TABLE III

Pharmacological data of some compounds described in Table II

Compound Nos.	ALD_{50}	Gross CNS observations at 1/5 of ALD_{50}				Mobility counts	0 hr	½ hr	1 hr	2 hr	3 hr
		SMA	Reactivity	Writhing	Hypothermia						
						Controlled	137	115	105	90	82
9.	681	↓	↓	(+)	0·4° C	Treated	104	89	44	28	26
13.	>1000	↓	↓	—	0·6° C		147	70	65	27	26
14.	>1000	↓	↓	—	0·7° C		136	109	85	77	74
16.	>1000	↓	↓	(+)	1·1° C		151	101	92	79	69
17.	>1000	↓	↓	(−)	0·8° C		176	92	67	44	41
19.	>1000	↓	↓	—	0·5° C		140	103	78	62	56

↓ = decreased; (+) = present; (−) = not effected.

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ASSESSMENT OF HEAVY METAL TOXICITY

I. Effect on Microbial Population, Mineralization and Soil Respiration

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ABSTRACT

For the assessment of heavy metal toxicity on microbial population in the soil, three heavy metals (mercury, zinc and cadmium) were mixed in the soil samples in the range of 200–500 ppm. Soil respiration, C/N ratio and total microbial counts in soil were measured and a remarkable toxic effect especially on higher concentrations was observed. Mercury was found most toxic followed by zinc and cadmium. Experimental observations were supported by predicted linear regression equations.

INTRODUCTION

SOIL fertility is primarily governed by microbial activity which is highly sensitive to environmental conditions. The disturbance of cryptic ecological equilibrium reflects on the biotic activity. Introduction of heavy metal pollutants[1], being largely toxic and non-degradable, lowers the microbial populations and renders them inactive, especially at higher concentrations. Microbial activities are susceptible to the heavy metals consequently reflecting on the soil

respiration and mineralization of organic matter. The microbial activities in presence of pollutants should be investigated[3,4]. The present investigation was initiated in order to monitor the impact of heavy metal pollutants (mercury, zinc and cadmium) on microbial populations and their activity.

Technique

In order to overcome limitations involved[2], soil samples were mixed with 200-500 ppm of Hg, Zn and Cd each, wetted and placed in 1 kg polythene bags under constant environmental conditions (moisture level 60–70% at 29 ± 2° C) for one month and then analysed.

For assessment of overall activity the rate of respiration[5,7], carbon/nitrogen ratio[6] and total counts of microbial propagules[8] were measured.

Results and Discussion

Soil respiration was measured as mg CO_2 kg^{-1} soil hr^{-1}. In the control the respiration rates were as high as 2·5 to 3 mg CO_2 kg^{-1} soil hr^{1}. In contrast, the lowest value of 0·3 mg CO_2 kg^{-1} soil hr^{-1} was found in Hg, while 0·4 and 0·5 in Zn and Cd, respecitvely, at the highest concentration (500 ppm). CO_2 evolution at lowest concentration (200 ppm) was 1·8, 2·4 and 1·9 in Hg, Zn and Cd, respectively. Regression values :

$Y = 2·7 - 0·0050\,X$
$Y = 3·82 - 0·0072\,X$
$Y = 2·74 - 0·00044\,X$

for Hg ($R = -0·98$, $P < 0·05$), Zn ($R = 0·83$), and Cd ($R = -0·98$), $P < 0·05$), respectively, where Y is the soil respiration (mg CO_2 kg^{-1} soil hr^{-1}) and X is the concentration (ppm) of Hg, Zn and Cd, respectively.

The results depict that the CO_2 evolution was maximum at lowest concentration. These values being very close to control values support a view that below this concentration, the effect of pollutants will be negligible. However, at the highest concentration, the CO_2 evolution is considerably less

Mineralization was measured in terms of C/N ratio of the soil. In control the ratio was 0·2 to 0·3. In treated samples at 500 ppm the ratio was 2·2 in Cd, while 1·9 and 1·6 in Hg and Zn, respectively. At 200 ppm the ratio observed was 0·8 for Zn, while the corresponding values of Hg and Cd were 1·2 and 1·3 respectively. Regression values :

$Y = 1·32 + 0·0012\,X$
$Y = 0·71 + 0·0024\,X$
$Y = 0·24 + 0·0026\,X$

for Cd ($R = 0·43$),
Hg ($R = 0·99$, $P < 0·01$),
and Zn ($R = 0·98$, $P < 0·05$) respectively,

where Y is C/N ratio and X is the concentration (ppm) of Cd, Hg and Zn respectively.

The data reflect undoubtedly that less mineralization due to impact of pollutants results when the ratio remains more than one and reverse when less than one.

