteristics. The DDSC curves of these materials shown in Figure 3b agree with the obtained DSC results. TGA and DTG analyses have been performed to estimate the homogeneity of the β-CDP hydrogels (0.5% and 1.5% β-CDP) and their thermal stability results depicted in Figure 4a and 4b. In the temperature range of 260 to 400 °C, the hydrogel having 0.5% β-CDP loses 50% of its weight, whereas the hydrogel containing 1.5% loses 60%. This indicates degradation of the hydrogel. These data revealed that the introduction of amount of β in β-CDP polymer increased the thermal stability.

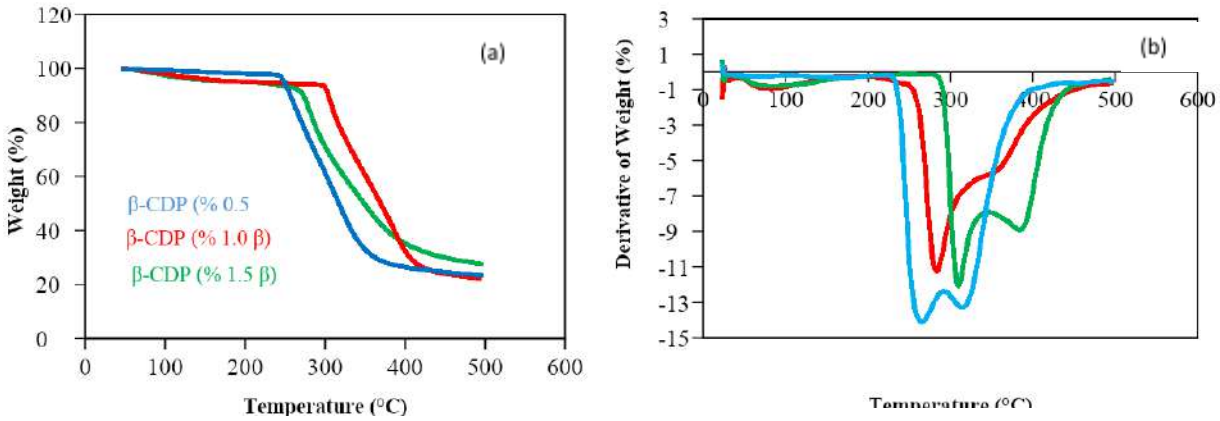

Figure 4. a) TGA and b) DTG spectra of β-CDP (0.5% and 1.5% β-CDP).

Swelling behavior of the hydrogels

One of the properties of β-CDP hydrogel is its ability to absorb water up to several times its weight and swell due to the holes with a hydrophilic nature in its network structure. By comparing the amount of water absorbed by β-CDP hydrogel with different ratios hydrogel, it can be concluded that with an increase of 1.5 percent β cyclodextrin added to the copolymer increases the amount of water absorption significantly due to the increase in the hydrogen bonds.

Swelling properties of hydrogels in the simulated media of the body

Sensitive hydrogels, known as intelligent systems, are susceptible to external stimuli, including physical, chemical, and other stimulus types such as temperature, pressure, pH, magnetic field and so on. Solution pH is crucial to surface adsorption. In this research, an attempt was made to investigate the water absorption by hydrogel in the simulated media of the body. The selected pHs were 3, 7, and 10 corresponding to the pHs in the acidic media of the stomach, the neutral media of the blood plasma, and the alkaline media of the intestine, respectively. A 0.1 M potassium hydrogen phthalate solution and 0.1 M HCl solution were used to prepare a buffer with pH = 3. Instead, K_2HPO_4/ NaOH (0.1 M/0.1 M) were mixed to provide a pH = 7 buffer. Finally, a pH-10 buffer was made from $NaHCO_3$/NaOH (0.05 M/0.1 M). The hydrogel with 1.5 % β-CDP absorbed the most water at pH = 7 for 1 hour. The result shows that the synthesized hydrogel is suitable for absorbing water in a neutral medium, i.e., blood plasma. The method used in this study can be extended to develop new drug delivery systems.

Removal of methyl orange from water

β-CDP hydrogels can form a complex with polluting molecules due to the many holes in their structure so that they can be used in water purification systems. Methyl orange is soluble in water due to its SO_3 group and is an anionic compound. This dye pollutant can be easily absorbed by β-CD hydrogel by forming hydrogen and ionic bonds. The amount of absorbent is an important parameter in determining the absorption capacity. For this mean, various amounts of adsorbent (5, 10, 15, 20, and 25 mg) have been investigated to optimize this parameter, and the results are presented in Figure 5 a.

