

## GENETIC RELATIONSHIPS AMONG LENTIL (*LENS CULINARIS* MEDIK.) LOCAL POPULATIONS ASSESSED BY AFLP AND I-SSR

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*biodiversity, ecotype, Lens culinaris, molecular markers*

Lentil (*Lens culinaris* Medik.) is an important seed legume crop cultivated worldwide as human food and dating back to pre-historic times. In the last century, lentil was widely cultivated in Italy, providing a cheap source of dietary proteins and allowing spreading of a lot of local biotypes. Socio-economic changes which occurred in the last 50 years in Italy had conducted to a drastic reduction of lentil cultivation (by 93%) resulting in the disappearance of several local populations and exposing the ones still in cultivation to a high risk of genetic erosion. In order to prevent disappearance of genetic variation inside landraces it is important the improvement and the conservation of the already existing biodiversity. To estimate the level and distribution of genetic variation in endangered local populations using molecular markers is a primary objective of conservation genetics. The aim of the current research was to investigate the level of genetic variation within and among three of the most appreciated Italian common lentil ecotypes: Onano, Altamura and Villalba.

For Altamura, Onano and Villalba, 29, 30 and 25 plants respectively were analysed at individual level by fluorescent AFLP (Amplified Fragment Length Polymorphism) markers using six primer combinations and by means of bulks using I-SSR (Inter-Simple Sequence Repeats) markers utilizing 14 primer. Out of the 643 discernible DNA fragments generated by AFLP, 565 (87.87%) were polymorphic. The percentage of polymorphic bands within populations ranged from 49.92 to 62.99. Genetic diversity ( $H$ ) within populations ranged from 0.147 to 0.167. The fixation index ( $G_{st} = 0.219$ ) showed that about 78% of the total genetic variability observed can be attributed to within population differences and approximately 22% is due to differences among the three landraces. The estimated gene flow ( $N_m = 1,779$ ) confirmed the condensation of a common gene pool.

Genetic similarity between individuals estimated by Dice coefficient was calculated in all possible pair-wise comparisons and the correspondent matrix was used for the construction of an UPGMA dendrogram, showing that genotypes belonging to the same landrace clustered in the same group. The genetic similarity estimates within and between populations ranged from 0,82 to 0,86 and from 0,71 to 0,75, respectively. The low level of genetic diversity exhibited by Altamura, Onano and Villalba suggests a common origin for them. Our results also show the ability of AFLP markers to distinguish the genotypes analyzed into different clusters according to their geographic origins.

The comparison between the AFLP dendrogram obtained from markers performed at individual level and the one provided by I-SSR markers performed by bulked DNA showed a high correlation

(96%) suggesting a good efficiency of both methods with a greater discriminative ability of AFLP markers in comparison with I-SSR.