THESES OF THE DOCTORAL (PhD) DISSERTATION

THE GENETIC STRUCTURE OF THE ANGUS POPULATION IN HUNGARY AND THE PERFORMANCE TRAITS OF ITS SUBPOPULATIONS

AUTHOR:
JUDIT MÁRTON

MOSONMAGYARÓVÁR
2025.

SZÉCHENYI ISTVÁN UNIVERSITY
ALBERT KÁZMÉR FACULTY OF AGRICULTURAL AND FOOD SCIENCES
WITTMANN ANTAL MULTIDISCIPLINARY DOCTORAL SCHOOL OF PLANT, ANIMAL AND FOOD SCIENCES
UJHELYI IMRE DOCTORAL PROGRAM IN ANIMAL SCIENCE

HEAD OF THE DOCTORAL SCHOOL:
Dr. László Varga, doctor of the Hungarian Academy of Sciences (DSc), university professor

SCIENTIFIC SUPERVISOR:
Dr. Ferenc Szabó, doctor of the Hungarian Academy of Sciences (DSc), professor emeritus

SCIENTIFIC CO-SUPERVISOR:
Dr. István Anton, doctor of the Hungarian Academy of Sciences (DSc), professor emeritus

THE GENETIC STRUCTURE OF THE ANGUS POPULATION IN HUNGARY AND THE PERFORMANCE TRAITS OF ITS SUBPOPULATIONS

AUTHOR:
Judit Márton
Mosonmagyaróvár
2025.

1. SUMMARY OF THE RESEARCH OBJECTIVES

1.1. Introduction

Beef cattle farming and breeding play a prominent role in global food production and the provision of high-quality protein sources. Its versatility results in various tangible and intangible benefits to society. The beef sector faces several challenges that need to be addressed from a sustainability perspective. Meeting the growing demand for food and increasing beef production volumes with current less sustainable systems would result in greater environmental impacts and could directly damage ecosystems. To achieve more sustainable beef production, it is essential to develop genetic and management strategies that improve productivity while reducing the environmental footprint.

The main limitation of the beef sector lies in its suboptimal reproductive performance, significantly lower productivity, and longer production cycles compared to other livestock species. The economic sustainability of beef cattle herds is influenced by a number of traits that directly affect the reproductive and productive performance of cows. Increasing efficiency, reducing dependence on subsidies, improving profitability, and complying with sustainability requirements are key factors for the long-term competitiveness of the sector.

In Hungary, the economic significance of beef cattle farming is primarily determined by calf sales, which form a major export base under current market conditions. Although the price position is favourable, the continuous rise in production costs presents increasing challenges for beef cattle farmers.

Angus is one of the oldest and most widespread beef cattle breeds worldwide. Numerous international studies and practical experiences confirm that, compared to larger-framed beef breeds, Angus is less demanding in terms of management, better adapted to climatic and environmental conditions, and more cost-effective to maintain, while still providing a high-quality end product. In addition, its calm temperament and ease of handling create a safer working environment.

There is limited data available on the genetic characteristics of the Hungarian Angus population, which restricts the development of targeted breeding and selection strategies. Genetic differences can be observed within the Angus breed that influence economically important traits, and their consideration can contribute to the optimisation of breeding strategies. Proper genetic selection and optimised breeding programmes for the breed can provide significant long-term advantages for both the Hungarian and international beef sectors.

1.2. Objectives of the study

In the course of my research, I set the following objectives:

1. To examine the population genetic structure and characteristics of Hungarian Angus nucleus herds, to determine the relative position and genetic distance of the subpopulations, and to map the level of inbreeding.
2. To analyse the effects of environmental and genetic factors on age at first calving.
3. To determine population genetic parameters related to age at first calving in the Hungarian Angus herds using the GLM sire and BLUP animal model, and to compare the results obtained from the applied models.
4. To estimate the breeding value of Angus sires in relation to age at first calving using the GLM sire and BLUP animal model.
5. To analyse phenotypic and genetic trends in age at first calving in the Hungarian Angus population.
6. To analyse traits that significantly influence sustainability and profitability (birth weight [BW], age at first calving [AFC], number of calves born alive [NCB], length of productive life [LP], weight adjusted to 205 days [WW]) among different Angus genetic groups.

