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VIRÁG ÁCS

SZENT ISTVÁN UNIVERSITY

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SZENT ISTVÁN UNIVERSITY

FACULTY OF AGRICULTURAL AND ENVIRONMENTAL SCIENCES
Institute of Animal Science
Department of Animal Sciences

Head of doctoral school:

PROF. DR. ANDRÁS SZABÓ DSc

Supervisor:

Prof. Dr. ISTVÁN NAGY DSc

Written by:

Virág Ács

POSSIBLE METHODS FOR IMPROVING MUSCLE MASS PRODUCTION IN THE PANNON LARGE AND THE PANNON WHITE RABBIT BREEDS

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LIST OF ABBREVIATIONS

ADG	Average daily gain
A	Additive genetic effect
abs(evst)	absolute standardized economic weight for a trait
AI	Artificial insemination
BLUP	Best Linear Unbiased Prediction
BW	Bodyweight
BrW	Birth weight
CAST	Calpastatin gene
CCW	Chilled carcass weight
CE	Common environmental effect
CT	Computer Tomography
CSkW	Commercial skin weight
CW	Californian white
DE	Digestible energy
DiFW	Dissectible fat weight
DL	Dorsal length
DLP	Drip loss percentage
DM	Double muscling
DNA	Deoxyribonucleic acid
DoP	Dressing out percentage
EBV	Estimated breeding value
EBW	Empty body weight
EGTW	Empty gastrointestinal tract weight
EV	Economic value
evr	Relative economic weight
EW	Economic weight
FCR	Feed conversation ratio
FGTW	Full gastrointestinal tract weight
GDF	Growth and differentiation factor
gsd_d	Genetic standard deviation for trait *i*.
GZ	German line of Zika rabbits
HCW	Hot carcass weight
hindp	Percentage of the hind part in the reference carcass
HLV	Hind leg muscle volume

IFaW	Inguinal fat weight
KiW	Kidney weight
LHW	Thymus, trachea, esophagus, lung and heart weight
LMV	Loin muscle volume
LvW	Liver weight
LW	Live weight
LW21	Litter weight at 21 years of age
MEV	Marginal economic value
MHC	Myosin heavy chain
MI	Mean of the selection index
midp	Percentage of the mid part in the reference carcass
MSTN	Myostatin
MW	Total meat weight
MW	Metabolic weight
NE	Netto Energy
PE	Permanent environmental effect
PFaW	Perirenal fat weight
PIXEL	Density range of muscle tissue
QTL	Quantitative trait loci
RCW	Reference carcass weight
REML	Restricted maximum likelihood
RI	Relative importance
RR	Number of reproduction cycles
SFaW	Scapular fat weight
SNP	Single nucleotide polymorphism
TL	Thigh length
TMV	Thigh muscle volume
TV_{AV}	Average value of a trait
TV_H	Higher value of a trait
TV_1	Trait decreased with one unit
TW	Total bone weight
valp	Percentage of valuable parts in reference carcass
YEARMONTH1	Year and month of kindling
YEARMONTH2	Year and month of CT measurement

1. INTRODUCTION

Animal breeding concentrates to improve the quality of certain products such as the lean meat quantity of the rabbits' carcass. Within the framework of breeding programs levels of selection pressure applied for the tissues (bone, fat, or muscle), can change the body composition (e.g. meat to bone ratio). The body size of the rabbits shows high variability from dwarf to giant. From the aspect of meat production, medium body size is preferred due to their growth rate and prolificacy. Meat quality and carcass yield of the various breeds also differ substantially.

Studies are focusing on the slaughter weight of the rabbit, measured in different breeds and age groups (Perrier and Ouhayoun, 1990; Lukefahr et al. 1982, 1983) determining the optimal slaughter age for the specific markets. The muscle tissue gives the largest part of the carcass weight regulated by ubiquitous and tissue-specific genes that can participate to expand fat and muscle tissue and thus, meat production. These genes can affect the cellular and biochemical composition of the muscle, thereby influencing not only the quality but also the quantity of the meat.

Achieving continuously improving performance through the successive generations is made possible by selection. For this reason, the whole process should not focus on the genetic merit of the current individuals but the expected merit of the next generation. To build an organized structure for the breeding process, the breeding goal has to be defined. This requires the specification of traits that can genetically improve the population. Thus, the accuracy of breeding value estimation plays an important role in the process, because it shows the amount of transmitted genetic value to the offspring.

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Therefore, the parental generation has to contain individuals with the best breeding values (Oldenbroek et al. 2015).

Direct estimation of breeding values requires specific technical background such as DNA markering, so breeders usually have to rely on phenotypic observations that combine genetic and environmental factors and use a linear model to evaluate the genetic merit of the animals (Henderson, 1975).

For breeding value estimation BLUP method is widely used in practical animal breeding. Making meat production more intensive, rabbit breeders frequently use three-way crossbreeding schemes, and select lines for paternal and maternal traits to take advantage of positive heterosis (Baselga, 2004). Some breeding programs operate with profit models, which can help the breeder to rank the traits by the mathematical relationship of inputs and outputs (Armero and Blasco, 1992). Therefore the profit function can easily form the breeding goal because it is expressed in terms of economic values of the desired traits (ie. the expected profit per one unit increase of the trait).

2.   LITERATURE REVIEW

2.1 Genetic background of muscle development

2.1.1 Postnatal muscle growth

The number of muscle fibers is mainly determined by genetic factors that differ between species (Hall et al., 2004) and sexes (Seidemen and Crouse, 1986) controlled by a special biochemical regulation system. Muscle differentiation yields the largest tissue mass in the organism committing approximately $\sim 10^{12}$ nuclei to the expression of muscle-specific genes.

Skeletal muscle involves muscle fibers from two distinct populations. Primary myofibres provide the framework of secondary fibers and they are formed during the initial stages of myoblast (Wigmore and Evans, 2002). The other population was firstly described by Moss and LeBlond (1971), called satellite cells, which are able to divide the myonuclei during postnatal growth. After birth, the total number of muscle fibers reported remaining unchanged in mammalian species, on the other hand, it is possible to increase the fiber number later as a result of maturation (Ontell and Kozeka 1984). This process results the proliferation of mononucleated myogenic cells to turn multinucleated (Reznik, 1976). However, it is assumed that a subpopulation of myoblasts is not assimilating in the development of the syncytia, in turn, associates in the exterior of all developing fibers (Feldman and Stockdale, 1992). These stem cells also can make cell renewal by the Pax7, thereby ensuring the muscle, growth, and repair *(*Kuang et al. 2007). Examining the satellite cell differentiation in rabbits Barjot et al. (1995) discovered that they differ according to their muscle type origin and slow-twitch and the fast-twitch originated satellite cells show different phenotypic properties. Many genetic markers can affect satellite cells, proliferating and differentiating myoblasts from distant anatomical locations.

2.1.2 Postnatal muscle composition

Muscle fiber type also can change during the maturation and the development of the skeletal muscle and affect meat quality. One of the major contracting proteins is the myosin heavy chain (MHC) containing a total of 11 isoforms revealing the existence of „pure" and „mixed" muscle fiber types depending on the number of the enclosed isoforms, accompanied by several proteins which can determine the functional properties (Staron and Pette, 1986). The genome includes at least 19 classes for the MHC gene superfamily comprising isogenes (Sellers et al., 1997). The phenotypic expression of these genes can be activated by thyroid hormone (Lompre et al. 1984; Izumo et al. 1986) passive stretch (Goldspink et al., 1992; Russell and Dix, 1992) and physical activity like electric stimulation (Pette and Vrbova, 1992). Besides, skeletal muscle fibers from different anatomical origins express various sets of genes adapting them to their required contractive activity. As an example, stretching and immobilizing the fast contracting *tibialis anterior* muscle of the rabbit results a 30% muscle growth within 4 days (Goldspink et al., 1992). Later, Yang et al. (1997) reported that IGF gene expression also has a serious impact on the muscle fiber length and the number of the sarcomeres of the rabbit.

Another regulator gene is *Myostatin* (MSTN), which is responsible for the regulation of muscle fiber types and sizes in the rabbit, acting as a negative regulator to muscle growth (McPherron and Lee 1997*;* Lee, 2004). It is a part of TGF-β superfamily, phylogenetically classified as a growth and differentiation factor (GDF) in the GDF8 subgroup (Lee and McPherron, 1999). In pro-domain form, it can affect the mature C-terminal ligand (Massagué, 1990), antagonize its biological activity resulting increased muscle mass (Thies et al. 2001, Young et al. 2001) and eventuates fat loss even if the animal was exogenously treated with it (Lin et al. 2002; et al.

2002). The double-muscling (DM) was firstly described in cattle (McPherron, 1997) resulting a serious increase in muscle fiber number, while the size remains unchanged. Thus, the amount of muscle mass thrives by almost 20% (Shahin and Berg, 1985; Wegner et al. 2000). The MSTN gene of the rabbit is composed of two introns and three exons. Kuang et al., (2014) studied the effect of MSTN to the *longissimus dorsi* and *biceps femoris* in Californian White (CW) and German great line of ZIKA (GZ) rabbits, where GZ rabbits showed less growth inhibition from MSTN which lead to 36% higher slaughter weight.

2.1.3 Molecular genetics serving the selection process

Microsatellite analysis

Microsatellite markers are widely used in animal breeding. Fontanesi et al., (2008*)* applied DNA markers to identify the genetic variability of the growth hormone (GH) and MSTN to the production traits of rabbits. While GH showed no mutations on the sequenced regions, the polymorphism on the MSTN (C>T on intron 2) can be used as a gene marker to the production traits according to its allele distribution. Linkage and quantitative trait loci (QTL) mapping of the rabbit genome to carcass traits was described by Sternstein et al. (2015*).* identifying the major QTL on chromosome 7 responsible for carcass weight.

SNP markers

Single nucleotide polymorphisms (SNPs) were also detected by several authors, affecting the skeletal muscle development of the rabbit. Qiao et al. (2014) found an SNP on the 476th locus of the 5'-regulatory region which had a significant effect on liver weight, carcass weight, and the weight of the forelegs. Fontanesi et al., (2011) found four SNPs in the MSTN gene of the rabbit, representing differences between breeds in conformation and muscle mass. Sternstein et al. (2014) reported a strong association between one, SNP

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(c. 373+234G>A), and 9 carcass composition traits. (hot carcass weight, reference carcass weight, dressing out percentage, fore-intermediate and hind carcass weight, meat weight for the fore and intermediate part, and bone weight for the intermediate part). According to Abdel-Kafy et al. (2016) a „G" allele of MSTN at the *194A>G SNP had positive effects on the growth performance and the carcass traits, on the other hand, did not produce any negative effects on reproduction.

SNP markers are also widely used for the genotyping of the meat quality traits. In this case, Calpastatin gene (CAST) and Myopalladin gene (MYPN) can be used (Wang et al., 2016, 2017), due to its allele frequency to the selection process. An SNP on the CAST gene (11th chromosome, g.16441502 C > T located at 67 bp in intron 3) determined the yellowness and the intramuscular fat content of the *longissimus dorsi* and *biceps femoris* muscles while a (g.18497416 G > A) was found at 229 bp in exon 13 of chromosome 18. showing strong correlations of the intramuscular fat content of the examined muscles.

CRISPR/Cas9

Genetically modified animal models are widely used in recent years. CRISPR/Cas9 gene-editing technology generated gene-targeted animal models in sheep (Crispo et al. 2015), mice (Horii et al. 2014) and pigs (Wang et al. 2015). Rabbits were firstly used by Qingyan (2016) creating successfully MSTN KO rabbits, where skeletal muscle hypertrophy and hyperplasia along with increased body weight was observed and inherited to the F1 generation.

2.2 Production traits in rabbit breeding

To set up a breeding goal, there are several ways to get information about the population. Food production requires a combination of traits, such as health, reproduction, or welfare traits which allows adapting the

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technological changes more easily. Production traits, however, are more informative because they can be measured by phenotype and be a part of selection criteria.

2.2.1 Reproductive and growth traits

In rabbit breeding, probably the maternal effect has the greatest impact on the progeny performance, even for carcass traits. The morphology of the genital tract, i.e. length and capacity of the uterine horn affects the number of implanted embryos (Dziuk, 1968) but it is not necessarily enhancing litter size since intrauterine crowding results reabsorbed embryos between implantation and birth (Adams, 1960, Webel and Dziuk, 1974). To reduce these losses, Blasco et al. (2005) applied divergent selection for uterine capacity. Increasing litter size in maternal lines resulted higher mortality rates of rabbit kits coinciding with decreasing litter-heterogeneity (Bolet et al. 1996). The weakest animals (under 35g) are most likely to die of starvation during the first week (Szendrő and Barna, 1984) so birth weight (BrW) is one of the most important traits measured in rabbit breeding. Large heterogeneity of individual body weight within the litter leads to disease sensibility, thus post-natal survival rate may diminish rapidly. Falconer, (1952) reported a stabilizing selection for birth weight to prevent prompt death. Heteroscedastic models were also developed assuming that genetic factors also can modify environmental variability (San Cristobal-Gaudy et al. 1998, San Cristobal-Gaudy et al. 2001, Sorensen and Waagpetersen, 2003). Later on, Bolet et al. (2007) selected rabbit lines to evaluate within-litter homogeneity by analyzing the uterine capacity. He observed, that fetus weight and elongation significantly affected birth weigh and they also had an impact on selection efficiency. To improve pre-weaning survival, Garreau et al. (2008a) applied divergent selection on two rabbit lines and reported lower kit mortality in the homogeneous line than in the heterogeneous line.

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The growth rate after birth (Figure 1) follows the characteristics of a sigmoid curve, with an inflection point between the 5th and the 7th weeks of age.
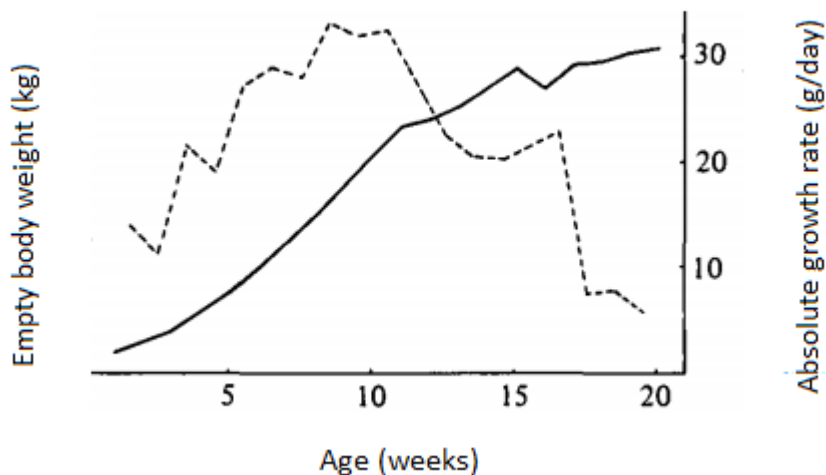
Figure 1. Evolution of empty body weight with age (——) and absolute growth rate (----). (Del Toro and Lopez, 1985)

From the 3rd week of age, milk is not enough to satisfy the high energy needs of rabbit kits so there is a break in the growth curve. Allometric coefficients of the rabbit (Table 1.) may change with age -also- numerous physiological modifications may occur.

