

by Shri J. D. Gadgil for oil estimation and hybridization.

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ON NEW RECORDS OF HOST PLANTS AND
SPECIES OF RHYPAROCHROMINAE
(LYGAEIDAE: HETEROPTERA) FROM INDIA

LYGAEIDAE is the second largest family of Heteroptera with more than 4,000 species recorded in the various zoogeographic regions of the world and nearly half of these species belong to the subfamily Rhyparochrominae. Distant¹⁻³ compiled the several scattered reports on Indian Rhyparochrominae and catalogued 89 species from the present Indian territory. But hitherto nothing is reported about the host plants of Rhyparochrominae from India.

During the present investigation (1974-79) on the bioecology of Rhyparochrominae from southern India the host plants recorded were, *Ficus bengalensis*, *F. glomerata*, *F. hispida*, *F. religiosa* and *F. retusa* (Urticaceae), *Arachis hypogea*, *Crotalaria verrucosa*, *Glyricidia maculata* and *Sesbania grandiflora* (Papilionaceae), *Acalypha indica* and *Euphorbia hirta* (Euphorbiaceae) and *Leucas aspera* (Labiatae) and these were found to be the most favoured host plants. A few monocotyledons, such as species of *Echinochloa*, *Andropogon*, *Eleusine* and *Setaria* were also frequented by these bugs in the field.

A few rhyparochromines were recorded for the first time in India. *Appolonius crassus* (Dist.), *Botocado signanda* (Dist.) and *Metochus n. lipes* Bred., previously reported only from Ceylon were found in several regions of southern India such as Coimbatore, Mysore, Madras, Trichur and Palhat. *Horridipamera niemei* (Dohrn) reported earlier from the Islands near Burma was recorded at Coimbatore and Madras. *Gonsalvus typus* Dist. reported earlier in Burma was seen distributed in southern India.

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AN ALCOHOL DEHYDROGENASE
VARIANT IN KHAPLI WHEAT
(*TRITICUM DICOCCUM* SCHÜBLER)

ELECTROPHORETIC variants of proteins and enzymes are of considerable interest for genetic, biochemical and evolutionary studies. While investigating the isoenzyme polymorphism in different species of wheat, variant forms of alcohol dehydrogenase (ADH E.C. 1.1.1.) were observed in one of the accessions of Khapli wheat [*T. turgidum* ssp. *dicoccum* (Schrank) Thell] or what is commonly known as *T. dicoccum* Schübler. *T. dicoccum*, a primitive, non-free threshing, tetraploid species, was the main wheat species grown in the prehistoric times¹. In India Khapli wheat is still grown in certain parts of Maharashtra, Gujarat and Karnataka States. In this communication variation observed in the ADH zymograms is described and its origin is traced to a single variant, and heterozygosity at one of the ADH loci.

The foundation seeds of Khapli wheat accessions used in this study were obtained from Dr. G. B. Deodikar of the Maharashtra Association for Cultivation of Science, Pune and from Wheat Research Station, Niphad. These were multiplied at the experimental field of this Research Centre.

Dry seeds were homogenized with cold 0.01 M Na-pyrophosphate buffer pH 9.5, in a chilled mortar and pestle. In all the extractions, the ratio of seeds to buffer was 1 : 5 wt/vol. The slurry was centrifuged at 12,000 g at 4° C for 30 minutes. The supernatant (200 μ l) containing about 360 μ g protein was used for electrophoresis. Disc electrophoresis was performed in 7% acrylamide gels essentially following the procedure of Davis². After electrophoresis, gels were incubated in the reaction mixture, the composition of which has been given by Brewer³.

