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AN INVESTIGATION BACTERIAL CONTAMINATION IN HOUSEHOLDS OF MEERUT REGION AT UTTAR PRADESH

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ABSTRACT
Microbial populations such as bacteria in indoor environments, where we spent our maximum time are indeed essential for public health. The presences of bacteria were discerned in 125 out of 200 samples of air of living room in rural and urban areas. The 75 samples (34 in rural and 41 in urban areas) of air of living room were found to be bereft of bacteria. The total number of bacteria isolates from the air of living room in rural and urban areas was 66 and 59 respectively, with 29 bacterial strains. The numbers of bacterial genus identified in living room of rural areas are 16 and in living room of urban areas are 13 and a total of 18 bacterial genus in which 9 each pathogenic and nonpathogenic were observed in the air of living rooms of rural and urban households respectively.

KEYWORDS: Microbial populations, Air borne diseases, Bacterial contamination, living rooms, rural and urban households.

INTRODUCTION

Global changes in environmental factors and excessive exploitation of natural resources leads to cause a major burden on human health as well as on climatic factors. These factors lead to cause a communicable and non-communicable disease in developing countries. Health can be negatively affected by all types of environmental pollution. Both the outdoor and the indoor environments are linked together. The two elements cannot be separated. Man spends around 85% -90% of a day in indoor activities. There are different categories of population like infants and young children, elderly people, sick people and convalescent which spend 100% of a day time indoor. Pathogenic organisms continuously enter the home with foods (food borne) or water (water borne), through foods prepared in the home by an infected person (person to person spread), through the air (airborne), by the insects or via pets[1]. There has been tremendous increase in the area of research and development to study the patterns of household infections caused among the population using statistical and fundamental analysis[2]. In order to reduce the effect of this infectious organism it is recommended to follow various hygienic practices like remain in isolated area during the period of illness so as to avoid contact with healthy person, cover the facial area to avoid contamination through sneezing, coughing, use of proper disinfectant to reduce the microbial population from exposed parts of body. Apart from this, good environmental and engineering practices can also be used to decrease the spread of pathogenic microorganisms[3]. Most of our time is spent indoors where we are exposed to a wide array of different microorganisms living on surfaces and in the air of our homes. Despite their ubiquity and abundance, we have a limited understanding of the microbial diversity found within homes and how the composition and diversity of microbial communities change across different locations within the home [4].

In many human activities micro-organisms in the environment represent a hidden but dangerous risk factor. Concern has increased with the introduction of advanced technologies in hospitals, industries and agricultural field. In recent years, many studies have been carried out on this topic, and nowadays the evaluation of the level of air microbial contamination in places at risk is considered to be a basic step toward prevention. However, there are still problems to be solved relating to methodology, monitoring, data interpretation and maximum acceptable levels of contamination[5]. The American Lung Association reports that there are nearly 10 million people in the U.S. with asthma. “Exposure to house dust mites, animal-related allergens (animal dander and cat saliva), and mold have been estimated to cause 200,00 or more emergency room visits a year by asthma patients (EPA)”. While pollutant levels from a single source may not be a health risk. People may be at greater risk of developing health problems by indoor air pollutants. The quality of indoor air has a great effect on keeping allergies and asthma under control. Therefore breathing in clean indoor air has an important impact on health. There is no simple way to sample the air in your home to determine the level of biological pollutants. The amount of most biological substances required to cause disease is unknown and varies from one person to the next. The present study carried out the experimental work to investigate and understanding the bacterial contamination of air of living rooms in rural and urban areas of Meerut district of Uttar Pradrsh.

MATERIALS AND METHODS

Sample procurement

A total of 200 different samples from living rooms of rural and urban areas of Meerut district surveyed from potentially harmful pathogens in the living rooms. The rural and urban areas cover 5 sites namely: Dorli, Palheda, SofiPur, Putha, PawaliKhas and Jawaher quarter, Inderlok, Begum Bagh, RajanKunj, Defence Colony respectively.