Table 1. Multiple correlation coefficients (r^2) and parameters of the allometric equations (log y = α log x + log b) for the carcass (Del Toro and Lopez, 1985)

Components (y)	Period (weeks)	Intervals of empty body weights (g)	Growth ratio $b \pm s^b$	r^2	RSD
		x = empty body weight			
Carcass	1-3	136-313	1.268±0.011	0.9969	0.0114
	4-20	464-2460	1.049±0.001	0.9991	0.0067
Bone	1-5	136-596	1.032±0.014	0.989	0.0267
	6-20	786-2460	0.986±0.006	0.9789	0.0211
Lean	1-5	136-596	1.324±0.016	0.9916	0.0296
	6-20	786-2460	1.208±0.003	0.996	0.0117
Fat (males)	1-6	136-786	0.859±0.050	0.8299	0.0853
	7-20	983-2460	1.080±0.045	0.5914	0.0845
Fat (females)	1-6	136-786	0.789±0.046	0.8708	0.0733
	7-20	983-2460	1.397±0.032	0.8778	0.0614
Head	1-5	136-596	0.787±0.011	0.9881	0.0212
	6-20	786-2460	0.729±0.005	0.9753	0.0181
Breast and ribs	1-8	136-1179	0.955±0.004	0.9983	0.0122
	9-20	1412-2460	1.334±0.008	0.9824	0.0124
Loin	1-3	136-313	1.395±0.022	0.9856	0.0414
	4-20	464-2460	1.077±0.004	0.9928	0.0145
Forelegs	1-5	136-596	1.085±0.016	0.9874	0.0301
	6-20	786-2460	0.967±0.004	0.9902	0.0301
Hind legs	1-5	136-596	1.395±0.022	0.9856	0.0414
	6-20	786-2460	1.077±0.004	0.9928	0.0145
Abdominal wall	1-5	136-786	1.357±0.013	0.9938	0.0298
	6-20	963-2460	1.169±0.009	0.9717	0.0233

Where x is body size, y is organ size, log b is the intercept of the line on the y-axis and α is theslope of the line, also known as the allometric coefficient, RSD is the relative standard deviation

The allometric growth is an essential element for the management of animal resources butalso a tool to guide the work to the selection of animals for rapid growth. In addition, relativegrowth of different tissues determines the economic yield of the carcass. The allometric coefficients

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are constant between 5-6 and 10-11 weeks of age, thus it is advisable to carry out measurements for selection in this period, as there are no significant physiological changes. When comparing rabbit lines or breeds, contrasts between them can be caused by age or genetic differences, thus they can be only accurately highlighted if they are measured in the same stage of maturity. Taylor et al. (1985) reported, that there are two genetic size-scaling rules in mammalian growth:

1.   Treat all age and type variables for the ith genotype as directly proportional to $A_i^{0.27}$, where A_i is the mature body weight of the ith genotype

2.   At every age-standardized, treat all cumulated inputs and outputs for the ith genotype as directly proportional to A_i

In commercial lines, when adult weight is not available comparisons at the same age can be used, but it has to be taken into account, that different-sized lines may have dissimilar maturity states, even at the same age (Pascual et al., 2015). Bodyweight of the growing rabbits has a wide range. Thus rabbits with the same weight are not necessarily in the same developmental stage. To determine skeletal development more precisely, body length is a more accurate assessment (Masoud et al. 1986).

Between-breed contrasts can be determined by the average daily gain (ADG). This trait is a useful tool to establish growth rates since breeds with a high growth rate can make more profit with the same maintenance costs. Breeding programs also commonly operate with feed conversion ratio (FCR) as a selection criteria trait. Intensive rabbit farming improved FCR from 3.8 to 3.4 respectively (Gidenne et al. 2017) in the past 15 years.

FCR is defined as the ratio of feed consumed/kg weight gain of rabbit (finishing weight/weaning weight). After the age of 11 weeks, the feed efficiency of rabbits deteriorates drastically.

However, in sire lines feed efficiency was not targeted by selection for a long time. The concept to add this trait to the breeding goal was firstly described by Brody (1945), who suggested to limit the feed costs by-product unit. This ratio has no biological interpretation and considering selection the relative selection pressure is unknown.

The concept of residual ingested energy was proposed: energy importation and exportation compartments are related to each other. His concept was extended by Tixier-Boichard et al. (2002) to the residual feed efficiency to select on the fraction of feed intake unexplained by maintenance requirements and production level, i.e. modifying feed efficiency without any change in the level of performance.

2.2.2 Genetic parameters for reproductive and growth traits

The heritability estimates of weaning weight, slaughter weight, and average daily gain of the different breeds varied between 0.12 and 0.67. In general, body weight is considered to be highly heritable. Some authors mention dissimilar results due to large standard errors or applied models. Besides, environmental variance greatly differs among farms and non-additive variability (maternal effects, epistasis, dominance) may take part in some estimations to modify heritability (Blasco et al. 2018). Heritability estimates for body weight (BW) at 10 weeks of age ranged from low to moderate (0.12-0.2) (Estany et al. 1992, Lukefahr et al. 1996).

In the Pannon white breed Matics et al. (2014) also reported moderate heritability for BW (0.2-0.26) and for ADG (0.3), similar to Lukefahr et al. (1996), Gómez et al. (1998) and Baselga and García (2002). On the other hand, Moura et al. (1997) estimated higher heritabilities (0.29-0.48) for growth traits. Peiró et al. (2019) found low heritabilities for weaning weight, growth rate, and slaughter weight (0.09, 0.14 and 0.13) and positive

correlated response with ovulation rate. They also mentioned that selection for ovulation rate and litter size did not modify the variability of growth traits using independent culling levels. Piles et al. (2004) found lower genetic correlations between FCR and growth traits than in other species (-0.49 to -0.47).

For growth traits, Wu et al., (2018) found a single nucleotide polymorphism (SNP) at the 9120 bp (*g.9120A>C*) in the 3′ untranslated region of *TAS1R1* gene, showing greater body weight at 70 and 84 days of age (P<0.01 and P<0.05). Between 28 to 84 days of age (P <0.05) this SNP also pointed out higher ADG for genotype AC, than for genotype AA.

2.2.3 Carcass traits

In rabbit breeding, the quality of the carcass represents great economic value. In Europe, the rabbits' carcass weight varies between 1-1.8 kg (differences may occur due to consumer demands), while slaughter yield is 51-66% of live weight according to Ouhayoun (1989), Dalle Zotte and Ouhayoun (1998) and Milisits et al. (2000). In 1994 the World Rabbit Science Association (WRSA) harmonized the criteria and terminology in rabbit meat research and production, where the commission set the standard measurement methods on rabbit meat and carcasses. For slaughtering data, the following parameters are measured till present:

- Commercial skin weight (CSkW)
- Full gastrointestinal tract weight (FGTW)
- Empty gastrointestinal tract weight (EGTW)
- Hot carcass weight (HCW)
- Chilled carcass weight (CCW)
- Drip loss percentage (DLP)
- Dressing out percentage (DoP)

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For the prediction of carcass composition, the measured parameters are:

- Total meat weight
- Meat percentage
- Meat to bone ratio
- Total dissectible fat
- Chilled carcass composition:
- Liver weight (LvW)
- Kidney weight (KiW)
- Thymus, trachea, esophagus, lung and heart weight (LHW)
- Reference carcass weight (RCW)

The characteristics of the reference carcass are:

- Perirenal fat weight (PFaW)
- Scapular fat weight (SFaW)
- Inguinal fat weight (IFaW)
- Dissectible fat weight (DiFW)
- Total bone weight (TW)
- Total meat weight (MW)
- Linear measurements
- Dorsal length (DL)
- Thigh length (TL)
- Lumbar Circumference (LC)

The retail cuts yield of the loin joint exposes 23-28%, (Ouhayoun, 1989), and the hind legs 27-29% of the chilled carcass (Parigi Bini et al. 1992). The meat-bone ratio of the carcass is 4.2-6.0 (Ouhayoun, 1989; Pla and Cervera 1997, Dal Bosco et al. 2000). The fatness of the chilled carcass

is expressed as the percentage of dissectible fat (3-6% of the reference carcass) Dalle Zotte and Ouhayoun (1998).

Rabbit breeds have short generation interval, thus meat quality and carcass traits may change rapidly. Based on consumer expectations the animals are usually slaughtered at a fixed weight, rather than at a fixed age. In this case, carcass traits are mainly influenced by maturity and adult weight (Pla et al., 1996; Piles et al., 2000). However, selection for growth rate caused slaughtering rabbits at a lower age. Consequently, the degree of maturity of the rabbits is reduced affecting carcass and meat quality. Carcass characteristics may also be affected by sex (Cavani et al., 2000). Szendrő et al., (2012) examined the effect of age to the slaughter weight and concluded, that 74-day old rabbits were not mature enough. On the contrary, the age of 84 days was ideal for slaughter, considering the value of the loin fillet, thigh meat, and the whole carcass. The highest values were observed at the oldest age and the heaviest weight (9.1-9.31 €/ carcass for the whole and the total valuable parts of the carcass).

2.2.4 Genetic parameters for carcass traits

Estimated heritabilities for carcass traits were moderate (h^2= 0.29-0.39). (Al-Saef et al. 2008; Ferraz et al. 1992). Since estimating heritability for carcass traits requires the slaughter of many individuals the available literature is scarce.

The carcass ratio traits (e.g. meat-bone ratio, the ratio of the fore/mid/hind part to the reference carcass) had higher heritability values than the carcass composition and carcass parts. The highest heritability estimations were observed for the perirenal fat percentage; h^2= 0.64-0.68 (Larzul et al. 2005; Nagy et al. 2016). For the valuable meat parts of the carcass, thigh muscle volume showed moderate heritability (Gyovai et al.

2008; Gyovai et al. 2012; Nagy et al. 2010a; 2013). On the contrary, the L-value (average surface of the CT estimation of *Longissimus dorsi et lumborum* (LTL) muscle), showed higher heritability estimates. This parameter was also measured using an ultrasound device by Lenoir and Morien, (2016) getting similar results. For the carcass components and muscle traits, the random litter effects were low in all cases (Krogmeier et al. 1994; Gyovai et al. 2008, 2012; Nagy et al. 2010a, 2013). For the dressing out percentage due to the different slaughter ages (63 vs. 96 days), the results of different studies can only be compared with caution. Nevertheless according to a large number of studies (Krogmeier et al. 1994; Garreau et al. 2008b; Larzul et al. 2005) the heritability of this trait was moderate.

In order to obtain precise genetic correlations coefficients, a large number of rabbits should be slaughtered. However, almost all published papers reported with values together with relatively large standard errors therefore these estimates must be taken with caution.

2.3 Selection index method

Genetic improvement of animals involves several traits simultaneously thus setting up a breeding goal is not possible based on a single source of information. In the late 1930s and early 1940s Smith (1936) and Hazel (1943) were the first authors, introducing selection index theory in plant breeding, and in animal breeding, respectively. Hazel (1943) optimized various traits by their performance to select individuals in the most appropriate combination.

2.3.1 Construction of a selection index

The selection index is in the form of multiple regressions of breeding values of the phenotypic values as a deviation from the population mean. Noting, that breeders have several traits to improve, the breeding values of these traits $(X_1, X_2 \ldots X_i)$ have to be measured to make a proper selection index. X_i-s may come from different sources such as own performance records, performance records from ancestors (pedigree data) and performance records of descendants (progeny data), (e.g.: X_1 can be an own performance data, X_2 might be the average performance of the individual's paternal half-sibs for the same trait, X_3 might be the average performance of the individual's progeny, and X_4, X_5, and X_6 might represent the performance of the individual, half-sibs, and progeny respectively, for a correlated trait) (Kempthorne and Nordskog 1959; Smith, 1967). Applying selection indices requires the knowledge of fixed effects, variances, and covariances (phenotypic and genetic) alongside with economic values of the examined traits. The traits and the economic values are combined in the selection objective: H, Based on the parameters mentioned above, the selection index is as follows:

$$Selection\ index = b_1X_1 + b_2X_2 + \ldots b_mX_m$$

Where the selection index is expressed in matrix notation: b'X and denoted as: I (for the selection index); b' is the partial regression coefficient of the individual's breeding value of each measurement. This weighting is done by finding the maximal correlation (r_{IA}) between the index and the breeding value, leading to a set of simultaneous equations (as many as the measurements) and the solution gives the best b' value used in the index (Pesek and Baker 1969; Casey 1970).

Breeding programs operate with these selection criteria traits and also with selection objective traits. These parameters do not have to be the same, however, the number of traits in the selection criteria and the selection objective is required to be equal, thus the indexing method determines the selection index coefficients that maximize the response in the selection objective (H), with the selection index (I). Relationships between the traits and genetic/phenotypic levels are in matrix form were previously described by Kempthorne and Nordskog (1959) as follows:

P: Phenotypic variance-covariance matrix of traits in the selection index

G: Genetic variance-covariance matrix between traits in the selection objective and the selection index

C: genetic variance-covariance matrix of traits in the selection objective. P and C matrices are symmetric, on the contrary, G matrix is only symmetric, when the number of traits measured is equal to the number of traits improved.

To predict the genetic merit, the derivation of selection criteria coefficients is more simple with matrix algebra. Thus, the variance of the selection index is:

$$var(I) = var(b'X) = b'var(X)b = b'Pb$$

The variance of the selection objective is:

$$var(H) = var(a'Y) = a'var(Y)a = a'Ca$$

Where: Y is a trait in the selection objective and a is the relative economic value of a trait.

The covariance of the selection criteria and the selection objective is:

$$cov(b'X, a'Y) = b'cov(X,Y)a = b'Ga$$

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With P, G matrices and the weighting factors b', the selection criteria coefficients can be determined as the coefficients that minimize the squared difference between the selection objective and the genetic merit. Where the squared difference is:

$$\frac{\partial (H - I)^2}{\partial b} = 2Pb - 2Ga$$

Which, when equated to zero, results:

$$b = P^{-1}Ga$$

The selection index method can be separated into two types

1.   Economic selection indices: Where information of traits is used to predict genetic merit for overall economic value

2.   Family selection indices: Where information is combined from different types of relatives (sire, dam, offspring, etc.) to predict the genetic merit of an individual for a given trait.

2.3.2 Economic selection index

All traits in the breeding goal have economic importance, thus the breeding objective aims to maximize this economic merit. For economic indices, the additive genetic value of traits of interest forms the aggregate genotype (A).

$$A = v_1 g_1 + v_2 g_2 + \cdots v_n g_n$$

Where: g_i is the additive genetic value of the ith trait, and v_i is the economic weight, and A is the aggregate genotype.

Economic weights (EW) are economic values (EV) of a unit of a trait (Falconer and Mackay, 1996) and can be calculated from the profit function as the difference of cost per unit of a trait and the incomes (if the profit function is linear). However, Smith et al. (1986) characterized profit as the

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ratio of income/costs to calculate economic weights, while Amer and Fox (1992) derived it from marginal cost curves.

Non-linear profit functions are also used in animal breeding, and they can be computed with the Taylor series (Taylor, 1715) by linearising the profit.

Smith (1984) described the process as the profit increase done by a small improvement of the trait of interest, thus economic weights need to be recalculated after a few generations when the means of the traits are going to be different due to selection.

