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# Reflection of Grain Yield Variability in Pearl millet on Biochemical Indicators of Soil Fertility

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**Abstract**: Development of efficient N-utilizing genotypes can be an important strategy to increase pearl millet productivity in N-deficient soils of arid region. Therefore, 30 genotypes of pearl millet (*Pennisetum. glaucum* (L) R. Br.) were studied for determining the amount of genetic variability for $NO_3$-N content and activity of nitrate reductase and dehydrogenase in the rhizosphere and their association with the grain yield. Significant variability existed among genotypes for these traits. Estimates of heritability in broad sense were high for all the traits. Genetic advance was high for $NO_3$-N, followed by nitrate reductase and dehydrogenase. Study revealed significantly high and positive association of grain yield with nitrate reductase and dehydrogenase, while it was negative between grain yield and $NO_3$-N. This suggested that high activity of nitrate reductase and dehydrogenase in the rhizosphere of pearl millet genotypes can be used along with other yield component traits for improving pearl millet productivity in the nitrogen-deficient production system of arid regions.

**Key words**: Nitrate reductase, dehydrogenase, pearl millet, genetic variability.

Low fertility, especially with reference to nitrogen, is wide spread in Indian arid zone (Praveen-Kumar and Aggarwal, 1996). This often limits the yield of pearl millet, a major summer cereal of this zone. An economic and efficient way to improve productivity in these soils would be to breed pearl millet genotypes capable of utilizing the available soil nitrogen more efficiently.

N utilization by pearl millet can theoretically be reflected in terms of depletion of plant-available $NO_3$-N in soil and activity of enzymes involved in N utilization pathways. Nitrate reductase (NR) is a major enzyme in N utilization pathway of plants. It is an inducible enzyme (Devlin, 1972). Therefore, its activity in plants increases with availability of $NO_3$. Changes in plant NR activity are also reflected in NR activity in the rhizosphere (Praveen-Kumar and Tarafdar, 1997). Therefore, we hypothesized high yielding pearl millet genotypes to have higher NR activity in rhizosphere. Further, we also expected better performance of genotypes to be reflected by higher soil dehydrogenase activity. This hypothesis was derived from the fact that better performing genotypes synthesize more C-based metabolites and this could lead to higher exudation of C-rich compounds by roots, which in turn would promote microbial acitity and hence dehydrogenase activity (Praveen- Kumar and Tarafdar, 1997; Praveen-Kumar *et al.*, 2000). Hence, NR and dehyderogenase activities were estimated in the rhizosphere of 30 genotypes of pearl millet to find out whether enzyme activity and $NO_3$-N can be indicative of crop performance in terms of grain yield. The variability and heritability for these traits were also assessed for possible use as selection criteria in crop improvement program.

## Material and Methods

Thirty genotypes of pearl millet, namely CZH-IC-511, CZH-9614, CZH-9623, CZH-962, HHB-67, CZ-IC-923, CZP-9401, CZP-9604, CZP-9603, CZP-9602, CZ-IC-315, RAJ-171, HAU-IC-9501, GIC-KB-95754, MP-316, RCB-IC-9, RCB-IC-956, GIC-KB-95107, MP-318, GIC-KP-95753, PCB-157, HMP-9401, UCC-17, PPMP-473, PCB-158, GIC-KV-94135, UCC-23, MP-171, ICMV-221 and ICTP-8203, were planted at research farm of CAZRI, Jodhpur, in a randomized block design with three replications on July 30, 1997 after 24.2 mm rainfall. Each genotype was planted in four rows of 4 m length. Row to row distance was 60 cm, while plant to plant spacing was maintained at 15 cm. Soil samples were taken from the rhizosphere and non-rhizosphere soil of each genotype at full bloom stage to quantify $NO_3$-N and activity of NR and dehydrogenase in soil. $NO_3$-N was estimated in 2 M KCl extract of soil (Bremner, 1965) using flow injection analyzer (Tecator 5010). NR and dehydrogenase activities were estimated by the methods described by Abdelmagid and Tabatabai (1987), and Tabatabai (1982), respectively. Crop was harvested on maturity and grain yield recorded for each genotype.

Data were subjected to analysis of variance. Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated as suggested by Comstock and Robinson (1952) and Johnson *et al.* (1955). The broad sense heritability was calculated as ratio of total genetic variance to phenotypic variance. Genetic advance was worked out as suggested by Falconer (1960). Simple correlations were calculated according to method suggested by Snedecor and Cochran (1967).

