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Prevalence of microorganisms of hygienic interest in goat carcasses in organized and unorganized abattoirs of Jammu region, India

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Abstract

Meat borne diseases are of utmost importance in humans especially in high meat consuming developing countries due to poor health of animals, poor hygienic conditions in abattoir and lack of surveillance networks. Monitoring the food borne pathogens and indicators of contamination in primary production at abattoirs is imperative for creating data bank and for effective control of such pathogens before they enter the food chain. In the present study, the micro-organisms of hygienic interest in respiratory tract were screened for prevalence at organized and un-organized abattoirs of Jammu region. Samples were collected from nasal cavity, trachea and lungs of both diseased and apparently healthy goats by use of cotton swabs and kept in transport media. A total of 230 samples were collected and analyzed for *Streptococcus* spp., *Staphylococcus* spp., *Pasteurella* spp., *Pseudomonas* spp. and *E. coli*. Apparently healthy animals and diseased animals showed prevalence of microbes as 32% and 70.66% respectively. Nasal swab, tracheal samples and lung samples respectively showed prevalence of 54.05%, 39.19% and 32.00% respectively. *Staphylococcus* spp. showed highest percentage (46.60%) while *E. coli* represented the lowest (3.88%). *Streptococcus*, *Pasteurella* and *Pseudomonas* respectively, represented 24.27%, 15.53% and 9.70%.

Keywords: Prevalence, micro-organisms, goats, abattoir

Introduction

Meat borne diseases pose great threat to public health worldwide including India. Besides having repercussions on the health, it also has economic consequences from the loss of business over food safety concerns. Developed countries have advanced mechanisms for timely identification of meat borne pathogens and the zoonotic diseases caused by them. However, in developing countries, there is paucity of related data due to lack of precise health care infrastructure and data management (Bhandare *et al.*, 2010) [4]. In developing countries, nearly 1.8 million children die due to acute microbial diseases with food or water being the major causes of many of these illnesses (World Health Organization, 2005) [18]. Emerging/ re-emerging zoonotic food borne and water borne diseases as well as diseases caused by multi-resistance organisms are the major public health threats in India (Chugh, 2008) [6]. However, the magnitude of food borne illness in India is unknown due to the lack of coordinated surveillance network.

Jammu and Kashmir needs special mention since the meat consumption in this state is high and was 2.70 kilograms per capita per year in 2011-12 (Economic survey, 2013) [8]. Meat in this part of the state is obtained from organized, unorganized and retail shops. Hardly any emphasis is being laid on hygienic meat practices and the consumers are forced to consume potentially threatening micro-organisms along with meat. Monitoring the incidence and prevalence of micro-organisms of hygienic interest in primary production at abattoirs is imperative for creating data bank and for effective control of such pathogens before they enter the food chain. Therefore, present study was undertaken at organized and unorganized abattoirs of Jammu region to determine the prevalence of micro-organisms of hygienic importance.

Material and Methods

The present study was conducted on goats, both apparently healthy and diseased, that were slaughtered routinely as a source of food in neighboring areas of the Jammu division from organized and unorganized abattoirs of Gujjar Nagar, Dogra hall, Bishnah and Nagrota. The suspected samples were collected from nasal cavity, trachea and lungs by use of cotton swabs kept in transport media. A total of 230 samples were collected. Sterile cotton swabs (3 cm long and 1 cm in diameter) held by wooden sticks and moistened by with 0.1% peptone were

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rubbed on the sites for 30 seconds and transferred to a screw capped test tube containing 10 ml of sterile maintenance medium (0.85% NaCl and 0.1% peptone). The screw capped test tubes were brought to laboratory in thermos flask containing ice and processed immediately