In economic indices, the base units for economic weights should be the same as the units forthe breeding value (eg.: body weight is expressed in kg, then economic weight should bedemonstrated in €/kg). It is worth noting, that traits of the aggregate genotype and traits in the index do not have to be the same, such as edible meat on the hind legs can be a part of the aggregate genotype due to its economic importance, but not measured because of the duration of the measurement. Wolfová and Wolf (2013) previously described strategies to calculate economic values in animal breeding, and reported, that traits in the breeding goal are not usually identical with traits in the selection criteria. Besides, EVs of traits need to be defined with complete information on assumptions used in analytical models, and details on interrelationships between traits are needed to be documented for better comparability. In animal breeding, many authors have addressed the economic index approach to selection for pigs, (Armer et al. 2014; Houška et al. 2004; Houška et al. 2010; Quinton et al. 2006; Wolfová et al. 2017), poultry (Kumar et al. 2006) dairy cattle (Wolfová, 2007) and aquaculture species (Janssen et al. 2017). However, the number of articles calculating EWs in rabbit breeding is very limited (Armero and Blasco, 1992; Prayaga

and Eady, 2000, Krupová et al., 2020). Re-calculation of these index weights is necessary for the changes in the industry.

2.3.3 Family selection index

For this index type, the information originates from different types of relatives, to make them more accurate estimation to the aggregate genotype.

$$A = g_1$$

Where g_1 is the genetic value of the trait of interest and A is the aggregate genotype.

In some cases, the economic importance of the trait is unclear (eg.: birth weight), and breeders usually interested in improving a questionable trait at the desired level. Yamada et al. (1975) created a selection index with desired gains based on the intended genetic changes from the breeder's point of view, where the means of *m* traits are changed by the amount of Qj,= *1,2,...,m*, and Q is the *m x 1* vector of the intended genetic changes.

The selection is made by the following index:

$$I = b'X$$

Where b is a weighting factor, and X is an n x 1 vector of sources of information.

The traits in the Q matrix are not necessarily the same as the traits in the index, and the genetic gains are calculated as follows:

$$\Delta G^* = \frac{i_I}{\sigma_I} G^{*\prime} Rb$$

Where: ΔG^* is a vector, consisting of $\Delta G_{k,I,} = 1,2, \dots m, l$; G^* is an *n x 1* matrix of genetic covariance elements (σ_{Gik}) σ_I. is the standard deviation of

the index $(b'Pb)^{1/2}$) and l is the selection intensity. The total changes of the examined traits after q generations of selection are:

$$Q^* = q\Delta G^* = G^{*\prime}Rb$$

Where: R is an $n \times n$ diagonal matrix of r_i, which is Wright's coefficient of relationship between the candidate and its relatives, who provide information about X. R matrix consists of coefficient of coancestry or Wright's inbreeding coefficient in the main diagonal, and the covariance of the additive genetic effect between two individuals.

Difficulties may occur for these desired gain indices when choosing the optimum set and level of traits in the selection objective. Thus, each trait can reach a maximum genetic gain by its relative importance (RI). However, adding desired gains for secondary important traits is not expedient (Cruz et al., 2014).

2.3.4 Selection index method in rabbit breeding

Management, nutrition, and genetic changes required to introduce the selection index method into rabbit farming. Matheron and Rouvier (1977) created a family index to increase the rate of response to litter size. Later, Estany et al. (1988) implanted a mixed-model method to the selection of dam lines. First economic weights in rabbit breeding ware described by Armero and Blasco (1992) for the main production traits and they defined profit function as follows:

$$PROFIT = RETURNS - COSTS$$

The weights -calculated below- were the partial derivates of the profit function applied to the mean value of the traits.

$$w_i = [\frac{\partial PROFIT}{\partial X_i}]$$

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When creating the index mortalities, the number of deliveries per year, replacement rate, and body weight were taken into account. Later, Prayaga and Eady, (2000) estimated economic weights (Table 5.) for production traits in Australian rabbit breeding, where the mean values for the variables are summarized in Tables 2, 3 and 4.

Table 2. Mean values of traits in rabbit meat production

	Mortality rates	
WM*	Mortality rate from birth to weaning	21%
FM*	Mortality rate from weaning to slaughter	10%
MM	Mortality rate for adult rabbits	5%
	Prices	
P1	Price per kg of live young rabbits	$2.60
P2	Price per kg of culled rabbit	$2.00
P3	Purchase price for bucks and does	$20.00
P4	Price per kg of food	$0.36
	Pregnancy and lactation	
L	Days of lactation	35
G	Days of pregnancy	30
	Weights	
MBW	Liveweight at maturity	4.0 kg
WS	Liveweight at slaughter	2.75 kg
BW	Weight at birth	0.05 kg
WW	Weight at weaning	0.68 kg
	Reproductive variables	
LS*	Litter size	8.4
DY*	Number of litters per year	7.6
RR*	Replacement rate of the farm per year per doe	1.2

Table 3. Mean values of feed consumption

	Feed consumption	
FMM	Maintenance requirements of a male during its reproductive life	44kg
CREP	Feed consumption of rabbits for replacement from 2-4 months	7.2 kg
PRM	Maintenance requirements during pregnancy	160 g/day
LRM	Maintenance requirements during lactation	190 g/day
ERRG	Extra requirements of the doe for each gestated rabbit	5g/day
ERRL	Extra requirements of the doe during lactation per each kitten	25 g/day
DCL*	Daily consumption per kitten during lactation	10.3
DCF*	Daily consumption per young rabbit during the fattening period	46 g/day

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Table 4. Mean values of health costs and other variables

	Others	
HC	Health costs per adult rabbit per year	$2.50
NM	Proportion of slaughtered adult rabbits not sold	0.1
RATIO	Ratio of bucks to does	1:07
FFC/MFC	Female or male fixed costs per year	$2.50
FC rep	Fixed costs for holding the replacement stock	$12.99
FCF	Fixed costs at fattening per rabbit	$0.01

Table 5. Economic weights per doe per year (for improvement of a unit of a trait)

Trait	Economic value ($)
LS - increase by 1	24.16
DY - increase by 1	26.32
RR - decrease by 1%	0.37
WM - decrease by 1%	2.74
FM - decrease by 1%	3.11
DGL- increase by 1g	0.34
DGF- increase by 1g	1.38
DCL- decrease by 1g	0.64
DCF- decrease by 1g	0.78

The profit was calculated from the index by breeding doe per year, by estimating the returns from a doe. Later, these authors compared systems in Spain to the Australian meat production and remarked differences in slaughter weight, depending on consumer's demands (Prayaga and Eady, 2000). The feed costs of the different countries are very diverse (10:1 for Spain and 6.5:1 for Australia) therefore it is advisable setting up the breeding objectives for the specified populations.

Cartuche et al. (2014) also computed a linear profit function for production traits. The fixed costs were summarized as labor, utilities, amortization, and administration costs and divided per doe, per replacement doe and per litter weaned per year. In this study, the authors declared, that litter size and feed conversation ratio are the most important traits from the economic aspect.

Conclusions from the literature

The selection has the primary role in improving the performance of the subsequent generations. The process should always focus on the genetic merit of the future progeny yet to be born. To build an organized structure for the breeding process, the breeding goal has to be defined. This requires the specification of traits that have to be improved genetically in the population. Thus, the accuracy of breeding value estimation plays an important role in the process, because it shows the amount of transmitted genotypic value to the offspring. Therefore, the parental generation has to contain individuals with the best breeding values.

Direct estimation of breeding values requires specific technical background such as evaluation of DNA markers, which is not available or too expensive, breeders have to use phenotypic observations combining genetic and environmental factors to evaluate the genetic merit of the animals using linear models (BLUP).

In animal breeding, BLUP is a widely used procedure predicting breeding values. Making meat production more intensive, rabbit breeders frequently use three-way crossbreeding schemes, and select lines for paternal and maternal traits to take advantage of positive heterosis (Baselga, 2004). Some breeding programs operate with profit models, which can help the breeder to rank the traits by the mathematical relationship of inputs and

outputs (Armero and Blasco, 1992). Therefore the profit function can easily form the breeding goal because it is expressed in terms of economic values of the desired traits, so several equations can be calculated if the trait is improved by one unit, how much more profit can be expected. Other models are able to operate without the necessity of knowing precisely the economic importance of the traits in the breeding goal and focus on the desired genetic gain per generation.

3. Aims of the present work:

1.   Analyzing the Pannon Rabbit Breeding Program from the aspect of efficiency. The optimal selection procedure needs to be found for achieving a desired genetic gain of a trait in the breeding goal. As the breeding goal contains multiple traits, the selection procedure can be performed in two steps or using a selection index, that combines these traits.

2.   Calculating aggregate genotype/desired gain index (BLUP index) for the production traits of the Pannon white and Pannon large rabbit breeds. Selection indices with desired gains are useful tools in practical animal breeding because they can predict the genetic progress of traits in the breeding goal without the necessity of calculating economic calculations.

3.   Calculating economic index for the production traits of the Pannon white rabbit breed by applying the newly developed software package EcoWeight Rabbit 2.1. The last aim of this thesis is to demonstrate economic modeling for the Pannon white rabbit breed, which can spread more widely in the future in order to support rabbit farms. Traits in the selection criteria are not always identical with traits in the breeding goal. This software package is a good solution for creating selection indices of traits that are not measured directly (such as traits measured with CT).

4. MATERIALS AND METHODS

The doctoral thesis contains two main chapters in connection with advanced selection decisions. First, genetic parameters and breeding values were estimated for the current selection criteria traits. Desired gain indices were then developed to improve selection efficiency. In the second part of the dissertation, a software package was used, to maximize the profit in rabbit farms by determining economic weights and to define economic indices.

The logical order of the three parts is demonstrated in Figure 2.

EcoWeight Rabbit 2.1 software for calculating economic selection indices of the Pannon white rabbit breed

Desired gain selection index from the current breeding objective

Estimating genetic parameters for the examined traits
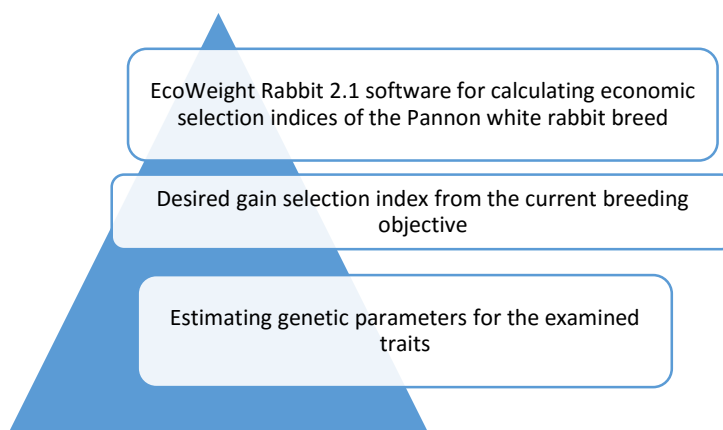
Figure 2.: The logical order of studies in the thesis

4.1 Selection process of the Pannon white and the Pannon large rabbit breeds

4.1.1. Selection process of the Pannon white

Pannon white breed was initiated from New Zealand white and Californian white rabbits since the late 1980's at Kaposvár University. Selection for carcass traits based on CT evaluations began in 1992 (Szendrő et al. 1992), where L-value (the average surface of muscle longissimus dorsi between the 2nd and 3rd, and 4th and 5th *lumbar vertebrae*) was the first carcass trait in the breeding goal.

From 2004, L-value was replaced by TMV (thigh muscle volume), due to its bigger surface and the breeding program was completed by a reproductive trait :LW21 (litter weight at 21 days of age) in order to maintain an optimal reproduction. The selection procedure of the Pannon White breed is conducted in two consecutive steps for every kindling batch. In the first step, the expected LW21 breeding values of the growing rabbits are predicted based on the ancestors' performances. Based on this prediction whole litters can be ranked within every population subgroup (ie. all full-sibs have the same expected breeding value). In the first step of selection from a given litter with a high LW21 breeding value generally, 1-2 males and 2-3 females are selected for the second selection step unless the parents of this litter already contributed a sufficient number of breeding animals (2 breeding males per buck and 5 breeding females per doe) to the population. The second step of selection is performed based on the TMV breeding values following CT scans. A more detailed description of the selection procedure was given by Matics et al. (2014).

This selection process provides an opportunity to create a selection index for both selection steps.

To controll the rate of inbreeding, a circular mating sheme is applied for both breeds (Matics et al., 2014), where each breed is divided into 4 buck groups Females from one group are always mated with males from another group (1♀×4♂; 2♀×1♂; 3♀×2♂; 4♀×3♂).

4.1.2 Selection process of the Pannon large

Pannon large is a terminal line, basically created for an optimal paternal crossing partner. The breed was established in 2005, and its selection process also operates with two selection steps. In the first step, a phenotypic measurement takes place to calculate ADG (average daily gain) between 5 and 10 weekss of age without breeding value estimation, and HLV (hind leg muscle volume) is measured in the second step. Inserting the selection index method to the breeding program is only possible in the second selection step, where genetic evaluations are performed with BLUP method.

4.2 Desired-gain selection index in the Pannon white rabbit breed

4.2.1. Data collection

This analysis was based on the 22 002 21-day litter weight (LW21) and the 8124 thigh muscle volume (TMV) records of the Pannon White does and growing rabbits, respectively. The experimental data was collected between 1992 and 2016 at the Experimental Rabbit farm of Kaposvár University. The total number of animals in the pedigree file was 14 124. The applied reproduction rhythm was 49 days and the generations were overlapping. To avoid a high inbreeding rate per generation a circular mating scheme was applied dividing the population into four subgroups. This method was described in detail by Nagy et al. (2010b).

TMV data were determined at the Kaposvár University Health Center Institute of Diagnostic Imaging and Radiation Oncology. A Siemens Somatom Cardiac type multidetector CT was used to make the scans with

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the following settings: tube voltage: 120 kV, current: 140 mAs, data collection mode: spiral. The scanned rabbits were 11 weeks old and before scanning they were fixed with belts in a special plastic container without anesthesia. During the CT measurement, the scans were taken of the whole body and segmented with 3D Slicer's automatic segmentation module (Fedorov et al., 2012) between the *crista iliaca* of the *os ilium* and the *patella* with 2 mm slice thickness. The muscle tissue was determined as the summed voxels between 0 and 140 on the HU (Hounsfield) scale of the CT scans.

4.2.2 Animal models

REML and BLUP methods were used to estimate the genetic parameters and breeding values for LW21 and TMV, and these traits were analyzed jointly using a two-trait animal model. PEST software (Neustadt, Germany) (Groeneveld, 1990) was used for data coding and the variance components were estimated with VCE 6 (Groeneveld et al. 2008). The matrix equation of the applied model was as follows:

$$\begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} x_1 & 0 \\ & x_2 \end{pmatrix}\begin{pmatrix} b_1 \\ b_2 \end{pmatrix} + \begin{pmatrix} z_1 & 0 \\ & z_2 \end{pmatrix}\begin{pmatrix} a_1 \\ a_2 \end{pmatrix} + \begin{pmatrix} w_1 & 0 \\ & w_2 \end{pmatrix}\begin{pmatrix} c_1 \\ c_2 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \end{pmatrix}$$

Where: y_i= vector of the observations of the ith trait, b_i =vector of the fixed effects of the ith trait, a_i= the vector of random additive genetic effects for the ith trait, c_i= vector of common litter effects for the ith trait, e_i= vector of random residual effects for the ith trait. X_i, $Z_{i,}$ and W_i are the incidence matrices relating to the records of the ith traits to fixed effects.