Ten accessions of Khapli wheat were examined for ADH zymogram, nine accessions had three closely spaced ADH bands of which the middle band was the most intense (Fig. 1A). This pattern was similar to the one observed earlier in most of *T. durum*^{4,5} and *T. dicoccum*⁶ wheat accessions. As this is the most frequent pattern, it is considered as the wild type. One accession Khapli 2-9-8 showed a different ADH pattern with 5 bands (Fig. 1C). On repeated gel electrophoresis using bulk seed samples three variant patterns were observed in 2-9-8. Essentially these were 5 bands but the zymograms differed from each other in band intensities (Fig. 1C, D and E). Single seed analyses of this stock gave all the 5 ADH patterns shown in Fig. 1. This suggests that the variant zymograms observed in the extracts of bulked seed samples were due to heterogeneous population.

The ADH band pattern with 3 widely spaced bands observed on single seed analyses (Fig. 1B) was almost similar to the one reported by Hart⁶ in CI 4013 of *T. dicoccum* from the U.S.D.A. wheat collection, except that the band intensities were different. In CI 4013 the relative intensities of the bands from the anode were 1:2:2. The relative intensities in the present variant were in the ratio of 1:2:1.3 (Fig. 2B) and were similar to the variant observed in several Indian accessions of *T. durum*⁵. The intensity variations suggest that the variant observed in Khapli 2-9-8 may have a different origin from the one found by Hart⁶ in CI 4013. However, further genetic and biochemical characterization would be necessary to establish dissimilarity or identity of the two variants.

