

A review of bacterial diversity and zoonotic potential in snakes

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Abstract

Snakes harbour diverse bacterial communities associated with different anatomical sites, including the oral cavity, venom glands, internal organs, gastrointestinal tract, blood and cloaca. These microbial communities play important roles in host ecology, disease transmission, venom-associated interactions and the emergence of pathogenic or antimicrobial-resistant bacteria. Understanding the bacterial diversity associated with snakes is therefore essential for both wildlife health and public health perspectives.

This review summarizes the current knowledge of bacterial communities reported from various snake derived samples, including oral, venom, organ, gut, blood and cloacal sources. The available literature demonstrates considerable variation in bacterial composition among snake species and sampling sites, with microbial diversity influenced by host species, geographic distribution, habitat, diet and environmental conditions. Several bacterial taxa have been identified as normal commensals while others are associated with opportunistic infections and potential zoonotic risks.

The review highlights the ecological significance of snake-associated microbiota and the importance of advanced molecular approaches for understanding bacterial diversity, functional roles, and antimicrobial resistance patterns. Further research integrating metagenomic and comparative studies is required to improve knowledge of snake microbiomes and their implications for animal and human health.

Keywords: Snake microbiota, bacterial diversity, zoonotic bacteria, oral microbiota, venom microbiota, antimicrobial resistance, snake-associated pathogens, one health

Introduction

Recently reptile interest is increasing recent decades [18]. Reptile are silent carrier of infection [20]. Nowadays reptiles as a pet demand increasing day by day [6]. One of the most neglected tropical disease was snakebites as every year approximately 2.7 million people worldwide suffer snakebite and around 81,000 to 1,38,000 of them die as snake oral cavity contain certain bacteria which harmless while some of them causes serious health issue to human resulting necrosis which affect the muscle as well as skin tissue [1]. This review summarizes the overall Oral, Venom, Organ, Gut, Blood and cloacal bacteria.

Oral Bacteria

Researcher conducted study in southern Taiwan were six species of snakes included 354 *Naja atra* (54.5% males, 45.4% females), 159 *Bungarus multicinctus* (60.3% males, 39.6% females), 216 *Trimeresurus stejnegeri* (40.7% males, 59.2% females), 118 *Protobothrops mucrosquamatus* (40.6% males, 59.3% females), 76 *Boiga kraepelini* (61.8% males, 38.2% females) and 181 *Elaphe taeniura friesi* (45.3% males, 54.6% females) were oropharyngeal (oral) swab was collected. Around 744 (67.4%) snakes were positive for *Enterococcus faecalis* bacteria. In *Morganella morganii* bacteria present in 348 (31.5%) snakes, 85(7.7%) snakes shows *Pseudomonas aeruginosa* bacteria followed by 90 (8.2%) snakes showed *Aeromonas hydrophila* bacteria [1]. Eighteen Burmese pythons' snakes was imported from Vietnam to Korea where the oral and cloacal swab was collected from the snakes. The bacterial strain found in only oral swab sample namely *Acinetobacter* sp., *Bacillus brevis*, *Enterobacter aerogenes*, *Escherichia coli*, *Klebsiella*

oxytoca, *Micrococcus rasenes*, *Pseudomonas aeruginosa*, *Pseudomonas putida* and *Pseudomonas* sp. *Aeromonas hydrophila*, *Citrobacter freundii*, *Corynebacterium jeikeium*, *Enterobacter* sp., *Enterococcus* sp., *Klebsiella pneumonia*, *Morganella morganii* ss. *Sibini*, *Proteus mirabilis*, *Proteus vulgaris*, *Providencia rettgeri*, *Pseudomonas* sp., *Staphylococcus lentus*, *Staphylococcus* sp. and *Staphylococcus xylosus* were the bacterial strains detected in the oral and cloacal samples [2].