The structure of the applied model is summarized in Table 6.

Table 6. The structure of the applied animal model

Effect	Type	Levels	Traits	
			LW21	TMV
PARITY	F	4	x	
YEARMONTH1	F	261	x	
AGE21	C	1	x	
LITTERSIZE21	C	1	x	
PE	R	11 594	x	
SEX	F	3		x
CT_WEIGHT	C	1		x
MUSCLE DENSITY	F	4		X
YEARMONTH2	F	94		x
CE	R	4 178		x
A	R	14 124	x	x

PARITY: Parity number of the doe; YEARMONTH1: Year and month of kindling; AGE21: Exact age of the kits at 21 days of measurement; LITTERSIZE21: Litter size at 21 days; PE: Permanent environmental effect; SEX: Sex of the growing rabbits; CT_WEIGHT: Bodyweight at CT measurement; MUSCLE DENSITY: Applied density ranges during 20 years of selection YEARMONTH2: Year and month of CT measurement; CE: Common environmental effect of the doe; A: Additive genetic effect

For muscle density, 4 ranges were used in the past 2 decades:

1. 10-100 HU

2. 20-200 HU

3. 40-120 HU

4. 50-130 HU

4.2.3 Construction of the selection index

To test the modification possibility of the breeding program a two-trait BLUP index (involving LW21 and TMV) was calculated using the software SEL-ACTION *(*Rutten and Bijma, 2001). The settings of the indexing are summarized in Table 7.

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Table 7. Settings of the selection index

Population size	
Number of selected male parents	12
Number of selected female parents	28
Number of male selection candidates per dam	100
Number of female selection candidates per dam	40
Total selected proportion male parents	0.13
Total selected proportion male parents	0.13
Characteristics of the used groups	
Full sib group 1 with	7 animals
Half-sib group 1 with	1 dam producing 8 animals
Progeny group 1 with	1 dam producing 8 progeny

The contribution of each trait was set to 50%. Following the practice developed in pig breeding, the final selection index was standardized with Z transformation, where the calculated index values were subtracted by their average and divided by the standard deviation. Then the so-called Z-values were multiplied by 20 and finally, 100 was added to this product. Thus, the index means were obtained to 100 and a standard deviation of 20, in each buck group respectively.

4.2.4 Testing the efficiency of the selection index

The selection process was tested on a chosen kindling batch where the date of insemination was 29th of January 2016. At that time, the population consisted of 160 does and 60 bucks. In the kindling batch, 928 kits were born from 121 dams. Using both selection alternatives in the first step of selection 69 litters (122 individuals) were selected for CT scan (2nd step of selection) either based on either the expected breeding values of LW21 or on the calculated BLUP index scores. As the two methods resulted in different rankings, altogether 139 rabbits were sent to CT scan. Regardless of the method of the first step's selection, after the CT scans the second step of

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selection was accomplished based on TMV breeding values. Comparing selection methods was carried out using Welch-test due to unequal sample distribution variance, and the rank correlation coefficient was also calculated. All the mentioned statistical analyses were performed using the R-software package.

4.3 Desired-gain selection index for the Pannon Large breed

4.3.1 Data collection

The analysis based on the records (collected between 2014 and 2018) of 312 randomly chosen Pannon Large rabbits breed at the Kaposvár University, Hungary. In the first step of data collection, average daily gain (ADG) was measured, and animals with the best ADG were selected for the CT examination. During the evaluation, three rabbits were fixed in a special plastic container without any anesthetics at 11 weeks of age. The used acquisition parameters were: tube voltage 140 kV, X-ray radiation dose 90 mAs, spiral data collection mode with pitch 1, field of view 500 mm, slice thickness 2 mm. Overlapping slices were recorded of the rabbits from head to toe during the measurement. For the segmentation process, masks were made for the loin muscle and the hind legs, and registered to the CT images for each animal.

4.3.2 Animal models

To estimate genetic parameters, REML and BLUP methods were used for the LM and HL in a two-trait animal model. The pedigree file consisted of 2758 individuals. PEST software (Neustadt, Germany) (Groeneveld, 1990) was used for data coding and the variance components were estimated with VCE 6 (Groeneveld et al. 2008). The structure of the applied model is summarized in Table 8.

Table 8. The applied animal model

Effect	Type	Levels	Trait	
			LMV	HLV
Sex	F	2	X	X
Year_month	F	17	X	X
CT_weight	C	1	X	X
A	A	2758	X	X

Where: LMV: Loin muscle volume; HLV: hind leg muscle volume; Sex: sex of growing rabbits; Year_month: year and month of kindling; CT_weight: bodyweight at the CT measurement; A: additive genetic effect

4.3.3 Selection index

After the calculation of the genetic parameters, a two-trait desired gain selection index was created by MIX software (Nath et al. 2002).

The final index was Z-transformed to get 100 as mean of the index and 20 for standard deviation.

The number of generations required to attain the goal (t) was calculated as:

$$t=\sigma_I/i_I=(b'Pb)^{1/2}/i_I.$$

Where: t is the number of generations required to attain the breeding goal, i_I is the selection intensity, σ_I is the standard deviation if the index, P is the n x n matrix of phenotypic variance-covariance and b is the n x 1 vector of weighting coefficients.

In the last step, a correlation matrix of the examined traits and the standardized index was created to test the efficiency of index selection.

4.4 Economic selection indices for the Pannon white rabbit breed

The economic model for the rabbit selection was introduced by Krupová et al., 2020. This model is deterministic and static, similar to modeling in

pig-breeding systems (Wolfová et al. 2017), where performances were represented by population means. Fractions of animals are allowed, thus the model is a non-integer, besides it contains calculations of the doe population, the progeny population, and total feed and non-feed costs for all age groups. Digestible energy (DE) feed and water requirements of the different age groups were also calculated, however, the scope and magnitude of this thesis don't permit to present all of these topics in detail. Major steps of the modeling process contained collecting information of measurable traits or features (phenotypic data) of the population, then transform these data into equations via algorithms, which can be solved by a computer program. In the last step, these model estimations were validated with actual results from a base year, where no health or financial problem occurred.

4.4.1 Management system of the rabbitry

The production system of Kaposvár University is quite special. Since the breeding program operates with 3 breeds, the rabbitry must work as space-efficient as possible. Thus, in our case 150 does are kept on the farm per breed, besides their offspring along with 80 bucks per breed to maintain genetic diversity. As a purebreeding system, replacement is produced via artificial insemination (AI) and surplus progeny goes to the slaughterhouse. Culling occurs for does due to health problems and bad mothering behavior, while all other female animals are mated post-partum. The length of pregnancy is fixed in 31 days, besides non-culled does are kept to the next reproduction cycle. The number of re-matings is assumed to be 1 in the model and weaning of kits is made at a fixed age. The breeding unit, nursery, the AI station, and the fattening unit are sometimes concentrated on different

farms however, all of these units are located to one farm at Kaposvár University.

The structure of the production system (kindling, weaning, mating, conception, culling) is illustrated in Figure 3.
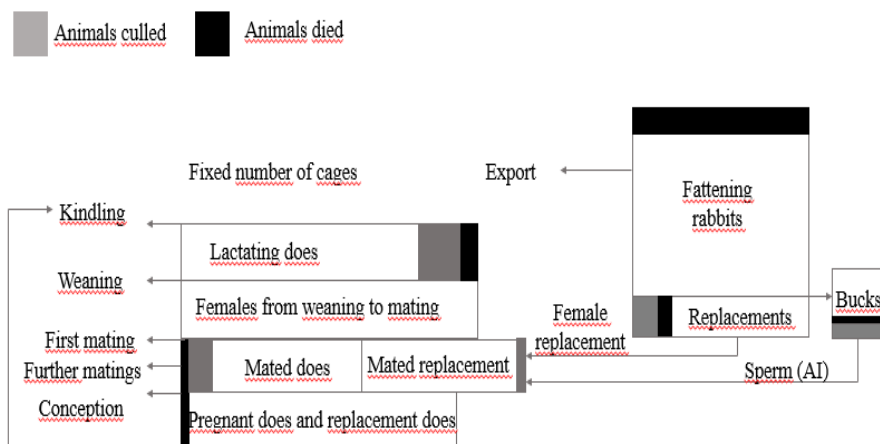
Figure 3. Rabbit production system of Kaposvár University (adapted from Wolfová et al., 2017)

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Structure of the herds was calculated by the Markov chain model, previously described by Jalvingh et al. (1992), and the herd dynamics were characterized in terms of doe categories (states a doe can pass during her life) and the probabilities between them. The doe states are mainly related to the reproductive cycles (interval between kindlings). The number of reproduction cycles is 7, while the reproduction rhythm is maximized in 49 days. Young does are mated at a specific age with a target body weight, the replacement does are placed into the herd at their first kindling and stay until culling or has reached the maximum number of reproduction cycles. Moreover, survival classes of progeny and bucks were added to the model.

Survival classes of rabbits are defined in Table 9:

Table 9. Categories of Pannon white rabbits

Category	Name of category
	Categories of does within reproductive cycles
1	Does died between kindling and kits weaning
2	Does culled after kit weaning due to health problems
3	Does culled for failure to conceive
4	Does not conceived but kept in the herd for the next reproduction cycle
5	Does conceiving and completing the current reproductive cycle
6	Barren does culled after kit weaning for age
7	Does during pregnancy
8	Does during lactation
9	Does during kindling
10	Open does
	Categories of progeny
11	Stillborn kits
12	Suckling kits
13	Kits died from birth till weaning
14	Kits survived from birth to a fixed age after weaning
15	Animals died during fattening
16	Animals finished to target slaughter weight
17	Doe replacement died during the rearing phase
18	Young breeding does sold
19	Doe replacement in rearing
20	Doe replacement from weaning to 1st mating
21	Doe replacement from 1st to 2nd mating
22	Doe replacement not conceived after first mating but kept in the herd and mated for the 2nd time
23	Doe replacement mated but not conceived and culled
24	Doe replacement mated once or twice and had kindling
25	Buck replacement for sperm production but died during rearing
26	Buck replacement different from the doe genotype
27	Buck replacement used for AI
28	Buck replacement used for purebreeding systems
29	Buck replacement sold
30	Young bucks sold after weaning
	Categories of breeding bucks
31	Adult breeding bucks used for AI
32	Adult breeding bucks used for natural mating

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4.4.2 Costs, revenues, and profits

4.4.2.1 Feeding costs

Total costs of the rabbitry were divided into feeding costs and non-feeding costs, later these categories were further divided into specific and non-specific costs. Feeding costs included feed and water. These total costs are calculated per doe and reproductive cycle. Specific non-feed costs were in association with special animal groups (i.e.: insemination of does, vaccination of growing rabbits, etc.). Non-specific-non feeding costs were in connection with buildings, labor costs, and maintaining facilities for the rabbits.

Feeding costs were calculated by categories in Euros (€) and the price of water was added per cubic meter to price per liter. Feeding costs for does were calculated with a general equation, thus does were fed with 6 types of diets *(k=1 to k=6)* according to their energy requirement levels.

The number of diets was used as an index number when calculating the nutrition requirements of different categories.

1.   Lactation diet (For doe replacement during lactation and pregnancy)

2.   Supplementary diet for kits from 21 days of age until weaning

3.   Fattening diet (If two-phased fattening is applied, the first phase is diet 3)

4.   Fattening diet (2nd phase)

5.   A specific diet for rearing replacement does

6.   Diet for open does

4.4.2.2 Non-feed costs

Specific and non-specific non-feed costs were not dissected. Specific non-feed costs were the following:

- Healthcare costs of does
- Insemination costs
- Healthcare costs for young animals
- Healthcare for fattening animals
- Costs for disposal
- Cost for supplies (i.e. bedding)
- Marketing costs
- Costs for breeding animals (from other farms, when natural mating was applied)
- Costs for purchasing doe replacement

Non-specific non-feed costs are fixed costs and treated as variable costs. As an example, a shorter finishing period due to better growth performance causes decreasing fixed costs. Annual costs are usually:

- Depreciation of buildings, cages, and equipment
- Repair costs
- Fuel and energy costs
- Labor costs
- Cleaning water costs

These costs were expressed by day for each animal group. Non-feed costs were calculated by progeny categories per does, and per breeding bucks. To calculate the differences between feeding and non-feeding costs, a paired t-test was used (after checking the normality of the difference of these costs).

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4.4.2.3 Calculation of revenues

Revenues of production systems include:

- Culled does and bucks
- Fattened animals
- Breeding bucks
- Rabbit skin and manure

Revenues mainly depend on the weight of the animals (live weight and carcass weight). Pricing system for culled and replacement does was added by live weight and carcass weight however, culled does could not be sold for the slaughterhouse due to the hormonal treatment, thus costs for disposal result in a negative value. For fattening animals, the pricing system was given per kg of live weight and carcass weight by fore mid and hind part.

4.4.3 Marginal economic values and economic weights

Marginal economic values were added per unit of a trait, per doe and per year. When changing the trait means, a fixed number of does was assumed. The simple partial derivate was replaced with complex bio-economic modeling i.e. by a numeric derivate. The profit was calculated based on the economic values for the whole production system per breed. Numeric derivate of the profit function was computed by increasing and decreasing the average value of a trait (TV_{av}) by 0.5%. TV_h was considered as the higher value of the trait while TV_l was the trait decreased with the same proportion. Thus, the partial derivate of the traits was as follows:

$$ev = \frac{TP_h - TP_l}{TV_h - TV_l}$$

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Marginal economic values were expressed in euros per doe and per year. The definition of traits was separated for calculating economic values.

4.4.4 Measured traits of the Pannon white

4.4.4.1 Functional traits (reproduction and survival)

- Conception rate of young does at first mating
- Conception rate of does after the first parity
- Total number of kits born per litter
- Number of kits born alive per litter
- Number of weaned kits per litter
- Stillborn rate (percentage of stillborn kits per litter over parities and genotypes)
- Survival rate of kits born alive
- Litter weight at 21 days of age

4.4.4.2 Survival traits

- Mortality rate of does over all parities
- Doe productive lifetime (in years)
- Doe productive lifetime (in reproductive cycles)
- Survival rate of young rabbits

4.4.4.3 Growth traits

Growth traits were modeled with a multi-phase growth curve for the individual phases:

- Growth of kits from birth till 21 days of age
- Growth of kits from 21 days of age till weaning
- Growth of rabbits from weaning till slaughtering
- Growth of young replacement from weaning till first mating

- Growth of young replacement does not conceive at the 1st mating but kept until 2nd mating

- Growth of young replacement does during pregnancy

- Growth of young replacement bucks from weaning to maturity

- Growth and body weight changes during reproductive cycles

After, the following traits were differentiated:

- Daily gain of kits between 21st day after weaning

- Litter weight at weaning averaged over parities

- Average daily gain of rabbits in fattening

For feed efficiency traits, residual feed intake and feed conversation in fattening were calculated. In the software, predicted feed intakes were computed by animal categories on actual growth data.

4.4.4.4 Carcass traits

- Dressing out percentage

- Percentage of the hind part in the reference carcass (hindp)

- Percentage of the mid part in the reference carcass (midp)

- Percentage of valuable parts in reference carcass (valp)

$$valp = midp + hindp$$

Calculating economic values for carcass traits and the hind part the value of hindp increased and decreased keeping the percentage of fore and mid part constant, assuming, that changes of the hind part mean alterations in the fat depots in reference carcass.

