Report about the OTKA project’s results (106175- 2013-2015)

According to the workplan between 2013-2015 the data of the reproductive, growth and carcass traits were continuously collected for all rabbit breeds (Pannon White, Pannon Ka and Pannon Terminal) bred at the Kaposvár University.

Genetic parameter estimation for the reproductive traits

In order to evaluate 18.398 kindling records of 3.883 Pannon White rabbit does, different animal models used. To estimate the genetic parameters for number of kits born alive (NBA), number of kits born dead (NBD) and total number of born kits (TNB) of the Pannon White rabbits were the following:

A + D; A + D + F; A + Pe; A + Pe + F; A + Pe + D; A + Pe + D + F;

Where, A = additive genetic effects, F = inbreeding coefficients of the does and litters, D = dominance effects, Pe = permanent environmental effects.

The most complete model estimated VA and VD to contribute 5.5±1.1% and 4.8±2.4%, respectively, to total phenotypic variance (VP) for NBA, the corresponding values for NBD were 1.9±0.6% and 5.3±2.4%, for TNB, 6.2±1.0% and 8.1±3.2%, respectively. These results indicate the presence of considerable VD. Including dominance in the model generally reduced VA and VPe estimates. Including inbreeding coefficients as covariates did not affect estimates of any variance component.Based on the pattern of the obtained results for the Pannon White breed for the Pannon Ka and Pannon terminal breeds only two models were used. These models differed only in the inclusion of the dominance effect (A + Pe, A + Pe + D). Besides, NBA and NBD were also evaluated together using two two-trait models for each breed and similarly to the single trait models these models differed only in the inclusion of the dominance effect.

A slightly smaller dataset was used (17.018) to evaluate the litter weight at day 21 of the Pannon White breed. The different models were:

A + Pe (Basic model); A + D (Reduced extended model); A + Pe + D (Extended model)

Where all elements were the same as above. Based on the performance records of the Pannon White breed using the basic models heritability estimate was 0.08 (0.01) for LW21. For the Pannon terminal breed this estimate was 012 (0.04). The relative importance of the permanent environmental effects for LW21 for the examined breeds were 0.17 (0.01) and 0.29 (0.04). Compared to the basic model using the extended models the Pannon White breed showed very similar heritability estimate for LW21: 0.07. Similar tendency was received for the Pannon Terminal breed where the heritability estimated by the extended models was: LW21: 0.12 (0.04). The relative importance of the permanent environmental effects for LW21 for the same breeds were 0.15 (0.02) and 0.27 (0.04). Based on the extended models the ratios of the dominance components compared to the phenotypic variances were 0.23 (0.01) and 0.07 (0.04) for LW21 in the Pannon White and Pannon Large breeds. When the reduced extended models were used for the Pannon White breed the heritability estimate was0.08 (0.01) for LW21. For the Pannon terminal breed this estimate was 0.032 (0.04). Concerning the dominance effects for the Pannon White and Pannon Terminal breeds the relative importance of dominance effects were 0.42 (0.01) and 0.46 (0.03) for LW21. It was clear that the magnitudes of the dominance effects were extremely high but this was the result of the confounding effects between the dominance effects with other random effects (and permanent environmental effects).

For the Pannon Ka breed 11.583 kindling records of 2620 rabbit does were analysed. Using the basic single-trait and two-trait models heritability estimates were 0.094±0.018 and 0.090±0.016 for NBA, 0.037±0.010 and 0.041±0.012 for NBD and 0.117±0.018 for TNB, respectively. For the Pannon terminal breed these estimates were 0.05±0.03 and 0.06±0.03, 0.01±0.01 and 0.01±0.01 and 0.03±0.02, respectively for the same traits using the same models. For the Pannon Ka breed the relative importance of permanent environmental effects was 0.069±0.014 and 0.069±0.012 for NBA, 0.025±0.011 and 0.023±0.010 for NBD and 0.060±0.013 for TNB, respectively. For the Pannon terminal breed the relative importance of the permanent environmental effects were 0.14±0.03 and 0.14±0.02 for NBA, 0.07±0.03 and 0.07±0.03 for NBD and 0.15±0.02 for TNB. Using the extended single-trait and two-trait models the ratios of the dominance components compared to the phenotypic variances were 0.048±0.008 and 0.046±0.007 for NBA, 0.068±0.006 and 0.065±0.006 for NBD and 0.005±0.0073 for TNB, respectively for the Pannon White breed. Using the data of the Pannon terminal breed the dominance variance components for NBA, NBD and TNB were 0.16±0.02 and 0.15±0.01, 0.06±0.02 and 0.08±0.01 and 0.16±0.02, respectively. Genetic correlation coefficients between

NBA and NBD were 0.401±0.171 and 0.521±0.182, for the Pannon Ka and -0.82±0.58 and -0.31±0.55 for the Pannon terminal breed, respectively.

