OPEN ACCESS INTERNATIONAL JOURNAL OF SCIENCE & ENGINEERING

ENRICHMENT OF THE MICROBIAL POPULATION IN THE VERMICOMPOST PRODUCED FROM WATER HYACINTH

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Abstract: ***Water hyacinth, an aquatic weed plant has occupied the Sambhaji tank, Solapur, Maharashtra, India. This weed is removed from the tank periodically and dumped on the open ground and not disposed properly. Therefore, the present investigation was carried out to recycle this aquatic weed into useful by-product by vermicomposting technique with the help of earthworm, Eudrilus euginae. The final product, i.e. vermicompost was subjected for the microbial population analysis. The results obtained from the analysis revealed the maximum enrichment of the microbial communities in the vermicompost. The colony morphology study revealed the presence of diverse species of bacteria and fungi in the vermicompost whereas, the microscopic study showed the presence of both Gram positive and Gram negative bacteria in the vermicompost. Hence, it is concluded that the water hyacinth weed waste can be converted into enriched by-product by vermicomposting.***

Keywords: *Water hyacinth, Eudrilus euginae, vermicompost, microbial population, colony morphology.*

I INTRODUCTION

Water hyacinth is a perennial hydrophyte. It is considered as a 'Blue devil' because it grows very fast and forms a dense mat over the stagnated aquatic bodies (Sakthika and Vimala, 2018) [20]. Sambhaji tank or Kambar Lake, located in the Solapur, Maharashtra, India is a natural fresh water body and recreational point. Water hyacinth plant has occupied this lake and causes interference in various activities. Therefore, these plants are removed from the water and dumped on the open ground which causes the accumulation of weed waste. For healthy environment, the proper management of this weed waste is highly important (Ankaram, 2013) [2].

Recycling of water hyacinth waste by vermitechnology minimises the problem of its disposal and also converts this weed waste into usable form. Vermicomposting is a biological process where earthworm and microorganisms interact, work together and convert the organic waste into rich vermicompost (Sakhivel*et al*., 2017) [21].Earthworm are considered as a bioengineers. They produce castings which is rich in nutrients and microbial population. Microorganisms of vermicompost help to enhance the plant growth by releasing plant growth promoting factors in the soil (Edwards and Fletcher, 1998) [3].

Various workers have assessed the microbial communities from vermicompost. Rastegari*et al*., (2017) [19] studied the microbial composition of vermicmpost produced from mixed sesame crust and cow manure. Pingale (2015) [16] given a detail account on the bacteria present in the vermicompost and the role played by them in conversion of waste into vermicompost. Indumathi (2017) [6] studied microbial conversion of vegetable waste into bio-fertilizer. The author also observed the impact of this bio-fertilizer on growth parameters of green gram plant.

Zhang *et al*., (2020) [24] while studying the vermicomposting of dewatered sludge observed the effect of different temperatures on vermicompost quality and microbial diversity of vermicompost. Pathma and Natarajan (2012) [13] have studied the microbial diversity of bacteria

from vermicompost and their potential role in waste management as well as use in agriculture.

In the present study an attempt has been made to recycle the water hyacinth weed waste into vermicompost and understand its microbial population.

II MATERIALS AND METHODS:

A. Preparation of Vermicompost:

Water hyacinth plants were collected from Sambhaji tank, Solapur, sundried and grinded into fine powder by mechanical pulveriser. This dried powder (ORM- organic raw material) was used as substrate for the production of vermicompost. The earthworms *Eudrilus euginae*were used for thevermicomposting and the mixtures were decomposed by pot and heap method. The treatments made for the vermicompost production are as follows

T1-ORM - Dried powder of water hyacinth,**T2**- Decomposed ORM,

T3- Vermicompost-(50% ORM+ 50% cow dung + *Eudrilus euginae*)produced by pot method and
T4- Vermicompost- (50% ORM + 50% cow dung + *Eudrilus euginae*)produced by heap method.

