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Control of inbreeding in Banija spotted pig population using Optimisation methods

Kontrola uzgoja u srodstvu u populaciji banijske šare svinja pomoću optimizacijskih metoda

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ABSTRACT

The aim of the study was to estimate genetic diversity parameters for Banija spotted pig population and to apply optimisation methods to control the inbreeding in the population in three different scenarios. The first scenario consisted of minimizing inbreeding by minimizing the average kinship without considering breeding values. The second scenario was to minimize inbreeding by minimizing the average kinship accounting for breeding values. The third scenario was to apply traditional optimal contribution selection by maximizing the breeding value of the offspring. A total of 5 boars and 49 sows were selected to create mating plan minimise inbreeding in the next generation. The average inbreeding coefficient in the population was 6.97, while effective population size was 8.47. In the first scenario, different kinship constrains between candidates resulted in a change in the number of selected animals and a change in the average breeding values, such that the number of selected candidates increased when the constraint on kinship was stronger, with a simultaneous decrease in breeding values. The second scenario resulted in increased inbreeding when additional weight was placed on genetic gain. The Maximisation of breeding values resulted with drastically increased average inbreeding coefficient in the next generation. Due the small total and effective population size, the application of optimisation methods demonstrated that genetic improvement is possible at a high cost of loss of the genetic variability and preservation of diversity remains the first objective in the breeding programme for Banija spotted pig.

Keywords: Banija spotted pig, inbreeding, selection, optimal contribution selection

SAŽETAK

Cilj istraživanja bio je procijeniti parametre genetske raznolikosti za populaciju banijske šare svinje i primijeniti metode optimizacije s ciljem kontrole uzgoja u srodstvu u populaciji u tri različita scenarija. Prvi scenarij bio je minimizirati uzgoj u srodstvu minimiziranjem prosječnog srodstva u populaciji bez uključivanja uzgojnih vrijednosti. Drugi scenarij bio je minimiziranje uzgoja u srodstvu minimiziranjem prosječnog srodstva uzimajući u obzir uzgojne vrijednosti. Treći scenarij bio je primijeniti tradicionalni pristup selekciji s optimiziranim doprinosima doprinosa maksimiziranjem uzgojne vrijednosti u potomstvu. Ukupno je odabrano 5 nerastova i 49 krmača za izradu plana sparivanja koji će omogućiti minimiziranje inbreedinga u sljedećoj generaciji. Prosječni F u populaciji bio je 6,97, a Ne 8,47. U prvom scenariju različita ograničenja srodstva između kandidata rezultirala su promjenom broja odabranih životinja i mijenjanjem prosječnih uzgojnih vrijednosti tako da se broj odabranih kandidata povećavao kada je ograničenje srodstva bilo jače, uz istodobno smanjenje uzgojnih vrijednosti. Drugi scenarij rezultirao je povećanim uzgojem u srodstvu kada je dodana dodatna težina na genetski napredak. Maksimiziranje uzgojnih vrijednosti rezultiralo je dramatičnim povećanjem koeficijenta uzgoja u srodstvu u sljedećoj generaciji. Zbog male ukupne i efektivne veličine populacije, primjena metoda optimizacije pokazala je da je genetski napredak moguć uz veći gubitak genetske varijabilnosti, a očuvanje raznolikosti ostaje prvi cilj u uzgojnom programu analizirane pasmine.

Ključne riječi: banijska šara svinja, uzgoj u srodstvu, selekcija, selekcija s optimiziranim doprinosima

INTRODUCTION

Conservation of livestock populations is a challenging process in which sustainable use of livestock is the ultimate goal of conservation. Although maintaining genetic diversity is the primary objective of breeding programs in local pig breeds, breed sustainability is based on the ability to derive economic benefits from these breeds (Barker 2001). Thus, breeding programmes for such breeds that include both breeding goals into conservation process must be established, with a balance between genetic diversity and genetic improvement of economically important traits.

