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VARIABILITY OF GENE EXPRESSION IN
NATURAL POPULATIONS.

In *Muscaria atlanticum* Boiss. et Reuter there exists three esterase isozymes, A, B, and C, each one codified by the structural genes Est-1, Est-2, and Est-3, respectively (1). The close species *Urginea maritima* (L.) Baker present also three esterase isozymes, codified by three structural genes Est-1, Est-2, and Est-3, in the same way.

Electromorphs variability in the isozymes of both species have been detected. In both species these structural genes show also a differential expression pattern when different organs of plant are analyzed (Figs. 1 and 2).

In *M. atlanticum* three pentaploid populations have been found. In other four populations there are three ploidy levels living together (tetra, penta and hexaploid) (2). In one of these localities (TV) the individuals 5n and 6n show a differential expression pattern of isozymes respect to remainder populations: in the flowers of those individuals the isozyme C is not present; however, this isozyme is present in the roots and leaves of these individuals (Fig. 1).

In *U. maritima* 18 hexaploid populations from Iberian Peninsula have been analyzed. The general expression pattern in different organs of these plants is shown in the Fig. 2. However, in one of these populations (IF) the expression pattern is distinct of the remainder: in the roots of all these individuals the three isozymes, A, B, and C, are presents.

We think both events can be explained by changes in the gene expression control systems. Perhaps these changes could be originated by position effects due to the great amount of chromosomal rearrangements detected in natural populations of both species (3, 4).

On the other hand, we believe these changes in the gene expression control systems play a very important role in the population differentiation of these species, since, as some authors have been postulated (5, 6), the evolutionary changes at the organismal level of the living beings have been based more frequently in mechanism alterations of gene expression controls, than in changes of protein amino acid sequences.

REFERENCES