For the Pannon Large breed 6269 records of 1469 does were examined. NBA, NBD and TNB was evaluated by 12-12-12 single trait models testing the best model structure based on the available environmental factors. The tested factors included parity, year-month, year-season of kindling, age and age square of the does. Heritability estimates were low for all traits and ranged between 0.074-0.084 (0.018-0.021) for NBA, 0.015-0.021 (0.009-0.009) for NBD and 0.038 and 0.056 (0.015-0.018) for TNB (standard errors of estimates are given in brackets). The ratios of the permanent environmental and the phenotypic variances exceeded that of the heritability estimates and ranged between 0.111-0.160 (0.016-0.018) for NBA, 0.059-0.074 (0.014-0.015) for NBD and 0.113-0.169 (0.014-0.017) for TNB (standard errors of estimates are given in brackets). Characterizing the models' fit bias values were practically zero for all traits and models. Mean squared errors and correlation coefficients between the observed and predicted values were consistent for all traits and showed that the best fit was observed when beside the obvious random effects (animal and permanent environmental effects) the model considered parity, age of the doe and year-month of kindling effects, respectively.

After the models showing the best fit were selected for NBA, NBD and TNB, dominance effects were included. Heritability estimates were 0.056 (0.028) for NBA, 0.017 (0.012) for NBD and 0.019 (0.022) for TNB (standard errors of estimates are given in brackets). The relative importance of the permanent environmental effects was 0.094 (0.031) for NBA, 0.048 (0.024) for NBD and 0.069 (0.028) for TNB (standard errors of estimates are given in brackets). Ratios of the dominance effects exceeded that of the heritability estimates and were 0.274 (0.024) for NBA, 0.047 (0.013) for NBD and 0.382 (0.025) for TNB (standard errors of estimates are given in brackets). Compared to additive model including dominance showed some confounding with additive genetic and with permanent environmental effects and reduced the calculated genetics trends (0.035 vs 0.03, -0.0017 vs -0.003 and 0.016 vs 0.01 for NBA, NBD and TNB, respectively).

Genetic parameter estimation for the growth and carcass traits

As the most important grwoth trait in rabbit breeding average daily gain (ADG) of Pannon White (125.511) and Pannon Large (31.366) rabbits was evaluated. Three different types of models were used:

A + C (Basic model); A + D (Reduced extended model); A + C + D (Extended model)

Where all terms were the same as above. Based on the performance records of the Pannon White breed using the basic models heritability estimates were 0.21 (0.03); 0.29 (0.01) and 0.08 (0.01) for TMV, ADG and for LW21, respectively. For the Pannon terminal breed these estimates were 0.22 (0.03); 0.17 (0.02) and 012 (0.04) respectively for the same traits using the basic models. Using the basic models for the Pannon White and Pannon Terminal breeds the relative importance of random litter effects were 0.09 (0.02) and 0.09 (0.02) for TMV; 0.24 (0.01) and 0.22 (.001) for ADG. The relative importance of the permanent environmental effects for LW21 for the same breeds were 0.17 (0.01) and 0.29 (0.04). Compared to the basic model using the extended models the Pannon White breed showed very similar heritability for ADG: 0.29 (0.01) and TMV (0.20) (0.01). Similar tendencies were received for the Pannon Terminal breed where the heritabilities estimated by the extended models were the following: TMV: 0.22 (0.03), ADG: 0.17 (0.02). Using the extended models for the Pannon White and Pannon Terminal breeds the relative importance of random litter effects were 0.07 (0.02) and 0.08 (0.03) for TMV; 0.24 (0.01) and 0.22 (.001) for ADG. The relative importance of the permanent environmental effects for LW21 for the same breeds were 0.15 (0.02) and 0.27 (0.04). Based on the extended models the ratios of the dominance components compared to the phenotypic variances were 0.03 (0.01) for ADG. The magnitude of the estimated dominance effects for the Pannon Terminal breed were 0.05 (0.03) for TMV, 0.01 (0.01) for ADG, respectively. When the reduced extended models were used for the Pannon White breed the heritability estimates were 0.21 (0.03); 0.22 (0.01) for TMV and ADG, respectively. For the Pannon terminal breed these estimates were 0.22 (0.03); 0.17 (0.02). Concerning the dominance effects for the Pannon White and Pannon Terminal breeds the relative importance of dominance effects were 0.27 (0.02) and 0.28 (0.02) for TMV; 0.74 (0.01) and 0.76 (.001) for ADG and 0.42 (0.01) and 0.46 (0.03) for LW21. It was clear that the magnitudes of the dominance effects were extremely high but this was the result of the confounding effects between the dominance effects with other random effects (random litter effects and permanent environmental effects).