4.4.5 Standardised, absolute and relative economic weights

Economic weights were calculated for the *i* traits in specific breeds combining the marginal economic values to the proportion of genes transferred to progeny. Production systems is not taken into account due to the short generation intervals and reproductive cycle when a trait affected costs and revenues.

4.4.5.1 Standardized economic weights

When economic weights cannot be compared to each other (e.g. traits have different units) they are referred to the genetic standard deviation of the trait given per doe and per year.

This can be described as:

$$evst = evp \ x \ gsd\_d$$

Where: *evst* is the standardized economic weight for the trait, *evp* is the absolute economic weight of trait, and *gsd_d* is the genetic standard deviation for trait *i.*

4.4.5.2 Absolute economic weights

They can be calculated in any production system however, in this work, it was only calculated for purebred progeny.

4.4.5.3 Relative economic weights

They are calculated from the standardized economic weights as the sum of all standardized weights if they have the same units with positive and negative values.

$$sevst = \sum_{ie\Omega} abs(evst)$$

Where: *sevst* is the sum of the absolute values of the standardized economic weights over all selected traits, *abs(evst)* is the absolute standardized economic weight for trait i, and $ie\Omega$ is the sum of selected traits (Krupová et al., 2020), and the relative economic weight is calculated as:

$$evr = 100 \; x \; \frac{abs(evst)}{sevst}$$

Where *evr* is the relative economic weight, *abs(evst)* is the absolute standardized economic weight for trait *i*, and *sevst* is the sum of the absolute values of the standardized economic weights over all selected traits.

As this dissertation is focusing on meat production in the Pannon breeding program, correlation coefficients previously described by Nagy et al. (2015) were used to determine the selection criteria traits, because CT traits are not easy to measure economically. Thus, traits in the breeding goal were hind leg muscle volume (HLV) and litter weight at 21 days of age (LW21), while in the selection criteria, HLV was replaced with the percentage of the hind part on the carcass due to the strong genetic correlation (r=0.95) of the traits.

Table 10. Correlation coefficients of slaughter and CT data (Nagy et al., 2015)

	TB	FV	TM	TMM	MMF	MMH	LD	SP
TBM		0.1	0.84	0.8	0.73	0.81	0.6	NS
FV	-		0.37	0.47	0.34	0.47	0.4	NS
TMV	0.4	0.2		0.92	0.71	0.95	0.7	NS
TMM	0.14	0.0	0.63		0.73	0.97	0.7	NS
MMF	0.11	0.2	0.11	-0.18		0.74	0.6	0.17
MMH	0.17	0.0	0.76	0.81	-0.26		0.7	NS
LD	0.05	0.0	0.01	0.11	-0.15	0.09		0.26
SP	0.21	0.1	0.1	-0.09	0.02	-0.1	0.1	

TBM: Total body muscle volume; FV: Fat volume; TMV: Thigh muscle volume; TMM: Thigh muscle mass; MMF: Muscle mass of the forepart; MMH: Muscle mass of the hind part; LD: Muscle mass of the longissimus dorsi muscle; SP: Slaughter performance

Data collection for calculating the economic importance of traits was based on previous studies made on the Pannon white (Ács et al., 2018). 122 litters were examined with a 49-day reproduction rhythm and 139 individuals were sent to CT. The following parameters were recorded to calculate relative economic values and economic weights:

- Number of reproductive cycles
- Conception rate of does after mating
- Average weight of does entering in each reproduction cycle
- Total Number of kits born/born alive/weaned
- Kindling interval
- Mating type
- Average productive lifetime
- DE requirements of rabbits
- Feeding and non-feeding costs of the rabbit farm
- Pricing system for fattening
- Selection criteria traits
- Breeding goal traits

4.4.6 Base inputs for the Pannon white breed

4.4.6.1 Inputs describing reproduction

Module 1 (production system for purebreeding) was used for calculations of MEVs of traits that were carried out on the database (base years 2017-2018) of Kaposvár University. Fattened rabbits accounted for approximately 86% of the Pannon white population. Does were selected

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as a replacement at 11 weeks of age and inseminated at 16.5 weeks with 3.2 kg bodyweight (BW). All females were mated after 11 days *postpartum*.

Reproduction inputs of the breed are summarized in Table 11.

Table 11. Base reproduction inputs of does in Pannon white breed

Variable/parity	1	2	3	4	5	6	7
Total kits born per litter	11	12	14	12	12	11	11
Kits born alive per litter	9	10	12	11	10	10	11
Kits weaned	8	9	9	9	9	9	9
Doe weight after kindling (kg)	3.2	3.3	3.35	3.4	3.45	3.5	3.6
Doe weight at 21st day of lactation (kg)	3.25	3.2	3.25	3.3	3.3	3.45	3.6
Doe weight at weaning (kg)	3.2	3.25	3.3	3.35	3.4	3.45	3.5

Source: Own investigation on the rabbitry of Kaposvár University between 2017-2018

The conception rate and the kindling rate was hard to define in the reference years due to *dermatomycosis* disease (the number of animals had to be minimized), thus base years were changed from 2017-2018 to 2013-2015 since no disease occurred on the rabbit farm during that time. Conception rate of firstly mated does was 85% and increased to 91% at the second mating and half of the non-pregnant does were kept for the next mating period. Table 12. summarizes the kindling rate in the Pannon white breed.

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Table 12. Kindling rate of the Pannon white breed between 2013-2015

Parity number	Number of does mated with AI	Number of does with kindling	Kindling rate %
1	582	483	83.0
2	522	399	76.4
3	466	362	77.7
4	383	307	80.2
5	315	242	76.8
6	245	194	79.2
7	189	145	76.7
8	138	108	78.3
9	109	80	73.4
10	84	62	73.8
11	57	49	86.0
12	45	32	71.1
13	26	18	69.2
14	17	13	76.5
15	10	7	70.0
16	4	3	75.0
17	1	1	100.0
1-17	3193	2505	78.5

The mortality rate and culling rate for health problems and bad mothering behavior were 2% in each reproduction cycle respectively, while it was 1,5% for bucks due to unsuitability for sperm collection. The number of sperm doses per young (18 to 22 weeks of age) and mature buck (>22 weeks of age) produced per reproductive cycle was 10. While the average productive life of bucks was 360 days. Kits were weaned at 35 days of age and fattened to a target slaughter weight.

4.4.6.2 Inputs for growth and nutrition

Input parameters for progeny until weaning and fattening are provided in Table 13.

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Table 13. Growth and survival of Pannon white growing rabbits

Variable/unit	Value
Average weight	
A newborn kit (g)	65
A kit at 21st day of age (kg)	0.5
A weaned kit (kg)	0.8
Slaughter weight of fattened rabbits (kg)	2.5
ADG of fattened rabbits (g/day)	40
Mortality rate in fattening (%)	5

*ADG: Average daily gain

Literature data by Xiccatio and Trocino (2010) were used to calculate digestible energy (DE) requirements of does and growing rabbits. Chemical composition of kits (888g water, 120 g protein, 55 g fat, 22g ash, and 5 MJ NE/kg) was used to determine fetal growth and net energy retained in fetuses. Suckling kits did not get any supplemental feed until weaning, therefore weaning weight at 21 days of age could be used to estimate milk production. From weaning to slaughter, DE was calculated also according to Xiccatio and Trocino (2010), where empty body gain (EBG) consisted of 610g water, 210g protein, 150g fat, and 30g ash per kg EBG. Daily feed intake was 0.18-0.2 kg for lactating does and 0.05-0.06 kg for growing rabbits from 5 weeks of age, while the average daily amount of water consumption was 0.4 l for does and 0.25 l for growers. Input parameters for calculation of DE are described in Table 14.

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Table 14. Main parameters for calculation of DE

Variable/Unit	Growing rabbits	Does
Coefficient for the calculation		
EBW from LW	0.87	0.92
MW from LW	0.75	0.75
Net energy retained		
Body protein (MJ NE/kg)	23.2	23.2
Body lipid (MJ NE/kg)	35.6	36.5
Doe milk (MJ NE/kg)	-	8.5
Net energy retained in EBW of does at	-	10.5
DE requirement for maintance per day and	0.43	0.43
The efficiency of utilization of DE from the		
Protein gain (MJ NE/ MJ DE)	0.4	0.4
Lipid gain (MJ NE/ MJ DE) or for doe milk	0.65	0.65
Foetus growth (MJ NE/ MJ DE)	-	0.3
The efficiency of utilization of body energy		
Non-pregnant	-	0.8
Pregnant	-	0.76
Coefficient of feed wasting in fattening	1.15	1.1

LW: live weight, EBW: empty body weight, MW: Metabolic weight, NE: Net energy,

DE: digestible energy

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4.4.6.3 Feeding and non-feeding costs of the rabbitry

Feeding and non-feeding costs were also calculated by the reference years 2017-2018 in Euros (€). Mean of costs for doe feed for the 6 phases were 11.7 € per day, 8.1 € for 60 Pannon white bucks and 32.4 € per day for growers respectively. The price of water was 2 €/m^3.

Non-feeding costs included the salary of 6 workers of the rabbitry. Due to the special working conditions (frequent measuring, ID tattoos of growing rabbits, etc.) salaries represented almost 30% of the total costs, while wages are approximately 5-10% at one of the Hungarian companies. Non-feeding costs per animal are reported in Table 15.

Table 15. Non-feeding costs of the rabbitry

Variable/Unit	Value
Costs for artificial insemination including hormonal treatment of does if it is applied (€/insemination)	1
Costs for health care of does including kits till weaning (€/doe and kindling interval)	1.66
Costs for health care of doe replacements from weaning to 1st mating (€/ doe replacement)	0.2
Costs for health care of doe replacements from 1st to 2nd mating (€/ doe replacement)	0.1
Costs for health care of buck replacements from weaning to selling to AI stations or to include in the herd for natural mating (€/ buck replacement)	0.5
Costs for health care of young breeding bucks intended for selling, in the interval from weaning to selling (€/ buck replacement)	0.2
Cost for supplies and misceallaneous of does including kits till weaning, e.g. bedding material (€/doe/day)	0.01
Fixed cost for does including kits till weaning (€/doe/day)	0.09
Fixed cost for doe replacement (€/doe/day)	0.002
Fixed cost for buck replacement (€/buck replacement/day)	0.0012
Fixed cost for animals during fattening (€/animal/day)	0.0012
Costs for disposal of dead animals (€/kg of live weight)	0.5

4.4.6.4 Pricing system for fattening

For calculating the revenues of the rabbit farm pricing system for fattening was adapted from Szendrő et al. (2016)

Table 16. pricing system for fattening

Variable/ Unit	Value
Price for slaughter rabbits(€/ kg of liveweight)	1.95
Average price for whole chilled carcass of slaughter rabbits (€/kg of carcass weight)	3.26
Average dressing out percentage of chilled carcass of purebred fattened rabbits (%)	59.3
Weight of reference carcass of purebred progeny given as percentage of chilled carcass (%)	84.5
Average percentage of fore part in the reference carcass of purebred progeny (%)	30
Average percentage of mid part in the reference carcass of purebred progeny (%)	30.9
Average percentage of hind part in the reference carcass of purebred progeny (%)	36.8
Price for dried rabbit skin (€/kg)	0.49
Price for rabbit manure (€/kg)	0.67

5. RESULTS AND DISCUSSION

5.1 Desired-gain selection index in the Pannon white

The Z transformed final selection index was the following:

*Index = -244.458 + 522.523 * LW21 + 6.017 * TMV.*

The descriptive statistics of the examined traits are summarized in Table 17.

Table 17. Descriptive statistics of the examined traits

Trait	N	Minimum	Maximum	Mean	SD
LW21 (kg)	22 002	0.32	5.51	2.64	0.65
TMV (cm^3)	8 124	176	534	326	40.50

LW21: Litter weight at 21 days of age, TMV: thigh muscle volume, SD:Standard deviation

The difference between the record number of the traits can be explained by the commencement of the data collection. Measurements of LW21 started in 1992, while CT examinations for TMV only began in 2004. The mean value of TMV (326 cm^3) is in accordance with previous studies (Gyovai et al. 2008, 2012) where the mean of TMV records were 334.8 cm^3 and 338 cm^3 respectively.

5.1.1 Heritabilities, genetic correlations and standard errors

The estimated heritabilities, genetic correlations (±SE) are presented in Table 18.

Table 18. Estimated heritabilities, permanent environmental effect, and genetic correlations between the traits.

Trait	h^2	PE	r_g LW21-TMV
LW21	0.1±0.02	0.18±0.01	-0.24±0.07
TMV	0.21±0.03	-	-

h^2: Heritability of the trait; PE: Permanent environmental effect; rg LW21-TMV: measured genetic correlation between traits in the breeding goal

For the heritability of thigh muscle volume in Pannon white rabbit breed Gyovai et al. (2008) and Nagy et al. (2013) observed similar results (0.21 ± 0.03). Our findings are also inaccordance with Lukefahr and Hamilton (1997) and Khalil et al. (2008) where heritability estimations ranged between 0.02 and 0.17. These results show that the non-genetic andenvironmental factors represent the major source of the trait's variability. For TMV, heritability estimations were lower than expected (as a carcass trait), however it washigher than LW21. These results are also similar with Gyovai et al. (2008) and Nagy et al. (2013).

The estimated correlation between the selection index and the examined traits are provided in Table 19.

Table 19. Correlation coefficients between the desired-gain selection index applied for the Pannon white and the examined traits

Trait	LW21	TMV	Index score
LW21	1	-0.24	0.28
TMV	-	1	0.84
Index score	-	-	1

LW21: litter weight at 21 days of age; TMV: Thigh muscle volume

The magnitude of permanent environmental effect exceeded that of the heritability resulting moderate repeatability of LW21. On the contrary, the common environmental effect had the same magnitude as the additive genetic effect. Rastogi et al. (2000), Gyovai et al. (2008, 2012), and Al-Saef et al. (2008) reported also low magnitude for the permanent environmental effect for litter weight with repeatability animal models.

5.1.2 Consequences of changing the current selection method to the index-based selection

In order to examine, weather index-based selection is more efficient, than the current selection method, litters with the best LW21_EBVs (estimated breeding value of litter weight at 21 dyas of age) were selected, and compared to the best index valued litters. TMV_EBV (estimated breeding value of thigh muscle volume) and index values were also compared during the process. After the CT examinations, these parameters were re-examined individulally. Table 20. summarises the results of the Welch-test.

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Table 20. Differences of the selection methods after Welch-test

Selection	Trait	t-value	DF	Significance
1st step	LW21_EBV	12.89	112.65	p < 2.2e-16
	TMV_EBV	-5.44	135.04	p= 0.0000002042
	Index	-2.54	123.22	p=0.012
2nd step	LW21_EBV	3.07	61.19	p=0.003
	TMV_EBV	-16.47	64.77	p < 2.2e-16
	Index	-3.86	73.24	p=0.0002363

LW21_EBV: Estimated breeding value of litter weight at 21 days of age, TMV_EBV: Estimated breeding value of Thigh muscle volume, DF: degrees of freedom

Tables 21. and 22. represent the differences between the selection methods in the first and the second step.