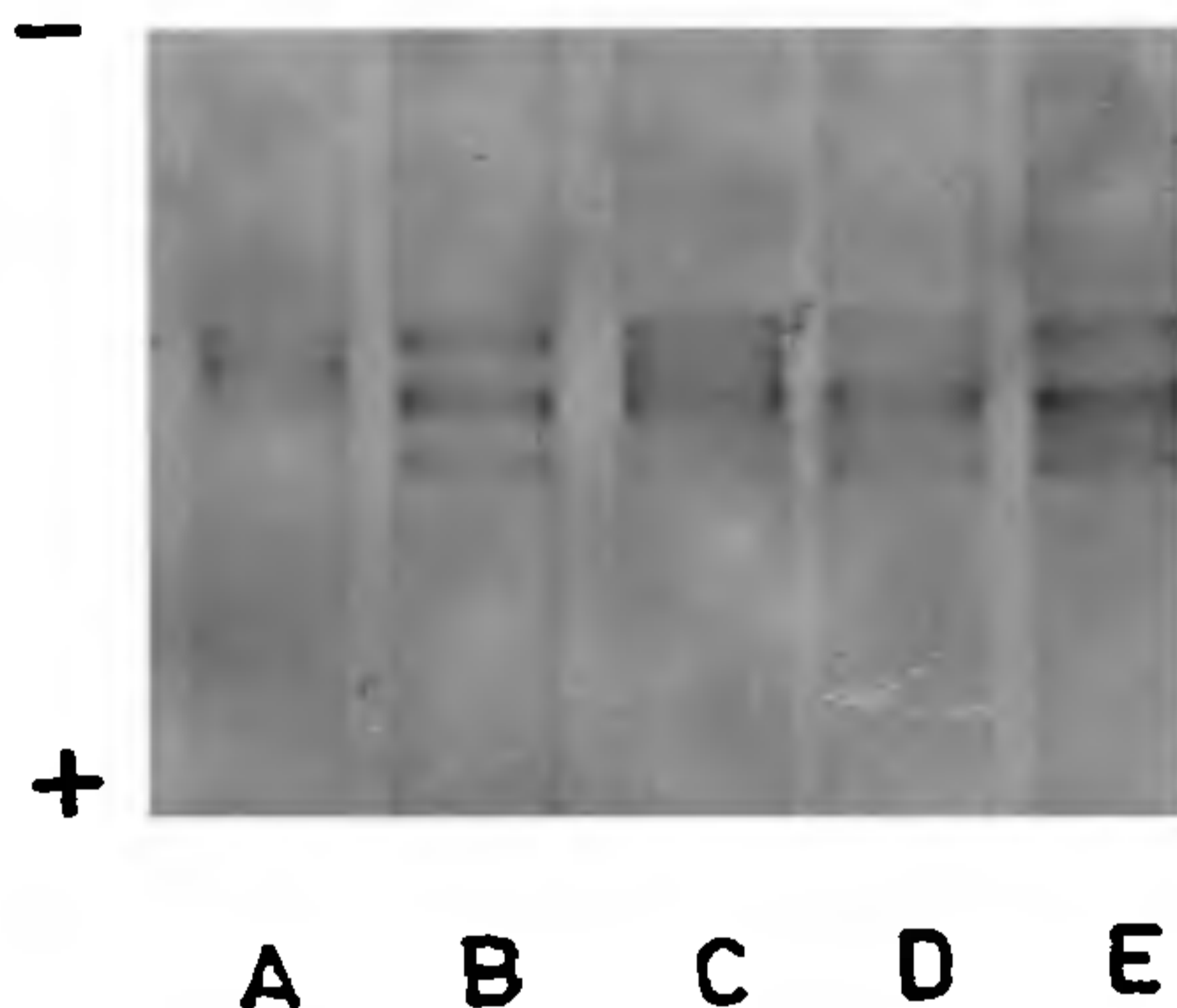


FIG. 1. ADH zymograms, A, wild type; B, mutant type; C, D and E, variant types observed in Khapli 2-9-8.

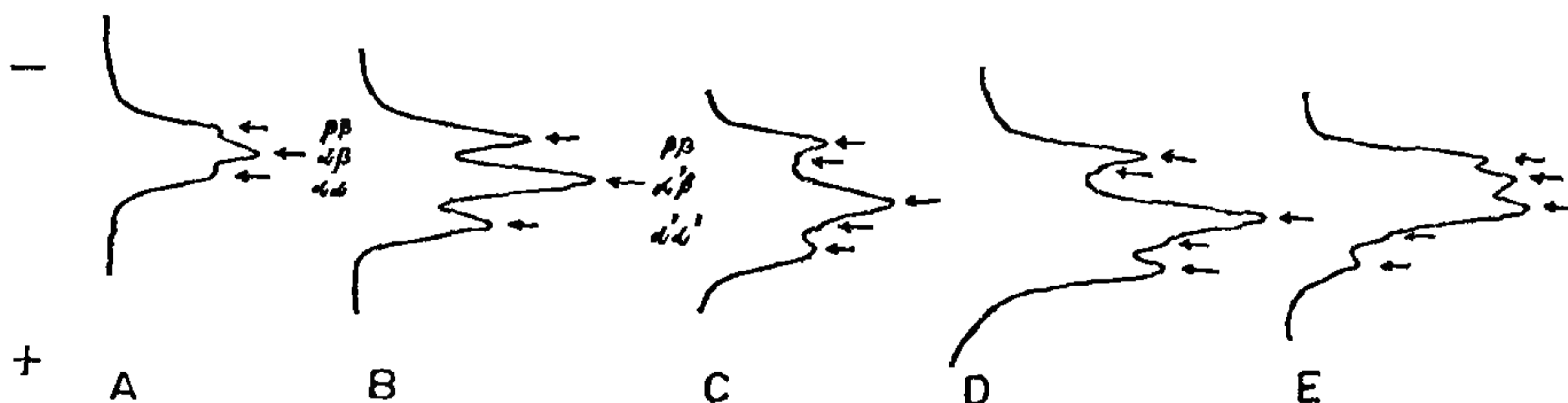


FIG. 2. Densitometer recordings of ADH zymograms, A, wild type; B, mutant type; C, D and E, variant type of Fig. 1. Reduced activity of the $\alpha'\alpha'$ peak relative to $\beta\beta$ peak was always observed in the mutant.