During vermicomposting process, optimum temperature and moisture (70% - 80%) was maintained by sprinkling water as per the requirement.Initially the mixtureswere partially decomposed for fourty five days and later the mixtures (T3 and T4) were introduced with earthworms, *Eudrilus euginae* and allowed for further decomposition for ninety days and final vermicompost was harvested.

Microbial analysis:

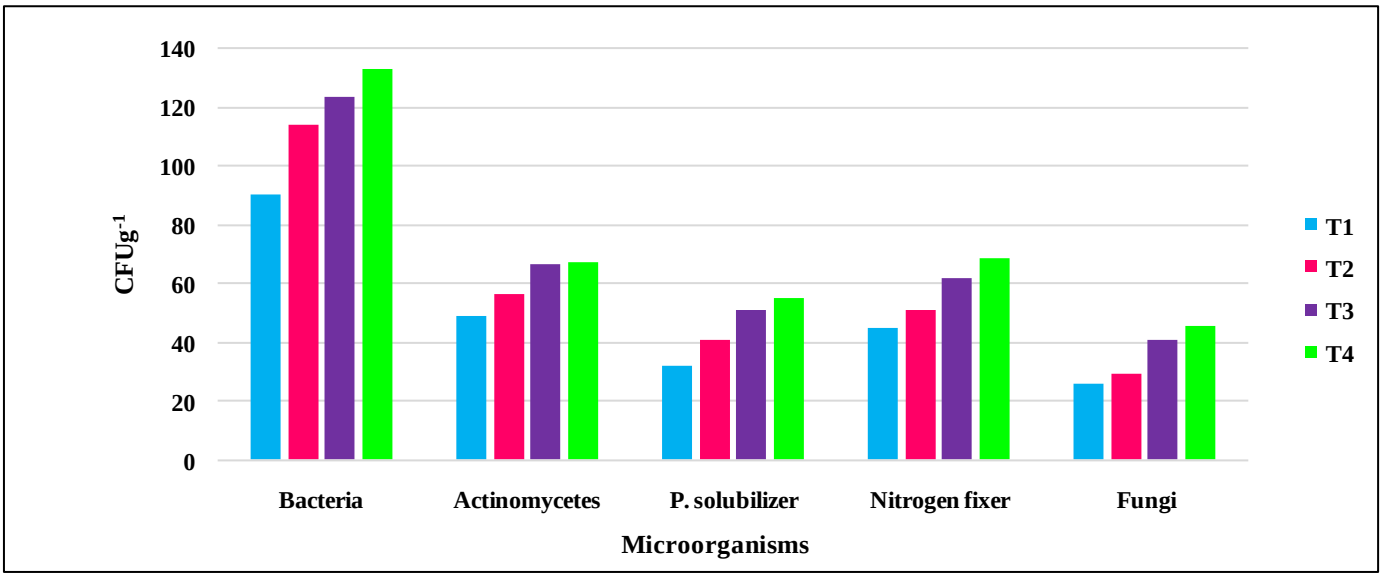
After production of vermicompost, all the above samples were subjected for microbial analysis. Microbial analysis of sample was done by 'Spread plate method' (Aneja, 2008) [1]. A stock solution was prepared by adding one gram of sample into 10 ml of sterile distilled water in test tube and shaken well. From this stock solution, 10^{-3} dilution was made. Different microorganisms were grown on different growth media as mentioned in the table 1. Digital colony counter was used for counting the microbial colonies and given in terms of Colony Forming Units ($CFUgm^{-1}$/ml).

Identification of microorganisms was done by observing the colony morphology. For convenience, the two distinct colonies from a single growth media were given name sequentially and by first alphabet and serial number like A1, A2, B1, B2 and so on. Microorganisms were also observed under the microscope. Gram staining was carried out for understanding the gram nature of bacteria whereas the fungi were identified by staining with Lacto phenol cotton blue stain.

