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Review Article

Human Fluid Microbiota, Benefits And Associated Biohazards

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ABSTRACT

Human life relies on fluids to transport various metabolites which include nutrients and wastes into and out of various organs and tissues. Consequently, body fluids are inhabited by various resident microorganisms depending on the state of health of a particular tissue or organ. Both commensal and pathogenic microorganisms have therefore been detected in various human fluids. This paper sought to review literature on their relevance; factors that affect their composition and expose potential biorisks associated with them. Published literature on breast milk, blood and stool; oral, vaginal and penile fluid microbiota revealed the presence of diverse bacteria, fungi, protozoa, archaea and viruses. Some of which are found in more than one body fluid. Their diversity is determined by factors such as age, gender, health condition, medication, geography and diet. A good number of these species are commensal and benefit the host in digestion, immunity and synthesis of micronutrients while others are pathogenic. Certain beneficial commensal bacteria especially *Lactobacillus* and *Bifidobacterium* among others are used in the formulation of probiotics while some bacteriophages are used as biopharmaceuticals. On the other hand, pathogenic ones such as HIV and Ebola viruses pose health risks. Though a good number of these microorganisms were detected in these fluids, functional analyses are yet to be done on a majority of them. Maximizing beneficial effects while minimizing potential health risks require more information on these microorganisms and; therefore further research is recommended.

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Introduction

Humans produce and secrete various fluids which include blood, saliva, stool, nasal, penile and vaginal fluids among others. These fluids differ in biochemical and microbial composition even in normal healthy persons[1][2]. Given the interdependent nature of life, normal and infectious microorganisms existing in a given gland or organ usually mix with fluids produced there upon shedding. Depending on the composition of a given body fluid, some of these microorganisms survive and thrive while others don't. Therefore the microbial composition of a given body fluid is dependent on various factors such as: environmental, nutritional and health status, medication, age and gender among others[3][4][5][6][7][8].

The normal microflora play important roles which include nutritional and provision of innate immunity among others[9]. Imbalance in the composition of some of these microorganisms can have medical implications. For example reduction in the number of vaginal *Lactobacillus* species can lead to overgrowth of opportunistic bacteria and *Candida* which results in Bacterial vaginosis and candidiasis among others[5][10].

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Therefore a balance between beneficial and harmful microflora is important. Maintaining this balance and alleviating medical conditions associated with dysbiosis requires information on the microbiome composition and factors that influence it.

On the other hand, infectious bacteria, fungi, protozoa and viruses survive or are shed into some of the glands that secrete or harbor these body fluids[1][2]. This contaminates and makes the affected body fluids a health hazard if these infectious agents can be transmitted via that particular body fluid[11][12]. Infections arising from accidental exposure to contaminated body fluids have been reported [13]. Transmission of highly infectious agents can strain personal and national economies[14][15]. These burdens can be reduced by good health practices that are informed by research[16][17]. While there are several reports on the microbial composition of individual body fluids[5][18][19][20][21][22][23][24][25][26][27][28][29][30][31]among others, reports entailing all human fluid microbes that give a holistic picture are still scarce. This study therefore sought to review literature on known microbiomes and microbes in various human body fluids under normal and disease conditions. Information on the microbiome composition of breast milk, blood, oral, penile, vaginal, and fecal fluids regardless of their transmission routes and their inherent health hazards is presented. This information is of great benefit to the general public, biomedical researchers and health practitioners.

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2.1 Oral fluid

Saliva is the main oral fluid though it's sometimes mixed with other fluids originating from the nasopharynx, gastrointestinal tract (GIT) and tonsils among others. Saliva contains various enzymes important for digestion of food and protection of the oral cavity against microbial agents [32]. This notwithstanding, several microorganisms which include viruses, bacteria and fungi were reported in the saliva of healthy persons and individuals with medical conditions. Some of the species that have been identified by different methods in samples from various healthy and disease conditions are provided in Table 1 below.