Nutrient agar Media Preparation

Nutrient agar powder (12.6g) was mixed in 450ml of cold demineralised water in an 800ml beaker and gently stirred. After addition of agar mixture was autoclaved and allowed to cool to 50 °C. The prepared agar was then poured into clean Petri dishes, cooled to caste and stored at 4°C until use [6].

Incubation

Incubation of the inoculated culture media plates was done in incubator at 28-30°C for 24 hours. The growth was observed on the successive day and it was different biochemical analysis were made positive samples. These tests were carried out to categorize the type of infection in a particular area and also the level of infection. The level of drug resistance parasites/infection was also determined using by biochemical techniques using different parameters [7].

Sample analysis

All samples were analyzed by conventional techniques as described by Buchanan and Gibbons [8]; Carter and Cole [9]; Tyagi and Tyagi [10]. After collection of samples, culture plates were incubated in BOD incubator at 30 to 34°C for 24 h. After incubation samples were analyzed by morphological or biochemical methods. Microbiological direct analysis of air requires quantitative determination, that is, total population of microorganisms. The densities of cells, spores/conidia of microorganisms were measured in the laboratory through several methods of direct microscopic or colonies counter. In the direct microscopic counts, a known volume of liquid is added to the slide and the numbers of microorganism are counted by examining the slide with the bright field microscope. For colony counter Neubauer or Petroff-Hausser counting chamber, breed smears or electric cell counter (or Coulter counter) were used.

Identification of isolates

After 24 h of incubation, the colonies that appeared morphologically dissimilar were chosen, counted, subcultured to fresh appropriate culture media and incubated at 30 to 34°C for 24 h. Identification of microorganisms did not commence, due to the fact that inhibition was evident that a pure culture had been obtained. Colonies identifiable as discrete on the different agar medium (EMB, Blood agar, MacConkey agar, XLD etc) will carefully examined macroscopically for culture characteristics such as the shape, color, size texture and hemolytic reactions. Colonies are gram stained and individual bacterial cell were observed. The bacteria were speciated using their isolated colonies (Beumer et al., 1996). Further identification of enteric organisms was done using different taxonomical methods given by Aneja [11].

RESULTS AND DISCUSSION

Total 125 samples (62.5%) were found to be positive for bacterial contamination out of 200 samples from different experimental sites of living rooms of rural and urban areas. The contamination was more pronounced in rural region 66% as compared with urban areas 59% (Table 1). On the basis of primary characterization, the samples were subjected to morphological and biochemical analysis to confirm the identification of bacteria. The presence of bacteria was discerned in 125 samples of air of living room in rural and urban areas out of 200 samples. The 75 samples (34 in rural and 41 in urban areas) of air of living room were found to be bereft of bacteria. The total number of bacteria isolates from the air of living room in rural and urban areas was 66 and 59 respectively, with 29 bacterial strains.

The numbers of bacterial genus identified in living room of rural areas are 16 and in living room of urban areas are 13 (Table 2). In rural area living room, *Streptococcus spp.*and *Pseudomonas spp.* contributed the major fraction of bacteria followed by *Lactobacillus spp., Bacillus spp., E.coli spp., Paenibacillus spp., Proteus spp., Micrococcus spp., Staphylococcus spp., Corynebacterium spp., Clostridium spp., Salmonella spp., Enterococcus spp., Aeromonas spp., Shigellaspp and Alcaligenes spp.*However, in urban area living room, *E.coli spp. and Micrococcus spp.* contributed the major fraction of bacterial genus followed by *Lactobacillus spp., Streptococcus spp., Shigella spp., Bacillus spp., Haemophilus spp., Campylobacter spp., Psedomonas spp., Salmonella spp., Clostridium spp., Enterococcus spp. and Proteus spp.* It is a notable fact that 8 pathogenic bacterial genus such as *Proteus spp., Salomonella spp., Clostridium spp., Streptococcus spp., Pseudomonas spp., Corynebacterium spp.,Enterococcus spp. and Shigella spp.* were found in living room of rural areas with 8 non-pathogenic bacterial genus such as *E.coli spp., Micrococcus spp., Bacillus spp., Alcaligenes spp., Lactobacillus spp., Paenibacillus spp., Staphylococcus spp., Enterococcus spp., Aeromonas spp.*(Figure 1a&b). On the other hand, 8 pathogenic bacterial genus such as *Proteus spp., Salmonella spp., Clostridium spp., Streptococcus spp., Pseudomonas spp., Campylobacter spp., Shigella spp.*,and *Enterococcus spp.* were found in living room of urban areas with 5 non-pathogenic bacterial genus such as *E.coli spp., Micrococcus spp., Bacillus spp., Lactobacillus spp.* and*Haemophilus spp.* (Figure 2a&b).

