



Figure 3. IR spectrum of the antibiotic AB(E)-6 in nujoll mull.

R_D values were 1.00 and 1.07 with actinomycin D and the antibiotic AB(E)-6 respectively in a solvent system of chloroform : methanol :: 95:5 (v/v).

The MIC values against different gram positive, gram negative bacteria and human and plant pathogenic fungi were determined (table 2). The antibiotic was particularly active against the gram positive bacteria. The antibiotic AB(E)-6 is a toxic compound, the LD_{50} being 1.25 mg/kg body weight in Swiss mice (ip route).

On comparison with Actinomycin D and other reported Actinomycins from the literature^{6,7} the antibiotic AB(E)-6 could not be correlated with any one of them and hence assumed to be a new type of actinomycin compound.

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COMPARATIVE BOD REMOVAL EFFICIENCY OF CERTAIN MICROORGANISMS ISOLATED FROM A STABILIZATION POND

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THE stabilization pond harbours a heterogeneous community of microorganisms consisting of viruses, bacteria, algae, fungi and protozoa¹. The biodegradative abilities of some of these groups in terms of the percent removal of biochemical oxygen demand (BOD) have been reported²⁻⁵. The literature concerning a comparative BOD removal efficiency of pond microorganisms is meagre. Hence the present investigation has been undertaken.

Three species of bacteria, *Pseudomonas aeruginosa*, *Proteus vulgaris* and *Escherichia coli*, two species of fungi, *Aspergillus niger* and an yeast sp and a species of alga, *Chlorella vulgaris* were isolated from the stabilization pond situated in the Botanical Garden on the Karnatak University, Dharwad Campus. These species were grown individually and in various combinations in flasks containing 1500 ml of sterile domestic sewage collected from the sewers of the University Boy's Hostel. The complex pond community as it occurs in the pond was inoculated into another flask and an uninoculated flask served as control. These flasks were maintained under the laboratory conditions exposed to reflected daylight near a window. Samples were collected from each flask aseptically on every alternate day and analysed for BOD⁶. The experiment was continued for 15 days and at the end of

the experiment, the total percent reduction in BOD was calculated.

The results are shown in table 1. Amongst the individual species, the bacterium *P. aeruginosa* removed comparatively larger amounts of BOD. The fecal bacterium *E. coli* also accounted for a considerable reduction in BOD. This is indicative of the fact that the fecal bacteria are not inactive in the stabilization pond medium, as it was thought earlier⁷, but also play a significant role in the purification of incoming wastewater. The BOD removal efficiencies of the filamentous *A. niger* and the alga *C. vulgaris* were comparatively poor. Whereas the unicellular yeast accounted for a considerable removal of BOD comparable to that removed by bacteria. When the bacterial species were grown individually in association with *A. niger*, the BOD removal efficiency was slightly reduced, most probably because of the antagonistic activity of the fungus. However, when the bacteria were grown in association with *C. vulgaris*, or when the alga, the two fungi and the three bacteria were grown together or when the pond complex community was inoculated, the BOD removal efficiency was increased considerably. The maximum BOD removal was recorded with the complex pond community. There was a negligible change in the BOD of the control flask. From the foregoing results it becomes evident that a beneficial association between various groups of microorganisms prevailing in the pond is better with respect to the BOD removal efficiency than any of the combinations considered in

Table 1 BOD removal efficiencies of the microorganisms isolated from the stabilization pond individually and in various combinations.

Organism(s)	Percent reduction in BOD
<i>P. aeruginosa</i>	68.29
<i>P. vulgaris</i>	65.38
<i>E. coli</i>	63.05
<i>A. niger</i>	45.24
Yeast	65.10
<i>A. niger</i> + <i>P. aeruginosa</i>	66.00
<i>A. niger</i> + <i>P. vulgaris</i>	63.10
<i>A. niger</i> + <i>E. coli</i>	61.57
<i>C. vulgaris</i>	47.81
<i>C. vulgaris</i> + <i>P. aeruginosa</i>	77.14
<i>C. vulgaris</i> + <i>P. vulgaris</i>	73.90
<i>C. vulgaris</i> + <i>E. coli</i>	66.67
<i>C. vulgaris</i> + <i>P. aeruginosa</i> + <i>P. vulgaris</i> + <i>E. coli</i> + <i>A. niger</i> + yeast	78.33
Pond community	82.67
Control	04.76

the present study. Hence it appears that the presence of various groups of microorganisms is essential for a better purification of sewage in stabilization ponds.

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PROTOPLAST LIBERATION FROM *SACCHAROMYCES CEREVISIAE* USING THERMOMYCOLASE OF *MALBRANCHEA PULCHELLA* VAR. *SULFUREA*

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THE isolation of protoplasts from fungi using lytic enzymes, is now a well-established technique¹. Initially this was a very useful procedure in preparing cell-free extracts² and organelles³ for biochemical studies. More recently interest has been focussed on the use of protoplasts as genetic tool⁴. However, fusion and transformation system depends upon the availability of protoplasts in large numbers and in most cases protoplasts would seem to provide the means of isolating DNA from fungal cells for transformation. Clearly, a key factor for success in this area concerns the availability of suitable lytic enzymes for cell wall digestion.

During our detailed biochemical investigations of