Table 1: Microbes reported in oral fluids

Microorganism	**Associated disease**	**Microorganism**	**Associated disease**
Bacteria		**Viruses**	
Streptococcus salivarius *Lactococcus lactis* *[33][34]*	Beneficial used in probiotic, produce bacteriocins: Salvaricins and nisin	Human herpesvirus 6 Herpes simplex virus 1 Herpes simplex virus 2 [37] [42]	Herpes
Eikenella corrodens *Prevotella melaninogenica* *Streptococcus mitis[109][34]*	Opportunistic in immunocompromised individuals	Hepatitis A virus Hepatitis B virus Hepatitis C virus [37] [42]	Hepatitis
Aggregatibacter actinomycetemcomitans *Porphyromonas gingivalis* *Fusobacterium nucleatum* *Prevotella intermedia* *Tannerella forsythia* *Campylobacter rectus* *Treponema denticola* *Parvimonas micra* *Eubacterium nodatum* *Filifactor alocis* *Streptococcus gordonii* *Actinomyces naeslundii* *[110] [37][34][55][38][40][39]*	Periodontitis	Cytomegalovirus Polyomavirus Influenza A & B virus Parainfluenzavirus Human metapneumovirus Rhinoviruses Adenoviruses Bocaviruses Enteroviruses Measles virus Rubella viruses Severe Acute Respiratory Syndrome Corona Virus (SARS CoV) [37][42][41]	Respiratory diseases: Flu, common cold, bronchiolitis, pneumonia Measles Rubella Severe acute respiratory syndrome
Scardovia wiggsiae *Streptococcus mutans* *Bifidobacterium longum* *Rothia mucilaginosa* *[109][34]*	Dental caries	Human papillomavirus (HPV) Epstein Barr virus [42][37]	Cervical cancer Mononucleosis, Burkitt lymphoma
Streptococcus pyogenes *[41]*	Skin and soft tissue infections- cellulitis	Rabies virus [42]	Rabies
Streptococcus pneumonia *[41]*	Pneumonia	Mumps virus [42]	Mumps
Neisseria meningitidis *[41]*	Meningitis	Dengue virus Ebola virus [42][37]	Dengue Ebola
Mycobacterium tuberculosis *[41]*	Tuberculosis	Torque teno virus [42]	None
Bordetella pertussis *[41]*	Whooping cough	Human Immunodeficiency Virus (HIV) [42][37]	HIV AIDS (Acquired immunodeficiency syndrome)
Fungi *Candida albicans* *[37]* *[32]* *[109]*	oral candidiasis	Mpox[41]	Mpox

The Earth sequencing project and other studies revealed that the majority of these belong to six phyla *Firmicutes, Proteobacteria, Bacteroidetes, Fusobacteria* and *Actinobacteria,* with major representation from the genus *Streptococcus* and *Veillonella; Neisseria* and *Haemophilus; Prevotella* and *Porphyromonas; Fusobacterium* and *Leptotrichia; Rothia* and *Actinomyces* respectively. A majority of these constitute the normal oral microbiota while some are pathogenic. Commensal bacteria such as *Streptococcus salivarius* and *Lactococcus lactis* produce bacteriocins (salivaricin and nisin respectively) which maintain oral health by inhibiting the growth of other bacteria and development of oral cancer and as such they are used in the formulation of probiotics[33][34][35][36].

On the other hand, pathogenic oral bacteria such as *Aggregatibacter actinomycetemcomitans, Porphyromonas gingivalis, Fusobacterium nucleatum* and *Prevotella intermedia* among others were reported to cause periodontitis. Others such as *Streptococcus* mutans produce metabolites that lowers pH (to around 3.5) causing dental caries[37][38][39]. Other than periodontitis and dental caries some of these bacteria were associated with other health conditions such as endocarditis, rheumatoid arthritis and cancer among others [37][40].

Several viruses such as the Herpes, Influenza, Human papillomavirus (HPV), Ebola and Severe Acute Respiratory Syndrome Corona Virus-2 (SARS CoV-2)virus which causes oral and genital herpes, influenza, cancer, Ebola and Covid-19, were also reported in oral fluids especially at advanced viral infection when replication and shedding was very high[12][41][37][42]. On the other hand *Candida albicans* was the main fungus reported in saliva[32][37].

The diversity of this *microbiota* was reported to vary with the method of sample collection and processing [18], age [36], oral care[6], health condition and medication[37], lifestyle such as smoking and, geographical location of study population among others[43]. It should however be noted that, though all of these microorganisms were detected in saliva and oral fluids, saliva is not necessarily the main transmission route for most of them probably because of oral enzymatic activity that destroys surface biomolecules including antigens and receptors used for infection[32].

2.2 Penile and vaginal fluids

Several microorganisms were reported (Table 2) in urine, semen, vaginal discharge and amniotic fluid. Their composition was shown to vary with age, pregnancy and health condition among other factors[5][44][45][46]. For example, microbes detected in vaginal fluids of healthy non-pregnant women mainly consisted of *Lactobacillus Spp., Actinobacteria, Prevotella, Veillonellaceae, Streptococcus, Proteobacteria, Bifidobacteriaceae, Bacteroides* and *Burkholderiales* while the *microbiota* of healthy pregnant women mainly consisted of *Lactobacillus Spp., Actinomycetales, Clostridiales, and Bacteroidales*[45].