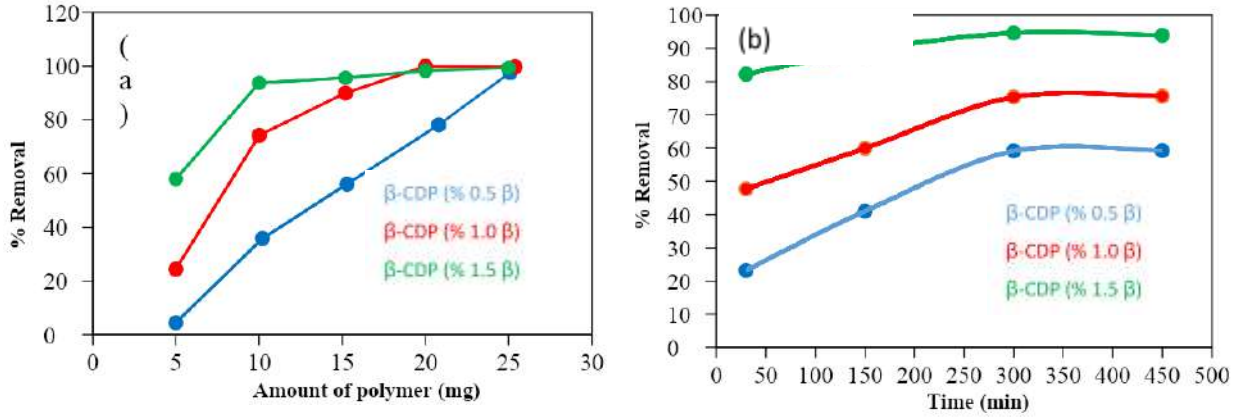

Figure 5. a) The effect of adsorbent dosage and b) absorption time on the methyl orange removal

The results showed that the available absorption sites for methyl orange absorption increase with the amount of absorbent up to 5 mg. In the higher amount of absorbent (>5 mg), the absorption sites are occupied by methyl orange, and there is no increase in the absorption. The contact time between the absorbent β-CDP (0.5, 1 and 1.5% β) hydrogels and the absorbate (methyl orange) is another important parameter in the absorption process. Thus, the absorption rate of methyl orange was investigated for 30 to 450 minutes by monitoring the color intensity of the solution (Figure 5b). According to the results, the remaining dye in the solution decreases with increased time absorption and reaches the highest value in 300 minutes. After this time, the absorption process reaches equilibrium.

Equilibrium adsorption isotherms

Adsorption isotherms examine the interaction between adsorbate and absorbents and the absorption mechanism. The adsorption results were analyzed with two isotherm models, including Langmuir and Freundlich to find a suitable model for describing the prepared hydrogel's adsorption behavior.

Langmuir isotherm

Langmuir isotherm implies monolayer adsorption in which all absorption sites have the same position in terms of energy level and absorption enthalpy. The relationship of the Langmuir model is as follows:

$$\frac{C_e}{q_e} = \frac{1}{K_L} + \frac{a_L}{K_L} C_e \qquad (3)$$

q_e (mg/g) is equilibrium absorption, C_e (mg/L) is methyl orange concentration after equilibrium, K_L is the Langmuir equilibrium constant, and a_L is the adsorption enthalpy constant. By plotting C_e/q_e in terms of C_e, the Langmuir equilibrium constant (K_L) is obtained from the intercept of the plotted line ($1/K_L$), and the Langmuir adsorption enthalpy constant (a_L) is derived from its slope (a_L/K_L). Equation (6) gives the maximal absorption capacity (mmol/g) according to the Langmuir equation:

$$q_m = \frac{K_L}{a_L} \qquad (4)$$

The calculated parameters are given in Table 1, and corresponding Freundlich isotherm diagrams are provided in Figure 6a.

Table 2. Langmuir equation constants in methyl orange absorption

Hydrogel type	K_L (dm^3/g)	a_L ($dm^3.mmol$)	q_m (mmol/g)	R^2
β-CDP (% 0.5 β)	18.51	0.44	42.06	0.999
β-CDP (% 1.0 β)	27.77	0.36	77.13	0.998
β-CDP (% 1.5 β)	55.55	0.44	126.25	0.997

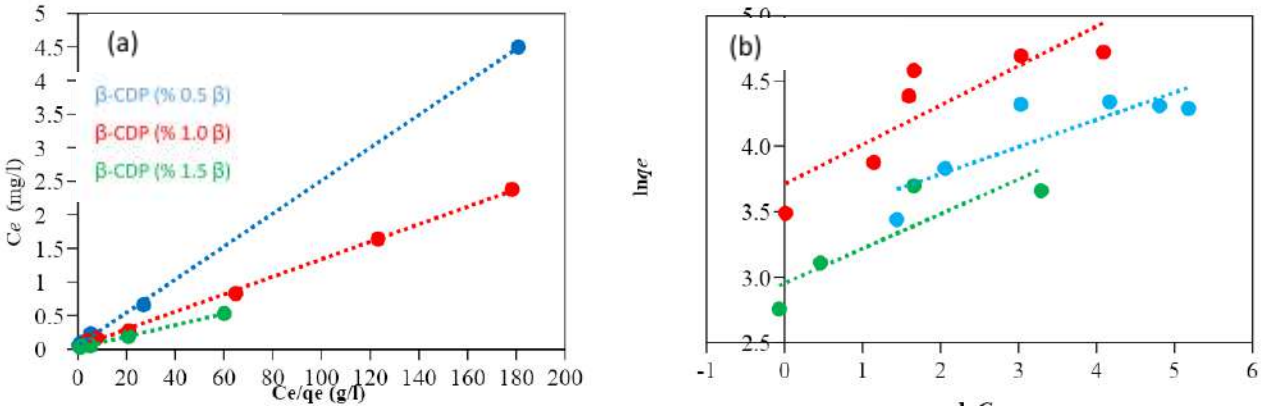

Figure 6 a) Langmuir isotherm diagram, b) Freundlich isotherm diagram.

