

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 species⁷; 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* (A⁹A⁹), *O. barthii* (A^bA^b), *O. longistaminata*, (A¹A¹) *O. punctata* (BB), *O. officinalis* (CC), *O. australiensis* (CE), *O. perleri* (?) and four tetra-

ploid 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 parenthesis 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

TABLE I

Amino acid profile in seed of some wild and cultivated species of genus Oryza (gm/100 gm protein)

Amino Acid	<i>O. sativa</i> sub sp. indica var. Tk.	<i>O. Sativa</i> sub sp. japonica var. Chowsung	<i>O. nivara</i> Ac. No. 100189-a	<i>O. glaberrima</i> Ac. No. 100297	<i>O. barthii</i> Ac. No. 100120	<i>O. longistaminata</i> Ac. No. 101410	<i>O. officinalis</i>	<i>O. punctata</i>	<i>O. minuta</i>	<i>O. schweinfurthiana</i> Ac. No. 100170	<i>O. ridleyi</i>	<i>O. perrieri</i> (<i>L. perrieri</i>)
Genomes	AA	AA	A''A''	A ^o A ^o	A ^o A ^o	A ^o A ^o	CC	BB	CCBB	CCBB	CCDD	?
Lysine	3.40	3.50	2.92	2.86	2.74	3.31	2.94	3.03	3.39	3.75	3.00	3.98
Histidine	2.11	2.18	2.23	2.17	1.77	2.10	1.59	1.95	2.42	2.30	1.90	2.07
Arginine	8.50	7.59	7.83	7.68	6.73	7.36	7.18	7.20	7.49	7.66	7.14	7.99
Aspartic acid	8.85	9.35	4.69	8.66	7.34	8.67	7.50	8.42	8.84	7.20	9.27	9.33
Threonine	3.16	3.17	3.09	2.89	2.49	2.71	2.76	2.62	2.62	2.35	3.12	3.08
Serine	4.41	4.81	4.61	4.25	3.78	4.03	4.80	4.03	4.28	3.80	5.30	3.87
Glutamic acid	18.76	18.87	20.84	20.02	18.33	18.53	20.93	18.65	19.01	19.69	19.04	19.46
Proline	3.90	4.19	4.92	4.82	5.62	7.12	6.66	7.34	6.87	7.68	3.53	6.94
Glycine	4.10	4.35	3.78	3.61	3.43	3.51	3.49	3.36	3.62	3.43	3.78	3.78
Alanine	5.66	5.70	5.97	5.49	5.13	6.48	5.35	4.92	5.04	4.85	6.11	4.75
Cystine	0.97	1.34	0.92	1.00	0.40	0.59	0.92	0.44	0.56	0.99	0.73	0.68
Valine	5.38	5.23	5.52	5.13	4.63	5.26	4.75	4.81	5.45	7.11	5.65	4.46
Methionine	1.64	1.17	1.32	1.25	2.40	1.16	0.95	0.91	0.92	0.83	1.23	1.08
Iso-leucine	3.55	3.48	3.76	3.58	6.01	3.77	3.44	3.63	3.43	3.51	4.84	3.75
Leucine	7.85	7.99	9.09	8.68	11.97	8.17	8.84	9.11	8.35	8.43	7.84	3.75
Tyrosine	3.38	2.59	3.71	3.51	3.21	3.05	3.51	4.04	4.28	2.42	3.37	2.85
Phenylalanine	4.33	4.53	4.85	4.39	4.03	4.20	4.42	4.69	4.33	4.02	4.37	4.49
Protein %	10.56	12.06	14.13	13.16	13.19	19.50	13.13	12.00	13.25	10.69	11.81	12.50

TABLE II
Analysis of variance

Source of variation	Degrees of freedom	Sum of Squares	Mean Square	F
Amino acid	16	153476.8	9592.302	4.03*
Species	13	152658.4	11742.95	4.93*
Residuals (Error)	208	495404.7	2381.753	..
Total	237	801539.8

* Significant at 1% level.

of different species statistically, an analysis of variance of 2-way classification was made².

Amino acid profiles of different species differed from each other considerably. The values ranged from 0.40 to 20.93%. The amino acid profiles of different wild and cultivated species are presented in Table I. The two cultivated sub-species, *O. sativa* L. ssp. *indica* variety *Tellakattera* and *O. sativa* L. ssp. *japonica* variety *Chousung* resembled very closely in their amino acid profiles. However, minor quantitative differences were observed in the contents of aspartic acid, serine, proline, cystine and tyrosine. When a comparison was made between Asian cultivated taxon *O. sativa* L. and its annual wild relative *O. nivara* it was found that they differ less markedly in their profiles, the minor differences observed being in the per cent content of lysine aspartic acid, glutamic acid, proline, glycine, and isoleucine. Similarly, the African cultivated rice, *O. glaberrima*, found to differ with its wild species, *O. barthii* and *O. longistaminata* in contents of a number of amino acids like lysine, histidine, arginine, glutamic acid, proline, alanine, cystine, valine, methionine, isoleucine and leucine (Table I).

The taxa belonging to *Officinalis* group namely, *O. officinalis* (CC) and *O. punctata* (BB), *O. minuta* (CCBB), *O. schweinfurthiana* (CCBB), and *O. latifolia* (CCDD) have also displayed differences in their amino acid profiles and also showed differences with AA genome species. The species *O. officinalis* and *O. punctata* differed from each other with respect to amino acid, like aspartic acid, glutamic acid, proline, cystine and lysine (Table I). Similarly the taxa, *O. officinalis*, *O. punctata*, *O. minuta* and *O. schweinfurthiana* found to differ in amino acid contents like, lysine, aspartic acid, serine, glutamic acid, proline, cysteine, valine, leucine and tyrosine (Table I). The allotetraploid taxa, *O. minuta*, *O. schweinfurthiana* and *O. latifolia*, differed from each other in the quantity of amino acids, namely, lysine aspartic acid, serine, proline, alanine, methionine, isoleucine, leucine (Table I). The taxon *O. ridleyi* differed from other species in the per cent content of amino acids like lysine, proline, alanine, valine, leucine and tyrosine. Similarly the species *O. perrieri*, which is now removed to another genus

*Leersia*³, does not differ markedly with other species but was observed to have differences in the contents of lysine and proline. The range of essential amino acid like lysine (up to 4.4% in wild species as against 3.5 in cultivated species) would be of considerable interest to rice breeders (Table I). The analysis of variance for amino acid profiles in seed of different *Oryza* species suggested a clear significant differences from species to species (Table II). The differences in the concentration of common amino acids have been used as criteria in the study of species affinities by several workers^{1,4,5,9,10}.

The significant differences obtained from species to species for the mean contents of amino acids in the genus clearly substantiates the earlier observation about the utility of this technique in assessing phylogenetic relationships^{6,8}. Further the present study of interspecific variability for amino acids clearly indicates the source of limiting amino acids for the improvement of the essential amino acid pattern of cultivated species. However, the possible utilization of this by wide interspecific crosses has to wait until the problem of crossability barriers is overcome, through somatic cell hybridization, in the genus.

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