Table 21. Differences between the selection methods in the first selection step

Selection method	LW21_EBV	TMV_EBV	Mean of index score
Current selection	0.21a	42.85a	105a
Index selection	0.17b	46.0b	111b

a, b: Significant differences between the examined groups (p=0.005)

Litters with the best breeding values for LW21 were selected in the current selection resulting in lower index scores due to the negative correlation between TMV and LW21.

*Table 22. Differences between the selection methods in the second selection step*

Selection method	LW21_EBV	TMV_EBV	Mean of index score
Current selection	0.17a	47.6a	111a
Index selection	0.15b	60.7b	128b

a, b: Significant differences between the examined groups (p=0.005)

After the CT measurements the estimated breeding values of the LW21 decreased by 11.4% with the index selection after the two-stage selection process, on the other hand, own TMV values increased substantially by 27.8%. TMV breeding values were significantly higher after both selection steps.

Ranking each selected individual, the Sperman's rank correlation coefficient between the selection index and TMV_EBV was 0.74. In the first step of the selection process, the litters were ranked by the LW21 data and the best bucks in the parental generation were selected which produced the best litters. The main criterion was that the dams of the selected litters had to be the most distant relatives. In some cases, the dams were half-sibs due to the lack of diversity. According to this sorting system, after the CT examinations maximum of two females and one male offspring went for further breeding from one sire. The consequences of the different selection strategies can be originated from the negative correlation between LW21 and TMV, which was reported in our study (Table 19.) and by Gyovai et al. (2012).

Figure 4. and 5. also demonstrates the differences between the selection methods.

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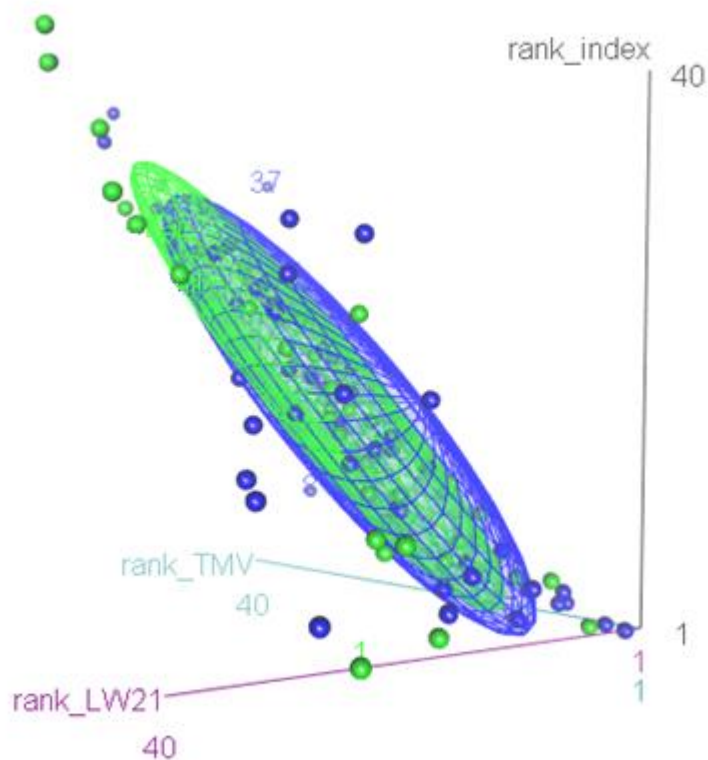
Figure 4. Rabbits selected with regular selection

Blue dots represent selected individuals, green dots represent non-selected animals. Rank_index: Rank numbers based on index points, Rank_lw: rank numbers based on the estimated breeding values of LW21, Rank_TMV: rank numbers based on estimated breeding values of TMV
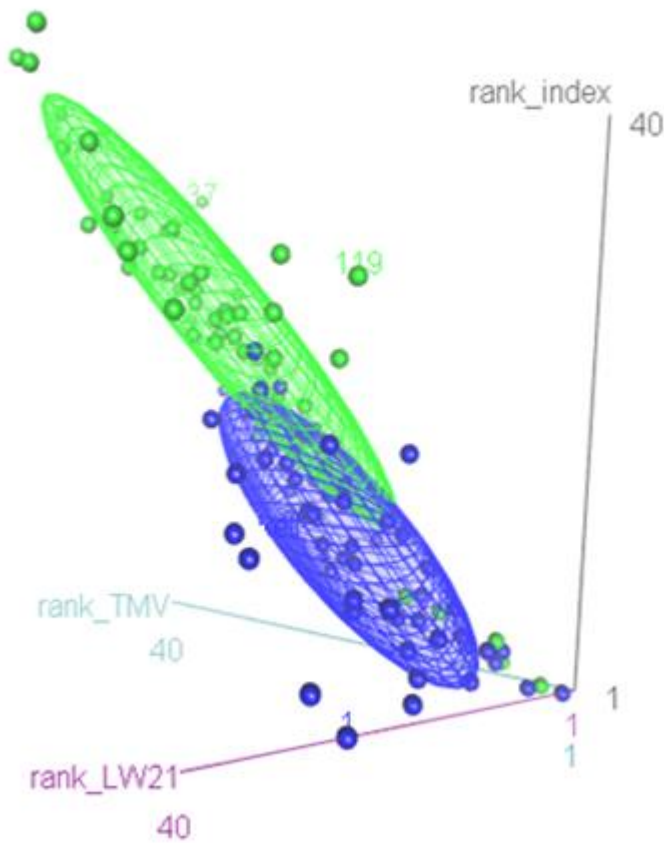
Figure 5. Rabbits selected with index selection

Blue dots represent selected individuals, green dots represent non-selected animals. Rank_index: Rank numbers based on index points, Rank_lw: rank numbers based on the estimated breeding values of LW21, Rank_TMV: rank numbers based on estimated breeding values of TMV

Despite the small reduction of the LW21, the economic efficiency of the selection process can be increased by using indexing LW21 and TMV in the pre-selection stage, since the economic importance of the LW21 is much lower than that of TMV, as reported previously by Szendrő et al. (2016).

Prayaga and Eady (2000) and Eady and Garreau (2008) reported the profitability of the price per kg of growing rabbits between 1.6 and 1.75€ in this case the thigh fillet produces 11 €/kg revenue which gives this trait great economic importance. In an earlier study, Mikó et al. (2010) reported the average weight difference of the thigh fillet based on a divergent selection experiment using Pannon White rabbits. These authors found that the weight of the thigh muscle was 8.5% higher in the positive groups, and there was also a 1.1% increase in the dressing out percentage compared to the negative group. These findings resulted in 0.1 €/kg additional revenue for the meat fillet and 0.03 €/kg for the whole carcass. Thus the benefits achieved by Mikó et al. (2010) and by this study can be substantial through a multiplier level from the aspect of the slaughterhouse. Considering 1 000 000 slaughtered rabbits per year the increased TMV can result 675 000€ profit for the slaughterhouse (Mikó et al. 2010).

5.2 Desired-gain selection index in the Pannon large

The Z transformed final index for the Pannon large was the following:

$$Index= 6.3 \times LMV + 4.13 \times TMV$$

Table 23. compiles the descriptive statistics of the examined traits

Table 23. Descriptive statistics of the traits

Trait	N	Minimum	Maximum	Mean	SD
LMV (cm^3)	312	98.58	232.68	157.11	23.99
HLV (cm^3)	312	278.91	478.48	374.33	39.43
CT_weight	312	2350	3620	2957	212.55

Where: LMV is the volume of the loin muscle; HLV is the volume of the hind legs; CT_weight: bodyweight at the CT measurement

Unsurprisingly, the volume of LMV (157.11 cm^3) is half of the volume of HLV (374.33 cm^3), however both traits are needed to be added to the breeding goal in order to contribute of the valuable meat parts.

5.2.1 Heritabilities, genetic correlations

The mean values of HLV are in accordance with the results for thigh muscle volume (TMV) of the Pannon white rabbit breed (Ács et al. 2018), however, the results are somewhat higher due to the breed differences and the slight changes in the CT segmentation method. The genetic correlations, estimated heritabilities are summarized in Table 24.

Table 24. Heritabilities, genetic correlations and standard errors of the measured traits

Traits	h^2	r_g LMV-HLV
LMV	0.4±0.01	0.68±0.08
HLV	0.42±0.02	-

LMV: Loin muscle volume; HLV: Hind leg muscle volume, h^2: estimated heritability of the examined trait, r_g LMV-HLV: estimated genetic correlation of the measured traits

LMV showed relatively high heritability ($h^2 = 0.4$), in contrast with Lenoir and Morien (2016), where CT evaluation was substituted with an ultrasound device due to economic reasons. They measured the surface of the *m. longissimus dorsi*, and observed a moderate heritability ($h^2 = 0.2$). However, because of the different methodologies of these studies, the direct comparison of the estimated genetic parameters should be treated with caution. In the Pannon White rabbit breed, previous selection criteria (L-value) was expressed in cm^2 and the heritability of the trait was $h^2 = 0.33$ (Matics et al. 2014), thus adding LMV to the breeding goal may result a more accurate selection decision. For the hind legs, the heritability of the muscle volume is also high ($h^2 = 0.4$). Heritability estimations were reported previously for thigh muscle volume in the Pannon large and the Pannon white breed, but these results were moderate ($h^2 = 0.21 - 0.25$) (Gyovai et al. 2012).

Figure 6. represents the correlation matrix of the selection index and the examined traits.

Linear correlations among the examined traits (LMV, HLV) and the standardized selection index
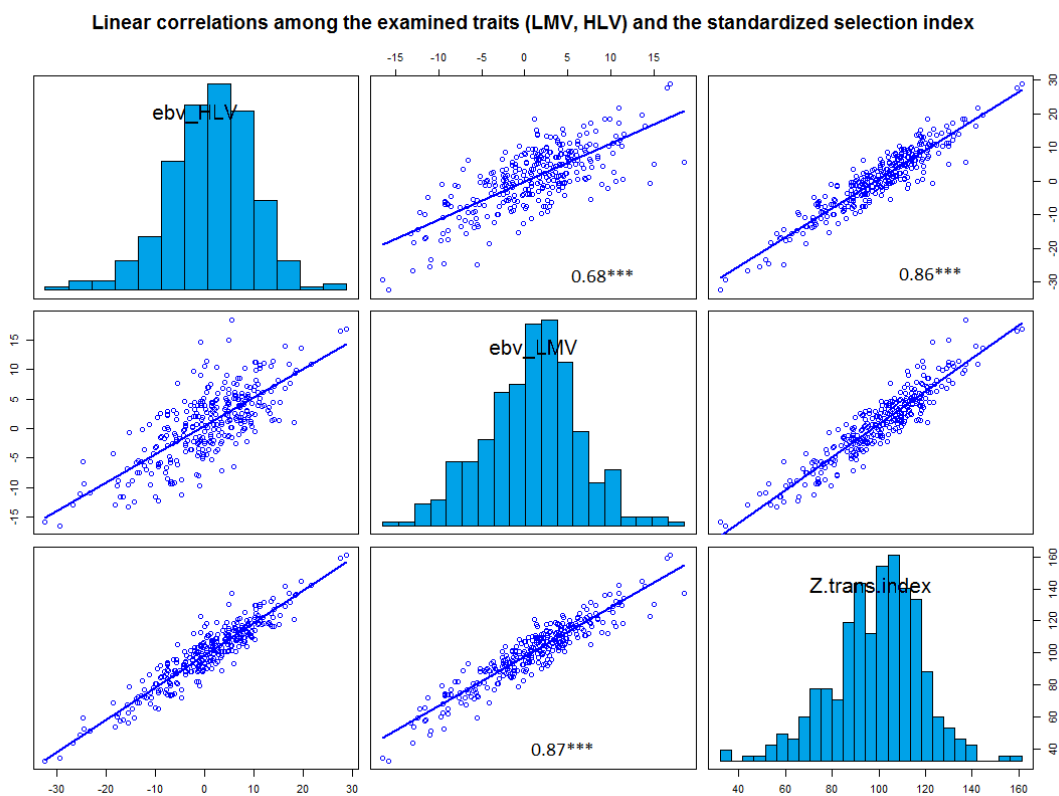
Figure 6.: Correlation matrix of the examined traits and the selection index

Where: ebv_HLV is the estimated breeding value of hind legs, ebv_LMV is the estimated breeding value of the loin muscle, Z.trans index is the standardized selection index

Matics et al. (2014) reported high genetic correlations between thigh muscle volume and the dressing out percentage (0.45–0.47). The number of generations required to improve the traits with one additive genetic standard deviation was 11.9, which can be achieved in approximately 5 years of selective breeding. After the Z transformation, the means of the estimated breeding values for the examined traits were somewhat higher (4.9 for LMV and 4.9 for HLV) than the index score (4.6). A favorable genetic correlation

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was found between LMV and HLV (0.68) and the correlation coefficients of both the LMV and the HLV were strongly positive (0.86 and 0.87, respectively) with the index scores.

5.3 Results of EcoWeight Rabbit

5.3.1 Structure of the doe herd

The structure of the doe herd in the stationary state is described in the following tables. The number of reproduction cycles was 7. The average conception rate of does was 0.86. Relative frequencies of does in reproduction cycles are demonstrated in Table 25.

Table 25. Relative frequencies of does in individual reproductive cycles

Number of the reproduction cycle	Relative frequency
1	0.187
2	0.177
3	0.169
4	0.149
5	0.131
6	0.104
7	0.083

Tables 26. and 27. demonstrate does with and without kindling as the proportion of does entered any parity.

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Table 26. Number of does that had kindling in the reproductive cycle, expressed as the proportion of does enter any parity

Number of the reproduction cycle	Proportion of does
1	0.188
2	0.168
3	0.144
4	0.135
5	0.118
6	0.104
7	0.083

At the end of the state, the doe is either died (or culled) followed by a transition to the system (parity number 1; e.g. replacing of the doe by a young doe) or kindling interval is completed and the doe is transited into the next reproduction cycle.