Freundlich isotherm

In this model, the absorption process is not a single layer, and each site's energy is different from another. This equation is expressed as follows.

$$\ln ln\, q_e = b_F \ln ln\, C_e + \ln ln\, K_F \qquad (5)$$

Q_e (mg/g) is equilibrium absorption, C_e (mg/L) is methyl orange solution concentration after absorption, K_F is the Freundlich constant, and b_F is the Freundlich exponent. By plotting Ln q_e versus Ln C_e, we can derive the Freundlich exponent (b_F) and Freundlich constant (K_F) from the slope and intercept of the plotted line, respectively. Table 3 shows Freundlich parameters, and Figure 6b presents Freundlich isotherm diagrams. The laboratory findings match the Langmuir equation better than Freundlich isotherm relation. Therefore, the absorption of methyl orange by hydrogels is a single-layer and homogeneous physical absorption.

Table 3. Freundlich isotherm constants in methyl orange absorption.

Hydrogel type	K_f	b_f	R^2
β-CDP (% 0.5 β)	11.94	0.264	0.825
β-CDP (% 1.0 β)	29.08	0.208	0.719
β-CDP (% 1.5 β)	40.85	0.301	0.752

Conclusion

In this work, β-cyclodextrin crosslinked with epichlorohydrin was prepared to remove methyl orange from aqueous solutions. Fourier-transform infrared spectroscopy and Scanning Electron Microscope were used to investigate the functional groups and morphology of the prepared hydrogel. The appeared peaks in FT-IR spectrum indicate the formation of β-CDP hydrogel (0.5% and 1.5%β CDP). The SEM image shows that the synthesized hydrogel has a porous surface with different pore sizes and β-cyclodextrin is cross-linked by epichlorohydrin. Differential scanning calorimetry and Thermogravimetric analyses were utilized to examine their thermal properties. Exothermic DSC spectra of β-CDP hydrogels (0.5 and 1.5 %β-CDP) at 250-300°C demonstrate desired exothermia. An approximate weight loss of 50% in the temperature range of 260 to 400 °C for the hydrogel containing 0.5% CDP and a 60% weight loss for the hydrogel containing 1.5% β-CDP in the temperature range of 270 to 400 °C is observed, which indicates degradation hydrogel in these temperature ranges. In addition, swelling properties of the β-CDP hydrogels were investigated in water and simulated body media (pH: 3, 7 and 10). Among the hydrogels, the hydrogel synthesized containing 1.5%β-CDP has the highest water absorption. The result shows that the synthesized hydrogel is suitable for absorbing water in a neutral medium, i.e. blood plasma. Finally, the hydrogels' methyl orange elimination capacity was examined. The effects of absorbent amount and absorption time on methyl orange removal were studied. Results indicated that methyl orange absorption sites increase with absorbent up to 5 mg. According to the results, the remaining dye in the solution decreases with increased time absorption and reaches the highest value in 300 minutes. The adsorption results were analyzed using two isotherm models, Langmuir and Freundlich. The Freundlich connection is less consistent with laboratory data than the Langmuir equation. Thus, hydrogels absorb methyl orange homogeneously and single-layer.

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Ajaja Godwin Stanley (Author)

Department of Microbiology/rivers State University

Examination of Oral Cavity for Pathogenic Bacteria Among University Students in Port Harcourt Rivers State.

Abstract

The study examined of oral cavity for pathogenic bacteria among university students in Port Harcourt Rivers State. Oral swab specimen was collected from the oral cavity (mouth) of each participant by inserting a sterile oral swab stick 1-2 inches into the mouth to gently swab the walls of the oral cavity including the oral mucosa, the teeth, area between the cheek and gum, as well as the tongue for one to two minutes. The swab stick was removed aseptically and corked immediately. All samples were transported to the laboratory inside a sealed plastic bag as soon as the collection was done. Samples were processed on the same day of collection. Results shows that the highest numbers of bacterial colonies were observed in the fifth sample (6.2±0.64 X 103) followed by Fourth (3.7±0.09 X 104) and first (2.9±0.45 X 106) samples. Third and second samples recorded (2.7±0.77 X 104) and (1.8±0.12 X 105) respectively. Similarly, five (5) bacteria genera isolated from the five (5) oral samples collected from students; these bacteria isolate was identified and confirmed as Streptococcus spp, Staphylococcus sp., Enterobacter sp., Pseudominas aeruginosa and Klebsiella Pneumonia. The highest prevalence of typhoid was recorded in 25-29 years, followed by 20-24, 15-19, 30-34, 2-14 and 35-above respectively. Lastly, the five samples were resistant to Cpx 10mcg, sample two showed intermediate zone of inhibition while the rest samples were resistant to PN 30mcg. Sample one was susceptible to GN 10mcg while sample 2, 3, 4 and 5 showed intermediate zone of inhibition. Sample one, two and four were susceptible to SXT 30mcg while sample three and five showed intermediate zone of inhibition. It is concluded that the bacteria recovered from oral cavity of students in Ignatius were Streptococcus spp, Staphylococcus sp., Enterobacter sp., Pseudominas aeruginosa and Klebsiella Pneumonia. It was recommended amongst others that proper sensitization on oral health should be done for students.