The procedure for isolation and identification of bacterial culture adopted for the present work was as per Holt (Holt, 1994) [10]. The samples collected from different areas were inoculated in Blood agar, Mannitol salt agar, and Nutrient agar and EMB agar and incubated at 37°C. After 24 hours of incubation, the colonies were purified and stained with Gram stain for microscopic examination as described by Beveridge (Biveridge, 2001) [3]. Respective cultures were identified on the basis of standard criteria and biochemical tests (Quinn *et al.*, 1998) [13]. Suspected growing colonies onto the surface of the above mentioned media were characterized on the basis of their colonial morphology and staining reactions. One single colony showed typical colonial appearance and morphological character was picked up, streaked into semisolid agar media, and incubated at 37°C for 24 hours for further identification (Cruickshank *et al.*, 1995) [7].

Results and Discussion

Food borne diseases of meat origin are of serious threat to public health worldwide, India being no exception (Rao Vemula *et al.*, 2012) [15]. Most important bacteria which cause food borne diseases include *Staphylococcus aureus*, *Bacillus cereus*, *Campylobacter jejuni*, *Pasteurella* spp., *Clostridium* spp., *Escherichia coli*, *Brucella* spp., *Listeria monocytogenes*, *Salmonella* spp., *Shigella* spp., *Vibrio cholera* etc. (Rao *et al.*, 1989) [16]. The present study was undertaken to study the prevalence of different meat borne bacteria in organised and unorganized abattoirs of Jammu region of Jammu and Kashmir state of North India. Results obtained revealed high prevalence of different bacteria under study. Prevalence of bacterial infection (%) from apparently healthy and diseased goats is shown in table 1. Out of 155 apparently healthy goats, 50 were positive for bacteriological infection with prevalence of 32.25% and out of 75 diseased goats, 53 were positive with prevalence of 70.66%. Table 2 depicts the total recovery rate (%) of bacterial microorganisms from apparently healthy and diseased goats. Of 230 specimens taken from nasal mucosa, trachea and lungs; 103 samples were positive with prevalence of 44.78%. In diseased goats, swabs taken from nasal mucosa showed the higher prevalence (30 isolates out of 38 swabs) with prevalence 78.94%, while the lowest prevalence rate was observed in samples taken from lungs (8 isolates out of 15 samples) with prevalence of 53.33%. In apparently healthy goats, the prevalence rate followed the same trend as that observed in diseased goats. Different bacteria isolated from goats were identified by cultural characteristics and biochemical tests (Holt, 1994; Biveridge, 2001) [10, 3]. Identified bacteria were Gram positive *Staphylococcus* spp., *E. coli*, *Streptococcus* spp., *Pseudomonas* and Gram negative *Pasteurella* spp., (Fig 1-10) and their prevalence is summarized in table 3. Staphylococci were found to be the predominant bacteria isolated with prevalence of 46.60%. Second and third position was occupied by *Streptococcus* spp. and *Pasteurella* spp. with prevalence rate of 24.27% and 15.53% respectively. The prevalence of *E. coli* was lowest at 3.88%.

The present data represents the prevalence of a diversity of micro flora in the healthy and diseased goat respiratory tract/carcasses. The data collected from government organised and unorganised local abattoirs showed bacteria (*Streptococcus* spp., *Staphylococcus* spp., *Pasteurella* spp., *Pseudomonas* spp. and *E. coli*) were involved in causing respiratory affections. The findings are in consonance with the findings of Azizi *et al.*, (2013) [2] who found prevalence of *Pasteurella* spp. to be 24.53% in sheep and goats. Slightly lower percentage of *Pasteurella* (13.8%) has been reported in goat by Raji *et al.*, (2000) [14]. Ugochukwu, (1985) [17] found the prevalence of Staphylococci to be (33.33%) which is comparable to results obtained in present study (46.60%). Azizi *et al.*, (2013) [2] and Momin *et al.*, (2011) [11] reported lower value as 20.75% and 24% respectively in slaughtered sheep. Yesuf *et al.* (2012) [19] found the prevalence of *Streptococci* spp. to be 13.79%. Similarly, in another study by Aden *et al.*, (2012) [1] prevalence of *E. coli* infection was 14.3% which is higher than the value of present study. Emikpe *et al.*, (2009) [9] found prevalence of *Pseudomonas* spp. infection to be 5.5%, which coincides with the present study. Özbey [12], 2004 too recorded lower percentage of isolation of *Pseudomonas* spp. with total percentage of its isolation as 5.85%.

