

Genetic parameters and genetic trends of reproduction traits in synthetic Pannon rabbits using repeatability and multi-trait animal models

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Abstract

Genetic parameters and genetic trends of total number of born kits (TNB), and number of kits born alive (NBA) were estimated in Pannon White and Pannon Ka rabbits for the first four parities. REML and BLUP procedures were applied using repeatability and multi-trait animal models (PEST and VCE software). Heritability estimates were low for both traits and breeds and ranged between 0.06-0.07 (0.01-0.02) and 0.04-0.06 (0.02-0.02) for TNB and NBA, respectively (standard errors of estimates are given in brackets). The estimated permanent environmental effects showed higher relative importance compared to the additive genetic effects and they ranged between 0.07-0.13 (0.01-0.02) and 0.08-0.14 (0.01-0.02) for TNB and NBA, respectively. High genetic correlation coefficients were found between TNB and NBA (0.97 ± 0.02 , 0.96 ± 0.02) for Pannon White and Pannon Ka, respectively. The genetic correlation coefficients estimated between TNB and between NBA of the successive parities (as separate traits) ranged between 0.64-0.97 (0.04-0.11) and 0.56-0.99 (0.03-0.10) for Pannon White and Pannon Ka, respectively. The estimated genetic trends for TNB and NBA were negligible for the Pannon White and small (0.03-0.02 [0.01-0.01]) for Pannon Ka. The mean squared errors (MSE) of the repeatability and multi-trait models were similar but the correlation coefficients of between the observed and predicted values were lower for the multi-trait (0.27-0.61) than for the repeatability models (0.43-0.65).

Keywords: rabbits, genetic parameters, genetic trends, reproduction traits

Zusammenfassung

Genetische Parameter und genetische Tendenzen bei Reproduktionsmerkmalen von synthetischen Pannon-Kaninchen unter Verwendung von Wiederholbarkeits- und Mehrmerkmalstiermodellen

Genetische Parameter und genetische Tendenzen der Gesamtanzahl von geborenen Kaninchenjungen (TNB) und der Anzahl von lebend geborenen Kaninchenjungen (NBA) wurden für Pannon-White- und Pannon-Ka-Kaninchen für die ersten vier Paritäten geschätzt. Dazu wurden REML- und BLUP-Verfahren unter Verwendung von Wiederholbarkeits- und Mehrmerkmalstiermodellen (PEST- und VCE-Software) eingesetzt. Die Heritabilitätsschätzwerte waren für beide Merkmale und Rassen niedrig und lagen

zwischen 0,06-0,07 (0,01-0,02) bzw. 0,04-0,06 (0,02-0,02) für TNB bzw. NBA (Standardfehler in Klammern). Die geschätzten permanenten Umweltauswirkungen zeigten eine höhere relative Bedeutung im Vergleich zu den additiven genetischen Auswirkungen und lagen zwischen 0,07-0,13 (0,01-0,02) bzw. 0,08-0,14 (0,01-0,02) für TNB bzw. NBA. Für Pannon White bzw. Pannon Ka wurden hohe genetische Korrelationskoeffizienten zwischen TNB und NBA ($0,97 \pm 0,02$; $0,96 \pm 0,02$) festgestellt. Die genetischen Korrelationskoeffizienten, die zwischen TNB und zwischen NBA der aufeinanderfolgenden Paritäten (als getrennte Merkmale) abgeschätzt wurde, lagen zwischen 0,64-0,97 (0,04-0,11) bzw. 0,56-0,99 (0,03-0,10) für Pannon White bzw. Pannon Ka. Die geschätzten genetischen Tendenzen für TNB und NBA waren für Pannon White vernachlässigbar und für Pannon Ka klein (0,03-0,02 [0,01-0,01]). Die mittlere quadratische Abweichung (MSE) für die Wiederholbarkeits- und Mehrmerkmalmodelle waren vergleichbar, aber die Korrelationskoeffizienten zwischen den festgestellten und vorberechneten Werten waren für die Mehrmerkmalsmodelle (0,27-0,61) geringer als für die Wiederholbarkeitsmodelle (0,43-0,65).

