In the course of the project 128 177 we have analysed both the Pannon White rabbit and the Hungarian Border Collie populations. The most important results obtained are the following.

Pedigree data of the Hungarian Border Collie dog breed was constructed, to examine genetic diversity within the breed and between its different lines. The database based on available herd books from the development of the breed (the late 1800s) until now. The constructed pedigree file consisted of 13 339 individuals from which 1567 dogs (born between 2010 and 2016) composed the reference population that are still alive and active from breeding aspect. Since the breed is visibly subdivided by appearance, the reference population was dissected according to the existing lines. The number of founders was 894 but only 8 individuals were responsible for contributing 50% of the genetic variability. The reference population had a pedigree completeness 99.6% until 15 generations and inbreeding coefficient of 9.86%, respectively. Due to the changing breed standards and the requirements of the potential buyers the effective population size substantially decreased between 2010 and 2016. Generation intervals varied between 4.09 and 4.71 years where the sire paths were longer due to the later ages when males begin their breeding carrier compared to females. Genetic differences among the existing lines calculated by fixation indices are not significant, nonetheless conventional and ancestral inbreeding coefficients are showing the segregation among subpopulations. Based on the calculated inbreeding the effect of inbreeding on hip and elbow dysplasia was determined for the same dog population. Ancestral inbreeding coefficients were calculated by using a gene dropping simulation method with GRain 2.2 software. Cumulative logit models (CLM) for CHD and CED were fitted using a logit-link Poisson distribution and the classical (F_W), and ancestral inbreeding (F_BAL, F_KAL, and F_KAL_NEW) coefficients as linear regression coefficients. The effective population size was calculated from F_W and decreased in the examined period along with an increase of F_W; however, slight differences were found as a consequence of breeding dog imports. CHD values were lowered by the expansion of F_BAL, as the alleles had been inbred in the past. For CHD, signs of purging were obtained. There was a positive trend regarding the breeding activity (both sire and dam of the future litters should be screened and certified free from CHD and CED), as years of selection increased the frequency of alleles with favorable hip and elbow conformation. Division of the ancestral inbreeding coefficient showed that alleles that had been identical by descent (IBD) for the first time (F_KAL_NEW) had a negative effect on both traits, while F_KAL has shown favorable results for alleles IBD in past generations. Some authors had proven this phenomenon in captive populations or experimental conditions; however, no evidence of inbreeding purge has ever been described in dog populations. Despite the various breeding practices, it seems that alleles of these polygenic disorders could be successfully purged out of the population with long-term selection.

Concerning the Pannon White rabbit populations in the closed selected small population with extremely informative pedigrees (up to 25 generations) and well recorded survival of kits at birth (22718) we have provided evidence for the purging of ID. In the first breeding period, rabbits born from 1992 to 1997, the significant litter ID for the survival of kits at birth has been estimated (standardized inbreeding effects bz.FL CI95% = [-0.10 to -0.06]; standardized new inbreeding bz.FNEWL CI95% = [-0.11 to -0.07]) and standardized lethal likelihood effects bz.LLL CI95% = [-0.10 to -0.06]). In the second breeding period, rabbits born from 1997 to 2017, significant ID have disappeared. The best model of the first period, with significant estimates of the new (negative) and ancestral inbreeding effects (positive), has provided additional evidence of purging of ID for the survival at birth. When survival is modelled as a binary variable and population is selected over many generations, analyses of ID and purging of ID require a demanding and complex modelling approach.

Besides, survival of rabbit kits at birth is modelled as a binary variable applying generalised linear mixed models (GLMM) based on the log link function. Modelling was performed taking into account the inbreeding coefficient of the kit, inbreeding coefficient of the dam, season of parturition, parity of the dam and animal. Based on the monthly averages of the survival of rabbit kits at birth the analyzed period (1992-2017) was divided to two periods (1992-1997 and 1997-2017). Altogether 22718 kindling records were analysed. The estimated regression coefficients for the inbreeding coefficients of the kits and for the dams were -0.20±0.27 and -0.41±0.36 and 0.05±0.08 and -0.01±0.09 in the first and second periods, respectively. This corresponds to the lethal equivalent of 0.2 in the first period which disappeared in the second period. Due to the large standard errors the results were not significant. Finally, the evolution of the survival at birth was evaluated applying the PurgeR software based on the inbreeding-purging model. In the period from 1992 to 2017, 22 718 kindling records were ana-lyzed. According to the heuristic approach, the purging coefficient reached the maximum possi-ble value of 0.5 when estimated between 1992-1997. Based on the expected fitness over genera-tions and on the expressed opportunity of purging the beneficial effects of purging could be ex-pected after 10 generations. The proportion of the purged genetic load could be between 20 and 60%. While the results obtained are not entirely conclusive, they do raise the possibility that some of the inbreeding load was caused, at least in part, by genes that could be successfully re-moved from the population by purging.

The utilisation of the information-theoretic approach and multimodal inference, with application of generalised linear mixed models based on the logit link function and considering polygenic random effects, was a rational option grounded in theory. The obtained evidence and modelling of purging of ID further enhance our knowledge in finding efficient breeding strategies that would lead to the elimination/reduction of inbreeding detrimental load in small selected mammalian populations.