GENETIC TECHNIQUES FOR DESIGNATION OF MAIN FLYWAYS OF THE WOODPIGEON (*COLUMBA PALUMBUS*) IN EUROPE AS A TOOL FOR CONTROL AND PREVENTION OF PATHOGENIC DISEASES

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Abstract. The population genetic structure of the Woodpigeon (*Columba palumbus*) in Europe was studied analyzing the distribution of different D-loop haplotypes among bird samples, collected in various breeding and wintering sites of the species (in Russia, Belarus, Lithuania, Sweden, Hungary, France, Spain and Portugal). Totally 89 different haplotypes ascertained as belonging to 5 haplo-groups were identified after examination of partial D-loop sequences consisting of 359 bp mtDNR fragments derived from 360 samples. The results of this study indicate that the Eastern Atlantic Flyway is used by Woodpigeons breeding in NW Russia, Belarus, Lithuania, Sweden and wintering mainly in the Iberian Peninsula. A distinct population genetic structure is characteristic of Woodpigeons breeding in Hungary and using the Mediterranean Flyway. The designation of main flyways of Woodpigeons in Europe is necessary for the control and prevention of potential spread of pathogenic diseases and parasites, as this species is the most important game bird in Europe.

Keywords: Woodpigeon, flyways, mtDNA D-loop, transmission of diseases, Europe.