The loss of genetic variability can be estimated from genealogical data in term of the increase of inbreeding through generations. The increase of inbreeding and impaired genetic diversity in pig populations can result with the manifestation of inbreeding depression: impaired fertility and functional traits, appearance of degenerative defects, causing economical losses in herds (Charlesworth and Charlesworth, 1999). The control of inbreeding can be achieved by the creation of adequate mating plans that avoid mating of related animals. Moreover, the control of the inbreeding rate in the population can include the selection of genetically superior animals ensuring simultaneous genetic gain and preserving genetic diversity of the population. This can be achieved using procedures within optimal contribution selection frame.

Optimal contribution selection (OCS) is a set of procedures based on optimisation algorithms that balance genetic gain for traits in the population with the loss of genetic variability. The concept of optimal contributions was proposed by Wooliams and Thompson (1993) and further developed by Meuwissen (1997), and Grundy et al. (1998). Practical implementation of the procedure in pigs is still rare, and the use of OCS in pig populations has been tested through simulations (Gourdine et al., 2015; Howard et al., 2018; Zhao et al., 2021), while it has been successfully applied in species such as dairy cattle (Kohl et al., 2020). Traditional OCS focuses on the maximising estimated breeding values (Wellman et al., 2019). However, in populations where primary goal is to maintain genetic variability, the optimisation algorithms can be used without taking breeding values into account, allowing a controlled increase of the inbreeding in the population. The most important prerequisite for a reliable estimation of population parameters such as the relatedness between animals and consequently for effective use of selection procedures is accurate genealogical information with sufficient pedigree depth and accurate records. Moreover, molecular information can significantly improve the estimation of diversity parameters.

Banija spotted pig was recently recognised as an indigenous Croatian breed of pigs after revitalisation that started in 2015 (Salajpal et al., 2017). At the same time, pedigree recording started. Banija spotted pigs have moderate fertility (Menčik et al., 2019) and are well adapted to semi-extensive and extensive systems. The number of animals in Banija spotted pig population shows a continuous increase with 30 boars and 139 breeding sows (Croatian Agency for Agriculture and Food, 2021). The increasing trend enables the establishment of breeding programme and setting up breeding goals, including genetic evaluation for economically important traits such as litter size or meat quality.

The aim of the study was to estimate population-specific parameters based on genealogical data for Banija spotted pig and to apply optimal contribution selection procedure to minimise the increase of inbreeding in the population.

MATERIAL AND METHODS

Data

Data set with litter records for Banija spotted pig was provided by the Croatian Agency for Agriculture and Food. The set contained 623 litter records on the number of piglets born alive (NBA). In addition to basic information (sow identification number and information about NBA), individual farrowing record contained information on herd, subsequent parity (from one to ten), service boar, and mating season (year/season interaction). After control of data quality, there were 31 seasons, 11 herds, and 71 service boar levels. The basic statistics for NBA can be found in Table 1.

Table 1. Descriptive statistics for number of piglets born alive in Banija spotted pig

N	Mean	SD	CV	Min	Max
623	6.84	2.61	38.12	0	15

Pedigree data file was created based on animals with phenotype and contained 323 animals.

Population parameters

Basic pedigree structure (Table 2) was determined using CFC software (Sargolzaei et al., 2006).

Table 2. Pedigree structure for Banija spotted pig

Item	N
Total number of animals	323
Total number of sires	46
Total number of dams	69
Sows with records	265
Number of inbreds	104
Founders	110
Non-founders	213

Pedigree quality

The pedigree quality was evaluated using:

- number of fully traced generations (NTG) – represents the number of generations separating an individual from its furthest ancestor,
- maximum number of complete generations (NCG) – identifies the furthest generation with two known ancestors,
- number of equivalent complete generations (NECG) – expresses the sum of all known ancestors counting how many generations have been traced. It is calculated for those individuals having at least one parent known following Maignel et al. (1996):

Following population parameters were estimated:

- coefficient of inbreeding (F) – it was determined by calculating F using Cholesky factorisation of the relationship matrix as proposed by Meuwissen and Luo (1992),
- mean rate of increase in coancestry (Cervantes et al., 2011),
- Effective population size calculated as:

  $$\Delta c_{ij}=1-\sqrt[\frac{g_i+g_j}{2}]{1-c_{ij}}$$

  where c_{ij} is the kinship between i and j, and g_i, g_j are the numbers of equivalent complete generations of individuals i and j,
- average relatedness.