ADH in wheat is known to be a dimeric enzyme and in the tetraploid wheat the three bands observed in the wild type results from random association of monomers governed by the structural genes Adh_A

and Adh_B located on chromosomes 4A and 4B producing respectively α and β monomers⁷. The three bands observed are due to $\alpha\alpha$ and $\beta\beta$ homodimers and $\alpha\beta$ heterodimers and are theoretically expected to show a ratio of 1:2:1 for $\alpha\alpha$, $\alpha\beta$ and $\beta\beta$ respectively. The observed ratio was 1:1.6:1 (Fig. 2A). The variant observed by Hart⁶ in CI 4013 was attributed to a mutation at the Adh_A loci leading to the formation of a monomer with faster mobility than $\alpha\alpha$ and was designated as $\alpha'\alpha'$. The present variant can also be explained on the basis of a mutation at the Adh_A loci on chromosome 4A. The densitometer recordings of the gels revealed that in the mutant relative activity of the $\alpha'\alpha'$ homodimers was less than the $\beta\beta$ homodimers (Fig. 2B). Type C, D and E (Fig. 1) zymograms can thus be explained on the basis of (1) differential activity of $\alpha\alpha$ and $\alpha'\alpha'$ dimers and (2) dosage effect of the maternal genes in the triploid (in fact 6x, in 4x wheat) endosperm which forms the bulk of seed. In the endosperm of the tetraploid wheat the maternal genes are present in 4 dosages while the paternal genes are in two dosages. Further, type C, D and E zymograms observed following single seed analyses were similar to those reported by Hart⁶ and Mahajan⁵ in the F_1 heterozygotes when the variants were crossed to the wild type. It is, therefore, inferred that Khapli 2-9-8 population examined was heterozygous for the Adh_A alleles.

The heterozygosity of Adh_A gene in the population of a highly self-pollinated species is of interest and this population will be investigated further. The occurrence of this ADH variant in Indian *dicoccum* wheat is also of interest. As mentioned previously, a similar variant was found in several accessions of Indian *durum* wheats⁵. *T. dicoccum* is considered to be

primitive and ancestor of the free threshing *durum* wheats.

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FACTOR ANALYSIS IN MEDICINAL YAM

MEDICINAL yam (*Dioscorea floribunda* Mart and Gal) is grown as a natural source of diosgenin. So far, experimental comparisons for this crop were made for individual single measurements only. This method of comparison leads to comparison in isolation and meaningful conclusions may not emerge. To obviate this, the multiple analysis of variance can be carried out. But such an analysis is very difficult even when micro computer sets are installed. Component or factor analysis has been suggested as an alternative by Holland¹, Pearce⁴ Mehra *et al.*³ and Ramachander *et al.*⁵. In this method, the number of characters under study are reduced to two or three factors by using the component analysis method and further comparisons are to be made for these factors if they can be ascribed any biological meaning. The centroid method of forming factors as suggested by Lawley and Maxwell² was used for this study. Tuber weight (X_1), stem diameter (X_2), vine length (X_3), number of branches (X_4), number of leaves (X_5),

leaf area (X_6), dry weight of shoot (X_7) and harvest index (X_8) were recorded for 70 plants which were grown under uniform conditions at Indian Institute of Horticultural Research, Hessaraghatta, during 1978-79.

The following factors were obtained as a result of the study :

$$\text{Factor I : } 0.5106 X_1 + 0.5084 X_2 + 0.2575 X_3 + 0.4658 X_4 + 0.4340 X_5 + 0.5251 X_6 + 0.4924 X_7 + 0.4539 X_8.$$

$$\text{Factor II : } -0.6133 X_1 - 0.7868 X_2 - 0.8362 X_3 + 0.7630 X_4 - 0.6625 X_5 - 0.6604 X_6 - 0.4668 X_7 - 0.7558 X_8.$$

The first factor explained away 21% of the total variation and second factor explained away 49% of the variation. Thus, both factors explain together 70% of the variation. While the first factor has positive loading to all characters under study, in case of second factor only number of leaves (X_5) had a positive loading. So the first factor can be taken as describing the general vegetative vigour and the second as antagonism of production of other parts of the plant to the production of leaves. Since the economic product in this case is the tuber, a low value of index 2 and higher value of index 1 would be desirable. These factors could be made use of in further statistical analysis.

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