In the domestic horse, the seven basic blood group systems *(A, C, D, K, P, Q,* and *U)* are distinguished. Due to the high level of polymorphism (the presence of 34 erythrocyte antigens determined by nearly 60 alleles), the knowledge of blood group inheritance has been used for decades in horse breeding, to verify their parentage. Currently, when this role is played by DNA markers, the variability of erythrocyte antigens is analyzed mainly to assess the likelihood of a serological conflict (and the resulting neonatal isoerythrolisis in foals) and to select an appropriate donor for blood transfusion. Although the equine blood group systems have been known for decades, the knowledge regarding their genetic background is scarce. Only the approximate chromosomal locations of the genes that determine the 4 group systems *(A, K, Q,* and *U)* are known. Unfortunately, due to the lack of knowledge regarding the molecular background of equine blood groups variability, their analyzes are based only on laborious and time-consuming serological techniques, which require the collection of fresh animals' blood and possession of test sera containing specific antibodies.

This research project aims to characterize the genetic basis of the equine erythrocyte antigens variability, with special emphasis put on the most immunogenic antigens (which are the main cause of serological conflict and determine the possibility of blood transfusion). This goal will be achieved by comparing the sequences of RNA isolated from the blood of horses with serologically defined, different blood groups. This comparison will allow the identification of genes and their polymorphic variants responsible for the observed erythrocyte antigens differentiation. The potential impact of the most promising polymorphisms will then be validated on the genomic DNA of a broad cohort of horses representing different breeds, with predefined blood types (resources of the Horse Genetic Markers Laboratory, Poznan University of Life Sciences). The collected data about erythrocyte antigens of over 36,000 horses and the collection of frozen biological material (blood or DNA) from these animals will allow the verification of the relationship between indicated polymorphisms and specific blood antigens.

The results obtained during the present project conducting will enhance the knowledge regarding the molecular background of equine blood groups variability. Defining specific genes and their variants determining the polymorphism of equine erythrocyte antigens may in the future result in the development of molecular tests allowing the determination of blood groups based directly on DNA sequence, without the need to conduct serological analyzes.