Using a small Pannon White sample (316) genetic parameters of other carcass traits (measured by computer tomography) were determined, using single trait models. The fat volume of the hind leg and the whole carcass showed high heritability estimated (0.58 (0.11) and 0.61 (0.12) but compared to these values the muscle volume of the whole carcas showed much lower value

(0.28 (0.10). After pooling the data of the three experimental slaughter and disclosing some erroneous records altogether slaughter records of 527 Pannon White rabbits were analysed. The examined traits were: thigh fillet (TMFILLET), dressing out percentage (DoP) calculated as the raito of the chilled carcass weight and live body weight at slaughter, hind part percentage (compared to the reference carcass) (HPP), and perirenal fat (RENALF). Becasue of the small dataset the basic model contained only one random factor (additive genetic effect) while the extended model also considered dominance effects. Thus the applied models were: A and A+D. Applying the basic model hereitability estimates were moderate 0.18 (0.07), 0.19 (0.06), 0.23 (0.07) for TMFILLET, DoP and HPP and high (0.68 (0.08) for RENALF. Extending the models with dominance effects the heritabilities did not change expect for RENALF (0.59 (0.16). Accordingly, the estimated dominance effects were practically zero for TMFILLET, DoP and HPP and moderate (0.16 (0.06) for RENALF.

Inbreeding depression

Due the size of the available reproductive datasets inbreeding depression for the reproductive traits was only evaluated of the Pannon White breed. Significant inbreeding depression due to litter inbreeding was observed for NBA (bFl=-0.41±0.11 per 10% increase in Fl) and TNB (bFl=-0.34±0.10 per 10% increase in Fl), while estimates related to doe inbreeding depression were not significant. For NBD, we observed significant inbreeding depression due to doe inbreeding (bFd=0.18±0.07 per 10% increase in Fd) but not due to litter inbreeding. Among the carcass traits 10% increase of the inbreeding coefficient resulted the most severe decrease (24.4 cm^3) for TMFILLET. DoP and HPP were less sensitive for inbreeding depression (-0.06% and -0.02%). On the contrary similarly to TMFILLET RENALFAT showed substantial depression (-2.88 g).