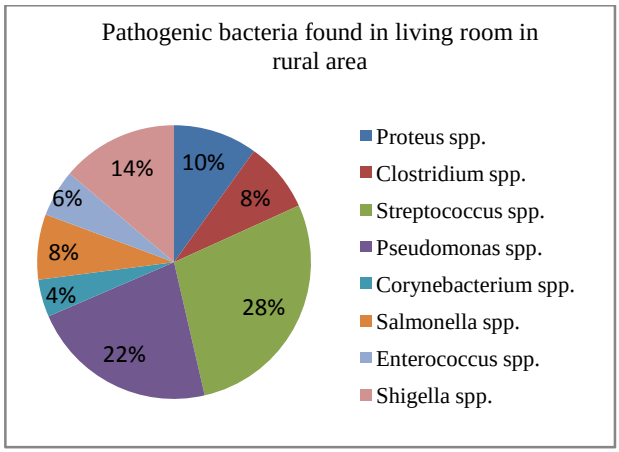

FIGURE 1a: Showing pathogenic bacteria found in living rooms in rural area

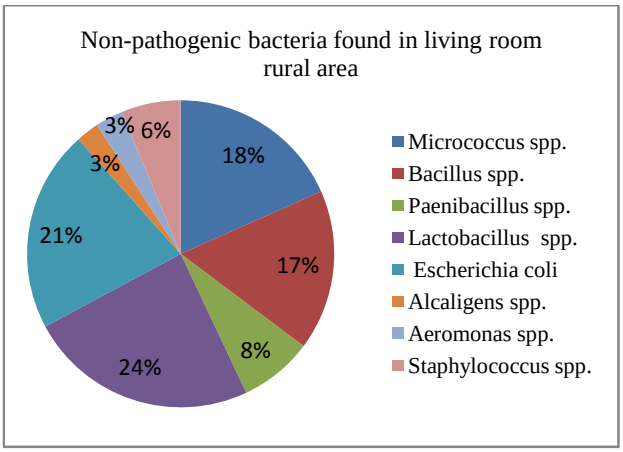

FIGURE 1b: Showing non-pathogenic bacteria found in living rooms in rural area

TABLE 1. Bacterial contamination analysis in the air of living rooms in rural and urban households of Meerut district

Types of samples	Experimental site	Total no. of samples processed	No. of samples devoiod of bacteria	No. of samples with bacterial growth	Total No. of bacterial genus isolated	Bacteria identified
Rural houses LRR	Dorli	20	4	16	8	[1]
	Palheda	20	4	16	7	[2]
	Sofipur	20	6	14	6	[3]
	Putha	20	11	9	5	[4]
	Pawlikhas	20	9	11	9	[5]
	Total	100	34	66	16	
Urban houses LRU	Jawahar quarter	20	7	13	7	[6]
	Inderlok	20	6	14	7	[7]
	Begum bagh	20	6	14	6	[8]
	Rajankunj	20	10	10	6	[9]
	Defence colony	20	12	8	4	[10]
	Total	100	41	59	13	