Keywords: Oral cavity, Pathogenic bacteria, University students, Rivers State.

I. Introduction

The oral cavity is a morpho-physiologically heterogeneous, dynamic environment with biotic and abiotic factors influencing with different intensity various specialized surfaces of its particular compounds (tongue, teeth, gums, etc.). Among these factors, temperature, pH of saliva (related to food substances), oral care agents and specific diet may impact oral cavity ecology. This environment creates an open system with dynamic ecological conditions promoting its colonization with many microbiota and influences their species composition. Resident species of the Gram positive Streptococcus viridans group are believed to be typical oral bacteria – inhabitants of healthy oral cavities, not related to any specific clinical pathological symptoms (Zawadzki, de Lucena, & da Silva, 2016). The oral cavity microbiome consists of a multi-species community with its complex relations to the human host. Single cells and their micro-colonies creating biofilm remain in a labile homeostasis; simultaneously, human immunological system activity inhibits microbiota multiplication (Thuy et al., 2013). Numerous factors, both environmental and hereditary, may influence the development of an oral pathology. An occupational specificity of generally healthy persons causing difficulties with the maintenance of good oral health, unfavorable economic, social, sanitary circumstances, and, also systemic disorders and congenital malformations of the masticatory system, are factors influencing poor oral hygiene and contributing in the appearance of dental difficulties. To date, dental caries and periodontal diseases are major health problem in Poland (Perkowski et al., 2014).

The oral microbiome, mainly comprising bacteria which have developed resistance to the human immune system, has been known to impact the host for its own benefit, as seen with dental cavities. The environment present in the human mouth allows the growth of characteristic microorganisms found there. It provides a source of water and nutrients, as well as a moderate temperature. Resident microbes of the mouth adhere to the teeth and gums to resist mechanical flushing from the mouth to stomach where acid-sensitive microbes are destroyed by hydrochloric acid (Sherwood et al., 2013).

The environment in the human oral cavity (water, nutrients, epithelial debris and as well as a moderate temperature) supports the growth and survival of a wide range of microorganisms, including bacteria, yeasts, viruses and occasional protozoans, with bacteria predominantly residing in the microflora. The prominent bacteria commonly found in the mouth include several genera such as: Streptococcus, Lactobacillus, Lactococcus, Enterococcus, Staphylococcus, Corynebacterium, Veillonella and Bacteroids. These numerous bacterial species undergo intense interspecies competition to form multispecies biofilm structure (Liu et al., 2016; Dahlen et al., 2019). The mouth's mucous membranes are often sterile at birth, but can be contaminated within 4 - 12 hours by passing through the birth canal. After birth, Streptococcus viridians became the most prominent member of the oral cavity's resident flora and remained so for life. The organism is thought to have originated in mother and birth attendants' respiratory tracts (Umar et al., 2015).

Aerobic and anaerobic Staphylococcus, Neisseriae, Moraxella catarrahalis, Diptheroids and occasionally Lactobacilli are added to the oral microbial flora early in life, before the eruption of the teeth. When teeth begin to erupt, however, anaerobic spirochete species such as Prevotella species, in particular Prevotella melaninogenica, Fusobacterium species, Rothia species and Capnocytophage species, together with some anaerobic Vibros and Lactobacilli, are found in the oral cavity. Actinomyces species are usually present in tonsillae tissue and gingivae in adults along with this load of bacteria (Majumdar & Singh, 2014).

Oral and dental problem such as tooth decay, tooth erosion, tooth sensitivity, tooth ache, calculus, gingivitis, periodontitis and plaque are common among many and it has been associated with poor oral hygiene (Haque et al., 2019). The dental plaque for instance is a dense, non-mineralized, complex mass of bacterial colonies that live in a gel-intermixing matrix and adheres to the tooth. It contains bacterial cells, salivary polymers and bacterial extracellular products. The dental plaque begins to accumulate within 24 hours without regular tooth brushing. The dental plaque has an extra polysaccharide that surrounds it and protects it from the penetration of an antibiotic. Plaque accumulation can be stimulated by increased production of gingival cervical fluid that contains growth factors of various bacteria including Gram negative anaerobes such as Porphyromonas gingivalis, Prevotella melaninogenica and Fusobacterium nucleatum (Vesna, 2018).

An individual's oral health depends on the existence of a healthy native microflora on the surfaces of their gums, teeth, and oral cavity linings (Gerald et al., 2013). The likelihood of the residing organisms surviving in an environment that is harmful to the hosts would be reduced. Several dental illnesses, including caries and periodontitis, begin to manifest when resident microorganisms experience a loss of homeostasis (Lim et al., 2020). Additionally, very little research has been done to comprehend the makeup of oral flora and the bacteria that make it up. The microbes are typically found on the surface tissues of all humans, such as the mouth cavity. The quantity and kind of these bacteria vary depending on a person's age, nutrition, and level of personal hygiene (Sharma et al., 2018). Numerous chronic diseases, including bacterial endocarditis, pulmonary pneumonia, pediatric osteomyelitis, preterm low birth weight, and cardiovascular disease, are brought on by these oral bacteria (Jorn et al., 2005). Streptococcus, Lactobacillus, Lactococcus, Enterococcus, Staphylococcus, Corynebacterium, Veillonella, and Bacteroids species are common in the normal oral cavity (Wang et al., 2012).

