

Allozyme Variation in Wild Rats *Rattus norvegicus* (BERKENHOUT 1769) (Mammalia: Rodentia) from Turkey

Nuri Yiğit^{1*}, Ercüment Çolak¹, Şakir Özkurt², Aydın Özlük³, Reyhan Çolak¹, Nursel Gül¹, Fulya Saygılı¹, Duygu Yüce¹

¹University of Ankara, Faculty of Science, Department of Biology, Ankara, Turkey

²University of Ahi Evran, Faculty of Education, Dept. of Primary Education, Kırşehir, Turkey

³University of Hitit, Faculty of Science and Art, Department of Biology, Çorum, Turkey

Abstract: The genetic diversity of 22 allozyme loci was investigated in 33 wild rat (*Rattus norvegicus*) specimens from 4 sub-populations. Eight of the 22 loci (*Pgm*, *Hk*, *Me-M*, *Ldh*, *α-Gpdh-1*, *α-Gpdh-2*, *Fum*, *Xdh*) were polymorphic. The level of genetic variation was measured by mean number of alleles per locus ($A = 1.18$), percentage of polymorphic loci ($P = 18.2$), mean heterozygosity per locus observed ($H_o = 0.007$), and mean heterozygosity expected under Hardy -Weinberg equilibrium ($H_e = 0.057$).

Mean F_{ST} value was 0.34, indicating 34% genetic variation and suggesting high-level differentiation between sub-populations of the Turkish wild rat. The number of migrants (N_m) was 0.48 and showed that gene flow was relatively low between sub-populations. Even though a high level of genetic variation was observed, the low N_m value and H_o could be evidence of the Wahlund effect or a genetic bottleneck for the sub-populations. It is also suspected that there might be some factors preventing gene flow from the sub-populations, which constitute their own genetic potential for new taxonomic units.

Key words: *Rattus norvegicus*, Allozyme, Turkey