The study conducted in Sichuan Province, China to investigate the bacterial communities present in oral regions of snakes. The snakes selected in the study was collected from different altitude ranges. *Protobothrops mucrosquamatus*, *Elaphe dione* and *Gloydius angusticeps* are snakes used for the study as researcher collected the oral swab sample for detect bacteria present in the mouth of snake. In oral sample of *Protobothrops mucrosquamatus* Proteobacteria is most dominant, *Labrys*, *Serratia*, *Pseudonocardia*, *Brevundimonas*, *Citrobacter*, *Mycoplasma*, *Delftia*, *Bacteroides* and *Fusobacterium* in *Elaphe dione* *Fusobacterium*, *Delftia*, *Citrobacter*, *Mycoplasma*, *Brevundimonas*, *Luteibacter*, *Pseudonocardia*, *Pelistega*, *Neisseria* and *Orthobacterium* similarly, in *Gloydius angusticeps* *Salinisphaera*, *Shinella*, *Luteimonas*, *Marmoricola*, *Mycoplasma*, *Rhodoplanes*, *Methylovirgula*, *Labrys*, *Serratia* and *Pseudonocardia*. In every species, Proteobacteria is the predominant microbiome [3].

Seven species of snake was study to find out the bacteria present in the mouth of snake were in *Naja atra* *Bordetella trematum*, *Mycoplasma fastidiosum*, *Phocoenobacter uteri*, *Pseudomonas helleri*, *Bisgaardia hudsonensis*, *Paia dinghuensis*, *Proteiniphilum acetatigenes*, *Serratia*

marcescens, *Morganella morganii* and *Haoranjiana flava*; in *Bungarus multicinctus* *Haemophilus felis*, *Stenotrophomonas maltophilia*, *Puia dinghuensis*, *Mycoplasma fastidiosum*, *Mycoplasma iguana*, *Bergeyella zoohelcum*, *Achromobacter insuavis*, *Acinetobacter bereziniae*, *Clostridium cylindrosporum* and *Comamonas testosterone* bacteria found. In the *Protobothrops mucrosquamatus* *Clostridium innocuum*, *Cupriavidus numazuensis*, *Puia dinghuensis*, *Klebsiella pneumoniae*, *Clostridium cylindrosporum*, *Sphingobacterium detergens*, *Luteibacter anthropic*, *Desulfovibrio desulfuricans*, *Epilithonimonas lactis* and *Oceanisphaera ostreae*; in *Trimeresurus stejnegeri* *Puia dinghuensis*, *Bacteroides fragilis*, *Citrobacter freundii*, *Yokenella regensburgei*, *Stenotrophomonas maltophilia*, *Morganella morganii*, *Phyllobacterium myrsinacearum*, *Beijerinckia fluminensis*, *Cupriavidus numazuensis* and *Tepidimonas aquatica*; in *Daboia siamensis* *Clostridium dakarensis*, *Cupriavidus numazuensis*, *Salmonella enterica enterica* serovar *Typhimurium*, *Sphingomonas paucimobilis*, *Bacteroides fragilis*, *Paracoccus chinensis*, *Stenotrophomonas pavanii*, *Chryseobacterium salipaludis*, *Mammaliococcus sciuri* and *Acinetobacter variabilis*; in *Deinagkistrodon acutus* *Morganella morganii*, *Providencia rustigianii*, *Puia dinghuensis*, *Mycoplasma fastidiosum*, *Rheinheimera pacifica*, *Cupriavidus numazuensis*, *Clostridium innocuum*, *Rheinheimera hassiensis*, *Acinetobacter proteolyticus* and *Rheinheimera aquimaris*. Finally, in *Trimeresurus gracilis* snakes *Cupriavidus numazuensis*, *Mycoplasma fastidiosum*, *Pseudomonas aeruginosa*, *Puia dinghuensis*, *Sphingomonas paucimobilis*, *Sediminibacterium lactis*, *Latilactobacillus curvatus*, *Comamonas testosterone*, *Paracoccus suum* and *Paenarthrobacter nitroguajacolicus* bacteria found [4].

In the study to detect the bacteria present in oropharynx of *Naja atra* found namely *Morganella morganii*, *Bordetella petrii*, *Corynebacterium freneyi*, *Proteus vulgaris*, *Proteus mirabilis*, *Enterococcus* spp., *Providencia* spp., *Bacillus* spp., *Staphylococcus* spp., *Streptococcus* spp., *klebsiella* spp., *Pseudomonas* spp., *Acinetobacter* spp., *Aeromonas* spp., *Paenibacillus* spp., *Microbacterium* spp., *Elizabethkingia* spp. and *Chryseobacterium* spp. [5].