## Results and Discussion

Statistical analysis of data revealed significant differences among genotypes for $NO_3$-N, NR and dehydrogenase and grain yield (Table 1). $NO_3$-N exhibited maximum range of variability. It was followed by NR and dehydrogenase. Association studies showed highly positive correlation of grain yield with NR ($r=0.620^{**}$), dehydrogenase ($r=0.745^{**}$) and $NO_3$-N ($r=-0.426^{*}$), which confirmed our hypothesis. Weaker correlation between grain yield and $NO_3$-N, as compared to that with NR and dehydrogenase, may be due to highly mobile nature of $NO_3$-N in soil solution that may

*Table 1. Range, mean and coefficient of variation for various traits in pearl millet*

| Trait | Range | Mean | CV(%) |
|---|---|---|---|
| $NO_3$-N ($\mu g\ g^{-1}$) | 0.14-4.41 | 1.66 | 78.9 |
| NR ($\mu g\ NO_2$-N formed $g^{-1}\ h^{-1}$) | 0.54-2.85 | 1.99 | 35.2 |
| Dehydrogenase (pKat) | 0.47-1.05 | 0.85 | 23.5 |
| Grain yield (kg $ha^{-1}$) | 639.5-1872.9 | 1397.1 | 18.3 |

*Table 2. Phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability and genetic advance in pearl millet*

| Traits | PCV | GCV | $h^2_{bs}$ | Genetic advance (% of mean) |
|---|---|---|---|---|
| $NO_3$-N | 58.75 | 54.91 | 0.87 | 98.8 |
| NR | 28.87 | 27.27 | 0.89 | 50.2 |
| Dehydrogenase | 29.43 | 21.32 | 0.76 | 29.4 |
| Grain yield | 21.78 | 19.14 | 0.77 | 30.5 |

alter with rainfall and limit a definite genotypic effect to develop. Among the genotypes studied in this experiment five were hybrids while the rest were open-pollinated genotypes. Incidentally NR activity in hybrids was higher (2.38-2.85) than observed for open pollinated genotypes (0.54-1.89) µg $NO_2$-N $g^{-1}$ $h^{-1}$. Comparable values for dehydrogenase activity were 0.83-1.05 and 0.47-1.05 pkat and for $NO_3$-N were 0.14-1.81 and 0.80-4.41 µg $g^{-1}$ for hybrids and open pollinated crop, respectively. The yield level among hybrids ranged from 1277 to 1872.9 and from 639.5 to 1415.0 kg $ha^{-1}$ in open pollinated genotypes. Higher activities of NR and dehydrogenase, coupled with low nitrate content in the rhizosphere and higher yield of hybrids is indicative of better N utilization than the open-pollinated genotypes. It could be the result of higher root biomass produced by hybrids due to hybrid vigor (Manga and Saxena, 1986).

The estimates of coefficients of phenotypic and genotypic variation, heritability and genetic advance expressed as per cent of mean are given in Table 2. $NO_3$-N had the highest values of phenotypic (PCV) and genotypic coefficient of variability (GCV), confirming high genetic variability for the trait. Moderate values of PCV and GCV for NR and grain yield indicated presence of genetic variability for these traits also. Broad sense heritability estimates were high for almost all the traits studied. NR had the highest heritability and was closely followed by $NO_3$-N, grain yield and dehydrogenase. This showed less influence of environment on these traits. Hence, selection for desired manifestation of these traits can be made successfully. The expected genetic advance, expressed as per cent of mean by selecting the 5% best individuals, was found to be highest for $NO_3$-N, followed by NR. Dehydrogenase and grain yield showed almost same quantum of genetic advance. Traits showing high genetic advance also had high heritability and genetic variability. Johnson *et al.* (1955) reported that heritability estimates, along with estimates of genetic gain, are more useful than heritability itself in predicting the resultant effect for selecting the best genotype for a given trait. Presence of high heritability and genetic advance for $NO_3$-N and NR indicated the role of additive genes for these traits. It should, therefore, be possible to select genotypes supporting higher activities of these parameters (Panse, 1957; Keller and Linkans, 1955).

Since NR and dehydrogenase were strongly and positively associated with grain yield, selecting genotypes with high NR or dehydrogenase activity in rhizosphere should indirectly improve grain yield in pearl millet. Thus, in the arid regions of India, where pearl millet crop frequently experiences terminal stress leading to reduced yields and large yield differences among genotypes, selecting genotypes supporting high NR and dehydrogenase activity in their rhizosphere, along with other yield component traits, could form a part of the selection procedure for improving pearl millet productivity under N-deficient production system. Such N-efficient genotypes can also be used as parent in the pearl millet improvement program.

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