Table 27. Number of does entered the reproduction cycle without kindling as a proportion of does enter any reproduction cycle

Number of the reproduction cycle	Proportion of does
1	0
2	0.008
3	0.025
4	0.013
5	0.012
6	0
7	0

Mortality and culling rate of does are presented in Figures 7. and 8.
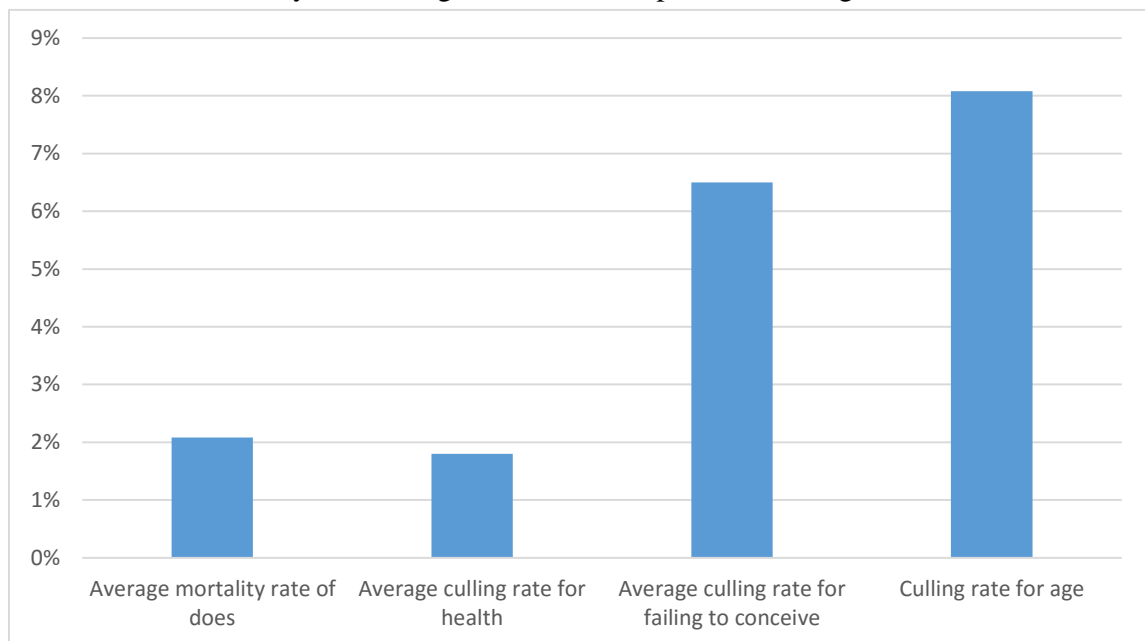
Figure 7: Percentage of does died or culled for different reasons during a reproduction cycle
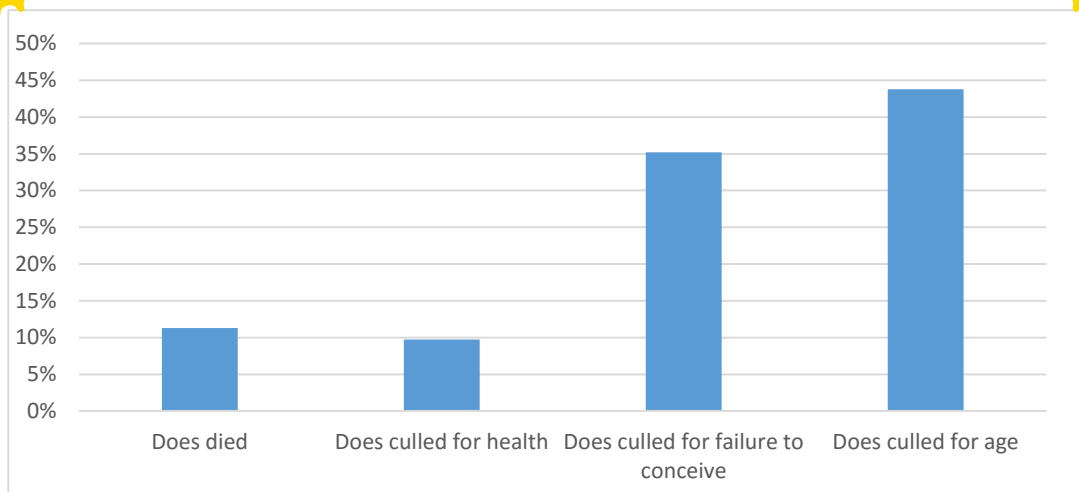
Figure 8: Does died or culled for different reasons as the percentage of does replaced

Rosell and de la Fuente, (2009) reported, that the highest mortality occurs at the first 3 kindlings, but remained stable thereafter. For breeding does, the main reason for culling was low productivity or infertility. The authors also mentioned that malocclusion, mastitis, myxomatosis, and respiratory disorders are the most common health problems for rabbits does. Reproduction specialties of the Pannon white are presented in Table 28.

Table 28: Reproduction characteristics of doe herds:

Average kindling interval of does	42
Average productive lifetime of does (number of kindling)	5.42
Average productive lifetime of does (years)	0.40
Average annual replacement rate of does (%)	160.5
Average number of litters per doe per year	8.70

The estimated values of litter size traits are summarized in Table 29.

Table 29: Litter size traits (number of kits per doe per kindling)

Parity	Total born	Born alive	Weaned	Stillborn	Died until weaning
1	9.5	9.3	8.5	0.2	0.8
2	9.6	9.4	8.4	0.2	1
3	9.7	9.6	8.5	0.1	1.1
4	10	9.8	8.8	0.2	1
5	10.2	10.1	9	0.1	1.1
6	9.8	9.7	9.3	0.1	0.4
7	9.3	9.1	8.7	0.2	0.4

Heritability of litter size components is low (less, than 0.2) in both repeatability (Garreau et al. 2000; Gyovai et al. 2008; Nagy et al. 2013), or multi-trait animal models (Nagy et al. 2011; Gyovai et al. 2012), as a consequence, there is a really slow genetic progress regarding these traits. Szendrő et al. (1997) noted, that the total number of kits born alive was 8.04 in 1992, increased to 8.55 by 1996. However, regarding this trait our outputs are in accordance with Cartuche et al. (2014), whose results are based on the databases of the Spanish rabbit sector. Mortality rate of kits was 9.08%, while the survival rate of the Pannon white rabbits in fattening was 95% in the current study.

Growth of does in the herd is demonstrated in Table 30.

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Table 30: Weights of does entering parity with kindling (kg)

Parity	After kindling	At 21th day of lactation	At weaning	Before parity
1	3.2	3.25	3.8	0.2
2	3.35	3.3	3.9	0.2
3	3.45	3.4	4.1	0.1
4	3.55	3.5	4.15	0.2
5	3.65	3.6	4.2	0.1
6	3.65	3.6	4.25	0.1
7	3.65	3.6	4.3	0.2

The age, weight, and weight gain of progeny categories are summarized in Table 30.

Table 31: Age and weight of the end of one period

Category	Age (days)	Weight (kg)	ADG (g)		
			live weight	body	body
12	0	0.1	-	-	-
13	15.5	0.4	-	-	-
14	31.0	0.8	30.0	5.5	3.9
15	52.2	1.6	40.0	-	-
16	73.5	2.5	40.0	7.3	5.2
17	73.0	2.0	28.7	-	-
18	-	-	-	-	-
19	115.0	3.0	28.5	5.2	3.7
20	157.0	3.5	7.14	1.3	0.9
21	133.5	3.3	7.14	1.3	0.9
22	149.1	3.2	-	-	-
23	151.1	3.2	56.4	-	-
24	153.0	3.4	54.3	-	-
25	73.5	2.3	30.7	-	-
27	115.0	3.5	56.4	10.3	7.36
28	117.0	3.2	48.97	8.94	6.39

ADG: Average daily gain

Some of the above-mentioned progeny categories were not measured related to the fact, that breeding does and bucks are not exported from the system (category 18, 26, 29, 30) and the rabbitry of Kaposvár University does not apply natural mating for bucks. ADG results for live weight were

somewhat lower than according to Szendrő et al. (2009) in categories 14 and 16. This may be the outcome of age differences in progeny categories.

Results of EcoWeight Rabbit also includes the feed requirements of rabbits in different categories, however, due to the magnitude of the dissertation, there is no place for this chapter.

5.3.2 Costs in the rabbitry

For progeny categories 13, 15, 17, and 25 (young replacement died from both sexes) feeding costs are not separated but assumed to be one-half of the feeding costs of the appropriate category alive (progeny categories 14, 16 and 19 or 20 and 27).

Table 32: Feeding and drinking costs per progeny (€/animal)

Progeny category	Costs per animal
12	0.0
13	0.0
14	0.1
15	0.0
16	2.2
17	2.1
19	2.0
20	0.7
21	1.6
22	2.6
23	3.1
24	3.1
25	1.7
26	2.0
27	2.0
28	2.1

In our system the calculated feeding costs for category 19 (breeding doe replacement) were 2€/doe while it was 3.5 €/doe according to Cartuche et al.
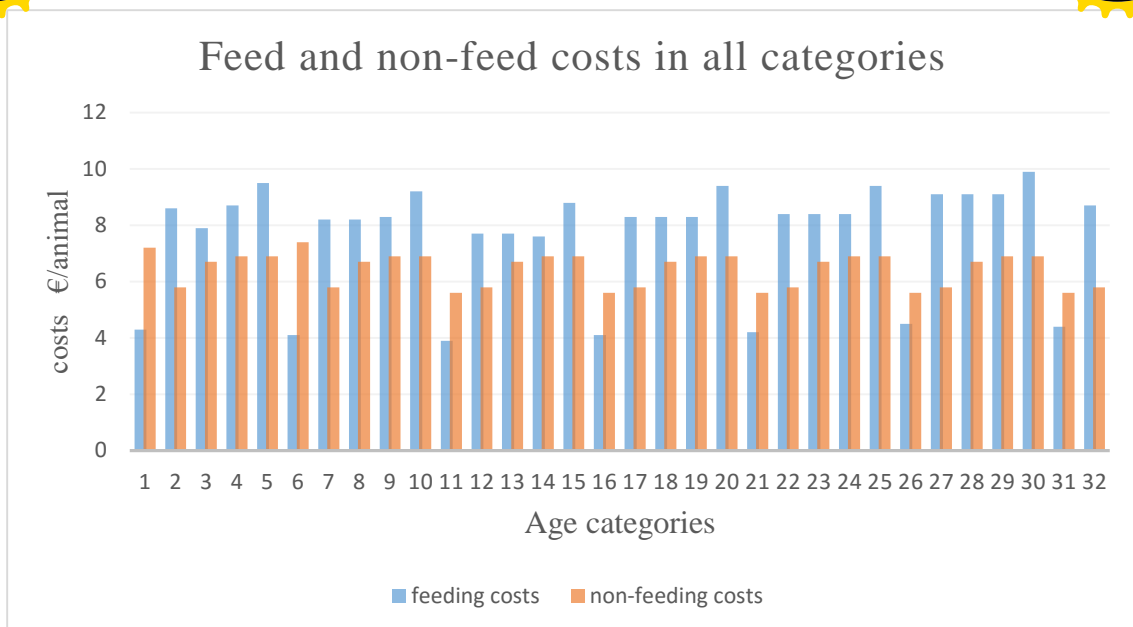
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(2014). Besides, the greatest proportion of feeding costs occurred during lactation (29.4%) and fattening (25.9%).

Non-feed costs of the rabbitry in progeny categories per doe are summarized in Table 33.

Table 33: Non-feed costs per animal (€/animal)

Progeny category	Non-feed costs
12	0.0
13	0.0
14	0.1
15	0.5
16	0.3
17	1.4
18	1.5
19	1.2
20	0.1
21	0.5
22	1.5
23	0.6
24	0.3
25	1.4
27	1.2
28	1.2

Figure 9. Feed and non-feed cost in the rabbitry (€/animal) in all categories

Comparing feeding and non-feeding costs a trend can be observed, that feeding costs are higher in almost all age-groups. This finding is in accordance with Cartuche et al. (2014) stating, that feeding costs represent 45% of the total costs, while health costs or expenses for replacement and administration are only depicted 6.9% and 3.9% in Spanish rabbit farms.

Detailed costs are demonstrated in Table 34.

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Table 34: Costs per doe in the 3rd reproduction cycle

Costs	€/doe per reproductive cycle
Costs for feed	8.79
Costs for water	0.03
Costs for health care	1.66
Costs for supplies and miscellaneous	0.42
Fixed costs	3.78
costs for AI	1.00
Total feeding costs	8.82
Total non-feed costs	6.86
Total costs	15.68

Non-feed costs for replacements (Table 33) were low, which fact implies, that longevity has slight economic importance in rabbit breeding. Fixed costs included relatively high amortization costs. Total feeding costs were 9.04 €/per reproductive cycle for does in our system, and 19.31 € for progeny in the same cycle, while non-feed costs were 6.73 € for does and 3.03 € for progeny.

Comparing these results with literature data; making a rabbit farm is a bigger investment per doe (38%) while investing money in swine or broiler production is much more favorable regarding the fixed costs and amortization costs (22% and 24%) according to ENESA (2009) and SIP (2012).

5.3.3 Revenues in the rabbitry

Revenues for the rabbit farm were calculated for does and for progeny. In our special case, there is no breeding does sold out from the system. Summarized revenues are in Table 35.

Table 35: Revenues of the rabbit farm

	Does	Progeny
Revenues from culled animals (€/doe)	0.57	37.83
Revenues from skin (€/doe)	0.07	0.54
Revenues from manure (€/doe)	7.36	0.58
Total revenues (€/doe/RR, €/kg slaughter weight	46.96	9

The summary economics of the rabbitry is demonstrated in Figure 10.
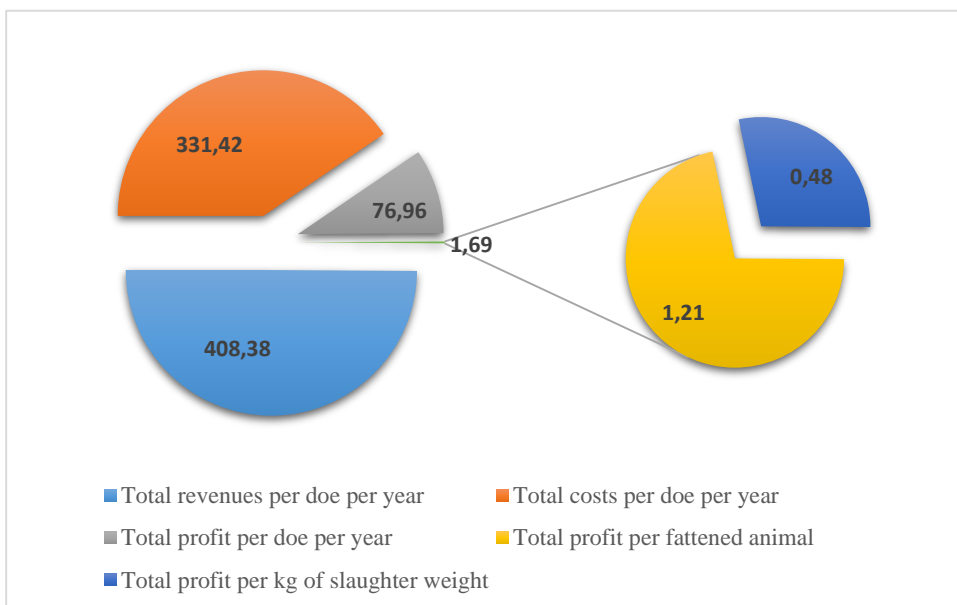
Figure 10: Summary economics of the rabbit farm in Kaposvár University (€)

This figure well demonstrates, as profit (23%) can only be obtained from fattened rabbits and does, thus rabbit farming may not be comparable with

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other species in intensive animal breeding. This simulation also represents an ideal situation, with good disease management and continuous and stabile reproduction rhythm.

5.3.4 Economic weights

Calculating with 15.15 € for the average volume of the hind part (350 cm^3) and 18.18 € for the valuable meat parts (550 cm^3), absolute, standardized, and relative economic weights of the selection criteria traits are summarized in Table 36.

