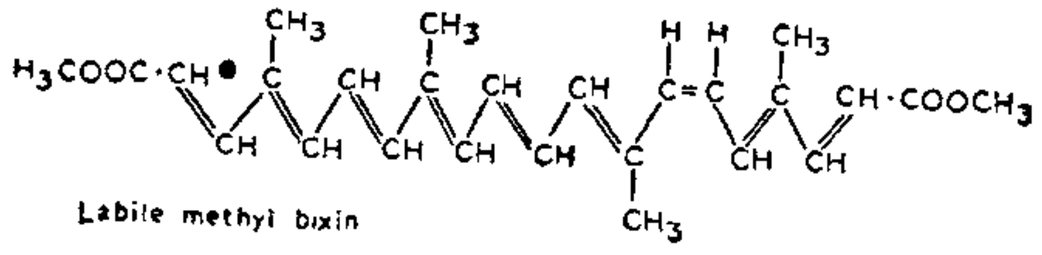
hydroxide with dimethyl sulphate. It is better prepared in good yield by the easier method of refluxing the acetone solution of bixin with dimethyl sulphate and potassium carbonate. After filtering off the potassium salts, the solution is concentrated, stirred with excess of water and allowed to stand when the crystalline labile methyl bixin is obtained. The ester is also easily formed when bixin is treated with ethereal diazomethane. It is obtained as red plates, m.p. 161–62°, $\lambda_{max.}^{CHCl_3}$ 502 (log ϵ, 2·72), 472 (2·79) and 446 (2·65) nm; $\nu_{max.}^{KBr}$ 1720 (s), 1650 (w), 1615 (s), 1560 (m), 1430 (w), 1310 (s), 1290 (m), 1265 (s), 1190 (m), 1165 (s), 1010 (m), 985 (m), and 965 (s) cm.$^{-1}$ This gives a blue colour with conc. H_2SO_4.



Labile methyl bixin

The nmr spectrum of labile methyl bixin in $CDCl_3$ showed a broad signal at 1·98 δ (12 H) indicative of four C-Methyl protons. A sharp singlet at 3·77 δ (6 H) was due to the protons of the two carbomethoxyls. In the olefinic region, a broad band centred at 6·57 δ (10 H) was observed. Apart from this, there were three doublets, each centred at 5·89 (2 H), 7·41 (1 H) and 7·98 δ (1 H). The first doublet belongs to the 2 α protons merging together and the β protons differ, one being at 7·41 and the other at 7·98 δ. Barber *et al.*[3] have earlier compared the nmr spectra of labile and stable methyl bixin. They noted that the two spectra agreed in all respects except one. In the stable methyl bixin, both the β-protons gave the same signal at 7·39 δ (2 H). The shifting of a β-proton in labile methyl bixin by 0·56 δ to the lower field was attributed to the proximity of the β-proton at one end of the molecule to the *cis* 6, 7 double bond. Thus, the nmr supports earlier fixation of the *cis* double bond by chemical methods.[4]

The greater solubility of methyl bixin in fats and fat solvents as compared to bixin which is rather sparingly soluble would suggest the use of ester as more suitable for colouring butter. Further, it will not add to the acid value of the butter. By the simplified method given above, it is very easily prepared. However, its tinctorial value is poor; though $\lambda_{max.}$ is the same as for bixin, log ϵ is markedly low and hence it is not suitable.

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INHERITANCE OF 'DYE BINDING CAPACITY' VALUE IN RICE

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RECENT work done at the International Rice Research Institute[1] and at the Indian Agricultural Research Institute[2] has convincingly proved that, in rice, considerable genetic variation exists for protein content and quality. A number of high protein genotypes have been identified at both places in the world germplasm collection. However, before such variation can be profitably exploited the estimation of heritability and the gene control mechanisms should be worked out under varying conditions to gain maximum genetic advance, through hybridization. Although numerous such studies have been performed in wheat,[3-6] there is no report available in rice on this aspect. In the present study, an attempt was made to evaluate the inheritance of protein quality and quantity using the micro dye binding technique described earlier.[7] The single grains of F_2 populations, derived from single plants from crosses between Tainan-3 × IR-8 (*japonica* × *indica* of subsp. *Oryza sativa*) and IR-8 × Basmati-370 (*indica* × *indica*) were studied along with their respective parents. Means and variances were obtained and the frequency distribution was plotted (Fig. 1). Parental variances were used to estimate the environmental component of variation. Before the data was used for estimating the heritability, scale was tested.[8] Means, vari-

TABLE I

Means, variances, heritability and genetic advance in two crosses

Generation	N	Mean (X)	Variance (V)	Heritability (h^2)	Genetic advance G_A
P_1 (Tainan-3)	48	0·143	0·00061	..	..
P_2 (IR-8) ..	51	0·160	0·00028	..	..
P_3 (Basmati-370)	48	0·176	0·00057	..	..
$P_1 \times P_2$ (F_2 population)	96	0·220	0·00089	50·000	0·029
$P_2 \times P_3$ (F_2 population)	92	0·245	0·00081	47·530	0·027

ances, heritability estimates and genetic advance (at 5% level of selection) are given in Table I.