Table 2: Microbes reported in penile and vaginal fluids

Microorganism	**Associated disease**	**Microorganism**	**Associated disease**
Vaginal bacteria		**Bacteria in human semen**	
Lactobacillus crispatus *Lactobacillus gasseri* *Lactobacillus jensenii* *[47][111][112]*	Beneficial- but can cause endo-carditis bacteremia	*Lactobacillus crispatus* [23][22][113]	Beneficial- improve sperm quality
Gardnerella vaginalis *Gardnerella piotii* *Gardnerella swidsinskii* *Gardnerella leopoldii* *Atopobium vaginae* *Mycoplasma hominis* *Lactobacillus iners Mageeibacillus in-dolicus Tannerella forsythia Prevotella intermedia* *[47][111][10][114][115][5][112]*	Bacterial vaginosis (BV)	*Pseudomonas stutzeri* *Pseudomonas fluorescens* *Pseudomonas putida* *Staphylococcus hominis* *Streptococcus agalactiae* *Staphylococcus epidermidis* *Finegoldia magna* *[23][22][113]*	Opportunistic: septic arthritis, endocarditis, pneumonia, bacteremia
Ureaplasma urealyticum *Sneathia amnii* *Sneathia sanguinegens* *[47][111][115][5]* *[112]*	BV, cervicitis, chorioamnionitis, preterm birth	*Staphylococcus haemolyticus* *Ureaplasma urealyticum* *Enterococcus faecalis* *Prevotella melaninogenica* *Escherichia coli* *[23][22][113]*	Urinary tract infections (UTI), chronic prostatitis,urethritis
Treponema denticola *[47][111][112]*	no vaginal disease	*Lactobacillus iners* *Prevotella timonensis* *[23][22][113]*	None in male urinary tract
Pathogens in urine		**Viruses in penile and vaginal fluids**	
Bacteria		Bacteriophages [52][53]	Beneficial
Escherichia coli [5]	Diarrhea, UTI	HPV [52][10][53][5]	Cervical cancer

Chlamydia trachomatis [10]	Clammydia and trachoma	Human Herpes viruses [10][53][5]	Herpes
Neisseria gonorrhoeae[10][5]	gonorrhea	SARS-CoV[20][53]	Severe acute respiratory syndrome
Protozoa		HIV [116][10][5]	HIV AIDS (Acquired immunodeficiency syndrome)
Trichomonasvaginalis[10][5]	trichomoniasis	Zika virus [53]	Zika
Dimastigella trypaniformis[117] *Colpoda Species [118]*	UTI	West Nile virus [53] Polyomavirus[53] Adenoviruses[53] Cytomegalovirus [53]	Flu-like /cold
Balantidium coli [119]	balantidiasis	Ebola virus [12]	Ebola
Fungi *Candida albicans*[111][5]	Candidiasis		

The *Lactobacillus Spp (L. Crispatus, L. gasseri and L. jensenii)* which dominate the normal microflora provides innate protection. They do so by producing bacteriocins, hydrogen peroxide and lactic acid which lowers vaginal pH (to 3.5 - 4.5) that negatively regulate survival and proliferation of many anaerobic bacteria such as *Gardnerella vaginalis, Atopobium vaginae, Mycoplasma hominis* and *Ureaplasma urealyticum* among others[10][45][47][48].

This composition changes during bacterial vaginosis which is characterized by a decline in *Lactobacillus Spp*. Consequently, there is a rise in vaginal pH(to 4.2 – 7.0). This change is conducive for the proliferation of anaerobic bacteria and thus results in a sudden rise in *Gardnerella (G. Vaginalis, G. piotii, G. swidsinskii* and *G. leopoldii), Prevotella, Atopobium (Atopobium vaginae), Mobiluncus, Bifidobacterium, Sneathia and Leptotrichia.*

In this condition *Gardnerella vaginalis* dominates *Atopobium vaginae, Mycoplasma hominis, Ureaplasma urealyticum, Lactobacillus iners* and *Mageeibacillus indolicus*[46][47]. Maintaining a healthy vaginal microflora is important to reproductive health and as such, research geared towards managing dysbiosis using vaginal probiotics from beneficial microbiota has shown success[49][50]. However since the roles played by only a few vaginal microorganisms are known, realizing the medical potential of the remaining microorganisms require more research.