Table 1: Microorganism grown on different growth media and their incubation temperature and incubation time.

Sr. No.	Name of the microorganisms.	Medium used for microbial growth.	Incubation temperature in ^{0}C	Incubation time (hours).
1	Bacteria	Nutrient agar	37	24
2	Actinomycetes species	Bennet's agar	30	48
3	Phosphate solubilizer	Pikovskyas agar	30	48
4	*Rhizobium* species	Congo red yeast extract calcium carbonate agar	37	48
5	Fungi	Sabouroud's agar	30	72

III RESULTS:



Graph 1: Microbial population of ORM (T1), D. ORM (T2), Pot vermicompost (T3) and Heap vermicompost (T4) at 10^{-3} dilution.

Table 2: Colony characteristics of some microorganisms from vermicompost.

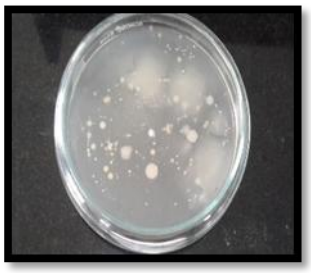
Growth media	Colony name	Size in (mm)	Shape	Colour	Margin	Opacity	Elevation	Consistency
Nutrient Agar	A1	2	Circular	White	entire	opaque	Flat	smooth
	A2	1	Circular	Yellow	entire	opaque	Flat	smooth
Bennet agar	B1	2	Circular	White	entire	translucent	Flat	smooth
	B2	3	Circular	White	entire	opaque	elevated	rough
Pikovskyas Agar	C1	1.5	Circular	White	entire	opaque	Flat	smooth
	C2	2	Circular	Cream	entire	opaque	Flat	smooth
Congo red Agar	D1	2	Circular	Pink	entire	opaque	Flat	smooth
	D2	1	Circular	Red	entire	opaque	Flat	smooth
Sabouroud's Agar	E1	4	Irregular	White	entire	opaque	elevated	rough
	E2	7	Circular	Black	entire	opaque	elevated	smooth

The microbial population count from ORM (T1), decomposed ORM (T2), pot vermicompost (T3) and heap vermicompost (T4) at 10-3 dilution showed maximum enhancement of the microorgamisms in the vermicompost (T3 and T4) when compared with ORM (T1). The number of bacteria showed incresing trend in T2 by 26.66%, in T3 by 46.97% and in T4 by 47.7%.

Similarly the actinomycetes also increased up to 15.30% in T2, 36.04% in T3 and 37.40% in T4. The Phosphate solubinizing bacteria found to be increased in T2, T3 and T4 by 27.09%, 61.83% and 68.33% respectively whereas the nitrogen fixers showed increasing trend up to 11.45% in T2, 36.91% in T3 and 51.30% in T4. Likewise, fungal population also increased maximum in T2 by 14.02%, T3 by 58.06% and 60.56% in T4 i.e. heap method vermicompost.

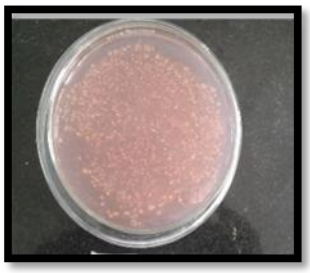
From our results, the maximum enrichmnt of microbial population was detected in both pot and heap method harvested vermicompost samples.The colony morphology showed the different types of bacteria and fungi in the vermicompost. The microrganisms were observed under the microscope and showed both Gram positive and Gram negative rods and cocci form bacteria in the vermicmpost.

Figure 1: Microorganism from water hyacinth vermicompost at 10-3 dilution.

