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Genetic variability of foxtail millet (*Setaria italica* P. Beauv.)

Electrophoretic study of five isoenzyme systems

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Summary. The genetic diversity of a world collection of foxtail millet strains (*Setaria italica*) and some samples of wild populations (*Setaria viridis*) was studied by means of electrophoresis on five enzymes (10 loci) Est, Acph, Got, Mdh, Pgd. In spite of an overall limited polymorphism, the diversity appeared to be clearly regionalized. The wild populations collected in France and China introduced new genetic variability to the cultivated forms. However, the interregional diversity within both species was greater than the between species (*S. viridis*/*S. italica*) diversity.

Key words: Foxtail millet – Enzymatic polymorphism – Genetic differentiation – Domestication

Introduction

This paper is a report of the analysis of genetic variability of foxtail millet (*Setaria italica* P. Beauv.) using the approach of enzyme electrophoresis. De Cherisey et al. (1985) have studied the genetic control of seven isoenzyme systems, five of which are treated here. Strains of cultivated *S. italica* and spontaneous green foxtail (*S. viridis* L.) were analyzed. It is commonly recognized that the cultivated species was domesticated from wild green foxtail, and crosses between these taxons have produced semifertile hybrids (Li et al. 1945). This same phenomenon has been observed for hybrids created in our laboratory (unpublished results). De Wet et al. (1979) reported obtaining a completely fertile hybrid.

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The material studied here was sampled from many regions of the world. The principal object of this study was to extract information about genetic variability, both intra- and interregional. Hypotheses pertaining to the domestication process are also discussed.

Materials and methods

Enzymes of 223 strains of *S. italica* and 45 strains of *S. viridis* were studied by electrophoresis. Five isoenzyme systems were observed: Esterase (Est), Acid Phosphatase (Acph), Glutamate Oxaloacetate Transaminase (Got), Malate Dehydrogenase (Mdh) and 6-Phosphogluconate Dehydrogenase (Pgd). All the strains were fixed lines. The *S. italica* samples originated from ten different regions and *S. viridis* from two regions (Table 1).

The methodology of electrophoresis and the genetic control of the enzymes have been described in a separate paper (De Cherisey et al., in press). The principal methods of data analysis used for this paper were the following:

1. The allelic frequencies, the number of polymorphic loci, the average number of alleles per locus, and the genic diversity were calculated in order to study interregional variability. The coefficient of genic diversity was obtained using the formula for heterozygosity proposed by Nei (1978). The coefficient of heterozygosity was initially intended for studying populations mating randomly. Foxtail millet is a cleistogamic plant and the material studied here consisted of samples of stocked seed, thus they are absolutely not randomly mating populations. However, Nei (1973) also suggested using this type of coefficient as a diversity index, with the remark that is would not have the same significance as heterozygosity.

2. Discriminant or Canonical Variable Analysis was used for studying interregional variability (Mardia et al. 1979).

Results

Polymorphism and genetic variability

As previously reported (De Cherisey et al. 1985), 10 loci with 26 alleles were observed for the five isoenzyme systems studied (Table 2).