2. MATERIAL AND METHOD

The analyses were carried out using the registration and performance testing data of the Hungarian Hereford, Angus, Galloway Breeders' Association (MHAGTE). The MHAGTE registry software was used for data extraction. Data preparation was performed using Microsoft Excel 2021 MSO and Microsoft Word 2021 MSO. Evaluation and correlation matrix construction were carried out using IBM SPSS Statistics for Windows, Version 27.0 (IBM SPSS 27.0, 2024).

2.1. Population genetic analysis of Hungarian Angus herds and evaluation of their economically important traits

The analyses were carried out using the registration and performance testing data of the Hungarian Hereford, Angus, Galloway Breeders' Association (MHAGTE). Genetic analysis and evaluation of economically important traits of Hungarian Angus herds, we analysed samples from 1,369 Angus cattle originating from 16 Hungarian nucleus herds. The individuals included in the analysis were pedigree-registered Angus cows and their offspring, with known maternal and paternal pedigree, and a high proportion of Angus blood (>75%). For genotype identification, 12 microsatellite markers were analysed (BM1824, BM2113, ETH3, ETH10, ETH225, INRA023, TGLA122, TGLA126, BM1818, MGTG4B, CSSM66, CSRM60) using an ABI 3500 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA).

To evaluate economically important traits, (birth weight, age at first calving, number of calves born alive, length of productive life) the production data of 4,082 cows were analysed. Based on genetic characteristics, four groups were distinguished among the 16 nucleus herds: – Blue (ACM): Canadian and American-type red, large-framed, modern type – Red (FJLNOP): Traditional red type – Green (BDEGHI): Traditional British type – typically black – Yellow (K): Traditional British black and American-imported red

Data processing and analysis were carried out using the following software: IBM SPSS Statistics 27.0 (data evaluation, correlation matrix construction), PowerMarker, Genalex 6.5, GDA-NT2021 (population genetic parameters), STRUCTURE (cluster number estimation), MEGA (dendrogram construction), Python Networkx 2.3 (betweenness centrality, genetic similarity network analysis).

2.2. Analysis of the age at first calving and population genetic characteristics of Angus cows bred in Hungary and the estimation of the breeding value of the sires

The age at first calving of cows born between 1998 and 2021 was examined. The database contained 2,955 registered Angus and high-percentage Angus (>75%) cows with known maternal and paternal pedigree, grouped into five different genetic categories. The population consisted of the progeny of 2,106 cows and 200 Angus sires. In determining AFC, only calves born alive were taken into account. Genetic groups were differentiated by origin, coat colour, size, and type: Group 1: Canadian and American-type red Angus, large-framed, modern type; Group 2: Traditional red Angus type; Group 3: Traditional Angus of exclusively British type; Group 4: Traditional British black and American-imported red Angus; Group 5: Miscellaneous group comprising mixed individuals from the above four groups. Population genetic parameters and breeding value estimation of sires were performed using both the GLM sire model and the BLUP (Best Linear Unbiased Prediction) animal model. The genetic trend of AFC was determined from the average estimated breeding values (EBVs) of the animals based on both models. Linear regression was used to evaluate genetic trends from three data sources: EBVs of sires estimated by GLM, EBVs of sires estimated by BLUP, and BLUP-based EBVs of the total population born in the same year. For phenotypic trend analysis, annual average AFC values were calculated by birth year, and linear regression was applied to determine the direction and magnitude of change.

2.3. Analysis of economically important traits among different Angus genetic groups

The analysed population consisted of 5,075 cows (born between 1990 and 2020) and 19,142 calves (born between 1997 and 2023; 10,629 male and 8,513 female calves). The individuals analysed were Angus and high-percentage Angus cows and their offspring. The six traits examined were: age at first calving, length of productive life, number of calves born alive, culling age, birth weight, and weight adjusted to 205 days. The genetic classification of Angus nucleus herds based on reproductive and longevity traits was established through DNA microsatellite-based identification. Individuals sold for further breeding were excluded from the database when determining culling age. For number of calves born and age at first calving, only live births were considered, while abortions and stillbirths were excluded. Birth weight was measured within 24 hours after calving, and weight adjusted to 205 days was calculated from the weight measured at 6–9 months of age. The analysis was performed using IBM SPSS Statistics 20 software. Kolmogorov-Smirnov test was used to assess normal distribution of the data, and Levene's test was used to evaluate the homogeneity of variances. Group comparisons were performed using the Kruskal-Wallis test, and differences between groups were evaluated using the Dunnett T3 post hoc test. For all statistical analyses, the significance level was set at $p < 0.05$.