OptiSel package (Wellmann, 2019) in the R programming environment (R Core Team 2020) were used to analyse the above parameters.

Genetic parameters and breeding values

Genetic parameters for NBA were estimated using following single trait repeatability model:

$$y_{ijklmno} = \mu + S_i + P_j + B_k + H_l + p_{im} + a_n + e_{ijklmno}$$

where effects of mating season (S_i), parity (P_j), service boar (B_k), and herd (H_l) were considered as fixed class effects. Permanent environmental (p_{im}) and direct additive genetic effect (a_{mn}) were included in the model as random effects.

In the matrix notation repeatability model can be written as:

$$y=X\beta + Z_p\, p + Z_a\, a + e$$

where y is a vector of observations, X is incidence matrix, for fixed effects, β is a vector of unknown parameters, for fixed effects, Z_p and Z_a are incidence matrices for permanent environmental and additive genetic effect, p and a are the corresponding vectors of parameters for random effects, and vector e presents residual. The following covariance structure was assumed:

$$\mathrm{var}\begin{bmatrix}\mathbf{p}\\ \mathbf{a}\\ \mathbf{e}\end{bmatrix}=\begin{bmatrix}I_p\sigma^2{}_p & 0 & 0\\ 0 & A\sigma^2{}_a & 0\\ 0 & 0 & I_e\sigma^2{}_e\end{bmatrix}$$

Estimation of the variance components for NBA was based on the residual maximum likelihood method using the VCE-6 software package (Groeneveld et al., 2008). Breeding values for NBA were estimated with the same statistical model.

Optimal contribution selection

To ensure the reliability of the OCS procedures, candidates were selected from the Banija spotted pig herdbook using following criteria:

- animals are still alive, as there is no elimination date in the herdbook,
- animals have sufficient pedigree depth (number of equivalent generations > 2),
- animals have an estimated breeding value.

Using all criteria, the total number of selection candidates was 76 sows and 4 boars.

Optimal genetic contributions were determined in three different scenarios. The first scenario was to minimize inbreeding by minimizing the average kinship of the population accounting without considering breeding values The second scenario was to minimize inbreeding by minimizing the average kinship of the population accounting also for breeding values, since inbreeding arises from mating of related parents. The third scenario was to apply traditional optimum contribution selection by maximising the breeding value in the offspring for NBA (Meuwissen et al., 1997). The optimisation problems were solved using the CCCP solver from the R package OptiSel (Wellmann, 2019). The package contains routines for solving cone constrained convex problems using interior-point methods that are partially ported from Python's CVXOPT and based on Nesterov-Todd scaling (Vandenberghe, 2010). The solver uses a primal–dual path following algorithms for linear and quadratic cone constrained programming.

RESULTS AND DISCUSSION

Population parameters

The genetic diversity parameters showed significant lack of population variability (Table 3).

Table 3. Genetic diversity in Banija spotted pig obtained from pedigree

Parameter	Value
Mean maximum number of generations traced back	4.12
Mean number of full generations traced back	1.17
Mean number equivalent generations	2.20
Coefficient of inbreeding (F), %	6.97
Rate of increase in coancestry (Δc)	0.06
Average relatedness (AR)	0.05
Effective population size (N_e)	8.47

The pedigree was characterised by low completeness, which is a consequence of the early stage of the conservation process. The coefficient of inbreeding was high compared to similar breeds such as Black Slavonian pig (Gvozdanović et al., 2020); Entrepelado line (F=2.50%) and Retinto line (5.80%) of Iberian pig (Casellas et al., 2019); Blonde (F=3.86%), Swallow-belly (F=3.29%) and Red Mangalitza pig (F=5.02%; Posta et al., 2016). The inbreeding coefficient was also higher compared to earlier studies on Banija spotted pig (Škorput et al., 2018; Zorc et al., 2022), as a results of increased amount of pedigree information. However, a measure that gives a better insight into dynamics of genetic diversity of the population is the change of average kinship between generations (Cervantes et al., 2011) and effective population size, resulting from the latter. According to FAO (2000), the effective population size of the population should not be lower than 50 and the inbreeding rate should not exceed 1%. According to FAO criteria (2007), Banija spotted pig belongs to the category of endangered pig breeds. In view of these criteria, the results of the pedigree data suggest that the breeding objective should be aimed at maintaining population diversity. This goal can be achieved by establishing valid mating schedules that avoid mating of related animals.