In Togo, West Africa the study was conducted on snake and feeder mice as oral and cloacal swab was collected. In Bacteria of ball pythons found *Acinetobacter*, *Bacteroides*, *Citrobacter*, *Enterobacter*, *Lysobacter*, *Proteus*, *Pseudomonas*, *Staphylococcus* and *Tsukamurella* similarly in feeder mice *Clostridium*, *Escherichia coli*, *Moraxella* and *Stenotrophomonas* found in feeder mice [6].

The study was conducted on nine healthy Russell's vipers (*Daboia russelii*) to check for their oral bacterial flora. Gram-positive bacteria like *Bacillus*, *Enterococcus*, *Staphylococcus*, and *Lysinobacillus* were found in the study, along with Gram-negative bacteria like *Proteus*, *Salmonella*, *Providencia*, *Pseudomonas*, *Alcaligenes*, *Morganella*, and *Escherichia coli* [7].

Overall the study plays important role in snakes oral microflora dominated by both Gram negative and Grampositive bacteria composition mainly include host species, environmental conditions and geographic distribution.

Venom bacteria

The study was demonstrating whether the snake venom is truly sterile, since it known for its anti-microbial properties

as researcher analysed venom from five snake species, including Puff adder (*Bitis arietans*), Black-necked cobra (*Naja nigricollis*), Fer-de-lance (*Bothrops atrox*), Western diamond rattlesnake (*Crotalus atrox*) and Taipan (*Oxyuranus scutellatus*). The researcher taken mouth swab, first venom sample followed by immediately second venom sample as the second venom sample contain less contamination as the first extraction might remove bacteria stuck on the fangs or venom-delivery system. In addition, Puff adder (*Bitis arietans*) Venom microbiota dominated by Gammaproteobacteria. Furthermore, *Naja nigricollis* they detected *Enterococcus faecalis* bacteria viable strains of *Enterococcus faecalis* were isolated from venom, suggesting they can survive this environment. They found venom is not completely sterile and contain some microorganism. Researcher found that *Enterococcus faecalis* strains carry different bacteriocin genes that act like antibacterial weapons helping them outcompete other microbes and survive in the venom environment [8].

The study explained that venom is not always sterile as further experimental study was needed to conform whether this bacterium are permanent residents of venom glands or transient contaminants introduced from oral or environmental sources.

Organ bacteria

Total 27 snake carcasses were examined through necropsy at university putra Malaysia. Organ sample was collected by aseptically and cultured on 5% blood and McConkey agar. Sample were taken from different body part including lungs, liver, kidney, stomach and intestine. Python accounted for the majority of cases about 81%. Across most of the snakes carry mixed infections, like more than one type of bacteria was present in the same snakes at the same time also same type of bacteria was found in the snakes. The majority of bacteria found were gram negative bacteria. The most commonly isolated bacteria were *Aeromonas* which was frequently found in pythons and anacondas. *Salmonella* bacteria most commonly found in the boa's snakes. *Salmonella* was Bacteria were most frequently isolated from kidney of pythons, Intestine of anacondas and stomach of boas. Hence, the study conclude that captive pythons harboured more bacterial species than anacondas and boas [9].

The study was conducted in a landscape Park in central Poland investigated 16 free-living snakes found dead. The snakes carcas was captured and analysis of internal organ detect that 14 individual snakes were positive for *Salmonella* spp., yielding 33 isolates representing multiple servars, including several rare types. Also 13 snakes were found to *Alaria alata* mesocercariae within muscle tissue. Unidentified nematodes are detected in 4 snakes for bacterial testing procedure. *Mycobacterium* spp. and *Yersinia* spp. was not found. Hence, finding of the study suggest that carcass of snakes with presences of bacteria may act as a potential source of infection for scavenging wildlife such as wild boars and fox's animal as the bacteria passes from it facilitating the transmission of zoonotic agents within the ecosystem [10].

In summary both captive and wild environments demonstrate that snakes can play a notable role in the maintenance and circulation of bacterial pathogens, particularly *Salmonella* spp. Variation in bacterial profiles between species and environments suggests that both

ecological conditions and host-specific factors influence microbial colonization. The findings underscore the importance of monitoring reptile-associated bacteria, especially in contexts where human–animal or wildlife interactions are frequent, due to their potential implications for public and veterinary health.