In the present study the highest prevalence was of *Staphylococci* spp. while the least prevalent bacteria was *E. coli*. This finding is due to the staphylococci being the normal commensals of the respiratory tract while *E. coli* being the abnormal residents of the respiratory tract. To evaluate the effectiveness of food safety programmes, base line studies are needed to determine the levels of indicator organisms and prevalence of pathogens (Bohaychuk *et al.*, 2009) [5]. The data depicts high prevalence and variety of micro flora on carcasses in the primary Indian production facility which might be due to lack of application of proper ante mortem and post mortem procedures in slaughter houses.

Conclusion

This study shows the prevalence of pathogens of zoonotic significance in edible meat and the need for adoption of good hygienic practices to prevent the entry of pathogens into the food chain. Application of effective food safety interventions is the need of the hour to reduce or restrict foodborne pathogens throughout the food continuum, from the farm to the table. However, current production and processing procedures applied in different abattoirs throughout the country do not have any sufficient robust food safety interventions to ensure pathogen free meat supply. Therefore, there should be emphasis on clean meat production which is prerequisite for the prevention of food borne diseases in the population.

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Table 1: Prevalence of bacterial infection (%) from apparently healthy and diseased animals (n= 230).

Animal	Apparently healthy animals			Diseased animals		
	No. of examined animals	No. of positive animals	%	No. of examined animals	No. of positive animals	%
Goats	155	50	32.25	75	53	70.66

Table 2: Total recovery rate (%) of bacterial microorganisms from apparently healthy and diseased goats (n=230)

Sites	Apparently healthy animals			Diseased animals			Total		
	No. of examined samples	No. of positive samples	% positive	No. of examined samples	No. of positive samples	% positive	No. of examined samples	No. of positive samples	% positive
Nasal swab	73	30	41.09	38	30	78.94	111	60	54.05
Tracheal samples	47	12	25.53	22	15	68.18	69	27	39.19
Lung samples	35	8	22.85	15	8	53.33	50	16	32.00
Total	155	50	32.25	75	53	70.66	230	103	44.78

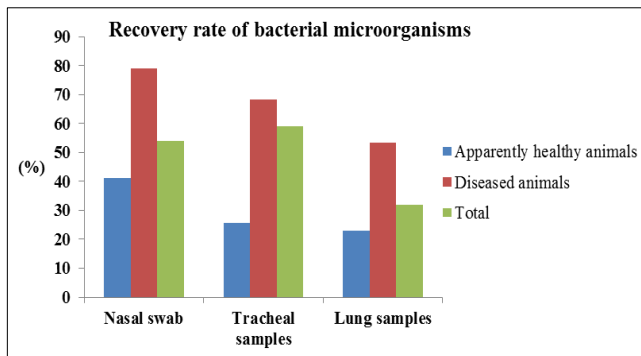


Fig 1: Total recovery rate of bacterial microorganisms from apparently healthy and diseased goats

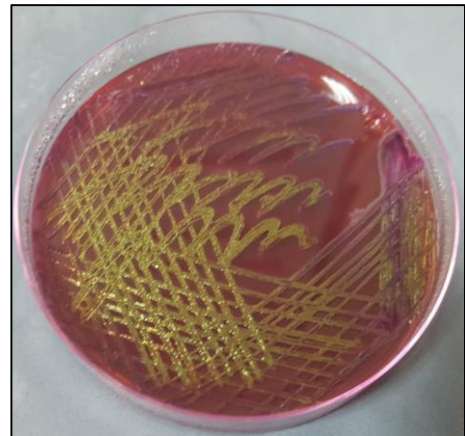


Fig 4: *E. coli*

Table 3: Identification of bacteria (%) from goats (n=230).