Schlüsselwörter: Kaninchen, genetische Parameter, genetische Tendenzen, Reproduktionsmerkmale

Introduction

Litter size is a more important trait in rabbit production than in other prolific species. Current genetic schemes for rabbit meat production are based in a three way cross, in which two lines are selected for litter size in order to produce the crossbred doe and the other line is selected for growth rate in order to produce terminal sires (Blasco 1996, Khalil & Al-Saef 2008). The different maternal rabbit lines of the different breeding programs are selected for different reproductive traits such as number of kits born alive, litter size at weaning or litter weight at weaning (or at day 21) (Khalil & Al-Saef 2008, Mocé & Santacreu 2010). Regardless of the chosen trait there is a general agreement in the literature that the heritability estimates of these traits are low (Blasco 1996, Khalil & Al-Saef 2008). Considering the low heritability estimates, in order to establish efficient selection programs the best possible model has to be defined. It has to be determined whether the litter size of the successive parities are the repeated measurements of the same trait (i.e. the genetic correlation between them is >0.8). Thus the litter size records can be evaluated using either repeatability or multi-trait animal models. Although this topic has been analyzed extensively in pigs (Hamann *et al.* 2004, Irgang *et al.* 1994, Noguera *et al.* 2002, Roehe & Kennedy 1995) in rabbits the available relevant literature is scarce (Baselga *et al.* 1992, Piles *et al.* 2006). Moreover the effect of the mating buck on litter size is analyzed only by few authors (Piles *et al.* 2006, Rastogi *et al.* 2000). Thus the first objective of the present study was the comparison of the repeatability and multi-trait animal models using the reproductive records of the different types of Pannon rabbits of the Kaposvár University. The second objective of this study was to analyze the relative importance of the mating bucks on the Pannon rabbits' reproductive performance.

Material and methods

Foundation populations

The development of the Pannon White rabbit breed was recently described by Nagy *et al.* (2010). The development of the maternal line at the Experimental rabbit farm of the Kaposvár University in Hungary started in 1995 with sperm import of a prolific genotype. The sperm was used inseminating Pannon White does but from the progeny only few breeding animals were selected. In 1999 beside individual sperm import 114 female and 48 male newborn kits of a genotype showing high reproductive performance were imported. These rabbits mated within genotype (and with Pannon White rabbits of high prolificacy) forming the base of the maternal line (called Pannon Ka). Pannon Ka was officially recognized as a new synthetic rabbit breed by the Hungarian National Institute of Agricultural Quality Control at 2003. Since then the genotype selected as a closed population (apart from individual sperm import of few bucks at 2004 and 2005) for number of kits born alive.

Population management and traits recorded

Breeding rabbits of both breeds were individually housed in a closed rabbitry (at the experimental rabbit farm of the Kaposvár University), in breeding cages. The basic area and the height of the wire net cage of the does were 84×38.5 cm (including the 26×38.5 cm sized nest box and feeder) and 35 cm, respectively. The same sizes of the wire net cage of the bucks were 55×43 cm and 40 cm, respectively. In winter the rabbitry was heated to a minimum temperature of 15-16 °C, while – although the rabbitry is equipped with cooling panel – in the summer the temperature occasionally reached levels as high as 28 °C. All bucks were fed by the same commercial pellet (10.3 MJ DE/kg, 15.1 % crude protein, 17.2 % crude fibre). During the first three weeks after kindling the does received lactation pellet (11.1 MJ DE/kg, 18.0 % crude protein, 15.5 % crude fibre) then it was gradually changed to starter pellet (10.4 MJ DE/kg, 16.1 % crude protein, 16.9 % crude fibre). Water was available *ad libitum* from nipple drinkers. The rabbits were first inseminated at the age of 16.5 weeks then using a 42-day long reproduction rhythm, AI occurred 11 days after kindling. The rabbits were inseminated with diluted semen (of single bucks) and at the same time they were injected 1.5 µg GnRH analogue (Ovurelin, Reanal) to their thigh muscle. Bucks began their reproductive performance at 20 weeks of age. Does which failed to conceive were reseeded 21 days after the unsuccessful inseminations. After 2 unsuccessful inseminations the does were culled.

To avoid mating of close relatives and high inbreeding, a circular mating system was used dividing the population of both breeds into 4 groups (Pannon White groups: 1-4, Pannon Ka groups: 5-8). After the matings all progeny received the group number of their bucks. The male progenies remained in the group but the female progenies were moved and mated with the bucks of the adjacent group: 1♀×4♂; 2♀×1♂; 3♀×2♂; 4♀×3♂; 5♀×8♂; 7♀×6♂; 8♀×7♂. The generations were overlapping.

