Eval uati on of quantitativ e charact er s correlati ons and distanc es in some Albanian wheat genotypes

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Twenty wheat genotypes from Albania Gene Bank were evaluated for some quantitative characters at experimental field of Agricultural University of Tirana (Albania). The study was carried out to analyze the variability of wheat genotypes conserved in gene-bank, and it is realized in a Randomized Block Design with four replications, during three years (2004–2006). Evaluated characters were: number of spikelet’s per spike, number of seeds per spikelet, number of seeds per spike, spike length, spike density, weight of the spike kernel, 1000 kernel weights, plant height, days to flower, and days to maturity. Correlation between ten characters and metric distances were also evaluated for all wheat genotypes. Days to flowering time and days to maturity ranged from 131 to 144 and from 173 to 200 days respectively. The differences between minimal and maximal values were small for the days to flower (13 days with standard deviation 2.764) and around three times more for the days to maturity (40 days with standard deviation 9.006). Differences between wheat analyzed genotypes and standard for yield characters were significant: in eight genotypes for number of spikelet’s per spike (differences ranged from 111% to 120%), and in four genotypes for number of seeds per spikelet (differences ranged from 119% to 140%); and in five genotypes for number of seeds per spike (differences ranged from 122% to 150%). There were also significant differences, in six genotypes, for weight of spike kernel where these differences were ranged from 120% to 163%. Correlation of characters were positive correlations between number of seeds per spikelet with number of seeds per spike (0.937), and weight of the spike kernel (0.922), and days to maturity (0.479). There were positive correlations between weight of the spike kernel with number of seeds per spike (0.908), and days to maturity (0.523).

Study results, using Agglomerative Hierarchical Clustering (AHC) method for dissimilarity between genotypes (Euclidean distances), grouped wheat genotypes into three classes: first class include 6; second class 9; and third class 5 genotypes. In conclusions Nikla-792; IKB-6 and LVS-93 were the promising genotypes useful to be used in the further developments of wheat breeding programs.