median; *m*, median and *St*, sub-terminal chromosomes. From the karyogram (figure 1a) it is clear that there is no medianly constricted chromosome. A single chromosome with secondary constriction was found and it belonged to the *Sm* category. The new chromosome number of $n=14$ establishes the occurrence of polyploid races of this taxon in India. In view of different chromosome numbers and distinct karyotype recorded in the present investigation, it can be assumed that *C. globularis* var. *leptosperma* f. *leptosperma* should be regarded as a distinct entity as was originally done by Braun[20] rather than considering it as a variety of *C. globularis* as recommended by wood[21], and Wood and Imahori[10].

The authors thank UGC, New Delhi for financial assistance.

14 April 1988; Revised 28 June 1988

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INDUCTION OF PROLINE ACCUMULATION BY GAMMA IRRADIATIONS IN BERMUDA GRASS [*CYNODON DACTYLON* (L.) PERS.]

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PROLINE accumulation in plants has been noticed as a result of water stress[1], water logging[2], temperature fluctuations[3–5], nutritional deficiencies[6], fungal infections[7] and even air pollutants[8]. Though different consequences of such accumulation have been visualized and roles suggested[9–13], its physiological significance remains speculative. Presently, while studying the effects of γ-irradiations on diploid ($2n=18$), triploid ($2n=27$) and tetraploid ($2n=36$) taxa of *Cynodon dactylon* (L.) Pers. in a bid to enlarge their gene pool, proline accumulation in these plants, growing under uniform nursery conditions, was noticed. The plants were raised from parts of rhizomes that were exposed to γ-irradiations of 5, 7.5 and 10 kr from ^{60}Co source that provided approximately 3.337 kr/min at the Department of Radiology of the Post-graduate Institute at Chandigarh. Preliminary observations indicated that in diploids doses beyond 5 kr, and in triploids and tetraploids, treatments beyond 10 kr were detrimental. The control and irradiated plants were grown in pots containing similar type of garden soil. Plants were sprinkled with water on alternate days. For free amino acid determinations[14,15], 3–5 leaves, just at the time of emergence of the inflorescence, were collected from erect culms.

Irradiation treatments were observed to be slightly promotory in respect of total free amino acid content. All the three taxa registered a marginal increase. The amount (mg/g dry leaf wt) increased from 10.80 ± 0.02 to 11.25 ± 0.03 in diploids, from 8 ± 0.08 to 10.10 ± 0.60 in triploids and from 10.50 ± 0.01 to 11.90 ± 0.06 in tetraploids. A linear relationship between the amount and intensity of irradiation was noticed in respect of some amino acids (figure 1). Whereas proline and arginine concentrations exhibited a progressive increase with