The present analysis was based on 12 494 and 3 413 kindling records of 4 629 Pannon White and 1 316 Pannon Ka rabbit does mated to 997 Pannon White and 297 Pannon Ka sires between 1992-2010 and between 2003-2010, respectively. The total number of animals

in the pedigree file was 6 226 and 1 965 for Pannon White and for Pannon Ka, respectively. Kindling records of each rabbit doe consisted of identity number, date of insemination(s), identity number of mating buck, date of kindling, total number of born kits (TNB) number of kits born alive (NBA), litter size and litter weight at 21 days after kindling. Due to the common practice of cross-fostering the analyzed traits were restricted to TNB and NBA. According to the literature the litter size of the latter parities have high correlations therefore only the first 4 parities were considered in the analysis. Descriptive statistics are presented in Table 1.

Table 1
Mean and SD of TNB and NBA in the Pannon White and Pannon Ka rabbit breeds

Trait	Parity	Pannon White	Pannon Ka	Pannon White	Pannon Ka	Pannon White	Pannon Ka
		No. of records		Mean		SD	
TNB	1	4278	1174	7.93	8.08	2.86	2.86
	2	3371	823	8.70	8.90	3.05	3.05
	3	2685	743	8.91	9.33	3.15	3.15
	4	2153	673	9.14	9.22	3.13	3.13
	1-4	12494	3413	8.56	8.77	3.38	3.38
NBA	1	4278	1174	6.95	7.10	3.31	3.31
	2	3371	823	8.09	8.33	3.29	3.29
	3	2685	743	8.23	8.71	3.39	3.39
	4	2153	673	8.56	8.57	3.32	3.32
	1-4	12494	3413	7.81	8.04	3.06	3.06

TNB: total number of born kits, NBA: number of kits born alive, SD: standard deviation

Statistical models

TNB and NBA were evaluated with the REML and BLUP procedures in order to estimate genetic parameters and genetic trends. In the first evaluation bivariate repeatability animal models were used. Then the TNB and NBA records of the successive parities (1-4) were analyzed as separate traits using multi-trait animal models. The applied software was PEST (Groeneveld 1990) and VCE 5 (Kovac & Groeneveld 2003).

In case of TNB and NBA the basic repeatability model was:

$$y = Xb + Za + Wpe + e \quad (1)$$

where y is the vector of observations, b is the vector of fixed effects, a is the vector of random animal effects, pe is the random vector of permanent environmental effects, e is the vector of random residual effects and X , Z and W are the incidence matrices relating records to fixed, animal and random permanent environmental effects, respectively.

Expected values of a , pe and e were $E(a) = E(pe) = E(e) = 0$. The variance-covariance structure was assumed to be $V(a) = A\sigma_a^2$, $V(pe) = I\sigma_{pe}^2$, $V(e) = I\sigma_e^2$, and $cov(a, e) = cov(e, a) = 0$, where A is the numerator relationship matrix. Also $cov(y, a) = ZA I \sigma_a^2$.

Regarding the model, the distribution of y was assumed normal, the traits were determined by many additive genes of infinitesimal effects at infinitely many unlinked loci. The alternative repeatability model contained the random effects of the mating bucks. Compared to the basic repeatability model the multi-traits models did not contain the permanent environmental

effect and instead of the parity effect the age of the does was used as covariate (other terms were the same). The structures of the used models are given in Table 2.

To compare the repeatability and multi-trait animal models' fit mean squared error (MSE) and correlation between the observed and predicted performances ($r_{\hat{y}_i, y_i}$) were calculated using the PREDICT option of PEST.

Table 2

The considered factors for the examined traits in the repeatability and multi-trait models

Factor	Type	TNB/NBA	TNB1-4/NBA1-4
Parity	Fixed effect	x	-
Year-month	Fixed effect	x	x
Animal	Animal effect	x	x
Permanent environment	Random effect	x	-
Age1-4	Covariate	-	x

TNB: total number of born kits, NBA: number of kits born alive, TNB1-4: TNB at the successive parities (1-4), NBA1-4: NBA at the successive parities (1-4), Age1-4: age of the does at the successive parities (1-4)

Results and discussion

Descriptive statistics

Comparing the mean values of TNB and NBA of the analyzed breeds it can be seen that the differences were small to the advantage of the Pannon Ka (maternal line) which may be explained by the different selection criteria of the breeds. However the observed NBA of Pannon White was also lower than the reported performances of this rabbit breeds some years ago (Lévai & Milisits 2002). Lévai & Milisits (2002) reported higher ratio of the dead born pups in the case of non-fatty rabbits. Because the CT-aided selection of the Pannon White breed results in an increased lean production this may caused the small decrease in NBA compared to the period mentioned by Lévai & Milisits (2002). It is worth mentioning that the highest TNB and NBA of the Pannon Ka was observed sooner (3rd parity) than recorded for Pannon White or for pigs (5th parity) (Cechova & Tvrdon 2006).