Gut Bacteria

The study was conducted on three Big-eyed Bamboo Snake (*Pseudoxenodon macrops*) for detecting gut microbiome. Phylum level bacteria found in stomach was dominated by *Pseudomonadota* (7.88% $\pm$ 0.40%), *Actinomycetota* (3.21% $\pm$ 0.09%), and *Bacillota* (1.07% $\pm$ 0.04%) in small intestine *Pseudomonadota* (6.52% $\pm$ 0.09%), *Actinomycetota* (3.34% $\pm$ 0.09%) and *Bacillota* (1.07% $\pm$ 0.04%). Similarly, in large intestine *Pseudomonadota* (19.90% $\pm$ 10.30%), *Bacteroidota* (13.04% $\pm$ 6.84%) and *Bacillota* (3.40% $\pm$ 1.16%). The dominant bacterial communities in stomach and small intestine were similar whereas in large intestine *Bacteroidota* was higher in abundance than stomach and small intestine. At genus level stomach was dominated by *Escherichia* (1.89% $\pm$ 0.05%) and *Mycobacteroides* (0.95% $\pm$ 0.03%) similarly small intestine showed similar dominant genera as stomach *Escherichia* (1.97% $\pm$ 0.03%) and *Mycobacteroides* (0.99 $\pm$ 0.01%). Large intestine was dominated by *Bacteroides* (11.2% $\pm$ 5.94%), *Kluyvera* (4.74% $\pm$ 4.49%) and *Citrobacter* (2.63% $\pm$ 1.66%). *Pseudomonadota* (phylum) and *Escherichia* (genus) are main bacterial group found followed by *Bacteroidota* second most abundant bacterial group found. Similarly, Region-specific taxa were also identified. *Cytophagia* was abundant in the stomach, while uncultured Gammaproteobacteria, *Bathymodiolus brooksi* methane-syntrophic bacteria, *Marinobacteraceae*, and *Micromonosporaceae* were found in the small intestine. Also, *Prevotella*, *Morganellaceae* were characteristic taxa of the large intestine [11].

The study was demonstrating on three wild *Rhabdophis subminiatus* gut section of each snakes were studied to find gut microbes. Researcher found that esophagus, stomach, small intestine had more bacteria species than large intestine and cloaca most common taxa found was *Proteobacteria* (65.30%), *Firmicutes* (9.5%), *Bacteroidetes* (9.03%), *Fusobacteria* (6.29%), *Tenericutes* (5.66%). *Actinobacteria* found high abundant in esophagus and stomach than large intestine. Bacterial genera include *Fusobacterium*, *Mycoplasma*, *Bacteroides*, *Acinetobacter*, *Pseudomonas*, *Rickettsiella*, *Aerococcus*, *Arenimonas* and *Trichococcus*. *Mycoplasma*, *Pseudomonas*, *Rickettsiella*, *Aerococcus* and *Tenericutes* (Phylum) found in upper gut and *Fusobacterium*, *Bacteroides*, *Trichococcus*, *Lachnospiraceae*, *Carnobacteriaceae*, *Bacteroidetes* (Phylum) and *Fusobacteria* (Phylum) found lower gut while *Proteobacteria*, *Aeromonadaceae* and *Enterobacteriaceae* found present throughout the gastrointestinal tract [12].

Researcher demonstrated to check the difference between dietary preferences based on vertebrate's eater snakes such as *Gonyosoma coeruleum* (GC), *Rhabdophis tigrinus* (RT) and invertebrate eater snake *Rhabdophis pentasupralabralis* (RP) to find the bacteria differentiation based on the diet. Three snakes of each species were collected and small intestine, large intestine and cloaca gut content taken and mixed it then used a DNA extraction kit (TIANamp Stool DNA Kit) then Amplify bacterial marker gene (PCR) target

a special gene 16S rRNA gene (V4 region) followed by Illumina HiSeq sequencing, bioinformatics the data. The finding of the study was vertebrate's eater snakes *Gonyosoma* dominant genera include *Cetobacterium* and *Bacteroides* were as subdominant genera included *Fusobacterium*, *Peptostreptococcus* and *Paraeggerthella*. In *Rhabdophis pentasupralabralis* dominant genera included Uncultured *Enterobacteriaceae* and Uncultured *Simkaniaceae* were as Subdominant genus was *Hafnia-Obesumbacterium*. Similarly, in *Rhabdophis tigrinus* *Cetobacterium* and *Fusobacterium* was dominant genera and subdominant genus was Uncultured *Enterobacteriaceae*. Bacterial biomarker in GC includes *Bacteroides*, *Paraeggerthella*, *Peptostreptococcus*, *Vagococcus*, *Erysipelothrix* and *Enterococcus*. Similarly, in RP biomarkers includes, Uncultured *Enterobacteriaceae*, Uncultured *Simkaniaceae*, *Hafnia-Obesumbacterium*, *Stenoxibacter*, *Lawsonia*, *Ureaplasma* and *Acinetobacter*. *Cetobacterium*, *Fusobacterium* and Uncultured *Barnesiellaceae* are biomarkers in RT [13].