Other than these microorganisms, the presence of several others such as *Tannerella forsythia, Treponema denticola, Prevotella intermedia, Leptotrichia amnionii/Sneathia amnii* and *Sneathia sanguinegens* otherwise predominant in oral and fecal fluids were attributed to contamination by these fluids [47][10]; while the presence of pathogenic and opportunistic microorganisms such *Escherichia coli, Chlamydia trachomatis, Neisseria gonorrhoeae, Trichomonas vaginalis* and viruses such as HPV, Human Herpes viruses, HIV, SARS- CoV-2 and Ebola virus were attributed to vaginal infections[5][10][12][20][46]. Levels of *Candida albicans* which is considered to be part of the normal microflora increases with immunodeficiency[5][51].

Microbiome analyses of human semen reported the presence of several bacteria which included *Lactobacillus iners, Pseudomonas stutzeri, Pseudomonas fluorescens, Pseudomonas putida, Escherichia coli, Streptococcus agalactiae* and *Staphylococcus hominis* among others[23]. Similarly, urine virome analyses reported various viruses which included, HPV, Polyomavirus, Adenoviruses, Cytomegalovirus, Zika virus and SARS-CoV among others[12][52][53].

2.3 Human anal fluid

The human gut is colonized by various normal and pathogenic microbes. The normal microflora is important in innate immunity, digestion and synthesis of micronutrients[54][55][56]. Subsets of these microorganisms from different sections of the gut usually mix with digestive fluids and end up in feces[21]. Reports on various studies of fecal microbiota showed that composition is influenced by lifestyle, diet, age, antibiotic use, geographical region and; sample collection and analytical methods used among other factors[8][36][56][57][58][59].

Various studies using methods such as metagenomic sequencing, PCR and culturing, reported numerous human pathogenic and nonpathogenic microbes in stool of healthy and infected individuals. A representative list in Table 3 shows that bacteria are by far the most represented group. The nonpathogenic bacteria such as *Bifidobacterium longum, Bacteroides uniformis, Lactobacillus reuteri, Akkermansia muciniphila* and *Faecalibacterium prausnitzii* among others play important roles that include maintenance of gut integrity, immunomodulation, digestion, metabolism and synthesis of nutrients among others[56][60][61][62][63][64][65][66]. Some of these beneficial bacteria were isolated and are used in probiotics[67].

Similarly, nonpathogenic viruses especially bacteriophages were reported to form part of the normal gut microflora. Bacteriophages are known to infect some of these bacteria including pathogenic one sand kill them by lysis. By so doing they modulate the population of their hosts[59][68][69]. Consequently some of them were isolated and formulated into specific biopharmaceuticals that target certain drug resistant bacteria[70][71][72]. Furthermore because of these beneficial microbes, there are attempts aimed at using human fecal transplants in the management of various human disease [73]. Though the role(s) of some of these microorganisms are known, the functions and effects of many more are not yet clear.

Several pathogenic bacteria, fungi, protozoa and viruses were also reported to be in human stool and sewerage (Table 3). The infectious bacteria which include *Salmonella typhi, S. paratyphi, S. choleraesuis, S. typhimurium, S. enteritidis; Vibrio cholerae, Shigella dysenteriae, S. flexneri, S. boydii* and *S. sonnei* among others cause typhoid, cholera, dysentery and enteritis among other bacterial diseases. The pathogenic protozoa included *Giardia lamblia, G. intestinalis* (which causes Giardiasis) and *Entamoeba histolytica* (which causes Amoebiasis)among others while pathogenic fungi included *Aspergillus niger* (which causes Aspergillosis) among others[74][75][36][56][57][76]. Similarly, infectious viruses such as Hepatitis A and E, SARS-CoV-2, Ebola virus, Poliovirus, Rotavirus and Adenoviruses among others were also reported in human feces[12][74][77][78].

