

## Microbiological Properties of Anaerobic Digestive System

P. RAJASEKARAN<sup>1</sup>

The study revealed that bacterial and other populations differed significantly among the samples examined. Methanogenic bacteria was found to occur in maximum numbers in samples collected from courtallam and least in Madurai. The methanogens are directly connected with the liberation of biogas. Total bacteria, fungi, actinomycetes and coliforms were found to decrease with increase in depth.

The usefulness of microorganisms in bringing about biodigestion of organic wastes under anaerobic conditions has been well established (Burbank *et al.* 1956., Toerien, 1967 and Bryant, 1976). Such a system seems to promote the biogeneration of methane, the much needed durning gas, which at present is attracting the attention of many scientists in different countries. (Burbank *et al.* 1956; Hobson *et al.* 1974 and Jewell *et al.* 1976). Apart from providing biogas, the utilisation of wastes not only helps to maintain a cleaner environment but also: at the end, results in good organic manure, rich in N,P,K content for application in the fields. This paper is an attempt to gain knowledge on the distribution pattern of microbial flora in the bioconversion of wastes through anaerobic digestive systems.

### MATERIAL AND METHODS

**Sampling :** The composite slurry samples from the anaerobic fermentative digestors located in 4 different places (Courtallam, Coimbatore, Madurai and

Gandhigram) were collected in 250 ml capacity, sterile, wide-mouthed ground-in stoppered glass containers for carrying out the microbiological examination. Care was exercised to avoid external contamination during sampling and transport. In order to compare the relative distribution of microorganisms, the slurry specimens from the anaerobic biogas digester designed by the Tamil Nadu Agricultural University at different depths viz. 40, 60 and 90 cm were collected and screened.

**Microbiological examination :** The different types of microorganisms in the various slurry specimens were estimated using various media favouring the growth of bacteria, fungi, actinomycetes, cellulolytic organisms, and methanogenic bacteria following the serial dilution plate technique (Timonin, 1940; Rajasekaran and Lakshmanan 1978). The bacterial, fungal and actinomycetes colonies were enumerated on the 3rd, 7th and 10th day respectively; the coliforms and fecal streptococci on the 2nd day after incubation at 37° and 44° C respectively by employing the MPN

1. Department of Microbiology, TNAU, Coimbatore-641 003.

multi-tube dilution technique, as described in Standard Methods (Anon, 1976). The methanogens were enumerated by counting colonies from plates that favoured the growth of organisms after incubation in a vacuum oven at 37°C, flushed with a gas mixture of 8% H<sub>2</sub> and 20% Co<sub>2</sub> (Zeikus, 1977). The populations

were computed and expressed per gram of oven-dry samples.

## RESULTS AND DISCUSSION

The microbial population enumerated from the slurry samples collected from various biogas generating digestors are presented in Table I. The relative

TABLE I. Maximum microbial population enumerated in slurry samples from various biogas plants (Population expressed per g on oven dry basis)

Organisms	Dilution	Location			
		Courtallam	TNAU Coimbatore	MADURAI	Gandhigram
Total bacteria	10 <sup>6</sup>	424.3	329.5	483.3	90.3
Fungi	10 <sup>1</sup>	6.6	3.2	21.7	4.0
Actinomycetes	10 <sup>4</sup>	38.6	1.7	1.3	9.3
Cellulolytic organisms	10 <sup>1</sup>	47.3	12.5	16.2	31.2
Coliforms	10 <sup>4</sup>	11.6	10.1	17.8	7.8
Faecal streptococci	10 <sup>2</sup>	9.3	11.8	8.5	4.5
Methanogenic bacteria	10 <sup>8</sup>	147.5	110.9	73.5	116.5

The figures represent the mean of two samples

distribution of organisms at different depths in the slurry samples from the mobile biogas plant designed at the Tamil Nadu Agricultural University is in Table II.

The total bacterial population was found to be more in the slurry specimen obtained from Madurai (369.70 x 10<sup>6</sup>/g) whereas the same in Gandhigram recorded the least (101.30 x 10<sup>6</sup>/g). The bacterial and other populations differed significantly from among the samples examined. Several factors such as temperature, pH and the type of raw material employed in biodigestion play a role in causing the differential distribution of various organisms enumerated (Sathianathan, 1975 and Mohan Rao, 1974).

TABLE II. Distribution of microorganisms at different depths in biogas plant (TNAU-Design) (Expressed in 10<sup>4</sup>/g of oven dry sample)

Organisms	Depths from where samples were collected		
	40 cm	60cm	90cm
Total bacteria	6750.0	5700.0	3950.0
Fungi	10.5	3.5	2.5
Actinomycetes	9.5	5.0	2.5
Cellulolytic organisms	16.5	6.0	4.5
Coliforms	9.8	6.2	3.4
Faecal streptococci	0.03	0.03	0.01
Methanogenic bacteria	5.23	6.23	7.64

However, methanogenic bacteria was found to occur in maximum numbers

( $125.1 \times 10^3/g$ ) in samples collected from Courtallam and least in Madurai ( $85.50 \times 10^3/g$ ). The methanogens are directly connected with the liberation of biogas. Increasing the gas production might be possible by selective incorporation of efficient strains of methanogenic bacteria. Studies on the qualitative characterization of methanogens and establishing a correlation between the gas produced and the type of methanogenic bacteria may be necessary.

The relative distribution of microorganisms at different depths from the mobile biogas digester gave interesting results. Total bacteria, fungi, actinomycetes, coliforms etc., found to decrease with increase in depth. Similar observations were recorded in soil. There is a declining trend in the different groups of organisms with the increase in depth. (Rose, 1954; and Oblisami, 1965) Same trend, might have been possible in an anaerobic digestive system. The methanogens increased from  $5.23 \times 10^4/g$  at 40 cm depth to  $7.64 \times 10^4/g$  at 90cm depth. This is probably due to more anaerobiosis maintained at the lower strata of the anaerobic digester. However elaborate studies are needed in this direction.

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