

Genetic Analysis of Cockchafer (*Melolontha* spp.) Species

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Cockchafers are widespread pest species throughout Central Europe. In genus *Melolontha* there are six species but economically important species comprise just the European cockchafer (*Melolontha melolontha* Linnaeus), the large cockchafer (*Melolontha pectoralis* Germar) and the forest cockchafer (*Melolontha hippocastani* Fabricius).

M. melolontha is divided into seven tribes in the Carpathian basin. The four Alpine tribes have a four-year life cycle while three lowland tribes complete their life cycle in three years and inhabit lowland areas of Hungary. In the present work we have investigated the genetic differences among the three economically important species and the three lowland tribes of *M. melolontha*.

Hundred-eleven individuals of *M. melolontha*, 15 of *M. hippocastani* and 16 of *M. pectoralis* from Central Europe (Hungary, Austria, Slovenia, Romania and Poland) were investigated. A 1188 bp fragment of the cytochrome oxidase (COI) gene of the mitochondrial DNA (mtDNA) was amplified by polymerase chain reaction (PCR), sequenced and aligned to construct phylogeny trees.

The three *Melolontha* species are different in both DNA and amino acid sequence. On the 1188 bp DNA fragment difference was 12.3% between *M. melolontha* and *M. hippocastani*; 13.0% between *M. hippocastani* and *M. pectoralis*; and 5.1% between *M. melolontha* and *M. pectoralis*. The tribes do not form separate or unique haplotypes. The maximum of pairwise distances in *M. melolontha* using Tamura-Nei method is 0.5% therefore we were not able to detect any difference between the lowland tribes of *M. melolontha*.

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