Table 36: Absolute, standardized and relative economic weights

	Absolute EVs	Standardized EWs (per genetic	Relative EWs (%)
Conception rate of young replacement after first mating	0.082	0.409	0.8
Conception rate of young replacement averaged all	0.716	3.366	6.55
NBA / litter averaged all parities (kits)	11.053	8.732	11
Percentage of stillborn kits (%)	-1.202	-7.211	5.32
Survival rate till weaning (%)	1.565	19.090	37.16
*LW21 (kg)	-4.856	-0.625	1.22
Number of reproductive cycles	4.093	1.637	3.19
Survival rate in fattening (%)	0.031	0.293	0.57
LW at weaning (kg)	0.022	0.040	0.08
Daily gain in fattening (g/day)	1.730	7.578	14.75
Feed conversion during fattening (kg feed/kg gain)	-40.593	-2.395	4.66
*HP	0.01	3.287	25.21
*VP	0.02	4.532	27.87

HP: Percentage of the hind part of the carcasses; VP: Percentage of valuable meat part of the carcasses

The created indices from the selection criteria traits were as follows:

Index 1= -0.625 LW21 + 3.287 HP

Index 2= -0.625 LW21 + 4.532 VP

Profit changes year-by-year however, response to selection depends on several factors such as selection intensity and genetic parameters. In rabbit breeding, only 3 studies are concentrating on economic weights and selection (Armero and Blasco, 1992; Prayaga and Eady, 2000; Cartuche et al. 2014). EWs for survival are relatively small, in addition, improving NBA is much more difficult, than feed conversion ratio. This finding is was also previously described by Cartuche et al. (2014). According to Piles et al. (2006) Sánchez et al. (2008) longevity- measured in the number of reproduction cycles- is an economically important trait. Nevertheless, our results show, that it has low importance. Eady and Garreau (2007) also came to this conclusion.

6. CONCLUSIONS AND RECOMMENDATIONS

Many factors can modify selection decisions in animal breeding. In case of rabbits, the number of kits and carcass traits are the most important. Implanting the selection index method in rabbit breeding is reasonable, especially when a breed is selected for both production and reproduction traits which are not positively correlated. The indexing technique with 'desired gains' can be available for those traits which were not determined before from an economic point of view. For the slaughterhouse, the valuable meat parts represent the main source of the profit, so it is feasible to put a selection index between the valuable meat parts and one of the reproduction traits, even if the only relevance of this trait is to maintain the breed as a possible crossing partner.

Economic indices are quite sensitive to the market changes and some of the extreme price changes, but they are robust to the variation of economic weights. Several traits in the breeding goal have a great role in profit incensement, but their heritability is low, so significant economic improvement is not guaranteed. Other traits are not part of the profit, but important for other reasons (such as meat quality traits), or only can be measured in one sex, or too expensive to measure in traditional farms (CT traits), so they can be part of the breeding objective, but not measured in the selection criteria.

7. NEW SCIENTIFIC RESULTS

1. A desired–gain selection index was created for the first time for the Pannon White breed using the aggregate genotype of the litter weight and the thigh muscle volume, which can be applied in the first selection step.

2. A desired–gain selection index was created for the first time for the Pannon Large breed using the aggregate genotype of the thigh muscle volume and the loin muscle volume.

3. Economic selection indices were created for the first time for the Pannon white rabbit breed, for the current selection criteria traits and the valuable meat parts. These indices are farm-specific, thus represent a new opportunity for rabbit breeders in terms of profitable selection.

8. SUMMARY

Animal breeding concentrates to improve the quality of certain products such as lean meat in case of the rabbit.

Selection programs of hybrid rabbits and breeds are based on growing the amount of the valuable meat parts of the carcass, making more profit to the breeder, and an extra amount of protein for the customer. For this reason, the whole process should not focus on the genetic merit of the current individuals but the expected merit of the next generation. To build an organized structure for the breeding process, the breeding goal has to be defined. This requires the specification of traits that can genetically improve the population. Thus, the accuracy of breeding value estimation plays an important role in the process, because it shows the amount of transmitted genotypic value to the offspring. The aims of the present work were the following:

1. Analyzing the Pannon Rabbit Breeding Program from the aspect of efficiency.
2. Calculating aggregate genotype/desired gain index (BLUP index) for the production traits of the Pannon white and Pannon large rabbit breeds.
3. Calculating economic index for the production traits of the Pannon white rabbit breed by applying the newly developed software package EcoWeight Rabbit.

A desired-gain selection index in the Pannon white rabbit breed

Genetic parameters for 21-d litter weight (LW21) and thigh muscle volume (TMV) were estimated, and based on these traits a two-trait selection index was created to increase the efficiency of the Pannon White rabbits' breeding program. Litter weight at 21 d of age (LW21, $n = 22{,}002$) and thigh muscle volume (TMV, $n = 8124$) measurements (based on computed

tomography – CT) were analyzed that were recorded between 1992 and 2016. The evaluated animals were reared in 4178 litters and the total number of rabbits involved in the pedigree file was 14,124. LW21 and TMV records were analyzed jointly in an animal model. The estimated heritability for LW21 and TMV was 0.10 ± 0.01 and 0.21 ± 0.02, respectively, and the estimated genetic correlation between these traits was -0.24 ± 0.07. The common environmental effect had the same magnitude (0.10 ± 0.01) as the additive genetic effect. The created selection index constructed to have 50 and 50% contribution of the measured traits. The application possibility of the created index was tested on a given kindling batch. In this case, the first step of the selection procedure was performed either according to the current breeding program (based on the LW21 breeding values) or based on the two trait selection index. The second step of selection was not changed (based on the TMV breeding values). The consequences of using index-based selection instead of the regular procedure were, that rabbits with 27.8% higher average breeding value for TMV were selected as a breeding animal. These rabbits also had 11.4% lower average breeding value for LW21, than animals than were selected by the current method. These results suggest that the introduction of the index may improve economic efficiency.

A desired-gain selection index for the Pannon large breed

Genetic parameters were calculated to hind leg muscle volume (HLV) and loin muscle volume (LMV), and a two-trait selection index was created to modify the current selection process of the Pannon large rabbit breed. The evaluated animals (n = 312) were randomly selected from 2014 and 2018, and the total number of animals in the pedigree file was 2758. LMV and HLV were analyzed in a two-trait animal model. The estimated heritability for LMV was $h^2 = 0.4 \pm 0.01$ and $h2 = 0.42 \pm 0.02$ for the HLV respectively. The selection index was created with desired gains by

improving each trait in the selection criteria with one additive genetic standard deviation and the final index was Z transformed. Correlation coefficients between the index and the examined traits were high, 0.86 for LMV and 0.87 for HLV, thus this method could be introduced into the breeding program.

Economic selection indices for the Pannon white rabbit breed

The program EcoWeight Rabbit 2.1 is an implementation of a bio-economic model of production systems of rabbits. This model is based on typical industrial rabbitry. The bio-economic model for rabbits can handle: In our case, production system 1: purebreeding which includes doe herds producing young does and bucks for own replacement (when natural mating is used) or bucks for AI stations (when AI is applied), and finishing surplus progeny for slaughter was applied. Selling (exporting) of surplus female or male replacement was also possible, but this function wasn't used. The model is mostly deterministic and static; performances of animals are represented by their population means. The model is non-integer, which means, fractions of animals are allowed. The average conception rate of does was 0.86. Detailed costs were used as input files of the rabbitry in Kaposvár University for the Pannon white breed. Revenues were calculated per doe per year and reproductive cycle. Difficulties occurred, regarding the current selection criteria trait (HLV) cannot be measured economically, thus genetic correlations were used with other carcass traits as selection criteria. Two economic selection indices were created, one for the current breeding goal traits, and one for implementing the valuable meat parts, along with the loin muscle volume to the breeding program.

9. ÖSSZEFOGLALÁS (SUMMARY IN HUNGARIAN)

A nyúlhús termelés célja a kiváló minőségű, sovány hústermékek előállítása. Mivel a tenyésztési programok a tenyészcélban szereplő tulajdonságok fejlesztését helyezik előtérbe, a szövetekre (csont, zsír, vagy izom) gyakorolt szelekciós nyomás nagy, mely különböző testtípusokat és hús-csont arányt eredményez. Így a nyúlfajták és hibridek testméreteinek varianciája rendkívül széles (a törpenyulaktól egészen az óriás vonalakig), azonban a hústermelés szempontjából a közepes testű vonalak a legnépszerűbbek, jó növekedési erélyük és szaporaságuk miatt. A hibridek és a hústermelésre specializálódott fajták szelekciós programjának lényege, hogy a lehető legnagyobb legyen a vágott testen az értékes húsrészek aránya, így több profitot termelnek a tenyésztőnek, valamint több húst jelentenek a vásárlónak. Így, a szelekciónak nem a jelenlegi generáció egyedeinek genetikai képességeire kell koncentrálnia, hanem a genetikai előrehaladás mértékére. Ahhoz, hogy felépítsünk egy szervezett tenyésztési struktúrát, meg kell határoznunk egy olyan tenyészcélt, mely a populáció genetikai értékét növeli. A tenyészérték-becslés pedig ehhez a folymathoz járul hozzá azáltal, hogy megmutatja az egyed genetikai átörökítő képességét a következő generációra. Ennek érdekében a disszertáció célkitűzései a következők voltak:

1. A Pannon Nyúltenyésztési Program vizsgálata a hatékonyság javításának szemszögéből.

2. BLUP index képzése a Pannon fehér és Pannon nagytestű fajták adatai alapján

3. Ökonómiai indexek képzése a Pannon fehér és Pannon nagytestű fajták adatai alapján az EcoWeight új szoftvercsomagja segítségével.

Kívánt-súlyos szelekciós index alkalmazása a Pannon fehér nyúlfajtában

Megbecsültem a 21 napos alomsúly (LW21) és a combizom térfogatának (TMV) genetikai paramétereit, majd létrehoztam egy kéttulajdonságos szelekciós indexet, a fajta tenyésztési programjának hatékonyság-növelése érdekében. Az adatbázis n=22,002 LW21 és n=8124 TMV rekordot tartalmazott, melyeket 1992 és 2016 között rögzítettünk. A vizsgált adatbázisban összesen 4178 almot vizsgáltam, a pedigrében 14 124 nyúl szerepelt. Az LW21 és TMV adatokat egy kéttulajdonságos egyedmodellben elemeztem, ahol a vizsgált tulajdonságok örökölhetőségi értéke 0,10 ± 0,01 és 0,21 ± 0,02 volt. A köztük becsült genetikai korreláció -0.24±0,07, a közös környezeti hatás mértéke pedig megegyezett az additív genetikai hatással (0,1±0,01). A szelekciós indexet úgy alakítottam ki, hogy a súlyok hozzájárulása a vizsgált tulajdonságokhoz 50-50% legyen. A létrehozott indexet egy adott fialási időpontban teszteltem, végrehajtottam az eredei, kétlépcsős szelekciót, illetve az első szelekciós lépés helyett (LW21), a szelekciós index alapján válogattunk és a két módszert összehasonlítottuk. Az index alapján szelektált egyedek combizom térfogat tenyészértékének átlaga 27,8%-al növekedett, a hagyományos szelekcióval válogatott tenyészállatokéhoz képest, az alomsúlyok tenyészértékének átlaga azonban 11,4%-al csökkent. Ezek az eredmények azt sugallják, hogy a szelekciós index módszer sikeresen beilleszthető a tenyésztési programba és javíthatja a gazdasági hatékonyságot.

Kívánt-súlyos szelekciós index alkalmazása a Pannon nagytestű fajtában

A hátsó láb izomtérfogatára (HLV) és a hosszú hátizom térfogatára (LMV) kiszámítottam a genetikai paramétereket, és a két tulajdonságot egy szelekciós indexben egyesítettem. A vizsgált állatok száma n=312 volt, melyeket 2014 és 2018 között a Pannon nagytestű populációból random választottam ki. A pedigrében szereplő egyedek száma 2758 volt. A tulajdonságok örökölhetőségi értéke 0,42±0,02 és 0,4±0,01; a szelekciós indexet pedig úgy hoztam létre, hogy mindkét tulajdonságot egy additív genetikai szórással kívántam megnövelni, majd a végső indexet Z transzformáltam. Az index és a vizsgált tulajdonságok közötti korrelációs együtthatók (0,86 és 0,87) mértéke megmutatta, hogy a módszer sikeresen alkalmazható a tenyésztési programban.

Ökonómiai súlyos szelekciós indexek kidolgozása a Pannon fehér nyúlfajtában

Az alkalmazott modell tipikusan intenzív tartási és tenyésztési technológián alapul, esetemben az EcoWeight Rabbit 2.1 első modulját használtam, hiszen ez a rendszer azokat a telepeket tudja kezelni, ahol fajtatiszta tenyésztés folyik, az ivadékokból kerül ki a tenyészutánpótlás, és a termékenyítés mesterségesen történik (a természetes pároztatás is beállítható). A másik két termelési rendszer keresztezett állományokat kezel, a dolgozat szempontjából nem volt releváns. A programban használt modell determinisztus és statikus, az egyedek teljesítményének mutatóit a populáció átlagaival számolja. A tenyészutánpótlás exportja lehetséges a programon belül, de ezt a funkciót nem használtam. A modell nem használ egész számokat, így az állatok frakcionálása megengedett. A részletes input paramétereket a Kaposvári Egyetem nyúltelepének adatai alapján készítettem el. A bevételeket kiszámítottam anyanyulanként és reprodukciós ciklusonként is. A jelenlegi tenyészcél (hátsó láb izomtérfogata, értékes húsrészek aránya) gazdasági jelentőségének kiszámítása a mérési módszerek

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miatt nehézkes, így helyettük a velük jól korreláló vágási tulajdonságokat választottam ki szelekciós célként. Ennek megfelelően két szelekciós indexet készítettem el, mely tartalmazza a 21 napos alomsúlyt, illetve vagy a hátsó láb izomtérfogatát vagy az értékes húsrészek arányát.

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12. SCIENTIFIC PAPERS AND LECTURES ON THE SUBJECT OF THE THESIS

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13. OTHER PUBLICATIONS

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14. Curriculum Vitae

Virág Ács was born in Komló on the 11th of May in 1991. She attended Babits Mihály high school affiliated with the University of Pécs from 2006 to 2010 on the faculty of biology and physics. She obtained her high school diploma in 2010 with an advanced final exam from biology and admitted to Kaposvár University in the same year.

From 2013 to 2015 she worked on a red deer farm, (Natur Agro Max Ltd.) as a farm manager. She had her BSc. Diploma in June of 2014 in Animal Science. On September, she took the entrance of her master studies in Animal Science in Kaposvár University. In the meantime, she started to work at Smart Farming Ltd. (headquartered in Germany) as a software developer and support in precision plant farming.

She started her Ph.D. studies in 2016 in Kaposvár University on the Department of Animal Sciences. In 2016 she became a member of the WRSA's Hungarian section. From 2017 till 2019 she was a member of a research group in connection with animal breeding and genetics. She obtained the" New National Excellence Program of the Ministry of Human Capacities" two times.

In 2018 she obtained the complex exam of the doctoral school. From December of 2018 to March of 2019 she took part in the translation of the book "Merle SINE insertion-The Incredible Story of Merle" written by Mary Langevin, summarizing the most recent studies of molecular genetic findings in connection with canine coat color. In 2019 she reviewed an article for Animal: An International Journal of Animal Bioscience. From 2017 to 2019 she participated 3 times on the International Symposium Animal Science Days in Brandlucken,

Piešťany, and Prague. From 2019 she is a member of the Hungarian Dog Breeder's Academy headquartered on the University of Veterinary Medicine, Budapest. Her publication list contains 7 peer-reviewed papers published in English, 11 proceedings in English, Hungarian and French and 5 abstracts. She was also a co-supervisor of 3 BSc. students and 5 students of the Scientific Student's Conference of Kaposvár University.