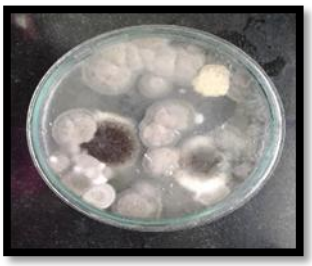


A. Microbes grown on Nutrient agar.

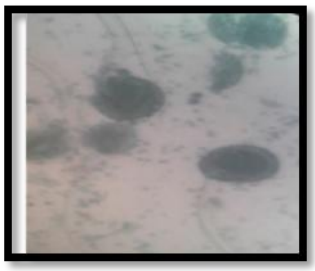
B. Microbes grown on Bennet agar.



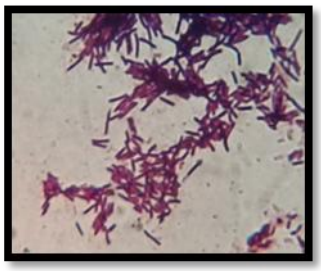
C. Microbes grown on Congo red agar.



D. Fungi grown on Sabouroud's agar.

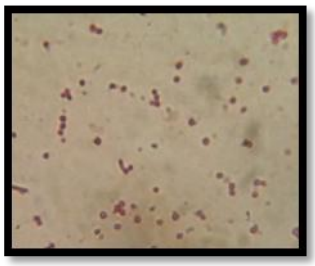


E. Stained fungi from vermicompost.



F. Gram positive rods from vermicompost.

G. Gram negative rods from vermicompost.



H. Gram negative cocci from vermicompost.

IV DISCUSSION:

Earthworm and microbes are active components of biodegradation process. Therefore, the quality of compost or vermicompost largely depends upon its microbial communities (Palm *et al*., 2004) [10]. Microorganisms maintain the stability of soil and increase its fertility which is cruicial for the plant growth (Pereira *et al*., (2014) [14].

In the present study, the water hyacinth weed waste was recycled into vermicompost by using earthworm, *Eudrilus euginae*. In our results, enrichment of the microbial community in vermicompost was observed mainly because of the earthworsms. The microorganisms flourish in the body of earthworm because the gut of the earthworm offers optimal environment for their activities. These microbes are released along with the cast. Hence the vermicmpost contains rich microbial population.

Similar results were also observed by Essakkiamal *et al*., (2015) [5] while studying the microbial diversity of vermicompst and vermiwash where they have stated that increased microbial population is due to the activity of earthworms. Our results are also in parallel with the findings of the other workers (Emperor and Kumar, 2015 [4]; Pramanik *et al*., 2007 [18] ; Mahanta *et al*., 2012) [7].

The isolation and identification of the microbial diversity was studied (Parle, 1963 [11]; Natalia and Victor, 2015 [9]; Emperor and Kumar, 2015 [4]; Pingale 2015 [16]; Minuara and Plabita, 2018 [8]; Shalyda *et al*., 2018) [22] from

compost, vermicompost and from earthworm gut. They have characteized bacterial communities of *Actinomycetes sp*., *Bacillus sp.*, *Staphylococcus*, *Azotobactor*, *Micrococcus*, *Pseudomonas*, *Enterobacter*, *Klebsilla*, *Streptomyces*, and fungi like *Aspergillussp.* and *Penicillium* etc.

Piyush Chandna *et al*., (2013) [17] isolated and characterized the different bacterial strains during composting of different agricultural residues. They have noticed that there was prominent increase in the microbial populaton occur during mesophilic phase of composting. Perungkottur and Koilraj (2015) [15] observed the enhancement of the microbial population in the vermicomost produced from cotton waste.

V CONCLUSION:

From our study it was observed that earthworms play cruical role during vermicomposting because their activities influence the microbial communities. Availability of rich microbial population makes it an excellent soil conditioner and can be used for plant growth.Hence it is concluded that the water hyacinth weed waste canbe transformed into another usable form by an ecofriedly vermicomposting technology.

ACKNOWLEDGEMENT:

Authors are thankful to Dr. S. V. Koti, Principal, Walchand college of arts and science, Solapur for providing all the necessay facilities to carry out the research work.

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