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Microbial Loads and Profiles of Poultry, Cattle and Pig Dung Produced In Owerri, Southeast Nigeria

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Abstract
Screening of raw poultry dropping (PD), cattle dung (CD) and pig manure (PM) collected from livestock farms at Owerri for their microbial loads were carried out using the pour plate method by selective enrichment technique. All samples were cultured on solid media with appropriate media and the isolates were identified based on their colonial and morphological characteristics. *Staphylococcus aureus, Staphylococcus albus*and *Pseudomonas spp* were isolated from all the raw animal dung, while *E. coli* was isolated frompoultry dropping and pig manure and *Salmonella typhi*and*faecalis*from pig manure only. Three fungi genera *Rhizopus oryzae, Aspergillus niger* and *Monascus* were isolated and identified. *Rhizopus oryzae* was common in all the samples, while *Aspergillus niger* was found to be common in cattle dung and pig manure. The colony forming unit (CFU) per ml for total heterogenous bacteria ranged from $3.25x10^5$ -$4.0x10^9$ in cattle dung, $1.27x10^5$- $2.0x10^9$ in poultry dropping and $2.38x10^5$-$7.4x10^9$in pig manure. The total coliform count ranged $2.25x10^2$-$1.7x10^9$, $6.4x10^5$- $2.4x10^9$ and $2.25x10^5$-$1.5x10^9$for cattle, poultry and pig manures respectively. Fungi colony count also ranges from 7.3x102-$0.5x10^9$, $1.50x10^2$-$0.3x10^8$and$7.3x10^2$ - $2.1x10^7$for cattle, poultry and pig respectively. There is the need to subject animal dung to further treatment before disposal since some of the microorganisms isolated are of public health and economic importance.

Keywords: Poultry dropping, pig manure, cattle dung, pathogenic organisms

Introduction

Animal production has continued to play vital roles in sustaining global agricultural systems, producing products such as meat, milk, egg needed in mitigating protein global malnutrition challenges (Wu *et al.,* 2014). However, according to Sillars (2000) while animals may be seen mainly as sources of these food products, in practice they produce more dung than anything else. Animal dung is a major source of soil nutrients, especially nitrogen, phosphorus, other minerals and organic matter needed by plants for optimal growth and yield (Abulude *at al.,* 2003). Animal dung has also been used to improve the physical and biological properties of soils, and forms a good substrate for bioremediation of toxic pollutants in farming environments (Udebuani *et al.,* 2012). Utilization of animal dung as bioenergy resource, gasification, liquefaction and direct combustion is also widely practiced (Wu *et al.,* 2010).

Recent increases in animal production have essentially led to increased animal dung generation, with consequent disposal challenges that now constituting major environmental hazards in livestock production environments (Alwaneen, 2016). Although endogenous microorganisms in animal dung contributes to the transformation of the wastes components intobeneficial products, some of the microbes are pathogens of public health and economic importance.

This study determined the microbial loads and profiles of poultry, cattle and pig dung produced at Owerri and environ in Southeast Nigeria.

Materials and Methods

Fresh poultry dung (PD), cow dung (CD) and pig manure (PM) used in the study were collected from the Teaching and Research Farm of School of Federal University of Technology, Owerri (FUTO),southeast Nigeria. The samples were collects from freshly voided dung with the aid of properly labelled sterile spatulas, while ensuring that the spatula did not touch any nearby material. Three samples of each dung type were collected and sent for microbial analysis according to standard methods.

Ten (10) grams of dung was added to 90 ml of physiological saline to obtain a 10^{-1} dilution. Serial dilutions were made thereafter made and inoculated unto differently labeled freshly prepared surface dried nutrient agar in other to determine the microbial loads of the dung. Total heterotrophic isolate count, isolation bacterial organisms on appropriate media and fungal organisms on potato dextrose agar (PDA) and their

iidentifications were carried out according to standard microbiological methods described by Cheesebrough (2000).

Data generated were subjected to simple descriptive statistics such as total and mean bacterial counts and presented in table formats.

