# ‘‘POLYMORPHISM IN MITOCHONDRIAL CYTB REGION IN CHOSEN FOREST AND FIELD GALLIFORMES SPECIES AND THEIR FILOGENETIC RELATEDNESS – STUDY IN SILICO”

**[1]JULIA KAŹMIERSKA, [2]BEATA GRZEGRZÓŁKA, [3]JOANNA GRUSZCZYŃSKA**

[1,2]Scientific Association of Experimental and Laboratory Animals, Warsaw University of Life Sciences – SGGW
[2,3]Department of Animal Genetics and Conservation, Institute of Animal Sciences, Warsaw University of Life Sciences - SGGW
E-mail: juliakazmierska42@gmail.com

Forest and field Galliforms belong to the order Galliformes, family Phasianidae. In Poland, we qualify as forest Galliformes the western capercaillie, black grouse and hazel grouse, while field Galliformes include quail, partridge and pheasant. Over the course of many years of observation, a decrease in the total population of the above mentioned species is noticeable, which is mainly due to the destruction of their natural habitats.
The purpose of this study is was to determine polymorphism of cyt b mitochondrial DNA region in selected forest and field Galliformes species – the western capercaillie, black groupe, hazel grouse, quail, partridge and pheasant and define their filogenetic relatedness.
Cytochrome b is one of three catalytic subunits found in the mitochondria of eucaryotes. The mtDNA sequence encoding this structure is highly conservative. For preliminary analise was used cyt b sequentions from the western capercaille (Tetrao urogallus) (AB120132.1), black grouse (Tetrao tetrix) (EF571183.1), hazel grouse (Bonasa bonasia) (NC_020591.1:14794-15936), pheasant (Phasianus colchicus) (AF028798.1), patridge (Perdix perdix) (AF028791.1) and quail (Coturnix coturnix) (L08377.1). The similarity of these sequences was compared with the bioinformatic programs BLAST and MUSCLE. The results obtained indicate that the differences between the sequences are at the level of 7 - 23%. The highest degree of genetic similarity (93.61%) was identified between the sequences of black grouse and western capercaillie. There are known cases of inter-species hybrids of these species. It was showed that the lowest level of genetic similarity of cytochrome b sequences (84.16%) occurs between black grouse and quail.
It was found that there is a need for further genetic studies to determine individual haplotypes of cytochrome b in Galliformes species. This will allow a better understanding of the genetic changes occurring within the species, which may enable to a correctly identification of the affiliation of individual haplotypes of cytb mtDNA to phylogenetic lines and clades.

**Keywords** - CYTB, Galliformes, polymorphis mtDNA, phylogenetics.