

EARLY STAGE IDENTIFICATION OF RUMEN MICROORGANISMS FROM SELECTED NIGERIAN BREEDS OF CATTLE O. I. Adeyosoye¹, A. K. Akintokun², Olanike Abiola-Olagunju³, K. D. Afolabi⁴

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SUMMARY

The necessity of microbiological assessment of members of rumen community is based on the kinetics of fermentative activities

Total heterophilic bacteria (THB) ranged between 9.1x10° cfu/g 125x10° cfu/g for female and male Dieli (Df and Dm) respectively.

Total heterophilic fungi (THF) recorded the highest count (6.0x10th spores/g) for female Bunaji (Bf) and no growth was observed for female Bokolo (Bkf). The pH ranged between 5.65-6.90 for female Futumi (Ff) and male Bunaji (Bm) respectively. Significant difference (p<0.05) was observed for pH and total microbial counts based on sex.

Bacterial species of the genera; Klebsiela, Proteus, Pseudomonas and Shigella were isolated and identified with Klebsiela occurring highest (24.24%). Fungal species identified include; Aspergillus, Botrytis, Cladosporium, Paecilomyces, Penicillium, Pullularia, Rhizoctonia and Trichophyton with A. glaucus and P. pullans both occurring highest (17%).

Breed as a factor influenced the total counts, type and occurrence of rumen bacteria and fungi.

INTRODUCTION

Domestic Cattle: Cattle are ungulates (Grubb, 2005) with a complex stomach system (Kudo et al., 1995). They are raised for meat production except in major parts of India and Nepal (http://www.guora.com), milk production and as draft nanufacturing industries such as; ceramics, feed mills, leather while carcasses and dung could be stabilized into organic manure and biogas production. (Rasi

Nigerian Breeds of Cattle: About twelve breeds have been reportedly found in Nigeria but extensive studies on origin, adaptation and management have been conducted on Kuri, N'dama, Muturu, Gudali and Red bororo/Fulani (DAGRIS, 2007).

Remen: The rumen is the first and the largest compartment where continuous naerobic fermentation takes place by a complex consortium of microorganisms (Kudo et al., 1995) thus, characterized as the World's largest cess (Weimer, 1992).

Objectives: This study was aimed at enumerating, identifying and de the percentage occurrence of the total heterophilic bacteria and fund hthonous to the rumen of cattle with respect to different breeds rais

MATERIALS AND METHODS

Fulani), Keteku (Futumi), Bokolo (N'dama) and Djeli (Sokoto Gudali) accorto the description of DAGRIS, (2007) were selected.

Sampling: Content was sampled immediately after opening the rumen of ea

Sterilization of Materials: The methods of Jacquelyn, (1993) were adopted. (1985) and Buchman and Gibbons (2000) were carefully adopted. Malt Extrac (ME) agar replaced NA for total heterophinic fungi (Bo the plates were incubated uninvertedly (Okore, 2004).

Isolation and identification of rumen bacteria and fungi: Colonia characteristics, cell morphology, spore formation and biochemical reacti led to the identification of resident bacteria and fungi (Cheesbrough, 2006). Statistical Analysis: Analysis of variance with means separated by the method



RESULTS AND DISCUSSION

for male Bunaji (Bm) (Table 1). Significant difference (p<0.05) in pH existed between male (6.71) and female (6.10) cattle.

optimal pH range of 6.0-6.9 at an optimum temperature of 39°C. The bacteria can tolerate a considerably higher level of organic acids without affecting

feed ingredients they were fed with, as feed rich in soluble sugars are capable of lowering the rumen pH when they are finally broken down (Yen and Brune, 2007; Orpin, 1977b).