Table 3: Microbes reported in human anal fluids

Microorganism	Associated disease	Microorganism	Associated disease
Bacteria		**Protozoa and nematodes**	
Beneficial Bacteria *Bifidobacteriumbreve[31]* *Bifidobacterium longum* *Bacteroides fragilis* *Bacteroides uniformis* *Parabacteroides distasonis* *Lactobacillus reuteri* *Akkermansia muciniphila* *Faecalibacterium prausnitzii* *Oscillibacter ruminantium* [57][56][67]	Digestion, produce bacteriocins, anti-inflammatory	*Entamoeba histolytica[74][77]* *Entamoeba dispar* *[74][77]* **Archaea** *Methanobrevibacter smithii[31]*	Amebiasis- diarrhea Enteritis
Alistipes finegoldii *[56]*	Beneficial but can cause bacteremia	*Giardia lamblia[74]* *Giardia intestinalis[77]*	Giardiasis- diarrhea, bloating
Staphylococcus leei[56]	gastritis	*Ascaris suum[77]* *Ascaris lumbricoides[77]*	Ascariasis
Fusobacterium nucleatum[56]	Colorectal cancer	*Cryptosporidium hominis[77]* *Cryptosporidium parvum[77]*	Cryptosporidiosis
Escherichia coli [56]	Diarrhea	**Viruses** Hepatitis A and E [79]	Hepatitis
Pathogenic bacteria *Salmonella species (S. typhi, S. paratyphi, S. choleraesuis, S. typhimurium, S. enteritidis)[74][75]*	Salmonellosis, typhoid, diarrhea	SARS- CoV-2 [78]	Covid- 19
Campylobacter jejuni[74][75] *Campylobacter coli* *Campylobacter fetus*	Campylobacteriosis, diarrhea, bacteremia	Ebola virus [12]	Ebola
Aeromonas caviae[75] *Aeromonas hydrophila* *Aeromonas sobria* *Aeromonas veronii* *Vibrio parahaemolyticus*	Gastroenteritis, diarrhea	Pecovirus[120]	Not known
Vibrio cholerae[74]	Cholera	Polyomaviruses[121]	Leukoencephalopathy, nephropathy, Merkel cell carcinoma
Shigella species (S. dysenteriae, S. flexneri, S. boydii, S. sonnei)[74][75][56]	Shigellosis- dysentery	Coronaviruses [121] Adenoviruses [81][74][122] Human Parainfluenza virus [77]	Common cold, gastroenteritis
Yersinia enterocolitica[75]	Yersiniosis- diarrhea	Caliciviruse- Sapovirus[77]Astroviruses[121][74][75][122]	Gastroenteritis
Yersinia pestis[75]	Plague	Parvoviruses [121][122]	Facial rash ('slapped chick') in children
Yersinia pseudotuberculosis[75]	pseudoappendicitis	Picornaviruses[121][122]	Common cold, poliomyelitis, hepatitis
Listeria monocytogenes[74][76]	Listeriosis- gastritis	Rotavirus[81][74][75]	Gastroenteritis, Severe diarrhea and vomiting in children
Clostridium botulinum[123]	Botulism	Human Poliovirus [81][77][122]	Polio

Fungi *Aspergillus niger[57]*	Aspergillosis	Coxsackievirus[77]	Hand foot and mouth disease, sore throat
Aureobasidium pullulans[57]	Soft tissue infections, abscesses	Echovirus [77]	Skin rashes, respiratory infections
		Human Cosavirus[77]	Not known
Eremothecium sinecaudum[57]	Not known	Human Parechovirus[77]	Fever, rash
Hanseniaspora uvarum[57]	Oral thrush, gastroenteritis, skin lesions	Bacteriophages [68]	Beneficial
Sporopachydermia lactativora[57]	Pneumonia		
Cyberlindnera jadinii[57] *Kazachstania barnettii[57]* *Rhodotorula mucilaginosa[57]*	Opportunistic		
Saccharomyces cerevisiae[57] *Wickerhamomyces ciferrii[57]*	Beneficial		

These viruses are known to cause hepatitis, corona, Ebola, polio and diarrhea among other viral diseases. While the risk of transmission of *E. coli, S. typhi, V. cholerae,* Hepatitis A and E and; Ebola among others via exposure to feces and sewerage is known[74][75][79][80], however transmission of many others via this route is yet to be proven [78][81][82] and therefore more research is required. Given that some of these infections are communicable, protective measures and care that minimizes exposure and transmission are important when handling anal fluids.

2.4 Human blood

Blood contains several immune cells, immunoglobulins, cytokines and chemokines among others which mediate the destruction of cells and particles having non self-antigens. This makes it difficult for commensals to survive. Consequently studies aimed at describing a sterile blood microbiome faced several challenges which included contamination, lack of proper controls and bias resulting from PCR and sequencing among others. These challenges created doubts in the existence of a consensus sterile human blood microbiome[26][83]. Nevertheless some of the reported microorganisms (Table 4) include *Fusobacterium nucleatum, Staphylococcus epidermidis* and *Lactobacillus crispatus* among others.

These microorganisms are residents of other body parts and though detected, their roles in blood is not clear [26][83][84][85]. In addition to this, human blood virome analyses reported the presence of various commensal viruses (Table 4). Among them is Torque teno viruses, Pegiviruses and Ekpoma viruses. However, clear information on their functions or pathological effects is scanty[84][86][87].