The formula, $\frac{VF_2 - VE}{VF_2}$ was used for the calculation of heritability in broad sense wherein, VF_2 = variance of F_2 population and $VE = \frac{VP_1 + VP_2}{2}$. The non-fixable components of variation and the genotype environment interactions have not been removed from the F_2 variance. The data clearly indicate that in both the crosses studied, there is considerable evidence for additive and cumulative gene action for the DBC values (Fig. 1). This is expected, since very diverse parents have been crossed in either case. A large number of genes must be responsible for the determination of 'DBC' values since moderate heritability estimates have been obtained. It is, however, remarkable that the two estimates are almost alike. The genetic advance calculated[9] indicates that F_3 lines derived from the 5% top F_2 selections would be 0·03 units higher than the mean of F_2.

The heritability estimates in the present study compare fairly well with similar studies done in wheat, soybean and other crops.[10-12] With larger population at hand, it should be possible to breed for high DBC value which in turn would result in genetic advance for protein content and quality.

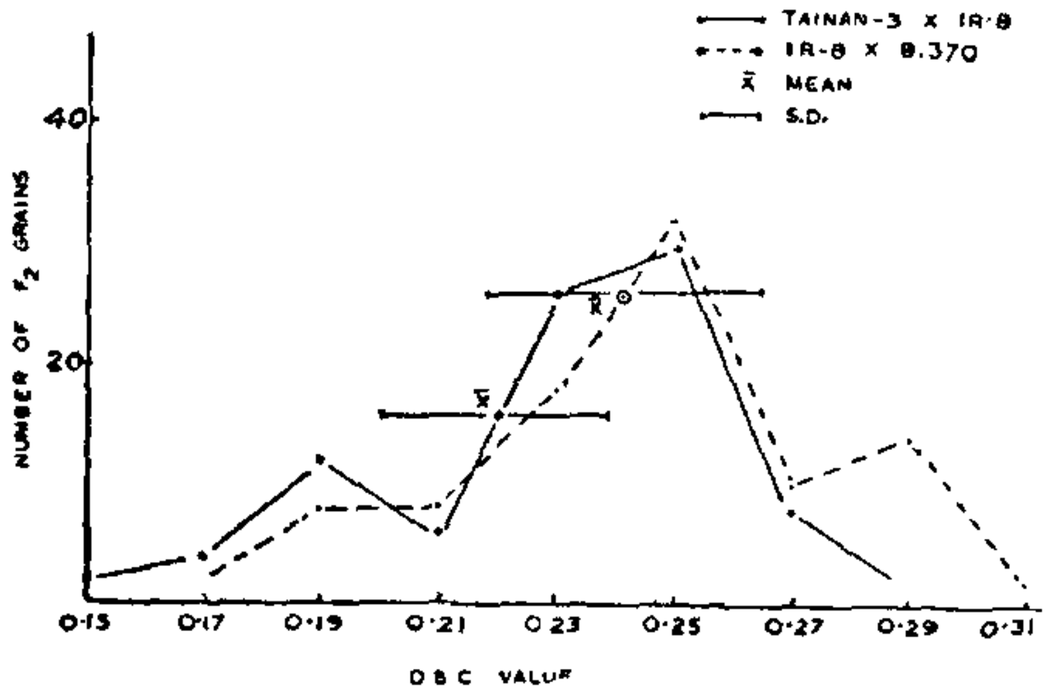

FIG. 1. Distribution of F_2 population of two crosses in rice for DBC value.

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RATE COEFFICIENT FOR TWO-BODY N-ATOMS RECOMBINATION

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THE recombination of N-atoms is important in many phenomena. During discharge through nitrogen, N_2 molecules are excited, ionized and/or dissociated. The dissociated N-atoms afterwards recombine and produce active nitrogen. Again, in the upper atmosphere, N-atoms are produced by dissociation of N_2 molecules by solar ultraviolet rays.[1] On reacting with constituent particles of the atmosphere—atoms, molecules, ions and electrons—they produce certain upper atmospheric phenomena. Data for two-body recombination of N-atoms[1] recombination are not available. In this note, two-body recombination of N-atoms is