Total microbial count (Bacteria, Fungi and Actinomycetes) was 8×10^{10} gm^{-1} soil in control. At 500 ppm the lowest value of matrix element C_{42} was detected in Hg, the corresponding values being C_{41} and C_{43} in Zn and Cd respectively. The highest value C_{11} was observed at 200 ppm in Zn while C_{12} and C_{13} in Hg and Cd respectively.

Matrix model for total microbial count

Concentrations ppm	Heavy metals		
	Zn	Hg	Cd
200	C_{11} (7·5)	C_{12} (4·4)	C_{13} (4·8)
300	C_{21} (4·0)	C_{22} (3·2)	C_{23} (3·8)
400	C_{31} (2·0)	C_{32} (2·2)	C_{33} (3·3)
500	C_{41} (1·6)	C_{42} (1·4)	C_{43} (1·8)

All the values of matrix element (C_{ij}) are in 10^{10} gm^{-1} soil. The order of matrix is 4 × 3. Regression values :

$Y = 8·99 - 0·0149\,X$
$Y = 6·3 - 0·01\,X$
$Y = 6·74 - 0·0095\,X$

for
Zn ($R = -0·97$, $P < 0·05$),
Hg ($R = -0·97$, $P < 0·05$),
and
Cd ($R = -0·98$, $P < 0·05$),
respectively,

where Y is microbial population (10^{10} gm^{-1}s oil) and X is the concentration (ppm) of Zn, Hg and Cd respectively.

Inclination of decreasing trend of the microbial propagules and their activity to higher dose response of pollutants being obvious which can be subjected to mathematical derivations in order to predict the con-

centration range responsible for absolute minimization of microbial population and their activity through the exponential function.

In view of these findings, it can be concluded that the pollutants have least interference in maintaining the fundamental relationship that microbial population is directly proportional to soil respiration and inversely proportional to C/N ratio. In addition, on the basis of the total microbial count, it can be ascertained that pollutants have toxic effect and mercury accounts for the highest level of pollution in the soil, the order of the toxicity being Hg > Cd > Zn.

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VARIABILITY OF AMINO ACID CONTENT IN SEED OF SOME WILD AND CULTIVATED SPECIES OF *ORYZA*

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ABSTRACT

The reserve seed protein composition of thirteen species of *Oryza* including two cultivated rice *O. sativa* L. and *O. glaberrima* Steud and the two principal geographical races of the former, *indica* and *japonica* has been studied using Amino Acid Analyser to assess the differences in the profiles of cultivated and wild species. The species differed from each other significantly for the different amino acid contents. Further, the results suggested a wide range of variability for essential amino acids like lysine among the *Oryza* species (upto 44% in certain wild species as against 3·5% in cultivars), which is of interest to rice breeders. The possible utilization of the wild species in breeding for superior protein quality in rice is suggested.

THE genus *Oryza* is represented by about twenty-two valid species[7]; of which only two species, *Oryza sativa* L. and *O. glaberrima* Steud are cultivated. The importance of the genus as a source of vital food crop, *viz.*, rice, hardly needs any emphasis. In view of the economic importance of the genus, an attempt has been made to study whether the amino acid profiles of different primitive wild species differ from that of evolved cultivated species. Furthermore the survey of interspecific variability for protein amino acids could possibly indicate the source of limiting amino acids for the improvement of the essential amino acid pattern in cultivated species by interspecific hybridization.

Nine diploid species, *O. sativa* (AA), *O. nivara* (AA), *O. glaberrima* (A^gA^g), *O. barthii* (A^bA^b), *O. longistaminata*, (A^lA^l) *O. punctata* (BB), *O. officinalis* (CC), *O. australiensis* (EE), *O. perleri* (??) and four tetraploid species *O. minuta* (BBCC), *O. schweinfurthiana* (BBCC), *O. latifolia* (CCDD), *O. ridleyi* (?) were used in the present study. The letters A, B, C, D and E mentioned in the paranthesis against names of the species refer to genomic constitution. All the species were grown in the net-house during Rabi season of 1976–77. For each accession 20 plants were raised in 10 large pots under uniform fertilizer level of 40, 20 and 10 kilograms per hectare of nitrogen, phosphorus and potash. Fully matured caryopsis of different species were dehusked and ground to a fine powder (100:120 mesh) and defatted prior to hydrolysis with 6 N HCl. The protein content was determined by microkjeldahl method. The separation and the analysis of amino acid was accomplished on a spinco automatic amino acid analyser, model 120 C (Spin Co. Division, Beckman Instruments Inc., Palo Alto, California). In order to assess the differences in amino acid profile