1. *Micrococcus spp., Bacillus spp., Paenibacillus spp., Lactobacillus spp.,* ***Proteus spp., Clostridium spp., Streptococcus spp., Pseudomonas spp.,***
2. *E. coli, Bacillus spp., Lactobacillus spp.,Paenibacillus spp.,* ***Streptococcus spp., Pseudomonas spp., Corynebacteria spp.,***
3. *Lactobacillus spp., Staphylococcus spp., Bacillus spp.,* ***Salmonella spp., Pseudomonas spp., Streptococcus spp.,***
4. *E. coli, Alcaligenes spp., Lactobacillus spp.,* ***Streptococcus spp., Pseudomonas spp.,***
5. Entero*coccus spp., Aeromonas spp., E. coli, Micrococcus spp., Bacillus spp.,* ***Proteus spp., Salmonella spp., Pseudomonas spp., Shigella spp.***
6. *E. coli, Micrococcus spp., Lactobacillus spp.,* ***Salmonella spp., Clostridium spp., Streptococcus spp., Pseudomonas spp.,***
7. *E. coli, Micrococcus spp., Bacillus spp., Lactobacillus spp., Haemophilus spp.* ***Campylobacter, shigella spp.,***
8. *E. coli, Micrococcus spp., Enterococuus spp.,* ***Proteus spp., Shigella spp., Streptococcus spp.,***
9. *E. coli, Micrococcus spp., Bacillus spp., Lactobacillus spp.,****Shigella spp., Streptococcus spp.,***
10. *Micrococcus spp., Bacillus spp., Lactobacillus spp.,* ***Streptococcus spp.***

A total of 18 bacterial genus pathogenic and nonpathogenic were observed in the air of living rooms of rural and urban households (Figure 3). The pathogenic bacteria were found common in both living room of rural and urban areas such as *Proteus spp., Salmonella spp., Clostridium spp., Streptococcus spp., Pseudomonas spp. and Shigella spp.* whereas *Corynebacterium spp.* was found in rural areas living room. On the other hand, *Campylobacter spp.* was found in urban areas living room (Table 2). The present result shows that bacterial genus isolated from living rooms in rural areas is more in percentage as compared to living rooms of urban areas in Meerut district. Bacterial contamination in kitchen spread out through sponges and washcloths used normally in kitchens and spread out upto living room were similarly reported [12, 13]. Bacterial contamination spread out into kitchens to living rooms and its surrounded areas through air and other factors such as dustbin, dusting cloth, utensils etc. were similarly reported [14].

Furthermore, a significant proportion of these infections are preventable by getting people to practice better hygiene in their own homes and in everyday life. This includes food and respiratory hygiene, and better hand, surface and laundry hygiene practices coupled with other practices such as safe disposal of refuse and wastewater. In communities that lack access to adequate sanitation and clean water, this may also involve ensuring water treatment and safe storage and the safe disposal of faeces. Recently Shruti et al. (2011) have found the bacteriological quality of air of kitchens in rural households was more pathogenic and virulent as compared to that of kitchen in urban households and they have suggested that these opportunistic pathogens may be harmful, especially in immunocompromised host.

TABLE 2. Morphological identification based on agar slant culture characteristics and number of colonies of the bacteria isolated from the air of living rooms in rural and urban households

Bacterial genus in living room	No. of colonies (%)/ 200 sample	Bacteria found in living room (rural / urban)
Micrococcus spp.	38	(N.P) rural /urban
Bacillus spp.	35	(N.P) rural /urban
Paenibacillus spp.	16	(N.P) rural
Lactobacillus spp.	50	(N.P) rural /urban
Proteus spp.	18	(P) rural/ urban
Clostridium spp.	15	(P) rural /urban
Streptococcus spp.	51	(P) rural/ urban
Pseudomonas spp.	40	(P) rural /urban
Escherichia coli	44	(N.P) rural / urban
Corynebacterium spp.	8	(P) rural
Salmonella spp.	14	(P) rural/ urban
Alcaligens spp.	5	(N.P) rural
Enterococcus spp.	10	(P) rural /urban
Aeromonas spp.	6	(N.P) rural
Shigella spp.	25	(P) rural /urban
Haemophilus spp.	7	(N.P) urban
Campylobacter spp.	7	(P) urban
Staphylococcus spp.	13	(N.P) rural