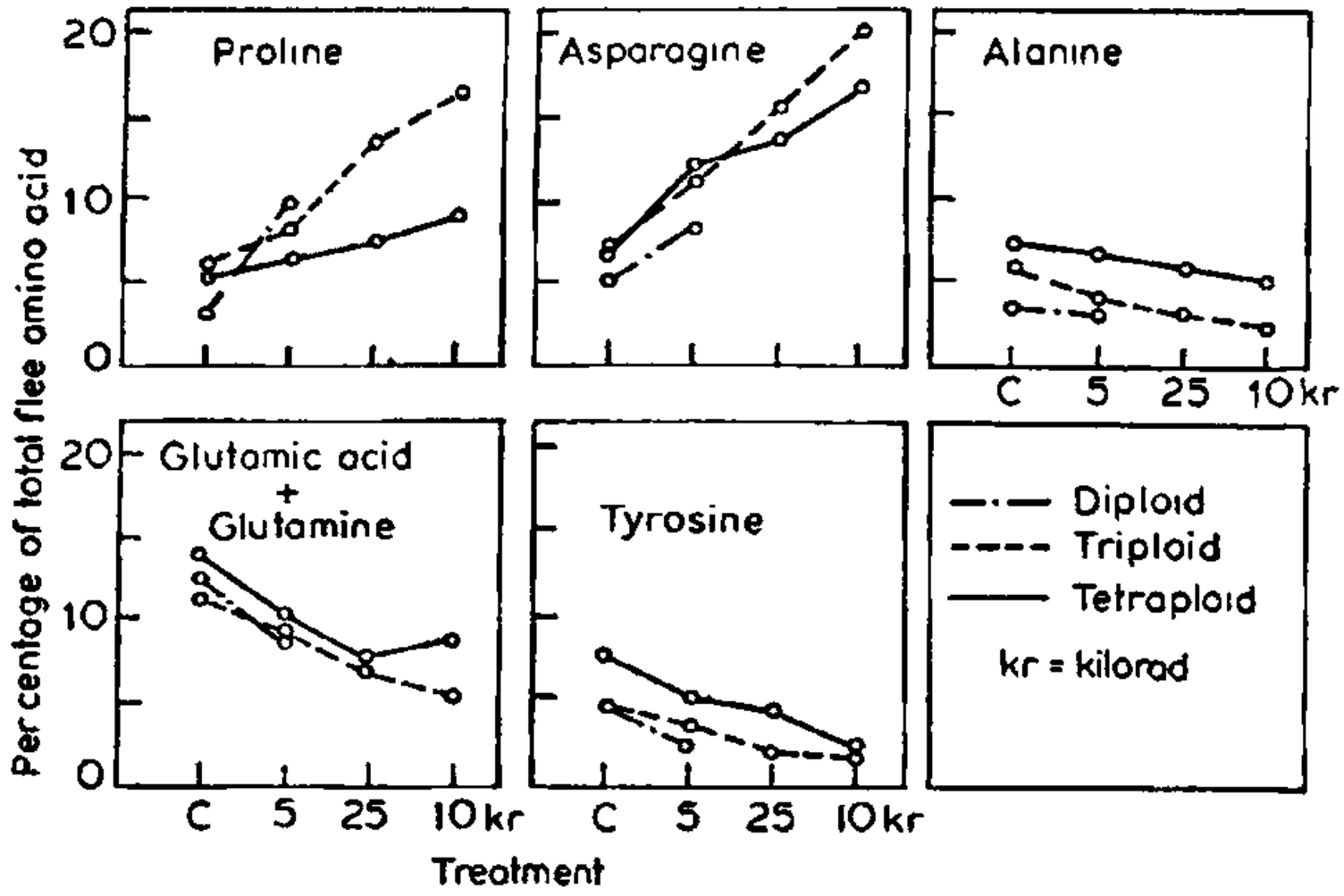

Figure 1. Levels of some amino acids in control and irradiated counterparts of diploid, triploid and tetraploid taxa of bermuda grass.

increase in irradiation dosage, a steady decline was apparent in tyrosine, glutamic acid + glutamine and alanine content. Possibly, radiations enhance the activity and/or synthesis of enzymes involved in proline formation from glutamate. Further, diploid, triploid and tetraploid genotypes differed in their capacity to react to varying irradiation treatments. To elaborate, whereas in diploids the proline content registered a three-fold increase with 5 kr treatment, the magnitude of accumulation of this amino acid was much lower in triploids and tetraploids. Maximum accumulation of proline was registered in 10 kr triploid plants. Enzyme levels thus seem to be affected differentially in the three taxa at different ploidy levels.

The resistance to desiccation was observed to increase when proline content of leaves was raised by artificial means[16, 17]. It has also been anticipated that increased proline accumulation serves to protect the plants from the stress of reduced water levels[18]. In the present case, the inherent property of triploids to accumulate more of this amino acid appears to be responsible for their prevalence in a variety of habitats and consequently for their wider distribution. The diploids and tetraploids, on the other hand, are quite restricted in this sense. Another interesting point worth mentioning is that irradiation-induced effect persists throughout the life of the individuals as proline level was never observed to decline in leaves from newer culms formed subsequently through vegetative propagation. The irreversible manner of increase in proline content and transmission of once attained levels to newly formed vegetative offshoots are suggestive of radiations acting at a genetic level.

26 April 1988; Revised 3 June 1988

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GENETICS OF PHENOL COLOUR REACTION OF SEED COAT IN PEARL MILLET [*PENNISETUM AMERICANUM* (L.) LEEKE]

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PHENOTYPIC markers, which have no apparent selective advantage, can serve as useful criteria in understanding the geographical and evolutionary paths of divergence that a system has undergone before it attained its present status. Colour change of the seed coat in response to treatments with phenol is one such character. This phenol colour reaction of seeds was first reported in wheats[1] and since then has been in use for testing the purity of a variety in seed testing procedures[2]. The test was reported to be indicative of the genotype and independent of the growth conditions, provided the grain ripens to $<30\%$ of moisture content[3].

Despite its suggested usefulness in understanding the phylogenetic differentiation and geographical distribution of plant systems, studies on the genetic basis of this character are limited to rice[4, 5], wheat[6, 7], rye[3], and foxtail millet[8] and no information seems to be available about the phenol colour reaction in pearl millet (*Pennisetum americanum* (L.) Leeke). In the present study eight inbreds of pearl millet are classified basing on the reaction of their seed coats to phenol colour test and the genetic basis of this character is analysed.

Dry and dehusked grains of pearl millet [*P. americanum* (L.) Leeke] (= *P. typhoides* Stapf. and Hubb.; $2n=14$) were placed on filter paper in a petri dish. The filter paper was moistened with 3 ml of 1% aqueous phenol solution. The petri dish was kept at 30 ± 2°C and was covered to prevent loss of moisture and left for 3 h for completion of the colour reaction. The grains were then gently dried by keeping on blotting paper and the colour of the treated grains due to the reaction—whether normal pearly or dark brown—was noted.

Since the site of colour reaction is a maternal tissue, the F_1 grains used for these studies were those borne by the F_1 plants and F_2 grains borne by F_2 plants. For example the F_2 population was formed by taking grains from each of the F_2 plants.

Concentration of the phenol solution and duration of the treatment were standardized after several trial experiments. With the particular staining schedule used in the present study, no loss in seed viability was observed and the percentage germination of the treated seed was comparable to that of the control (untreated). In plants raised from the treated seed, no chromosomal aberrations were observed either at root tip mitosis or at the PMC meiosis. The progeny of the treated seed was studied through four generations of selfing and no gene mutations were recorded.

Eight inbreds (Vg 212, Vg 587, IP 1746, IP 1475, IP 3128, LC.I, LC.II and CO_5) were examined for their reaction to phenol colour test and only one inbred (IP 3128) showed negative phenotype, in that the colour of the seed coat remained unchanged even after the test. The remaining seven inbreds showed positive reaction to the test and the colour of the seed coat turned dark brown after treatment. Both positive and negative phenotypes observed in different inbreds were quite stable since the character was observed through several generations of selfing. No seasonal differences in the expression of this character were observed. In all seven inbreds exhibiting positive phenotype, the intensity of dark brown colour developed, appeared to be identical.

To study the genetic basis of this character, reciprocal crosses were made between plants showing negative and positive phenotypes and the data are presented in table 1. The phenotype observed in F_1 was always positive. In the F_2 generation, segregation was observed for the positive and negative