## 2. Streszczenie w języku angielskim.

The Forkhead box transcription complex is a set of conserved genetic factors and their expression is associated with important physiological processes taking place at the level of various functional areas. Its name comes from the fork head gene first discovered in 1989 by Weigel et al. in the fruit fly mutant *Drosophila melanogaster*. Currently, the Forkhead transcription complex genes are referred to as the Fox genes. The Foxp3 box gene has been described in many mammals, including humans (NC000023), domestic dogs (NC006621), and domestic mice (NC000086). The indicated gene is responsible for the differentiation and modulation of the activity of CD4 + CD25 + Treg T cells (Fontenot et al., 2003; Sakaguchi et al., 2005). The transcription factor FOXP3 is also necessary for development and functions of CD4 + FOXP3 + T (Treg) regulatory cells (Seitz et al., 2022). Treg lymphocytes play an important role in autoimmonological processes and their expression level can be associated with cancer diagnosis (Biller et al., 2007). It is worth noting that the presence of the Foxp3 gene in mammals is associated general connection of forkhead genes with the functions of carbon life (Wojtaszczyk et al., 2013).

The current state of knowledge about the genome of the common fox is still incomplete. The genome of the common fox shows strong analogies to that of other canines including the domestic dog, but also shows phylogenetic similarities to less obvious species, such as pinnipeds (Arnason et al., 2006). It is worth noting that the common fox is a species living in natural conditions, but is also subject to inbreeding mechanisms resulting from its use also for breeding purposes. The canine genome was fully sequenced in 2005 (CanFam1 and CanFam2, Lindblad et al., 2005), but is now being further explored in the search for epigenetic factors determining the expression of specific coding regions. The aim of the research is to assess the differentiation of the expression level of the Foxp3 gene in the common fox compared to the domestic dog. Biological samples in the form of blood collected from foxes came from the Experimental Station in Chorzelów and animal farms in the Lublin and Ryki poviats, Poland. The biological material was collected under the conditions of euthanizing the animals for production purposes. Biological material in the form of blood from domestic dogs was collected during standard medical and veterinary activities undertaken in the Epizootiology Clinic and the Infectious Diseases Clinic of the Faculty of Veterinary Medicine in Lublin. The expression level of the Foxp3 gene in the common fox is 71% higher in females than in males, and this result is statistically significant, which may suggest the validity of the research hypothesis that this gene is located on the X heterosome. The level of HPRT expression in the common fox it is 64% higher in males

compared to females, and this result is not statistically significant. Obtaining the results of the HPRT expression level with stable SEM characteristics and the distribution of individual values may justify the assumption of the research hypothesis about the feedback of the levels of HPRT and Foxp3 expression. The level of expression of the Foxp3 gene in the common fox is higher by 138% in individuals up to 1 year of age compared to individuals above the age of 1 year, and mentioned result is not statistically significant. The common fox of the flamed variety was characterized by the highest level of HPRT gene expression compared to other breeds, and this result was highly statistically significant. The expression level of the Foxp3 gene was significantly higher in domestic dog compared to the common fox and this result was highly statistically significant. The results of the study confirm that the common fox and domestic dog are strongly different species, and at the same time they undermine the legitimacy of using canine primers in the fox genome in some cases. Due to the known functions of the Foxp3 gene in the immunological system, the results may be used to create a clinical trial calibration protocol compliant with the GCP guidelines for the development of solutions delivering immunodulation functions in the future.