Results and Discussion

The microbial count of the raw dropping PD, CD and PM used in this study are presented in tables 1 to 3. The microbial count per gram of samples varied with the different animal dung. Bacterial counts were observed to higher in raw cattle dung, followed by poultry dropping. The coliform counts were also higher in cattle dung than in any other dung. On the other hand, the fungal populations were higher in poultry dropping than any other animal dung. Expectedly the dung were high in their microbial loads confirming their value in transformation of the wastes components dung into beneficial products (Udebuani *et al.,* 2012).

Bacterial and fungal species isolated from the three-different animal dung were shown in table 4. *Staphylococcus aureus, Staphylococcus albus, Pseudomonas sp* were common to all the animal dung samples, while *E. coli* was found in poultry dropping and pig manure. *Salmonella typhi* and *Streptococcus faecalis* were found only in pig manure. The fungal species common in all the samples were *Rhizopus oryzae*, while *Aspergillus niger* was found to be common in two samples which include cattle dung and pig manure. Some of the microbes such as *S. aureus, S. typhi* and *S. faecalis* are pathogens of public health and economic importance and have been in animal dung by other workers (Ijah and Antai, 1988).

Table 1: Microbial load of pig manure used in the remediation process

Raw pig manure (PM)	Dilutions	Media	Total count	Mean count	Microbial cell/g
Bacterial Population					
	10^2	NA	238	119	2.38×10^5
	10^5	NA	206	103	1.03×10^7
	10^7	NA	148	74	7.4×10^9
Coliform Population					
	10^2	MAC	164	8.2	2.25×10^5
	10^5	MAC	48	24	2.4×10^7
	10^7	MAC	30	15	1.5×10^9
Fungal Population					
	10^0	SDA	180	90	7.3×10^2
	10^5	SDA	60	30	4.9×10^7
	10^7	SDA	42	21	2.1×10^9

Table 2: Microbial load in poultry dropping used in this remediation process

Poultry droppings	Dilutions	Media	Total count	Mean count	Microbial cell/g
Bacterial Population					
	10^2	NA	254	127	1.27×10^5
	10^5	NA	146	78	7.8×10^7
	10^7	NA	40	20	2.0×10^9
Coliform Population					
	10^2	MAC	128	64	6.4×10^5
	10^5	MAC	90	45	4.5×10^7
	10^7	MAC	48	24	2.4×10^9
Fungal Population					
	10^0	SDA	300	150	1.50×10^2
	10^2	SDA	98	49	4.9×10^4
	10^7	SDA	6	3	0.3×10^8

Conclusion

The animal dung was generally rich in endogenous microorganisms. However, there is the need to subject the dung to further treatment before disposal or use furthers use, since some of the microorganisms isolated are of public health and economic importance.

Table 3: Microbial load in cattle dung

Raw Cattle dung	Dilutions	Media	Total count	Mean count	Microbial cell/g
Bacterial Population					
	10^2	NA	650	325	3.25×10^5
	10^5	NA	258	129	1.29×10^7
	10^7	NA	80	40	4.0×10^9
Coliform Population					
	10^0	MAC	450	225	2.25×10^2
	10^5	MAC	240	120	1.20×10^7
	10^7	MAC	34	17	1.7×10^9
Fungal Population					
	10^0	SDA	146	73	7.3×10^2
	10^2	SDA	98	49	4.9×10^4
	10^7	SDA	10	5	0.5×10^9

Table 4: Bacterial and fungal species isolated and identified from three animal dung

Isolates	Poultry dung	Cattle dung	Pig dung
Bacteria	*Proteus sp, Staphylococcus aureus, Staphylococcus albus Pseudomonas sp, Streptococcus faecalis, E coli. Pseudomonas maltophila,Proteus sp*	*Serratis marcens, Pseudomonas sp. Enterobacter sp, Staphylococcus aureus, Klebsiella sp, Staphylococcus albus*	*Pseudomonas sp, Salmonella typhi, Shegella sp, E coli, Streptococcus faecalis, Bacillus cereus, Micrococcus roseus*
Fungi	*Rhizopus oryzae, Monascus rubber*	*Rhizopus oryzae, Aspergillus niger*	*Rhizopus oryzae, Aspergillus niger*

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