3. RESULTS AND DISCUSSION

3.1. Population genetic characteristics of Hungarian Angus herds

The number of alleles observed at the 12 loci ranged between 11 and 18. The average effective number of alleles was $N_e = 3.201$. The observed heterozygosity was $H_o = 0.710$, and the expected heterozygosity was $H_e = 0.659$. In the herds studied, expected heterozygosity ranged from $H_o = 0.6$ (herd M) to $H_o = 0.809$ (herd B). In all herds except herd D, more heterozygous animals were observed than expected. Six populations (BJMNOP) had an inbreeding coefficient of $F_{is} \leq 0.1$, while for population B, $F_{is} < 0.2$. Herd B exhibited the highest heterozygosity, while a lower degree of inbreeding was observed in herd D.

Herd classification was determined using three different methods. According to the STRUCTURE software, the most likely number of clusters was four. At $K = 4$, four genetically defined groups were identified from the 16 Hungarian Angus herds: blue (ACM), green (BDEGHI), red (FJLOP), yellow (K). Two of these groups, ACM and FJLNOP, were also confirmed by principal component analysis (PCA). Based on Nei's genetic distance, the dendrogram placed the ACM group on the same branch of the phylogenetic tree with bootstrap values exceeding 50. The FJLNOP group—particularly JLOP—showed strong genetic relatedness. According to data from the IBS (Identical By State) network analysis, individuals in herd A had the highest betweenness centrality, IBS = 0.624 (moderate-to-high genetic similarity), which was the threshold at which the network remained connected. Individuals in population A showed the highest degree of genetic similarity to one another. Genetic analyses were performed without knowledge of the animals' phenotypic appearance or performance data. A relationship was found between the defined production and performance data of the genetic groups and the clusters identified by genetic analysis, which can be attributed to differences in animal types. Significant differences were found among Angus individuals belonging to different types and genetic groups in terms of the traits studied. For birth weight, the blue group had a result of 25.9 ± 2.7 kg, while the red group showed 29.3 ± 5.3 kg, resulting in a difference of 3.4 kg. In terms of traits influencing economic efficiency, the best result for age at first calving was found in the red group (829 ± 156 days or 27.2 ± 5.1 months), while the worst result was found in the yellow group (945 ± 320 days or 31.1 ± 10.5 months), representing a difference of 116 days or nearly 4 months. Regarding the number of calves born alive, a notable difference of 3.6 calves was observed between the blue group (4.8 ± 3.5) and the yellow group (8.4 ± 4.1). In terms of productive lifespan, a substantial difference of 1,560 days (4.27 years) was found between the large-framed blue group (1996 ± 1535 ≈ 5.46 ± 4.2 years) and the traditional British-type group (3556 ± 1758 ≈ 9.74 ± 4.81 years).

3.2. Population genetic characteristics of age at first calving (AFC) in Hungarian Angus cows

3.2.1. Effect of different factors

The overall average age at first calving (AFC) in Hungarian Angus cows was 28.1 ± 0.1 months (SD = 5.3 months, CV = 18.9%). This result falls short of the optimal 22–24 months. In the study, the average age of Angus heifers at first breeding was 18.6 months, which is 5–7 months later than the ideal age of 12–15 months. The factors examined—sire ($p<0.01$), herd ($p<0.05$), year of birth ($p<0.01$), and calving season ($p<0.01$)—had a significant effect on AFC, while no significant difference was observed among groups based on coat colour. Pearson correlation analysis revealed a significant but weak correlation between AFC and herd ($r = 0.104$, $p < 0.01$), a negative correlation with coat colour ($r = -0.108$, $p < 0.01$), and a significant but weak positive correlation with season of birth ($r = 0.060$, $p < 0.01$), while year of birth showed a very weak negative correlation ($r = -0.063$, $p < 0.01$).

The percentage contributions of environmental factors to AFC variance were: season of birth 28.99%, year of birth 28.7%, sire 18.32%, herd 11.77%, and residual variance 4.12%. The most influential factors were season and year of birth, jointly accounting for nearly 60% of the variation in AFC. These effects are attributable to changes in management and feeding practices, weather, and grazing conditions. The sire's genetic effect explained 18.32% of the phenotypic variance in the offspring.