Genetic parameters

The relative importance of additive genetic and permanent environmental effects estimated with repeatability models are presented in Table 3.

The heritability estimates of TNB were low for both breeds. Mantovani *et al.* (2008) received very similar value (0.07) for TNB as in our study for an Italian synthetic rabbit line selected for maternal traits. Somewhat higher heritabilities (0.09-0.2) were reported by other authors (García & Baselga 2002a, García & Baselga 2002b, Piles *et al.* 2006, Rastogi *et al.* 2000). The differences among the heritability estimates of the different studies may be caused by the different rabbit breeds used for these studies. Moreover the applied repeatability models contained also different fixed and random factors. For the Spanish and French rabbit lines (García & Baselga 2002a, García & Baselga 2002b, Piles *et al.* 2006). A common fixed effect in the applied models was the physiological status of the does with 3 levels (nulliparous, lactating or non-lactating at mating). Contrary to these studies Rastogi *et al.* (2000) used

parity as fixed effect and other random effects (maternal genetic effects, mating sire effects) that were not used by the previously mentioned authors. The estimated heritabilities for NBA were even lower than that of TNB. This phenomenon was observed by several other studies (García & Baselga 2002a, García & Baselga 2002b, Mantovani *et al.* 2008, Piles *et al.* 2006, Rastogi *et al.* 2000) where the estimated heritabilities ranged between 0.05 and 0.175 thus mostly exceeding our estimate. Beside the possible explanations mentioned so far Rastogi *et al.* (2000) (conducting their study at Trinidad) mentioned that in tropical environments, rabbit populations often have a heterogeneous history involving multiple breed introductions and crossings which could explain the reported relatively high heritability value (0.12). Other authors (Moura *et al.* 2001, Lenoir & Garreau 2009) reported very similar values (0.04-0.05) compared to our study. The observed genetic correlation between TNBA and NBA was close to unity for Pannon White (0.97 ± 0.02) and for Pannon Ka (0.96 ± 0.02). This result was in close agreement with the finding of Mantovani *et al.* (2008) who reported a genetic correlation of 0.97 between these traits. This result suggests that increasing the NBA will also result in a higher number of stillborn kits. Moreover Mantovani *et al.* (2008) estimated an unfavourable genetic correlation (0.62) between NBA and mortality % up to weaning indicating a negative trend in decreasing the number of weaned kits with the enhancement of the NBA.

Table 3

Heritability estimates and relative importance of permanent environmental and mating buck effects in the Pannon White and Pannon Ka rabbit breeds (standard errors of estimates are given in brackets)

		Basic model		Alternative model	
		TNB	NBA	TNB	NBA
Pannon Wite	h^2	0.07 (0.01)	0.06 (0.01)	0.07	0.06
	pe	0.07 (0.01)	0.08 (0.01)	0.07	0.08
	mb	-	-	0.00	0.00
Pannon Ka	h^2	0.06 (0.02)	0.04 (0.02)	0.06	0.04
	pe	0.13 (0.2)	0.14 (0.02)	0.13	0.14
	mb	-	-	0.01	0.006

TNB: total number of born kits, NBA: number of kits born alive, pe: permanent environmental effects, mb: mating buck effects

The estimated heritabilities for TNB and NBA using multi-trait animal models are provided in Table 4.

It can be seen that the heritabilities showed no trend with the increasing parity number. The topic whether the genetic background of litter size was the same after the successive parities was first investigated in rabbits by Baselga *et al.* (1992). Baselga *et al.* (1992) conducted a series of univariate models for NBA of the first three parities and found the highest h^2 at the first parity (0.10-0.14) compared to the second and third parities (0.01-0.07). Based on these findings Baselga *et al.* (1992) suggested that genetic correlations among the NBA of the successive parities were possibly lower than unity. However, as Baselga *et al.* (1992) did not use multivariate models the observed results estimates may be biased for the latter parities because not all information on selection was used simultaneously in the analyses. In pigs using univariate or bivariate analyses Roehe & Kennedy (1995) and Irgang *et al.* (1994) found that heritability increased with advancing age which tendency was opposite compared to Baselga *et al.* (1992). In pigs Alfonso *et al.* (1997) conducted bivariate and multi-trait analyses

for TNB and NBA of the first 5 parities. Based on their results no trend was observed for the heritabilities with the advancing parity number. In accordance with Alfonso *et al.* (1997) Piles *et al.* (2006) did not find any tendency for the heritability estimates with the advancing age using multi-trait models.