Saliva plays a considerable role in influencing the oral microbiome. More than 800 species of bacteria colonize oral mucous, 1,300 species are found in the gingival crevice, and nearly 1,000 species comprise dental plaque. The mouth is a rich environment for hundreds of species of bacteria since saliva is mostly water and plenty of nutrients pass through the mouth each day. When kissing, it takes only 10 seconds for no less than 80 million bacteria to be exchanged by the passing of saliva. However, the effect is transitory, as each individual quickly returns to their own equilibrium (Kort et al., 2014). Most of the bacterial species found in the mouth belong to

microbial communities, called biofilms, a feature of which is inter-bacterial communication. Cell–cell contact is mediated by specific protein adhesins and often, as in the case of inter-species aggregation, by complementary polysaccharide receptors. Another method of communication involves cell–cell signalling molecules, which are of two classes: those used for intra-species and those used for inter-species signalling. An example of intra-species communication is quorum sensing. Oral bacteria have been shown to produce small peptides, such as competence stimulating peptides, which can help promote single-species biofilm formation. A common form of inter-species signalling is mediated by 4, 5-dihydroxy-2, 3-pentanedione (DPD), also known as autoinducer-2 (Al-2). The tooth surface is the only non-shedding surface in the oral cavity and therefore provides an ideal environment for bacterial growth and the formation of dental plaque. It has been shown that dental plaque has higher α-diversity, microbial richness, and evenness than samples of saliva and tongue (Ren et al., 2017). It is noteworthy that the plaque on the supragingival enamel surface is formed by the acquired pellicle (Lynge-Pedersen & Belstrøm, 2019), whereas at subgingival sites, the gingival crepuscular fluid acts as a special source of nutrition, and its serum proteins combine with salivary proteins to form a unique proteinaceous film. The physical barrier effect of the gingiva also significantly reduces the oxygen tension and shear forces at subgingival sites, causing the compositions and structures of the supragingival and subgingival plaque microbiotas to differ, for example, anaerobic bacteria, including Actinomyces, Fusobacterium, and Veillonella, are predominantly found in the subgingival plaque (Caselli et al., 2020).

II. Statement of the Problem

Oral bacteria pose a potential threat and danger to individuals with inadequate and poor toilet hygiene by penetrating the body through the mouth as a result of nail biting which can lead to various oral cavity infections. Since oral health is integral to general health and is essential to the overall health and wellbeing of all individuals, the early identification of oral disease may contribute to the early diagnosis and treatment for a number of systemic diseases. Bacteria in the oral cavity have been known to be the major cause of halitosis and other oral/dental problem like osteomyelitis, Ludwig angina, retropharyngeal abscess, parapharyngeal abscess, necrotizing mediastinitis, cavernous sinus thrombosis, meningitis, and subdural empyema. As a result of the above insinuations, it has become relevant to examine bacterial profile of university students' oral cavity in Port Harcourt Rivers State.

III. Aim and Objectives of the Study

This study was aimed at examining the oral cavity of university students in Port Harcourt Rivers State for pathogenic bacteria. The specific objectives of the study were to:

1. isolate bacteria in oral cavity of students
2. enumerate and Characterize bacteria isolate from oral cavity of students,
3. identify bacteria in oral cavity of students
4. carry out antibiotic sensitivity of bacterial isolates.

IV. Significance of the Study

Besides the need to examine the oral bacterial profile of students' oral cavity, this study will help determine the antibiotic sensitivity pattern of these oral bacterial pathogens due to emergence and reemergence of antibiotic resistance among bacterial population. This will guide empirical therapy for oral infection and dental problems. More also, this study will reduce the number of hospital visits, cost of treatment and risk of treatment failure. Also, identification of risk factors associated with oral infection and dental problems will be found very helpful in developing control and prevention programs aimed at reducing oral infection and dental problems.

V. Materials and Methods

The study was carried out in the main campus of Ignatius Ajuru University f Education, Rumuolumeni, Port Harcourt, Rivers State. Rumuolumeni is a community found in Obio-Akpor local government area in Rivers state. Obio-Akpor is a local government area in the metropolis of Port Harcourt, one of the major centres of economic activities in Nigeria, and one of the major cities of the Niger Delta, located in Rivers State. The local government area covers 260 km^2 and at the 2006 Census held a population of 464,789. Its postal code or ZIP code is 500102. Ikwerre is one of the largest ethnic nationality in Rivers State and occupies the largest land mass with an estimated population of 265,400.