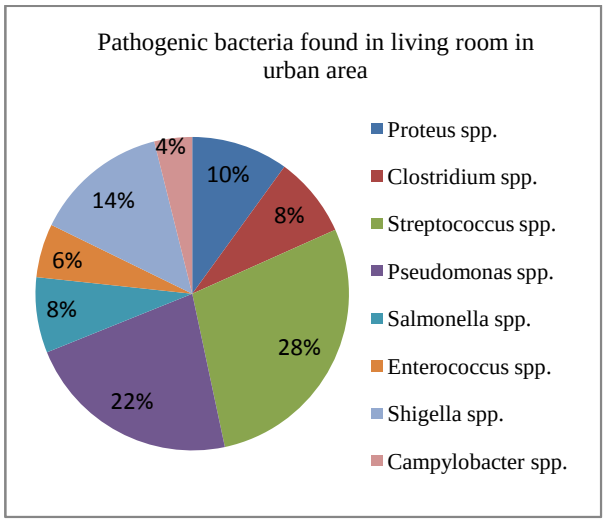

FIGURE 2a: Showing pathogenic bacteria found in living rooms in urban area

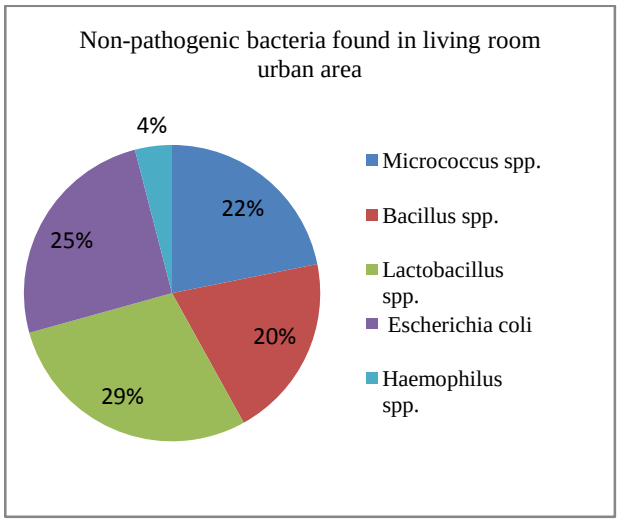

FIGURE 2b: Showing non-pathogenic bacteria found in living rooms in urban area

The results of our study have several implications on the preference for floor, carpet, tabletop in living rooms and unwashed hands, spoiled vegetables, dust bins, sink, washing areas, food shelves, cutlery and crockery, refrigerator, vegetables racks, floor, back side of door and near kitchen gas cylinder in kitchens. The primary sources of these bacteria are kitchens in which the food spoilage and stored dustbin contain for many days and directly entered vegetables (some infected with higher pathogens). After sometime, bacteria spread out to its surrounding areas which are more suitable for growth. In living rooms such as carpet, curtains, toilet doors, table top, dressing tables and ceiling fans etc. are the best places in which the bacterial growth are more conditional and when the favorable conditions start (seasonal variation) these bacteria infected the individuals. This explains why most

people experience a lot of respiratory symptoms from acute allergic rhinitis to pneumonia during climate changes. Avoiding these infections, we have made some arrangement in our kitchens, living rooms and its surrounding areas. When possible, floor carpeting in homes should be minimized or avoided, since this serves as habitat for opportunistic infection agents that pose harm to one's health.