Researcher collected 50 intestinal sample (Small and large intestine) from 29 snakes including two venomous snake species *Deinagkistrodon*, *Naja* and one non venomous snake species *Ptyas*. In *Deinagkistrodon* core genera found namely *Acinetobacter* (Y), *Aeromonas* (Y), *Bacteroides* (Y), *Citrobacter* (Y), *Clostridium sensu stricto* 1, *Lachnospiraceae_uncultured*, *Morganella* (Y), *Proteus* (Y), *Providencia* (Y), *Pseudomonas* (Y), *Saccharibacteria_norank*, *Salmonella* (Y), *Achromobacter* (Y), *Cetobacterium*, *Clostridium innocuum* group (Y), *Fusobacterium* (Y), *Lachnoclostridium*, *Parabacteroides*, *Romboutsia*, *Clostridium sensu stricto* 13, *Delftia*, *Epulopiscium*, *Erysipelotrichaceae_unclassified*, Family XIII_uncultured, *Lachnospiraceae_unclassified*, *Methylobacterium* and *Porphyromonadaceae_uncultured*; *Naja* core genera such as *Acinetobacter* (Y), *Aeromonas* (Y), *Bacteroides* (Y), *Citrobacter* (Y), *Clostridium sensu stricto* 1, *Lachnospiraceae_uncultured*, *Morganella* (Y), *Proteus* (Y), *Providencia* (Y), *Pseudomonas* (Y), *Saccharibacteria_norank*, *Salmonella* (Y), *Achromobacter* (Y), *Cetobacterium*, *Clostridium innocuum* group (Y), *Fusobacterium* (Y), *Lachnoclostridium*, *Parabacteroides*, *Romboutsia*, *Enterococcus* (Y), *Eubacterium fissicatena* group, *Hungatella*, *Shewanella* and *Xanthomonadaceae_uncultured* similarly in *Ptyas mucosa* core genera *Acinetobacter* (Y), *Aeromonas* (Y), *Bacteroides* (Y), *Citrobacter* (Y), *Clostridium sensu stricto* 1, *Lachnospiraceae_uncultured*, *Morganella* (Y), *Proteus* (Y), *Providencia* (Y), *Pseudomonas* (Y), *Saccharibacteria_norank*, *Salmonella* (Y), *Edwardsiella* (Y), *Erysipelothrix* (Y), *Myroides* (Y) and *Ureaplasma* (Y). (Y) indicate does't mean that snake is sick or that all bacteria in that genus are harmful it only means that some members of that bacterial genus are known to cause disease, so researchers consider them medically important [14].

The study conducted in Sichuan Province, china to investigate the bacterial communities present in gut were the cloacal sample is taken to detect bacteria. The predominant bacteria in *Protobothrops mucrosquamatus* were *Bacteroides*, *Mycobacterium*, *Pseudonocardia*, *Brevundimonas*, *Cytobacterium*, *Salmonella*, *Citrobacter* and *Fusobacterium*. Similarly, in *Elaphe dione* *Proteobacteria* dominant phylum, *Salmonella*, *Citrobacter*, *Fusobacterium*, *Mesorhizobium*, *Methylobacterium*,

Myroides and *Brevundimonas* where as in *Gloydus angusticeps* *Proteobacteria*, *Snodgrassella*, *Neisseria*, *Mycolicibacterium*, *Rhodoplanes*, *Lactobacillus*, *Methylovirgula*, *Oribacterium* and *Deinococcus* bacteria found ^[15].

In summary, gut microbes how that gut bacterial diversity varies according to snake species, gut region and dietary habits were *Pseudomonadota*, *Bacillota*, *Bacteroidota* and *Actinomycetota* with some potentially pathogenic genera such as *Salmonella*, *Pseudomonas*, and *Aeromonas* present as part of the normal gut microbiota. As snake gut microbiota plays an important role in digestion, host health and understanding potential zoonotic risks.