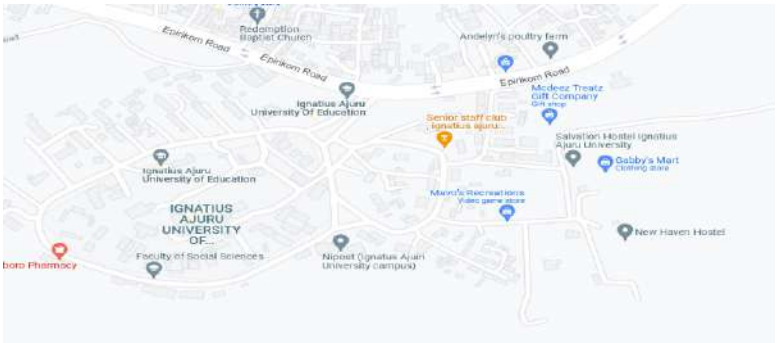

Fig 1: Map of the study Area

Collection and Processing of Samples

Oral swab specimen was collected from the oral cavity (mouth) of each participant by inserting a sterile oral swab stick 1-2 inches into the mouth to gently swab the walls of the oral cavity including the oral mucosa, the teeth, area between the cheek and gum, as well as the tongue for one to two minutes. The swab stick was removed in an aseptic manner and corked properly immediately. The samples were transported to the laboratory within 1 hours of collection. All samples were transported to the laboratory inside a sealed plastic bag as soon as the collection was done with. Samples were processed on the same day of collection.

Isolation and Enumeration of Bacterial Isolates

The pure bacterial cultures were obtained by inoculating the sample on nutrient agar media plates. For this purpose, the swab samples were aseptically streaked on nutrient agar plates and incubated in thermal incubator for 24 hours at 37^0C. Observed colonies were counted and recorded properly.

Media Preparation

Following the manufacturer's guide, the appropriate grams of nutrient agar, was weighed using the weighing balance; media was then poured into a 250ml conical flask holding the appropriate ml of distilled water needed for the preparation of the media and then sterilized using an autoclave for about 15 psi and 121°C for 15 minutes.

Enumeration of Bacterial Isolate

Standard techniques (macroscopy and microscopy) as described by Ochei & Kolhatkar, 2006 were adopted for the identification of the bacterial isolates. Morphological features of the colonies such as the size, shape, texture, elevation, pigmentation, margin and opacity were noted and recorded. Gram staining technique was performed to demonstrate their shapes and arrangement.

Pure Culture

After incubation the isolated bacterial colonies were picked from growth plates and quadrant streaking was done aseptically to new culture media plate in order to obtain pure strains of bacterial culture.

Cultural Identification and Biochemical Characterization of Bacterial Isolates

Catalase, oxidase, coagulase, motility, indole, methyl-red, vogue proskauer, citrate utilization, sugar fermentation were the biochemical tests conducted for identification and characterization of bacteria.

Catalase Test

Apparatus, material and reagent: Pasteur pipette, microscope slide, wooden applicator stick, hydrogen peroxide (3%v/v).

Procedures:

1. Place a drop of hydrogen peroxide (3%v/v) on a clean microscope slide
2. Use a wooden applicator stick to collect the colony of the investigated isolate
3. Smear the picked colony into the hydrogen peroxide drop
4. Observe for gas bubbles.

Expected result: catalase positive bacteria will produce bubbles of oxygen while catalase negative bacteria will not produce bubbles.

Oxidase Test

Apparatus, material and reagent: Pasteur pipette, filter paper, wooden applicator stick, 1% tetramethyl-p-phenediamine dihydrochloride (oxidase reagent).

1. Moisten a filter paper with few drops of freshly prepared 1% tetramethyl-p-phenediamine dihydrochloride.
2. Use a wooden applicator stick to collect a colony of the test bacterium
3. Smear the picked colony on the filter paper
4. Observe for colour change

Indole Production Test

Apparatus, material and reagent: nutrient broth, peptone water, protease or tryptone broth, test tubes, cotton wool, kovac's reagent

Procedures:

1. Prepare the medium (nutrient broth, peptone water, protease peptone or tryptone broth) according to manufacturer's instruction, dispense into test tubes sterilize in an autoclave at 121°C for 15 minutes.
2. After sterilization, allow to cool and then inoculate each test tube with a colony of the investigated isolates.
3. Incubate at 37°C for 48 hours.
4. After incubation, add 10 drops of kovac's reagent

Expected result: if indole was produced by the investigated isolate, a red/pink layer will form on top the broth, if indole was not produced, the layer will be yellow.

Methyl Red/ Voges Proskaurer Test

Apparatus, material and reagent: MRVP broth, test tubes, cotton wool, barrette's reagent A, barrette's reagent B, methyl red reagent.
The MRVP procedures:

1. Work out the volume of MRVP broth required for the number of isolates to be tested, noting that not less than 10ml is required for one test tube.
2. Dispense the broth into test tubes and cork with cotton wool.
3. Sterilize the tubes in an autoclave a 121°C for 10 minutes.
4. Allow the tubes to cool, isolate each tube with colony of the investigated isolate.
5. Incubate at 37°C for 48 hours.
6. After incubation, transfer about half of the broth culture into a clean test tube and use for VP test.

The VP (Vogue Proskaurer Test)

1. Add ten drops of freshly prepared barrette's reagent A to the broth culture in the clean test tube.
2. Immediately add ten drops of barrette's reagent B.
3. Shake the tube for 30 seconds.
4. Allow to stand, and then observe for the colour change.

Expected result: A positive test is indicated by a gradual formation of red colour (plates). A negative test is indicated by the formation of a yellowish or brown colour.