Identified bacteria	No. of positive samples	% positive
<i>Streptococcus</i> spp.	25	24.27
<i>Staphylococcus</i> spp.	48	46.60
<i>Pasteurella</i> spp.	16	15.53
<i>Pseudomonas</i> spp.	10	9.70
<i>E. coli</i>	04	3.88
Total	103	

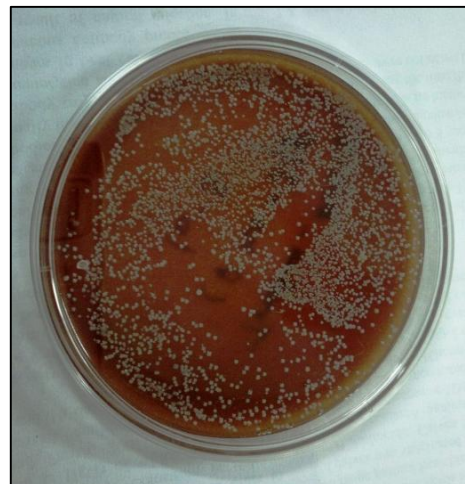


Fig 5: *Pasteurella* spp

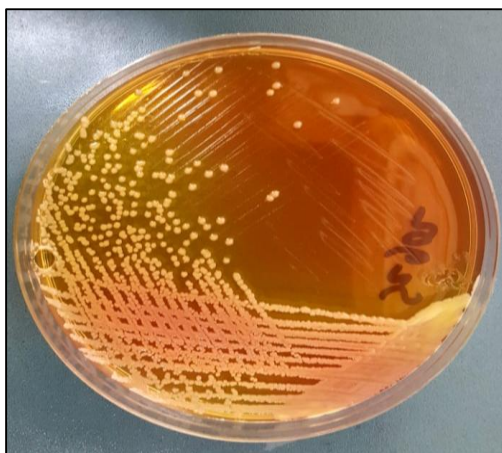


Fig 2: *Staphylococcus* spp



Fig 6: *Streptococcus* spp.

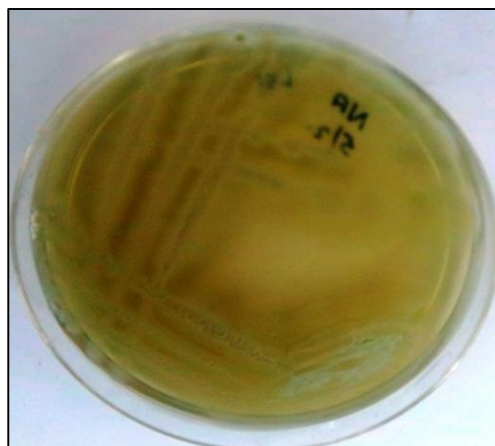


Fig 3: *Pseudomonas* spp

Figs: (1) *Staphylococcus* spp. grown on Mannitol Salt agar showing yellow colonies (2) *Pseudomonas* spp. grown on nutrient agar showing bluish-green colonies (3) *E.coli* spp. grown on EMB agar showing characteristic metallic sheen (4) *Pasteurella* spp. grown on sheep blood agar showing translucent colonies (5) *Streptococcus* spp. grown on sheep blood agar showing clear zone of beta haemolysis.