Blood Bacteria

The study was conducted on grounds of the Oklahoma City zoo where 15 free-ranging *Pantherophis obsoletus* (Western ratsnakes) were evaluated for aerobic and anaerobic blood culture. The study found that 12 (80%) snakes individuals tested positive for Gram-negative bacteria namely *Morganella morganii*, *Citrobacter freundii* and *Proteus vulgaris*. Presence of bacteria in bloodstream indicate infection of diseases but in this study showed no clinical signs of diseases. Therefore, these finding suggest that such bacteria may be represent part of normal physiological state not the indication of disease in this snake species ^[16].

In reptile market of Jemaa el-fna Marrakech market, Morocco total 118 reptile were examined for blood pathogen including 68 snakes Montpellier snakes (*Malpolon monspessulanus*), Puff adder (*Bitis arietans*), Egyptian cobras (*Naja haje*), Eastern Montpellier snakes (*Malpolon insignitus*) and Horsehoe Whip snakes (*Hemorrhois hippocrepis*) respectively. The microscopic examination showed that gamonts were detected only in snake's species. Molecular screening of blood sample was found to have positive results for *Anaplasma/Ehrlichia* spp., *Rickettsia* spp., *Babesia/Theileria* spp., and *Leishmania* spp. were obtained via molecular screening of pathogens in blood whereas all samples were negative for *Borrelia burgdorferi sensu lato*, Spotted Fever Group *Rickettsiae* or *Coxiella burnetii*. *Anaplasma phagocytophilum* found in two Montpellier snakes and other two species have *Anaplasma* spp. whereas four Puff adder snakes *Rickettsia asiatica* bacteria was found. *Leishmania tarentolae* parasite was found in Montpellier snakes. *Hepatoozon* spp parasite found in Montpellier snakes and puff adder snakes. Interestingly, puff adder's blood sample tested positive for *Candidatus Midichloria mitochondrii* bacterium found inside the ticks suggesting that snake was exposure to the tick vector ^[17].

The study indicate that snakes can harbor diverse blood-associated bacteria and hemoparasites across different environments while some bacterial presence may represent a non-pathogenic or commensal state other detected organisms highlight the potential role of snakes as reservoirs or incidental hosts in complex vector-borne pathogen cycles. This emphasizes the need to further investigate the ecological and epidemiological significance of blood-associated microorganisms in reptilian species.

Cloacal Bacteria

The study was conducted on eighteen Burmese python were snakes imported from Vietnam to the Korea from the cloacal sample the bacterial strain found namely *Acinetobacter baumannii*, *Acinetobacter calcoaceticus*, *Aeromonas* sp.,

Bacillus sp., *Chryseobacterium indologenes*, *Citrobacter koseri*, *Enterobacter cloacae*, *Enterobacter intermedium*, *Enterococcus faecalis*, *Flavobacterium indologenes*, *Gemella haemolysans*, *Kluyvera cryocrescens*, *Micrococcus roseus*, *Pseudomonas* sp. and *Shewanella putrefaciens* ^[3].

Researcher examined 29 healthy adult pet snakes in Bulgaria as snakes belong to different species such as *Python regius* (Ball python), *Python curtus* (Short-tailed Sumatran Python), *Python bivittatus* (Burmese python), *Morelia spilota* (Carpet python), *Acrantophis dumerili* (Dumerili's boa), *Boa constrictor* (Common boa), *Boaedon fuliginosus* (The African house snake), *Pantherophis guttatus* (Corn snake) and *Bothrops insularis* (Golden lancehead). The bacterial species found in snake cloacal swab was *Salmonella enterica* (27.59%), *Staphylococcus* spp. (62.07%), *Enterococcus* spp. (44.83%), *Bacillus* spp. (31.03%), *Enterobacteriaceae* spp. (27.59%), *A. denitrificans* (20.69%), *S. paucimobilis* (20.69%), *C. koseri* (20.69%), *Pseudomonas* spp. (27.59%) and *Klebsiella pneumoniae* (20.69%) ^[18].

In reptiles from the souks of Jemaa el-Fna, cloacal screening revealed the presence of opportunistic bacteria in snakes. *Morganella morganii* was detected in both *Malpolon monspessulanus* and *Bitis arietans*, while *Pseudomonas aeruginosa* was identified in the cloacal sample of an *Naja haje* ^[17].