The MR Test

1. Add 3-5 drops of freshly prepared methyl red solution to the remaining broth culture.
2. Observe for colour change.

Expected result: The formation of a red colour at the surface of the broth indicates a positive result, whereas the formation of a yellow colour indicates a negative result.

Citrate Utilization Test

Apparatus, materials and reagents: Simon's citrate agar, test tubes, cotton wool, inoculating needle.
Procedure:

1. Prepare the Simon's citrate agar medium according to the manufacture's instruction, boil and dispense into the test tube.
2. Sterilize in an autoclave at 121°C for 15 minutes.
3. After sterilization, allow agar in the test tube to cool and solidify.
4. Pick a colony of the investigated isolate using a sterile inoculating needle.
5. Stab-inoculate the picked colony into the agar tube, carefully following and retracting in a straight line.
6. Incubate the tubes at 37°C for 24 hours.

Sugar Fermentation Test

Acid and gas or only acid is produced during fermentative growth with sugar (glucose, lactose, sucrose, mannose etc). Acid production is detected by a pH indicator. Gas production is detected by placing Durham tubes in the fermentation tube.

Fermentation brought of a test compounded as follows: test compound e.g glucose-1%w/v, peptone water or nutrient broth-1%w/v, phenol red (0.005%w/v).

Apparatus, materials and reagents: test compounds e.g glucose, peptone water or nutrient broth, phenol red solution (0.04%w/v). Test tubes, cotton wool.

Procedures:

1. Assuming 100ml of the medium is required; compound a broth of test compound in question by transferring 1g of the test compound and 1g peptone water or nutrient broth into a 250ml conical flask.
2. Add 87.5ml of distilled water and 12.2ml of the phenol red solution to the content of the flask. The broth should color orange red or red.
3. Place Durham tubes into the test tubes and dispense the broth into the tubes.
4. Cork the tubes with cotton wool and sterilize in an autoclave at 121°C for 10 minutes.
5. After sterilization, allow the tube to cool, then inoculate each tube with a colony of the investigated isolate.
6. Incubate the tube at 37°C for 24 to 48 hours
7. After incubation, observe the test tubes for color change and for presence of gas in durham tubes.

Urease Test

Procedure:

1. Streak the surface of urea agar slant with a portion of well isolated colony or inoculate slant with one to two drops from an overnight brain-heart infusion culture.
2. Leave the cap on loosely and incubate the tube at 35°C to 37°C in ambient air for 48 hours to 7 days.
3. Examine for development of pink colour for as long as 7days

Positive reaction: development of an intense magenta to bright pink color in 15 minutes to 24 hours.

Antibiotic Sensitivity Test

Clinical Laboratory Standard Institute (CLSI) guidelines were used to assess and interpret the zones of inhibition (2016, 2018). A brand-new nutrient agar plate was used; the pure culture colonies were picked and evenly distributed on the new nutrient agar plate. The sensitivity drug pads containing both gram positive and negative antibiotics were placed on the plate and incubated for 48 hours.

Statistical Analysis

The statistical analysis was carried out using Statistical package for social sciences (SPSS) software.

VI. Results

Mean Total Heterotrophic Bacteria

The total heterotrophic bacteria of oral cavity samples collected from different students in Ignatius Ajuru University of Education are shown in Table 4.2 below. The highest numbers of bacterial colonies were observed in the fifth sample ($6.2\pm0.64 \times 10^3$) followed by Fourth ($3.7\pm0.09 \times 10^4$) and first ($2.9\pm0.45 \times 10^6$) samples. Third and second samples recorded ($2.7\pm0.77 \times 10^4$) and ($1.8\pm0.12 \times 10^5$) respectively.

Table 1: Mean Total Heterotrophic Bacteria

s/n	Oral Specimen	Total Heterotrophic Bacteria Count-THC (cfu/ml)
1	First	$2.9\pm0.45 \times 10^6$
2	Second	$1.8\pm0.12 \times 10^5$
3	Third	$2.7\pm0.77 \times 10^4$
4	Fourth	$3.7\pm0.09 \times 10^4$
5	Fifth	$6.2\pm0.64 \times 10^3$

Microscopic Morphology and Biochemical Characteristics of Bacteria Isolated

s/n	Color	Cell morphology	Margins	motility	Gram reaction	Spore	catalase	hemolysis	Indole	Citrate	Probable genera
1	Deep golden yellow	Round, raised and glistening	smooth	-	+	-	+	Beta-hemolytic	-	+	*Staphylococcus* spp
2	Whitish gray	Rods	smooth	-	+	-	-	Beta hemolytic	+	-	*Streptococcus* spp
3	gray	Rods	smooth	+	-	-	+	Alpha hemolysis	-	-	*Enterobacter* sp.
4	greenish	Rods,	entire smooth	+	-	+	+	Beta-hemolysis	-	+	*Pseudominas aeroginosa*
5	pinkish	Rod	Smooth	-	-	-	+	Beta-hemolytic	-	+	*Klebsiella Pneumonia*

Table 2 relates the microscopic morphology and biochemical characteristics of five (5) bacteria genera isolated from the five (5) oral samples collected from students in Ignatius Ajuru University of Education. These bacteria isolate was identified and confirmed as *Streptococcus* spp, *Staphylococcus* sp., *Enterobacter* sp., *Pseudominas aeruginosa* and *Klebsiella Pneumonia*

Table 2: Microscopic Morphology and Biochemical Characteristics of Bacteria Isolated

Antibiotic sensitivity

Table 3 represent result of the antibiotic sensitivity of the five samples collected from students of Ignatius Ajuru University of Education. The five samples were resistant to Cpx 10mcg, sample two showed intermediate zone of inhibition while the rest samples were resistant to PN 30mcg. Sample one was susceptible to GN 10mcg while sample 2, 3, 4 and 5 showed intermediate zone of inhibition. Sample one, two and four were susceptible to SXT 30mcg while sample three and five showed intermediate zone of inhibition.