THB: Dm and Df recorded both the highest (1.125x10") and the lowest (9.1x10") between them (Table 1). Significant difference (p<0.05), however, existed between male (5.8125x10") and female (2.4728x10"). The bacterial load obtained in this work agrees with the result obtained by Kamra, (2005) in which the efficiency of ruminants to utilize a wide variety of feeds (Stanton and Canale 1980) was based on a highly diversified rumen microbial ecosystem consisting of bacteria (1010-1011 cells/ml). All the microorganisms isolated from this study (1993). However, variations in microbial load have been extensively dealt with

| Breed of Animal | THIS | THE | piti Value |
|-----------------|------------------|----------------|-------------|
| žm. | 5.1610 1 12.069 | 1.563 (45.062 | 6.90 * 10.1 |
| Bf | 2.25610 1 ±5.068 | 6.0E5*±1.0E5 | 5.90*10.1 |
| fin | 3.4010 * ±1.509 | 9.564195.003 | 6.60110.1 |
| er. | 5.3510 7 ±1.059 | 3.005*12.505 | 5.65 t.05 |
| Bides | 3.6610 * 11.569 | 1.563125.062 | 6.60° ±0.1 |
| east. | 2.3E10 11.5E9 | NU.S | 6.10 * 10.1 |
| Des | 1.1011 * 61.509 | 1.563 * 15.062 | 6.75 10.05 |
| 90 | 9.168*±1.067 | 5.5631±5.062 | 6.75 10.25 |

Walues are means ± Sandard deviation of duplicate readings. Value on the same column with different appears; these are simplicantly differ (p=0.05). THE: Total Heterophilic Bacteria, THF: Total Heterophilic Pill: Yell Hydrogen in concentration, Br.m male Bungi, Bf. female Bungi, F. Bandle Putumi, Br.m male Bokolo, Br. film and Putumi, Br. film

agreement with fungal counts obtained by Kamra, (2005), standard error based on sex revealed a significant difference (p<0.05) male (2.4875x101) and female (2.26376x10°), implying that cows generally, are more loaded

Obligate anaerobic fungi found in the rumen are active in fibre degradation the lignocellulosic feeds over the cellulose-degrading bacteria due to the presence of different enzymes like proteases and esterases in combination with cellulases and hemicellulases (Founty and Joblin,

Population variation between bacteria and fungi could be due to the include; variation in pH resulting from C/N ratio (Yen and Brune, 2007). nutrient availability (Eze and Agbo, 2010), the toxic effect of phytochemicals in feeds (Akin and Rigsby, 1987) and the parasitic effect of Cladosporium herbarium on other fungi (Prior, 1966).

Fungi found in rumen are involved in the hydrolysis and acidogenesis by means of extra-cellular digestion of the substrates, depending on the nature of substrate (Atlas. 1984).

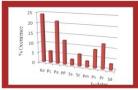
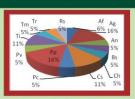


Fig. 1: % Occurrence of Bacterial Isolates in theRumens of selected Bree-Ke: Klebsiella edwardsii, Pc: Pseudomonas cepacia, Pa: Pseudo aeruginosa, Pp: Pseudomonas pseudomallei, Sa: Shigella sonn Shigella ceylonensis, Pm: Proteus morganella, Pa: Pseudomonas. Pr: Proteus retigeri, St. Shigella dysentariae.



Ruminal obligate anaerobic fungi make up only 5-10% of microbes but are

The partial digestion of microbial carcasses releases high quality protein to cattle and allows them to thrive on fibrous materials. The efficiency of utilization products (fissue accretion) is as low as 5% (Ferrell, 1993). Isolates: Species of Proteus, Klebsiella and Citrobacter are peculiar to cow dung (Vinneras et al., secies of all the identified breeds of cattle studied(Fig. 1). P. aeruginosa wa found in all the breeds studied except Dm(Fig. 2), the presence of P. aeruginosa is as a result of its ability to form acid from simple sugars (Ugoji and Bolarinwa, (Meirelles et al., 1996). P. morganella has been reported to have a comm relationship within the intestinal tracts of mammals and reptiles as normal flora

P. stutzeri, denitrifying bacterium resident in soil (Lalucat et al., 2006) which may be useful in bioremediation (Sepulveda-Torres et al., 1999)

Call et al. 2012). P. pullulans is a ubiquitous black yeast-like fungus and well known as naturally occurring epiphyte or endophyte of a wide range of plant species. It produces useful enzymes such as siderophores and pullans and has

RECOMMENDATION

Microorganisms as normal micro-flora of rumen play a vital role in sustaining

Breed as a factor, influenced the load, percentage occurrence and type of

The use of fistulated animals should be considered for further studies at different stages without sacrificing the animals.

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