

The genetic structure of the *Funaria hygrometrica* HEDW. populations in Sierra Nevada (Spain) using the sequence-related amplified polymorphism (SRAP) technique

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In the current context of global climate change and its effect on the biodiversity, studies on this subject have gained a special relevance. Many of them focus on economically important plants such as wheat, barley, rice, etc. However, there are other groups of organisms that represent a significant portion of the existing biodiversity, and whose reactions to climate change are obviously important. Within these, the bryophytes, with approximately 15,000 species, represent a very important part. We have selected the moss *Funaria hygrometrica* Hedw., (Funariaceae) as a model organism to study its population structure and the diversity among its sub-populations along the altitudinal gradient of Sierra Nevada mountains in Spain. The populations were divided in three groups: lowland populations (below-500m), middle altitude populations (500m - 1000m) and high mountain populations (1000m - 1800m). The population structure and genetic diversity of *F. hygrometrica* were determined by applying sequence-related amplified polymorphism (SRAP) molecular marker technique which uses pairs of primers with AT- or GC-rich cores to amplify intragenic fragments for polymorphism detection. Is a PCR based technique in which the first five cycles the annealing temperature is set at 35°C and the following 35 cycles are run at 50°C. Five of the 64 tested SRAP primer pairs were fully successful. A total of 57 samples from 10 locations were amplified. The band number amplified by each primer pairs ranged from 14 to 23. In total 98 bands were observed, of which 97 were polymorphic (98.88%). Within populations, a significant difference in the percentage of polymorphic loci, ranging from 33.67% to 86.73%, was observed among the heights, which indicated that a relationship can be established between genetic diversity and the altitude. The genetic variation found to be mainly caused by the variation within groups, accounting for 80.88% of the total genetic variation. Moreover, the gene flow of *F. hygrometrica* between the locations was 3.2348, and that relative high gene flow can prevent efficiently gene drift. Based on the Neighbor Joining (NJ) cluster dendrogram and Principal coordinate analysis (PCOOA) diagram, the 10 locations studied may be divided into pairs groups, while among the 57 samples a moderate separation and a relative high level of genetic diversity within the

populations of *F. hygrometrica* of Sierra Nevada (Spain) was found. This is the first report of the application of SRAP technique to Mosses (*F. hygrometrica*).

Keywords: Biodiversity, Bryophytes, Mosses, Funariaceae, *Funaria hygrometrica* Hedw., Bryophytes in-vitro cultivation, Sierra Nevada flora, SRAP molecular marker, genetic distance, Phylogenetic tree.

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