Table 3: Antibiotic sensitivity

	Sample one		Sample two		Sample three		Sample four		Sample five	
CONCENTRATIONS	ZONE OF INHIBITION (mm)	REMARK	ZONE OF INHIBITION (mm)	REMARK	ZONE OF INHIBITION (mm)	REMARK	ZONE OF INHIBITION (mm)	REMARK	ZONE OF INHIBITION (mm)	REMARK
Cpx 10 mcg	1.5±0.19	Resistant	1.34±0.11	Resistant	0.87±0.14	Resistant	1.33±0.14	Resistant	1.87±0.04	Resistant
PN 30 mcg	3.10±0.55	Intermediate	1.06±0.42	Resistant	1.18±0.13	Resistant	1.78±0.22	Resistant	1.23±0.12	Resistant
GN 10 mcg	5.00±0.91	Susceptible	2.56±0.09	Intermediate	2.18±0.19	Intermediate	2.56±0.09	Intermediate	3.48±0.19	Intermediate
SXT 30 mcg	5.05±0.16	Susceptible	5.12±0.17	Susceptible	3.45±0.56	Intermediate	5.14±0.17	Susceptible	2.45±0.16	Intermediate

VII. Discussion of Findings

Oral cavity of the human is a mini ecosystem which is comprised of different niche like dorsal and ventral side of tongue, buccal epithelium, hard palate, soft palate and supra-gingival plaque of tooth surfaces which is colonized by immense amount of microorganism including fungi, several types of virus and diverse bacterial fauna. Around 1100 different taxa were discovered from the oral cavity and recorded in the Human Oral Microbiome Database. The complex community of the buccal cavity principally contains *Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, Spirochaetes* and *Fusobacteria* with only 4% of species belong to other phyla (Bik et al., 2010). Some of these are very beneficial while other may cause some serious infections. Some of the worthy bacteria may shift their life style from the beneficial to harmful and cause serious oral infections (Ahn et al., 2012). So, the current study aimed at examining oral cavity of university students for pathogenic bacteria.

Results of this study shows that the highest numbers of bacterial colonies were observed in the fifth sample ($6.2\pm0.64 \times 10^3$) followed by Fourth ($3.7\pm0.09 \times 10^4$) and first ($2.9\pm0.45 \times 10^6$) samples. Third and second samples recorded ($2.7\pm0.77 \times 10^4$) and ($1.8\pm0.12 \times 10^5$) respectively. Also, the microscopic morphology and biochemical characteristics of five (5) bacteria genera isolated from the five (5) oral samples collected from students in Ignatius Ajuru University of Education was done and the bacteria isolated and identified were confirmed as *Streptococcus* spp, *Staphylococcus* sp., *Enterobacter* sp., *Pseudominas aeruginosa* and *Klebsiella Pneumonia.* This result in in concordance with a research carried out by Enitan et al., (2020) who worked on a total

of 200 oral swab samples. Oral swab samples were collected from 200 consenting participants (100 males and 100 females). The oral swab samples were cultured on Blood agar, MacConkey agar and Mannitol salt agar and incubated at 37^{o}C. Gram staining, motility test and routine biochemical tests were done for the identification and characterization of the bacterial isolates. Antibiotic susceptibility testing was carried out using the disc diffusion method. Data obtained were analysed using SPSS Statistics software package (version 18.0). Results showed that the bacterial species isolated include: *Streptococcus viridans, Staphylococcus epidermidis, Enterobacter spp, Streptococcus pyogenes, Enterococcus feacalis, Klebsiella pneumoniae, Staphylococcus aureus,* and *Escherichia coli.* The result of this study is not in line with a study conducted by Khadija et al., (2021) which reported the presence of *S. saprophyticus* in the oral cavity of 11.98% of women postpartum, although the clinical relevance in the oral cavity is still unclear. Additionally, Mueller et al., (2021) observed that babies born by C-section had lower microbial diversity and a higher abundance of *Clostridium* species.

VIII. Conclusion

The bacteria recovered from oral cavity of students were *Streptococcus* spp*, Staphylococcus* sp., *Enterobacter* sp*., Pseudominas aeruginosa* and *Klebsiella Pneumonia.* These bacteria are pathogenic and it is a cause for alarm. Frequent need for the observation of good hygienic practice during brushing or mouth washing and also the use of quality tooth paste is very relevant.

IX. Recommendation

Based on the findings of this investigation, the following recommendations are made;

1. Proper sensitization on oral health should be done for students
2. More work should be done using greater population size
3. More antibiotics should be used for the sensitivity to ascertain susceptibility and resistance level of bacteria isolated from oral cavity in further research.

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