Table 4

Estimated heritabilities (diagonals) and genetic correlations (off-diagonals) of TNB and NBA in subsequent kindlings of the Pannon White and Pannon Ka rabbit breeds (standard errors of estimates are given in brackets)

	1	2	3	4	TNB
Pannon White	0.12 (0.02)	0.89 (0.05)	0.68 (0.05)	0.64 (0.08)	1
		0.12 (0.02)	0.91 (0.04)	0.91 (0.05)	2
			0.19 (0.02)	0.93 (0.04)	3
				0.11 (0.01)	4
Pannon Ka	0.19 (0.03)	0.75 (0.11)	0.74 (0.08)	0.80 (0.09)	1
		0.23 (0.04)	0.82 (0.08)	0.92 (0.05)	2
			0.31 (0.03)	0.97 (0.02)	3
				0.24 (0.04)	4
	1	2	3	4	NBA
Pannon White	0.14 (0.02)	0.90 (0.04)	0.68 (0.06)	0.56 (0.10)	1
		0.14 (0.02)	0.91 (0.03)	0.86 (0.06)	2
			0.17 (0.01)	0.96 (0.05)	3
				0.12 (0.02)	4
Pannon Ka	0.13 (0.04)	0.98 (0.04)	0.71 (0.11)	0.79 (0.12)	1
		0.09 (0.02)	0.82 (0.13)	0.88 (0.12)	2
			0.26 (0.05)	0.99 (0.02)	3
				0.18 (0.04)	4

TNB: total number of born kits, NBA: number of kits born alive

The genetic correlations among the TNB and NBA of the successive parities were high (generally above 0.8) (Table 4) especially for the adjacent parities. For the Pannon White breed the estimated genetic correlation coefficients decreased with the increasing time gap between the different parities. The lowest estimates were obtained between the first and fourth parities for TNB (0.64) and NBA (0.56). For the Pannon Ka breed this tendency was less pronounced probably due to the lower amount of the available data. In a similar study conducted in pigs the genetic correlations reported by Alfonso *et al.* (1997) were high in case of the bivariate analyses (generally higher than 0.8) but were much lower when multi-trait models were used (0.16-0.74). In rabbits multi-trait models were used only by Piles *et al.* (2006) to analyze TNB and NBA of the successive parities. For the genetic correlations among TNB and NBA of the successive parities the authors found high estimates in the A-line generally equal or greater than 0.8. In the other two lines the estimates were much lower for TNB (0.53-0.84) and NBA (0.39-0.82). Based on these results different genes or combinations of genes could be involved in the determination of litter size at the first, second and successive parities. Therefore different parities may be treated as different traits when genetic evaluations are performed (Piles *et al.* 2006). However, Piles *et al.* (2006) also noted that BLUP is not robust to errors in the estimation of genetic parameters. Genetic correlations have greater errors than heritabilities and are

more difficult to estimate. Thus a multiple-trait model has a greater risk of giving wrong estimates than a repeatability model.

The estimated relative importance of permanent environmental effects was somewhat higher for TNB and NBA than that of the additive genetic effects (Table 3). The magnitude of our estimates were inside the range to that (0.07-0.22) of the previously mentioned authors. The alternative repeatability model that included the effects of the mating buck did not finished with optimal convergence status therefore the standard errors could not be obtained (Table 3). Nevertheless it can be seen that the relative importance of these effects were negligible for Pannon Ka and were zero for Pannon White. The mating buck effects were analyzed only by few authors in rabbits (Piles *et al.* 2006, Rastogi *et al.* 2000) and similarly to our study they reported that the relative importance due to random effect of service sire was very low (0.01-0.03). Piles *et al.* (2006) similarly to the present study decided not to use this effect in the multi-trait models. On the contrary in pigs although the effect of service sire was also very low authors suggested to include this effect in the model of TNB (Serenius *et al.* 2003) and NBA (Hamann *et al.* 2004) to improve accuracy of breeding value prediction and to get an efficient tool for phenotypic selection of AI boars due to poor piglet production.