Reported bloodborne pathogenic microorganisms (Table 4) included bacteria such as *Treponema pallidum, Brucella melitensis, Escherichia coli, Staphylococcus aureus, Streptococcus pneumoniae, Pseudomonas aeruginosa, Klebsiella pneumoniae, Mycobacterium tuberculosis* and *Enterococcus faecalis* among others which causes syphilis, brucellosis, pneumonia, tuberculosis, bacteremia and sepsis among others[25][88][89][90]. Also reported in blood are parasitic protozoa such as *Plasmodium falciparum, Babesia microti, Trypanosoma brucei (T. b. rhodesiense* and *T. b. gambiense)* and *Trypanosoma cruzi* which infect and circulate in blood. They cause malaria, babesiosis and trypanosomiasis(Chagas disease and sleeping sickness) among others[91].

Table 4. Microorganisms reported in human blood

Microorganism	**Associated disease**	**Microorganism**	**Associated disease**
Bacteria		**Protozoa**	
Bacteroides fragilis[89]	Digestion, produce bacteriocins, anti-inflammatory	*Plasmodium falciparum [91]* *Plasmodium vivax* *Plasmodium ovale* *Plasmodium malariea*	Malaria
Lactobacillus crispatus[26] *Neisseria flavescens[26]*	Beneficial- but can cause endocarditis bacteremia	*Babesia microti[91]* *Babesia divergens* *Babesia duncani*	Babesiosis
Fusobacterium nucleatum[26]	Periodontitis	*Trypanosoma brucei rhodesiense[91]* *Trypanosoma brucei gambiense* *Trypanosoma cruzi*	Trypanosomiasis (Chagas disease and sleeping sickness)
Neisseria subflava[26] *Haemophilus parainfluenzae[88][26]* *Staphylococcus epidermidis[26]* *Moraxella osloensis[26]*	Endocarditis, bacteremia	*Leishmania donovani[91]* *Leishmania infantum* *Leishmania tropica*	Leishmaniasis

Fannyhessea vaginae[26]	Bacterial vaginosis (BV)	**Viruses** **commensal** Bacteriophages [87] Human Torque teno Viruses [87] Human Pegiviruses[87] Ekpoma viruses [87]	 Beneficial Roles not clear Roles not clear Roles not clear
Acinetobacter baumannii[26]	Opportunistic- pneumonia, blood-stream infection	**Pathogenic** Human Adenovirus [93] Human Polyomavirus[93] Influenza A virus [93]	Respiratory diseases: Flu, common cold, bronchiolitis, pneumonia
Corynebacterium imitans[26]	Diphtheria-like infection, respiratory disease	Human Parvovirus B19 [93][87]	Facial rash ('slapped chick') in children
Treponema pallidum	Syphilis	Human Herpesviruses[93][87]	Herpes
Brucella (B. melitensis, B. abortus, B. suis)	Brucellosis	Zika virus [93]	Zika
Escherichia coli [88][89]	Diarrhea	HIV virus [93][87] Human T lymphotropic virus [93]	HIV AIDS Immunosupression
Staphylococcus (S. aureus, S. epidermidis) [88][89]	Skin disease- boils, endocarditis	Hepatitis A virus [87] Hepatitis B virus[93] Hepatitis C virus [93]	Hepatitis
Streptococcus pneumoniae[88][89] *Klebsiella pneumoniae[88]*	Pneumonia Pneumonia, UTI	Human Papillomaviruses [93] Merkel cell virus [93]	Cancer
Pseudomonas aeruginosa[88][89]	Folliculitis	Yellow fever virus [87] Dengue virus [87] Ebola virus [87]	Yellow fever Dengue Ebola
Mycobacterium (M. haemophilum, M. tuberculosis)[89]	Swollen leg and lymph nodes, tuberculosis		
Enterococcus faecalis[88]	Endocarditis, UTI		
Fungi *Candida (C. albicans, C. tropicalis, C. krusei)- [88][89]*	Candidemia		
Aspergillus (A. niger, A. flavus, A. terreus) [89]	Invasive blood stream infections		
Helminthes *Schistosoma mansoni[91]*	Schistosomiasis		

Several pathogenic viruses such as HIV virus, Hepatitis B virus and Hepatitis C virus among others were also reported in blood and cause bloodborne diseases such as HIV AIDS and hepatitis among others[92] [93]. Such pathogenic microorganisms can easily be transmitted via exposure to infected blood and via blood transfusion and so awareness is important.

2.5 Human breast milk

The composition of human breast milk microbiota was reported to be dynamic [30]as it changes over the lactation period[94]. It's also affected by factors such as diet [95], health condition (such as immunodeficiency and mastitis) [4][96] and antibiotic medication of the lactating mother [4] [94] and; experimental methods and conditions used to analyze the microbiota[97].

