SUMMARY

The aim of this study was to determine within breed genetic diversity in endangered Çine Çaparı sheep by Random Amplified Polymorphic DNA (RAPD) markers and to obtain genetic similarities and distances among animals within flock and also between flocks. Seventy two animals from 3 flocks (26 animals from ADU-ÇÇKP conservation flock, 32 animals from Erdoğan Aktürk's flock (EA) in Tatarmemişler village and 14 animals from Mustafa Vural's flock (MV) from Dereköy village) were genotyped with 24 arbitrary primers. Genetic similarities between and within flocks were investigated.

DNA was extracted from blood. DNA amplification was realized by PCR using 10'mer RAPD primers. PCR products was separated on agarose gels and photographed after ethidium bromide staining. Band sizes and profiles were obtained from gel photographs and a data matrix including band profiles were generated. Data were analyzed by using the formula of Nei for genetic similarities and distances.

The genetic similarities between individuals within a flock are ranged between 0.4468 and 0.8511 for ADÜ-ÇÇKP conservation flock, 0.4894 and 0.8723 for EA flock, and 0.5745 and 0.8723 for MV flock. Genetic distances were ranged between 0.1613 ile 0.8056 for ADÜ-ÇÇKP flock, 0.1366 and 0.7147 for the EA flock, and 0.1366 and 0.5543 for the MV flock. The similarities between flocks were ranged between 0.8439 and 0.9037 and, genetic distances were ranged between 0.0902 and 0.1698.

As a result, the similarity was highest between ADU-ÇÇKP conservation flock and the flock in Tatarmemişler than the flock in Dereköy village. This may be stem from higher animal flow between ADÜ-ÇÇKP conservation flock and flock in Tatarmemişler village. Mean genetic similarity between animals within flock were found highest for MV flock. This finding was also supported by fixation of frequency of nearly one-third of the loci in MV flock.