The estimated least squares mean of age at first calving using the GLM method was 28.3 ± 0.4 months. The average AFC differed among the herds studied. In herd 2, the average AFC was 30.0 ± 0.7 months (+1.7 months from the mean), while in herd 3 it was 26.8 ± 0.7 months (-1.5 months from the mean), resulting in a 3.2-month difference between the two herds. Herd 2 consisted of British-type red Angus, while herd 3 consisted of traditional British-type black Angus. In 1999, the AFC was 24.9 months, whereas in 2012 it was 31.6 months—a 6.7-month difference between years. These variations highlight the significant influence of environmental and management conditions on reproductive performance.

Spring-born individuals had a shorter AFC (27.7 ± 0.3 months), which was 1.3 months shorter than that of summer-born and 0.8 months shorter than autumn-born animals.

3.2.2. Population genetic parameters

The heritability (h^2) of AFC was estimated to be relatively high using both the GLM (0.51 ± 0.06) and the BLUP (0.38 ± 0.05) methods. The differences can be attributed to population structure, selection intensity, and environmental conditions.

3.2.3. Sire effect on age at first calving

Using the GLM method, significant differences were found in AFC means among the progeny groups of sires. The reliability coefficient ($r^2 = 0.9994$) of breeding values estimated for AFC using the BLUP animal model was extremely high, attributable to complete pedigree data, large sample size, and the inclusion of environmental effects in the model. Progeny of the sire with registration number 20716 calved first at an average age of 31.7 ± 1.1 months (EBVGLM = +6.8 months), while progeny of sire 20495 calved at 22.4 ± 1.0 months (EBVGLM = –11.7 months), a difference of 9.3 months. A similarly large difference was observed in EBVs for AFC between the sires.

Using the BLUP animal model, the two extreme EBVs for AFC were +6.0 months (sire 27934) and –6.2 months (sire 20495), a difference of 12.2 months. The Spearman rank correlation coefficient between the GLM and BLUP estimates was relatively high (rho = 0.86; $p < 0.01$), indicating good similarity in BVs. However, this correlation may not fully capture discrepancies in the ranking of sires with fewer offspring or outlier values. The results suggest that incorporating more detailed genetic information would improve the models and increase the accuracy of breeding value estimation.

3.2.4. Phenotypic and genetic trends in age at first calving

Based on the estimated data, the phenotypic change in AFC was minimal ($b = +0.03 \pm 0.05$) and not significant ($R^2 = 0.02$; $p > 0.05$), indicating that environmental and genetic factors, along with temporal changes, did not significantly influence AFC. The genetic trend, although showing a significant decline in AFC using the GLM model ($b = –0.20$; $p < 0.05$; $R^2 = 0.18$), but did not show any decline using the more reliable BLUP model, either in maternal or direct EBVs ($b = –0.00$ to $+0.01$; SE = 0.00 to 0.03; $p > 0.05$, $R^2 = 0.00$).

Thus, no phenotypic or genetic change in AFC was observed during the 23-year study period. However, the higher heritability estimates obtained suggest that selection based on age at first calving is feasible within the Angus population.

3.3. Performance traits of different Angus genetic groups

3.3.1. Age at first calving (AFC)

The AFC values showed slight differences among the groups. The average AFC of the four genetic groups was 2.35 ± 0.54 years. The lowest AFC was found in the red group (2.28 ± 0.49 years), while the highest value was observed in the yellow group (2.47 ± 0.68 years). The difference between the lowest and highest values was 0.19 years, approximately 69.4 days. The differences in AFC between genetic groups were statistically significant ($p < 0.01$).

3.3.2. Number of calves born alive (NCB)

The NCB values differed significantly among the groups. The average NCB of the four genetic groups was 5.89 ± 3.69. The differences between genetic groups were significant ($p < 0.01$). The lowest NCB was found in the blue group (5.3 ± 3.6), and the highest in the yellow group (8.85 ± 4.15), resulting in a difference of 3.6 calves.

3.3.3. Length of productive life (LP)

LP showed substantial differences among the genetic groups. The average LP of the four genetic groups was 6.85 ± 4.13 years. The differences among groups were significant ($p < 0.01$). The lowest LP was found in the blue group (6.14 ± 3.6 years), while the highest was observed in the yellow group (9.8 ± 4.6 years), resulting in a difference of 3.7 years, which corresponds to a difference of more than three calves, as also reflected in the NCB results.