Genetic parameters and breeding values

The analysis of genetic parameters for number of piglets born alive in Banija spotted pig (Table 4) showed higher phenotypic variance than estimates in other local breeds, such as Black Slavonian pig (Škorput et al., 2013) or Bissaro pig (Paixão et al, 2019) and similar to modern pig breeds (Ogawa et al., 2018).

The estimate of additive variance, which is the basis for selection for quantitative traits was lower than in modern breeds, such as Landrace and Large White (Ogawa et al., 2018), but higher than in Black Slavonian pig (Škorput et al., 2014) and similar to estimates in different strains of Iberian pig (Noguera et al., 2019). From the breeder's point of view, the additive variance and heritability obtained in this study could allow genetic improvement for NBA and consequently improve competitiveness of the breed with other breeds and achieve more effective and sustainable production results.

Permanent environmental effect is a characteristic of each individual sow and the accuracy of estimating this effect depends on the number of litters per sows obtained. The low estimates of permanent environmental effect are consequence of high proportion litter records from the first parity, and lower proportion of records from subsequent parities. Proportion of permanent environmental variance in total phenotypic variance is in range from 0.02 (Adamec and Johnson, 1997) to 0.361 found by Noguera et al. (2019).

Estimated genetic parameters indicate slow future genetic improvement for litter size. Litter size is strongly affected by environmental factors (Luković and Škorput, 2015) and an adequate management practices can significantly improve prolificacy. Škorput et al. (2020) observed the high variability in phenotypic expression for NBA in Banija spotted pig with strong effects of season and herd. This information, considered together with results obtained in this study clearly demonstrates the importance of good management practices in fertility management. Since the strong increase of NBA in the Banija spotted pig is not the main breeding goal, the genetic evaluation should be considered for other traits of interest. Gourdine et al. (2012) demonstrated that there is a clear possibility to preform optimal contribution selection for improved product quality in small local pig breeds. Thus, the future selection work should consider inclusion of additional traits that might improve the value of the final products of Banija spotted pig.

Optimal contributions

Optimal genetic contributions were determined in three different scenarios: minimising kinship without accounting for breeding values; minimising kinship accounting for breeding values; maximising breeding values. The parameters obtained from the first scenario are shown in Table 5. In total, 5 boars and 49 sows were chosen to create mating plan which will enable minimizing inbreeding in the next generation. Due to small number of boars that were declared as selection candidates, genetic contributions of female candidates were also managed. The average breeding value for NBA was -0.04, and thus no genetic progress is achievable within this scenario; however, the benefit is decreased average kinship in the next generation.

Table 4. Genetic parameters for number of piglets born alive in Banija spotted pig

Variances	σ^2_{ph}	σ^2_{p}	σ^2_{a}	σ^2_{e}
Number of piglets born alive	6.16	0.00	0.42	5.74
		p^2	h^2	e^2
Ratio of the phenotypic variance		0.00	0.07	0.993

Table 5. Number of selected breeding pigs, average inbreeding in offspring generation, minimum and maximum male and female contribution by minimizing the average kinship of the population without account on breeding values

BV	No. of selected candidates(M/F)	F	Kinship	Maximal male contribution	Maximal female contribution
-0.04	5/49	0.07	0.17	0.24	0.19

However, with the inclusion the breeding values in the optimisation procedure, the distribution of selection candidates changed, and the number of boars used was 5, and number of sows changed depending on the target breeding value. With the increase of target breeding value, the average kinship and inbreeding in the next generation increased (Table 6). The increase of average kinship is a consequence of favourising related animals with higher breeding values by animal model.