Collectively, these studies demonstrate that cloacal microbiota varies among snake species and environments. Several medically important bacteria, including *Salmonella*, *Pseudomonas*, and *Morganella*, were commonly identified.

Factor Influencing Bacteria

The factor influencing by bacteria mainly species, sex, temperature, season as in Taiwan snake's species the researcher found that in winter *Enterococcus faecalis* found less and highest in autumn as *Boiga kraepelini*, *Elaphe taeniura friesi* and *Bungarus multicinctus* snakes show high occurrences compared to *Protobothrops mucrosquamatus* and *Trimeresurus stejnegeri* show lowest occurrence of bacteria as there is no significant difference was observed in male and female within each snake species. *Morganella morganii* bacteria occurrences rate was lowest in summer and highest in autumn as *Naja atra* and *Trimeresurus stejnegeri* show higher occurrences and *Elaphe taeniura friesi* and *Protobothrops mucrosquamatus* show lowest occurrence of bacteria. Male *Naja atra* and *Bungarus multicinctus* show highest rate of bacteria than in females as no significant sex difference was observed in another species. Similarly, in summer the *Pseudomonas aeruginosa* found less and highest in autumn as *Boiga kraepelini* and *Bungarus multicinctus* show higher occurrences rate compared to another snake's species. There is no significant effect of season on *Aeromonas hydrophila* as occurrence remained fairly similar throughout the year as *Boiga kraepelini* and *Bungarus multicinctus* show high occurrences of the bacteria ^[1]. Many Anti biotics are resist to the bacteria ^[19]. Some of the bacteria were resistant to the antibiotic such as penicillin, Amoxyclav, oxacillin, methicillin and streptomycin while they are susceptible to imipenem, amikacin, norfloxacin, gatifloxacin, ciprofloxacin, gentamicin, tetracycline, chloramphenicol and azithromycin ^[9]. Similar to this, antibiotics including cephalosporins, penicillins, sulfonamide-trimethprim, and trgecycline are resistant to bacteria since salmonella can

contaminate reptile eggs through the cloaca, soil, or even the ovaries due to the thinness of the snakes' eggs ^[20]. Bacteria also contribute by feeder animal such as Mice when oral and cloacal sample test bacteria also found in it ^[6]. Quarantine procedure is also important while travelling snakes imported from Vietnam to Korea snakes found some bacteria in their oral and fecal sample ^[2].

Conclusion

Snakes harbour diverse bacterial communities in multiple anatomical sites, including the oral cavity, venom, gastrointestinal tract, internal organs, blood, and cloaca. These microbial communities comprise both commensal and potentially pathogenic bacteria, with several genera such as *Salmonella*, *Morganella*, *Pseudomonas*, *Aeromonas*, *Citrobacter*, *Proteus*, *Enterococcus*, and *Klebsiella* being repeatedly reported across different snake species and geographic regions. The composition of these bacterial communities varies according to host species, habitat, diet, geographic location, season, and environmental conditions, highlighting the dynamic nature of the snake microbiome.

The reviewed studies demonstrate that snakes can serve as important reservoirs of zoonotic bacteria with implications for snakebite-associated wound infections, reptile handling, the exotic pet trade, wildlife rehabilitation, and conservation programs. Emerging evidence also challenges the long-held assumption that snake venom is sterile, suggesting that viable bacteria may persist within the venom delivery system. Furthermore, the detection of antimicrobial-resistant bacteria in snake-associated microbiota underscores an additional public health concern.

Advances in high-throughput sequencing and metagenomic approaches have greatly expanded our understanding of snake-associated microbial diversity; however, significant knowledge gaps remain regarding the functional roles, transmission dynamics, persistence, and antimicrobial resistance of these microorganisms. Future research integrating culture-based methods, whole-genome sequencing, metagenomics, and comparative ecological studies across wild and captive snake populations will improve our understanding of host microbe interactions and zoonotic transmission. Such knowledge will support the development of evidence-based strategies for snakebite management, antimicrobial therapy, wildlife health monitoring, and One Health surveillance programs.

Authors Contribution

Anjali Khond conducted the literature search and prepared the original draft of the manuscript. Dr. Mrunal Ghag Sawant performed critical revision of the manuscript for important intellectual content and provided overall supervision of the study.

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