3.3.4. Culling age (AGE)

Culling age (from birth to removal from the herd) showed moderate differences among the genetic groups. The average AGE for the four genetic groups was 9.2 ± 4.26 years. The lowest AGE was found in the blue group (8.44 ± 4.11 years), and the highest in the yellow group (12.27 ± 4.53 years), representing a 3.83-year difference. This corresponds with the differences observed in LP and AFC. The AGE differences between genetic groups were statistically significant ($p <0.01$), indicating that individuals with different genetic backgrounds may reach different lifespans and herd retention times.

3.3.4. Birth weight (BW)

The BW values showed minor differences among the groups. The average BW across the four genetic groups was 29.4 ± 4.28 kg. Differences in BW between genetic groups were statistically significant ($p < 0.01$). The lowest value was recorded in the blue group (29.23 ± 4.2 kg), and the highest in the red group (31.35 ± 5.8 kg), a difference of 2.12 kg.

3.3.5. Weight adjusted to 205 days (WW)

The WW values varied considerably among the groups. The average WW of the four genetic groups was 176.90 ± 44.07 kg. The differences in WW among genetic groups were statistically significant ($p < 0.01$). The lowest WW was observed in the blue group (166.57 ± 41.1 kg), and the highest in the yellow group (212.56 ± 25.9 kg), a difference of 45.99 kg.

The results indicate significant differences in key reproductive and longevity traits between the genetically defined Angus groups identified by microsatellite markers. These findings can inform breeding programs and support selection decisions, contributing to more effective and sustainable breeding strategies for the breed.

3.3.6. Summary of results for economically important traits among genetically distinct Angus subpopulations

The average values for the six traits examined were as follows: AFC 2.35 ± 0.54 years, NCB 5.89 ± 3.69, LP 6.85 ± 4.13 years, AGE 9.2 ± 4.26 years, BW 29.4 ± 4.28 kg, and WW 176.9 ± 44.1 kg. The yellow group performed best in reproductive and growth traits (NCB, LP, AGE, WW), while the red group showed the best results in AFC and BW. The blue group had the weakest performance in NCB, LP, AGE, BW, and WW. The large-framed, modern-type red Angus herds significantly underperformed in key sustainability and profitability traits compared to the traditional, smaller British-type black and red Angus populations.

4. NEW SCIENTIFIC RESULTS

1. Using DNA microsatellite markers, I was the first to determine the genetic structure of Hungarian Angus herds. The number of alleles observed across the 12 loci ranged

between 11 and 18. The average effective number of alleles (N_e) was 3.201, indicating a moderately high level of genetic diversity. The observed heterozygosity (H_o) was 0.710, expected heterozygosity (H_e) was 0.659, and the inbreeding coefficient (F_{is}) was –0.079.

2. Based on network analysis, I demonstrated that the IBS (Identical By State) value at which the network remained connected was 0.624, indicating shared alleles in the DNA segments of the individuals.
3. I established that there were significant differences in the six traits examined (age at first calving, number of calves born alive, length of productive life, culling age, birth weight, and weight adjusted to 205 days) between the Angus genetic groups defined by microsatellite information.
4. I showed that the age at first calving of pasture-kept Angus cows was primarily influenced by weather-related environmental factors (season of birth 28.99%; $p < 0.01$), year of birth (28.7%; $p < 0.01$), and management-related herd effects (11.77%; $p < 0.05$).
5. Through linear regression trend analysis, I determined that the average age at first calving in the Hungarian Angus cow population did not change significantly over the 23-year study period, neither phenotypically (performance trend value, $b = +0.03 \pm 0.05$; $p > 0.05$; $R^2 = 0.02$) nor genetically according to the BLUP method (breeding value trend, $b = –0.00$ to $+0.01$; $SE = 0.00$ to 0.03; $p > 0.05$, $R^2 = 0.00$).