Breeding value stability

Concerning breeding value stability for the Pannon White breed Spearman rank correlations between breeding values estimated with the different models were close to unity for NBA (0.984-0.999), NBD (0.988-1.000) and TNB (0.978-0.998). This means that no substantial re-ranking with respect to breeding values occurs across different models. Concentrating on the top ranked animals our results showed high concordance of the top 100 and 1000 rabbits across different models. Including inbreeding coefficient in the model caused smaller changes (88-97) in the top 100 rankings for the various model pairs (A + Pe vs. A + Pe + F, A + D vs. A + D + F, A + D + Pe vs. A + D + Pe + F). Only moderate differences (86-94) were observed among the 100 top-ranked rabbits using the model (A + Pe) and the most complete one (A + D + Pe + F). Similarly moderate changes were observed among the 100 top ranked rabbits between model pairs A + Pe vs. A + D (85) and A + Pe + F vs. A + D + F (94). The decrease in concordance was greatest for NBD, which is also the trait that showed the largest ratio of dominance to additive variance (VD/VA) in our study. Results for the top 1000 rabbits were similar to results for the top 100 animals for that trait, though concordance of selected animals did not drop as much for a pair of the most extreme models as is it was in the case of the top 100 animals. Concerning the Pannon Ka breed based on the different single-trait models the estimated breeding values showed very high Sperman rank correlations for NBA, NBD and TNB (0.999, 0.992 and 0.999). On the contrary the two-trait models resulted lower (0.898) rank correlation of breeding values for NBA and it was low (0.384) for NBD. When Sperman rank correlations between the breeding values were estimated with single-trait and two-trait models the observed values were high (0.913-0.984) for NBA and moderate for NBD (0.681-0.793). Beside the overall stability the breeding value stability of the top 100 and 1000 rabbits showed that the common proportion of the highest ranked rabbits based on the different models was high (93-99 and 953-999) based on the single-trait models of all examined traits. However, in our study based on the other model combinations (single-trait vs. two-trait models; including or excluding the dominance effects) the re-ranking among the top ranked rabbits was substantial especially for NBD (30-84 and 525-700). Concerning LW21 of the Pannon White breed the following correlations were obtained: 0.93 (basic –extended) 0.96 (basic – reduced extended) and 0.96 (extended – reduced extended). These values were: 0.99 (basic –extended) 0.96 (basic – reduced extended) and 0.96 (extended – reduced extended) for the Pannon Terminal breed. Concerning Pannon Large rabbits spearman rank correlation coefficients between breeding values of the additive and dominance models were high for all NBA, NBD and TNB (0.96-0.98), when dominance effects were included in the models but some re-ranking was observed among the top ranked animals for every trait. The stability of the breeding values estimated with the different models (basic model; reduced extended model; extended model) were determined for all traits in both breeds as the Pearson correlation coefficient calculated among the breeding values of the same rabbits. For TMV the calculated correlation coefficient exceeded 0.99 for both breeds. The same phenomenon was found for ADG for the Pannon Terminal breed. The ADG breeding values showed somewhat lover correlation in the Pannon White breed. The correlations among the different models were 0.99 (basic –extended) 0.98 (basic – reduced extended) and 0.98 (extended – reduced extended).

Near-infrared spectroscopy (NIRS) analyses

The research focused on analysing the samples originating from 180 and 177 Pannon White rabbits, born and kept at the experimental rabbit farm of the Kaposvár University, Hungary. Rabbits were slaughtered at 11 weeks of age at the body weight of 2.2-3.3 kg, at the slaughter house of OLÍVIA Ltd. in Lajosmizse, Hungary. The carcasses were dissected according to the World Rabbit Science Association's recommendation. Total deboned left hind legs were collected in the slaughter house and were transported to the laboratory. The samples were chopped, homogenized (IKA A11 basic), and freeze-dried (Christ Alpha 1-4). Freeze-dried samples were re-homogenized before NIRS scanning. The calibration dataset of 2005 originates from different feeding and housing systems, the other three groups are from homogeneous datasets. The slaughter age, the slaughter method and slaughter traits collection agreed in all groups. Differences were observed in the sample preparation and sampling in the case of Group 2013. The whole hind leg meat was used in Group 2005, 2014 and 2015, while in the case of Group 2013 only the meat of the thigh muscle was utilized. Portions for freeze-drying and later NIRS scanning were picked up from the total amount of homogenized meat of an individual in all groups, except in Group 2013 where the portions were picked up after simple chopping, resulting a non-representative sampling of leg muscle in this case. The same instrument was used over the years, however, it was replaced several times, thus the laboratory where NIR spectra acquisitions were performed was different. Repeated scans of each sample were recorded and the average spectra per samples were used for further data analyses. Results of the NIRS prediction are presented in tables 1-4.