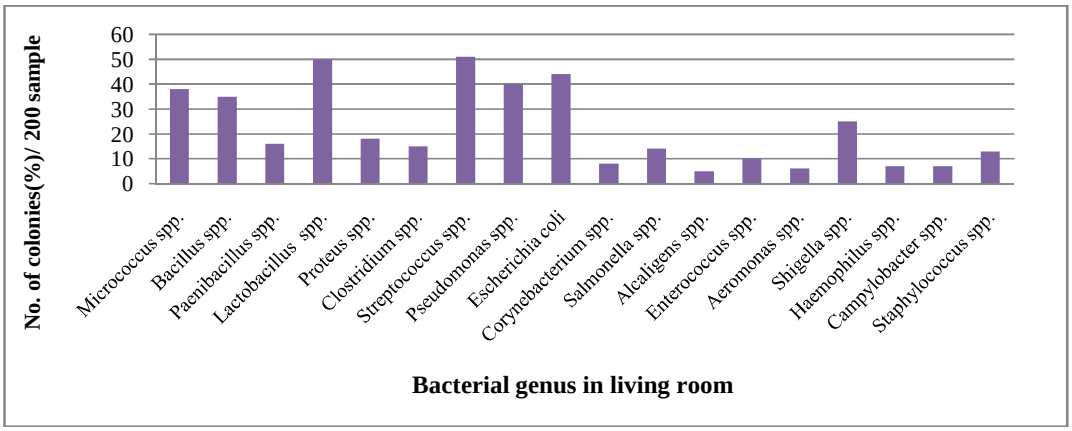

FIGURE 3: Showing bacterial genus found in living rooms in urban and rural households

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REFERENCES

[1]. Beumer, R.R., TeGiffel, M.C., Spooranberg, E., Rombouts, F.M. (1996) Listeria species in domestic environments. Epid. Infect., 117: 437- 442.

[2]. Rylance, J., Gordon, S.B. Nacher, L.P. (2013) Household air pollution a call for studies into biomarkers of exposure and predictors of respiratory disease. Am. J. Physiol. Lung. Cell Line Mol. Physiol. 304:I571-578.

[3]. Li, Y., Leung, G.M., Tang, J.W., Yang, X. (2007) Role of Ventilation in Airborne Transmission of Infectious Agents in the Built Environment – A Multidisciplinary Systematic Review. Indoor Air 17(1): 2-18.

[4]. Dunn, R.R., Fierer, N., Henley, J.B., Leff, J.W., Menninger, H.L. (2013) Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes. PLoS ONE 8(5): e64133.

[5]. Charnley, J., Eftekhar, M. (1969) Postoperative infection intotal prosthetic arthroplasty of the hip-joint with special reference to the bacterial content of air in theoperating room. Brit JrSurg; 56: 641–664.

[6]. Arulanantham, V., Pathmanathan, S., Ravimannan, N., Niranjan, K. (2012) Alternative culture media for bacterial growth using different formulation of protein sources. J. Nat. Prod. Plant Resour, 2 (6):697-700.

[7]. Sivashanmugam, A.1., Murray, V., CC Zhang Y, Wang J, Li Q. (2009) Practical protocols for production of very high yields of recombinant proteins using *Escherichia coli*. Protein Sci., 18(5):936-48.

[8]. Buchanan, R.E., Gibbons, N.E. (1974) Berge's manual of determinative bacteriology (8th Ed.) The Williams and Wilkins Co, Baltimor, p. 1246.

[9]. Carter, G.R., Cole, J.R. (1995) Diagnostic procedures in veterinary bacteriology and mycology (5th Edn.) Academic press inc., California

[10]. Tyagi, P.K., Tyagi, S. (2013) Bacterial contamination in kitchens of rural and urban areas in Meerut district of Utter Pradesh (India). African Journal of Microbiology Research, 7 (19): 2020-2026

[11]. Aneja, K.R. (2003) Experiments in Microbiology Plant Pathology, Tissue culture and mushroom production technology, pp. 245-282.

[12]. Tyagi, S., Tyagi, P.K., Panday, C.S., Kumar, R. (2011) Bacterial contamination: A comparison between rural and urban areas of Panipat District in Haryana (India). African Journal of Bacteriology Research, 3(3): 32-41

[13]. Tyagi, P.K., Tyagi, S., Kumar, R., Panday, C.S. (2011) Bacteriological analysis of air of kitchens in rural and urban areas of Panipat district in Haryana (India). Int. J. Pharm. Biol. Sci., 2(1): B247-256

[14]. Tyagi, S.,Tyagi, P.K., Mishra, M., Khan, N. (2014) Beware! Our home is Wonderland of Pathogenic Bacteria. International Research Journal of Biological Sciences, 3 (8): 69-76.