5. PUBLICATIONS RELATED TO THE DISSERTATION

5.1. Peer-reviewed article published in a foreign-language journal

- **Márton J.**, Bene Sz., Anton I., Zsolnai A., Szabó F.: Comparison of some economic traits by genetic cluster of Aberdeen Angus cattle. Archives Animal Breeding, vol. 68, issue 2, AAB, 68, 279–286, 2025 (Q2, IF: 1,75). https://doi.org/10.5194/aab-68-279-2025
- **Márton J.,** Bene Sz., Szabó F., “Heritability Estimates of Age at First Calving and Correlation Analysis in Angus Cows Bred in Hungary,” ANIMALS, vol. 14, no. 24, 2024. (Q1, IF: 2,94). https://doi.org/10.3390/ani14243715
- **Márton J.**, Szabó F., Zsolnai A., Anton I., “Genetic diversity and phylogenetic relationship of Angus herds in Hungary and analyses of their production traits,” ANIMAL BIOSCIENCE, vol. 37, no. 2, pp. 184–192, 2024. (Q1, IF: 2,4). https://doi.org/10.5713/ab.23.0157

- **Márton J.,** Szabó F., "Some Actualities and Challenges in Sustainable Beef Cattle Breeding and Husbandry," CHEMICAL ENGINEERING TRANSACTIONS, vol. 107, pp. 241–246, 2023.(Q3, IF: 1,2). https://doi.org/10.3303/CET23107041

5.2. Peer-reviewed article published in a Hungarian-language journal

- **Márton J.,** Bene Sz., Szabó F., "Néhány tényező hatása a Magyarországon tenyésztett angus tehenek első elléskori életkorára.," ÁLLATTENYÉSZTÉS ÉS TAKARMÁNYOZÁS vol. 74, no. 1, pp. 45–61, 2025.
- **Márton J.**, Bene Sz., Szabó F., "A fenntartható húsmarhatartás, húsmarhatenyésztés aktualitásai, kihívásai.," ÁLLATTENYÉSZTÉS ÉS TAKARMÁNYOZÁS, vol. 73, no. 1, pp. 47–58, 2024.
- **Márton J.**, Szabó F., Zsolnai A., Anton I., "A magyarországi angus állományok populációgenetikai vizsgálata, értékmérő tulajdonságaik elemzése.," ÁLLATTENYÉSZTÉS ÉS TAKARMÁNYOZÁS, vol. 73, no. 2 pp. 219–232, 2024.
- Szabó F., **Márton J.**, Szabó E., Bene Sz., "Húshasznosítású tehenek korai kiesésének, hasznos élettartamának néhány kockázati tényezője," MAGYAR ÁLLATORVOSOK LAPJA, vol. 143, no. 1, pp. 17–24, 2021.
- **Márton J.**, Márton D., Márton I., "Húsmarha tenyésztésünk lehetőségei, kihívásai = Possibilities and challenges of the Hungarian beef industry," ÁLLATTENYÉSZTÉS ÉS TAKARMÁNYOZÁS, vol. 66, no. 4, pp. 398–406, 2017.

5.3. Publications in Foreign Languages Published in Conference Proceedings

- Szabó F., **Márton J.**, Bene Sz., "Weaning results of Angus calves in Hungary," in 58th Annual Meeting of the European Association for Animal Production, 2007, p. 369.

5.4. Book Chapters in Hungarian Language

- Kádár L., **Márton J.**, A jövedelmező húsmarhatartás alapjai. Budapest: Vidékfejlesztési Minisztérium, 2013.
- **Márton J.**, "Húsmarha kalendárium," Versenyképes húsmarhatartás - A jövedelmezőség kulcstényezői a telepi gyakorlatban, 2013, pp. 145–160.

- **Márton J.**, “Alkalmazott tenyészérték-becslési eljárás,” Versenyképes húsmarhatartás - A jövedelmezőség kulcstényezői a telepi gyakorlatban, 2013, pp. 41–55.
- **Márton J.**, “Húsmarha kalendárium,” Versenyképes húsmarhatartás - A jövedelmezőség kulcstényezői a telepi gyakorlatban, 2012, pp. 201–217.
- **Márton J.**, “Alkalmazott tenyészérték becslési eljárás,” Versenyképes húsmarhatartás - A jövedelmezőség kulcstényezői a telepi gyakorlatban, 2012, pp. 53–72.
- **Márton J.**, “A fenotípusos teljesítmény alapján történő tenyészkiválasztás,” Versenyképes húsmarhatartás - A jövedelmezőség kulcstényezői a telepi gyakorlatban, 2012, pp. 50–52.