The reported human breast milk microbiota consisted of bacteria, fungi, protozoa, viruses and archaea, some of which originated from the skin and mouth among other body parts[31][98]. A representative list is provided in Table 5. Bacterial species were by far the largest group though the functions of most of them in health and disease are not known. They included *Bifidobacterium breve, Bifidobacterium longum, Bifidobacterium bifidum, Lactobacillus gasseri, Lactobacillus salivarius, Lactobacillus fermentum, Lactobacillus rhamnosus, Staphylococcus epidermidis, Staphylococcus aureus, Staphylococcus agalactiae, Staphylococcus hominis, Staphylococcus haemolyticus, Streptococcus mitis, Streptococcus salivarius, Streptococcus lactarius, Rothia mucilaginosa, Bacteroides fragilis, Bacteroides dorei, Phocaeicola vulgatus/Bacteroides vulgatus, Faecalibacterium prausnitzii, Acinetobacter johnsonii* and *Brucella melitensis* among others [30][31][95] [96][98][99][100][101][102].

Some of these bacteria influence the early development of the infants microbiome[100][103][104], gut immunity, synthesis of vitamins and digestion of biomolecules such as complex carbohydrates[31][61][94] [104] as well as pathogenesis [96][105]. Consequently some of these beneficial bacteria, such as *Lactobacillus fermentum, Bifidobacterium breve, Bifidobacterium longum, Faecalibacterium prausnitzii* and

Table 5:Microbiota reported in the human breast milk

Microorganism	Associated disease	Microorganism	Associated disease
Bacteria		**Fungi**	
Beneficial bacteria *Bifidobacterium breve[100][104][31][98]* *Bifidobacterium longum[104][31][98][102]* *Bifidobacterium bifidum[104][98]* *Lactobacillus gasseri[31][95]* *Lactobacillus salivarius[31][98]* *Lactobacillus fermentum[31][98]* *Lactobacillus rhamnosus[31][98]* *Streptococcus salivarius[96][98][102]* *Streptococcus lactarius[96][98][102]* *Bacteroides fragilis[96]* *Bacteroides neonati[95]* *Faecalibacterium prausnitzii[98]* *Acinetobacter johnsonii[96][95][102]*	Digestion, produce bacteriocins, anti-inflammatory	*Saccharomyces cerevisiae[31]* *Malassezia globosa[31][98]* *Debaryomyces hansenii[31]*	Beneficial Pityriasis versicolor Not clear
Staphylococcus epidermidis *Corynebacterium kroppenstedtii[30][95][98][102]*	Beneficial but can cause mastitis	**Protozoa** *Giardia intestinalis*[31][98]	Giardiasis- diarrhea, bloating
Pathogenic bacteria		*Toxoplasma gondii[31][98]*	Toxoplasmosis
Brucella melitensis[106]	Brucellosis	**Archaea** *Halomicrobium mukohataei[31]* *Haloarcula marismortui[31]* *Halorhabdus utahensis[31]*	Beneficial: antioxidant antimicrobial Not evidence, has beneficial biotechnological applications Not evidence, has beneficial biotechnological applications
Staphylococcus aureus[31][101][98]	Skin disease- boils, endocarditis	*Methanobrevibacter smithii[31]*	Generate methane during constipation in irritable bowel syndrome (IBS) persons
Staphylococcus agalactiae *[95][98]*	Group B strep disease especially in newborn babies	**Viruses** Bacteriophages [106] [105]	Beneficial
Staphylococcus hominis[95][98] *Staphylococcus haemolyticus[101][30]* *Streptococcus mitis[95][98][102]* *Acinetobacter lwoffii[96]* *Corynebacterium jeikeium[95]* *Pseudomonas fulva[95]* *Pseudomonas putida[95][98]* *Burkholderia gladioli[30]* *Pseudomonas fragi[95][98]* *Stenotrophomonas maltophilia[95][98]* *Streptococcus parasanguinis[95][98]* *Prevotella melaninogenica[30]*	Opportunistic infections: endocarditis, bacteremia	Papillomaviruses [106][105] Herpesviruses[106][105] Retroviruses- HIV [106][105]	Cancer Herpes HIV AIDS
Rothia mucilaginosa[30][102]	Dental caries		
Corynebacterium acnes [30]	Acne		
Corynebacterium fastidiosum[95] *Corynebacterium jeddahense[95]* *Pseudomonas panacis[95]* *Pseudomonas koreensis[95][98]* *Paracoccus marcusii[95][98]* *Pseudomonas viridiflava[95][98]* *Prevotella nanceiensis[96]*	Scanty information or nonpathogenic		
Corynebacterium simulans[96]	Chronic pyogenic spondylitis		
Lactobacillus iners[96][96][30]	Bacterial Vaginosis (BV)		

Streptococcus pneumonia [95][98]	Pneumonia		
Prevotella copri[30]	Inflammation and autoimmune diseases- rheumatoid arthritis		

Saccharomyces cerevisiae among many others have been used to formulate probiotics[61][67]. Full realization of the potential in many others call for more research on their role in health and disease.