Table 1: The prediction results of fat content of the prediction set of 2014 (n=180) by using PCR, PLS, Local PLS and MLR

Model	**PCR[1]**		**PLS[2]**		**LocalPLS[3]**		**MLR[4]**	
	Mean	**SD[5]**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**
2005ref87_2014pred80(Group1)	**9.77**	*2.04*	**9.78**	*2.04*	**10.4**	*2.29*	**9.56**	*1.80*
2013ref94_2014 pred 80(Group 2)	**11.1**	*1.84*	**11.4**	*1.80*	**10.8**	*1.99*	**10.7**	*1.93*
2005_2013ref181_2015 pred 180(Total)	**9.80**	*1.98*	**9.70**	*1.98*	**10.4**	*2.08*	**9.45**	*1.45*

[1]PCR: Principal component regression; [2]PLS:Partial least square regression; [3]Local: Local Partial least square regression; [4]MLR: Multiple linear regression; [5]SD: standard deviation

Table 2: The laboratory and prediction results of fat content of the prediction set of 2014 (n=21) by using PCR, PLS, Local PLS and MLR

LAB 1		**LAB 2**		**Model**	**PCR[3]**		**PLS[4]**		**LocalPLS[5]**		**MLR[6]**	
Mean	**SD[7]**	**Mean**	**SD**		**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**
10.8	*3.41*	**10.7**	*3.21*	**(Group1)**	**10.5**	*3.18*	**10.5**	*3.18*	**11.1**	*3.52*	**10.1**	*2.76*
				(Group 2)	**11.7**	*2.88*	**12.0**	*2.80*	**11.3**	*3.01*	**11.3**	*3.01*
				(Total)	**9.85**	*2.27*	**10.4**	*3.08*	**11.2**	*3.31*	**9.85**	*2.27*

LAB1: 1st measure of laboratory; LAB2: 2nd measure of laboratory [3]PCR: Principal component regression; [4]PLS:Partial least square regression; [5]Local: Local Partial least square regression; [6]MLR: Multiple linear regression; [7]SD: standard deviation

Table 3: The prediction results of fat content of the prediction set of 2015 (n=178) by using PCR, PLS, Local PLS and MLR

Model	**PCR[1]**		**PLS[2]**		**LocalPLS[3]**		**MLR[4]**	
	Mean	**SD[5]**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**
2005ref87_2015pred78(Group1)	**8.45**	*2.10*	**8.46**	*2.10*	**8.65**	*2.01*	**9.51**	*2.10*
2013ref94_2015pred78(Group 2)	**10.12**	*1.85*	**9.88**	*1.83*	**9.08**	*1.81*	**10.63**	*2.08*
2005_2013ref181_2015pred178(Total)	**8.68**	*2.03*	**8.69**	*2.02*	**8.86**	*1.85*	**9.40**	*1.57*

[1]PCR: Principal component regression; [2]PLS:Partial least square regression; [3]Local: Local Partial least square regression; [4]MLR: Multiple linear regression; [5]SD: standard deviation

Table 4: The laboratory and prediction results of fat content of the prediction set of 2015 (n=21) by using PCR, PLS, Local PLS and MLR

LAB 1		**LAB 2**		**Model**	**PCR[3]**		**PLS[4]**		**LocalPLS[5]**		**MLR[6]**	
Mean	**SD[7]**	**Mean**	**SD**		**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**
8.35	*2.41*	**8.72**	*2.69*	**(Group1)**	**9.81**	*2.49*	**9.82**	*2.49*	**9.21**	*2.69*	**10.70**	*2.24*
				(Group 2)	**11.3**	*2.22*	**11.1**	*2.21*	**9.58**	*2.42*	**11.83**	*2.34*
				(Total)	**9.99**	*2.41*	**9.99**	*2.40*	**9.41**	*2.54*	**10.30**	*1.76*

LAB1: 1st measure of laboratory; LAB2: 2nd measure of laboratory [3]PCR: Principal component regression; [4]PLS:Partial least square regression; [5]Local: Local Partial least square regression; [6]MLR: Multiple linear regression; [7]SD: standard deviation

The error of sampling influence the accuracy of the prediction more importantly than altering of the measuring place or differences in the time and number of measuring. As concern the applied multivariate statistical methods Local PLS eventuated the most accuracy results. From among the models the calibration set of 2005 seems to be the most convenient for predicted the unknown samples.

Besides, the achieved publications two manuscripts are submitted to Animal Science Papers and Reports (determining the best model for evaluating NBA, NBD and TNB of the Pannon Large rabbits and estimating the relative importance of the dominance effects, for these traits). One additional manuscript will be submitted for Animal Science Journal based on the results of the NIRS analyses. The project was succesful concerning Ms Henrietta Kiszlinger who owing to the OTKA project succesfully defended her PhD degree and received a permanent status at the Kaposvár University and became the lecturer of pig breeding.