Genetic trends

The estimated annual genetic trends were low for both traits in Pannon Ka (repeatability model) and were negligible for Pannon White (Table 5).

Table 5

Estimated genetic trends of TNB and NBA in the Pannon White and Pannon Ka rabbit breeds (standard errors of estimates are given in brackets)

		Repeatability model	
	Parity	TNB	NBA
Pannon White	1-4	0.008 (0.002)	0.01 (0.002)
Pannon Ka		0.03 (0.01)	0.02 (0.01)
		Multivariate model	
	Parity	TNB	NBA
Pannon White	1	-0.000002 (0.000003)	7.036062E-7 (0.000002)
	2	-0.000002 (0.000002)	9.695047E-8 (0.000002)
	3	0.0002 (0.0001)	0.0002 (0.0001)
	4	0.00002 (0.00001)	0.000021 (0.00001)
Pannon Ka	1	0.00003 (0.00003)	0.00002 (0.00004)
	2	-0.00005 (0.00004)	-0.000002 (0.00002)
	3	0.00007 (0.00003)	0.002 (0.001)
	4	0.00004 (0.00001)	0.0002 (0.0002)

TNB: total number of born kits, NBA: number of kits born alive

The latter breed is not selected for reproductive traits but the observed trend of the Pannon Ka breed is perhaps lower than expected. Moura *et al.* (2001) received the same annual trend for NBA (0.03 rabbits/year) and similar magnitude of correlated response (0.5 kits/10 generations) were found by Santacreu *et al.* (2005) as the result of selection for uterine capacity. On the contrary French and Spanish rabbit lines showed higher genetic trends for

NBA (0.11-0.17 rabbits/generation and 0.12 rabbits/year) (Garreau *et al.* 2005, García & Baselga 2002a, García & Baselga 2002b, Lenoir & Garreau 2009). The differences may be explained by the higher heritabilities found by these studies compared to our results. As de Rochambeau *et al.* (1998) demonstrated when heritability estimate increases the estimated genetic trend also goes up. Thus the small magnitude of the genetic trend of the present study was probably the consequence of the low NBA and TNB heritabilities estimated in the Pannon White and Pannon Ka populations. García & Baselga (2002a, 2002b) used a cryopreserved population to determine the selection response of NBA which was almost identical (0.086 vs. 0.09) with the estimated genetic trend according to García & Baselga (2002a) but the selection response and the estimated genetic trend differed greatly (0.085 vs. 0.175) according to García & Baselga (2002b). However, as Blasco (1996) and de Rochambeau *et al.* (1998) noted that when the heritability is small and when the generations do not overlap, the response estimated with a control strain (e.g. using cryopreservation) is preferable. The regression line through the average genetic values per generation/year fit better in case of overlapping generations (as it was the case for the Pannon rabbit populations).

Fit of the models

The fit of the used models are presented in Table 6. Generally the estimated MSE values of the repeatability and multi-trait models did not differ much but the correlation coefficient between the observed and predicted TNB and NBA were lower for the multi-trait models than that of the repeatability models.

Based on the genetic correlation coefficients estimated between the TNB and NBA of the successive parities and on the parameters evaluating the different (repeatability and multi-trait) models' fit the authors of the present study advocate the use of the repeatability models.

Table 6
Comparison of the different models' fit of TNB and NBA in the Pannon White and Pannon Ka rabbit breeds

		Repeatability model	
		TNB	NBA
Pannon White	MSE ¹	7.70	9.55
	$r_{\hat{y}_i, y_i}^2$	0.46	0.43
Pannon Ka	MSE	5.01	6.88
	$r_{\hat{y}_i, y_i}$	0.65	0.62
		Multivariate model	
		TNB	NBA
Pannon White	MSE	7.57; 8.75; 9.02; 9.22	7.21; 8.44; 8.65; 8.87
	$r_{\hat{y}_i, y_i}$	0.27; 0.30; 0.33; 0.41	0.27; 0.31; 0.34; 0.39
Pannon Ka	MSE	5.85; 6.79; 7.05; 6.45	4.75; 5.60; 4.85; 5.42
	$r_{\hat{y}_i, y_i}$	0.48; 0.32; 0.32; 0.36	0.59; 0.44; 0.61; 0.46

TNB: total number of born kits, NBA: number of kits born alive, MSE: mean squared error, $r_{\hat{y}_i, y_i}$: correlation between the observed and predicted performances

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