The human breast milk was also reported to contain Fungi such as *Malassezia globosa, Debaryomyces hansenii* and *Saccharomyces cerevisiae* which are beneficial. It was also reported to have, Protozoa such as *Giardia intestinalis* and *Toxoplasma gondii which are pathogenic* and; *Archaea such as Halomicrobium mukohataei, Haloarcula marismortui* and *Halorhabdus utahensis* which are likely to be beneficial. Human viruses such Papilloma viruses, Herpesviruses, Bacteriophages and Retroviruses such as HIV were also reported in human breast milk [31][98]. While Bacteriophages are beneficial, the others such as HIV and Herpes viruses are pathogenic.

Given that most of these microbiota originate from other parts of the body and depends on the health condition of the lactating mother [4], transmission of pathogens such as HIV virus by lactating mothers to their infants were reported [105][106]. These exemplifies potential health hazards associated with lactation and handling of human breast milk. Therefore, though human breast milk is very nutritious, confers health benefits to infants [94][103]and is thus recommended for exclusive feeding for the first six months, care aimed at minimizing transmission of pathogens to infants and accidental exposure to caregivers is important [105][107].

2.6 Biorisks associated with human fluid microbiota

Exposure to contaminated fluids can lead to infections depending on the transmission route for a given pathogen. Reports on laboratory, hospital and community infections of Ebola, HIV 1, Dengue, Hepatitis, Herpes, Yellow fever and Marburg viruses; *Brucella abortus, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Leishmania species, Plasmodium falciparum, Toxoplasma gondii* and *Trypanosoma brucei* among many other infectious agents exist [13][106]. Some of these pathogenic agents are listed in various fluids in preceding sections. If their transmission is not controlled on time it causes health burdens that strain personal and national economies [14][15]. These burdens can be reduced by good health practices that are informed by research [16][17].

Several commensals such as as *Aggregatibacter actinomycetemcomitans, Tannerella forsythia, Porphyromonas gingivalis, Rothia mucilaginosa, Enterococcus faecalis, Treponema denticola, Escherichia coli* and *Human papillomaviruses* were implicated in modulating signal transduction cascades that progress cardiovascular diseases, cancer, inflammatory bowel syndrome and; chronic kidney and liver disease [40][55]. Given that infants are inoculated with vaginal and breast milk microbiota during vaginal delivery and subsequent breast feeding [94] and; that transmission of commensals was also reported in hospitals [108], then the risk of spreading such microbes exists. *E. coli* and *E. faecalis* were listed among 85 pathogens that contribute to the global disease burden [15] and therefore commensals which pose detrimental health effects are potential biohazards and care must be taken to minimize exposure.

3.0 Conclusion and future perspectives

This study highlighted the diversity in microbiota of various body fluids. This diversity varies depending on the geographical location, age, diet, health condition and medication of the participant and; sample collection and analytical techniques used among other factors. Some of the microorganisms are uniquely found in one fluid while some commensal microorganisms such as *Lactobacillus gasseri, Bifidobacterium longum, Bacteroides fragilis, Tannerella forsythia,* and *Staphylococcus haemolyticus* among others, were reported in more than one body fluid. Similarly, transmissible pathogens such as Ebola, HIV and Hepatitis viruses among others were reported to exist in various body fluids.

Though some of these findings were mainly based on the analysis of nucleic acids and did not confirm the existence of live microorganisms, however, some were confirmed implying that such microorganisms can colonize other body parts. Therefore, though cross contamination during sample collection and analysis cannot be ruled out for some of them, however these findings emphasizes the need for sanitary awareness aimed at minimizing cross contamination and unnecessary biorisks at personal and at the laboratory level.

This study has also highlighted the beneficial impacts conferred by some of the commensal microorganisms especially on immunity, micronutrient synthesis and metabolism. These benefits have seen the development of various probiotics using species such as *Lactobacillus fermentum, Lactococcus lactis, Bifidobacterium breve, Bifidobacterium longum* and *Saccharomyces cerevisiae* among others and; formulation of biopharmaceuticals using human feces and bacteriophages.

However the functions of most of these commensals are not known and infact some of them are emerging as pathogenic or aggravators of certain health conditions. The benefits and health risks associated with commensal microorganisms are just starting to emerge. Their transmission and potential health risks are still not clear. Knowing their role is key to their utilization and management.Therefore future research aimed at elucidating their relevance is invaluable.

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