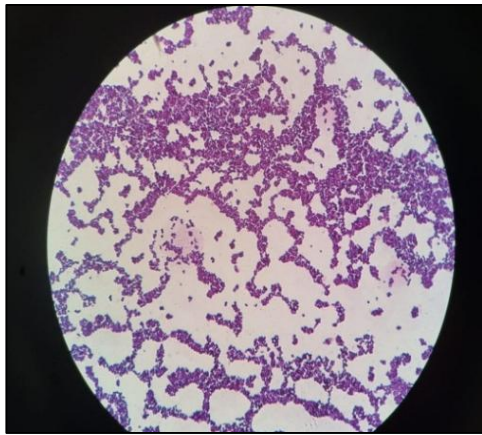


Fig 7: *Staphylococcus* spp

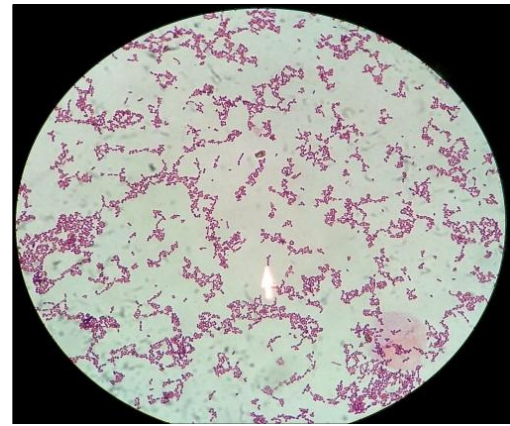


Fig 11: *Streptococcus* spp

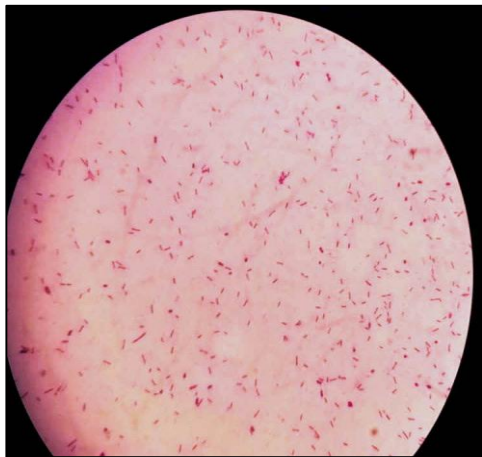


Fig 8: *Pseudomonas* spp

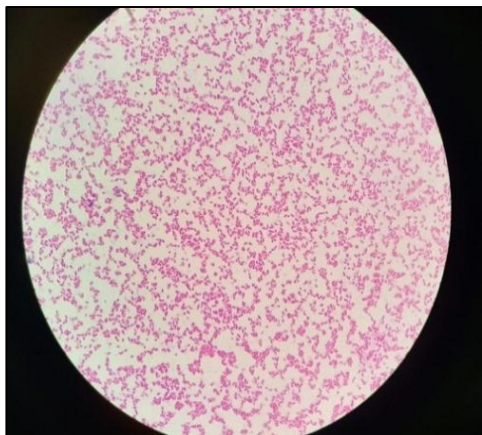


Fig 9: *E. coli*

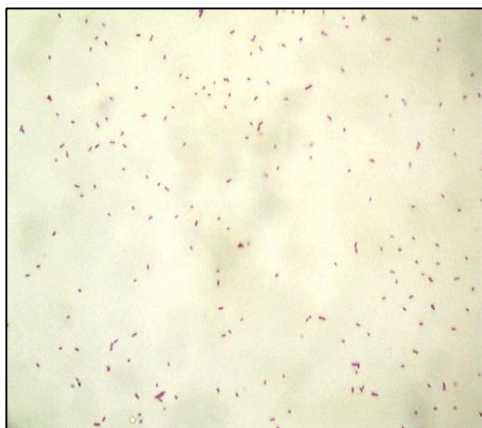


Fig 10: *Pasteurella* spp

Figs: (6) Bunch of grapes like colony characteristic of *Staphylococcus* bacteria (7) Gram -ve rods (*Pseudomonas* spp.) as seen under microscope (8) Gram -ve rods (*E. coli*) as seen under microscope (9) *Pasteurella* spp. showing characteristic bipolar staining (10) Long chain like colony of *Streptococcus* bacteria as seen under microscope.

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