Using the traditional approach to the optimal contribution selection procedure (maximising EBV's given constrains on kinship), the smallest upper bound of kinship with available solution was 0.17 (Table 7). However, the average inbreeding coefficient in the next generation is drastically increased, and the traditional approach with maximising EBV's would lead to a degradation of genetic diversity in the population.

Obtained genetic diversity parameters implicate that the primary breeding goal in the Banija spotted pig population is still to maintain genetic diversity. Although the primary breeding goal in Banija spotted pig population is to preserve genetic variability, the application of optimisation procedures is useful in creating mating planes for future selection candidates. The practical implementation of OCS in pig populations is not widely spread, however, the optimisation procedures are gaining great importance, especially in populations where genetic diversity is at risk, such as Banija spotted pig. This is particularly important if the genetic valuation is performed by pedigree-based methods, such as BLUP or genomic selection, which are expected to select more related animals with higher breeding values (Wooliams et al., 1999).

In such situations mating plans should be created to avoid mating of related animals. In this way, the optimisation between two opposite breeding goals in population may be achieved even in populations with impaired genetic variability by weighing risks and benefits of genetic improvement. The future implementation of optimal contribution selection in populations such as Banija spotted pig might be boosted by using genomic information which can improve the accuracy of prediction.

Zorc et al. (2022) gave the first insight in genomic background of Banija spotted pig, which can be considered as starting point in the application of marker assisted selection in the Banija spotted pig.

Table 6. Number of selected breeding pigs, average inbreeding in offspring generation, minimum and maximum male and female contribution by minimising the average kinship of the population with account on breeding values

BV	No. of selected candidates (M/F)	F	Kinship	Maximal male contribution	Maximal female contribution
0.05	5/7	0.10	0.18	0.17	0.16
0.10	5/7	0.11	0.19	0.14	0.13
0.25	5/10	0.18	0.24	0.17	0.15

Table 7. Number of selected breeding pigs, average inbreeding in offspring generation, minimum and maximum male and female contribution under different restrictions on average kinship using traditional OCS

Upper bound - kinship	No. of selected candidates (M/F)	BV	F	Maximal male contribution	Maximal female contribution
0.17*	5/7	0.05	0.09	0.17	0.15
0.25	5/8	0.27	0.19	0.24	0.19

* the least possible upper bound with solution

CONCLUSION

Specific population parameters of Banija spotted pig showed a low level of genetic diversity with high average inbreeding coefficients and a low effective population size. The application of optimisation methods resulted in lower average relatedness in selected individuals. Due to the low total and effective population size, the application of optimisation methods showed that genetic improvement is possible at a high cost of loss of genetic variability and that maintenance of diversity remains the first objective in the breeding programme for the analysis breed. Further goals objectives should be the improvement of pedigree and litter data as well as the inclusion of genomic information in the estimation process to ensure a more reliable estimation of population parameters.

REFERENCES

Adamec, V., Johnson, R.K. (1997) Genetic analysis of rebreeding intervals, litter traits, and production traits in sows of the National Czech nucleus. Livestock Production Science, 48,13–22. DOI: https://doi.org/10.1016/S0301-6226(96)01417-0

Barker J.S.F. (2001) Conservation and management of genetic diversity: A domestic animal perspective. Canadian Journal of Forest Research, 31 (4), 588-595. DOI: https:/doi.org/10.1139/cjfr-31-4-588

Casellas, J., Ibanez-escriche, N., Varona, L., Rosas, J. P., Noguera, J. L. (2019) Inbreeding depression load for litter size in Entrepelado and Retinto Iberian pig varieties. Journal of Animal Science, 97 (5), 1979–1986. DOI: https://doi.org/10.1093/jas/skz084

Cervantes, I., Goyache, F., Molina, A., Valera, M., Guitérrez, J. P. (2011) Estimation of Effective Population Size from the Rate of Coancestry in Pedigreed Populations. Animal Breeding and Genetics, 128 (1), 56-63. DOI: https://doi.org/10.1111/j.1439-0388.2010.00881.x

Charlesworth, B, Charlesworth, D. (1999) The genetic basis of inbreeding depression. Genetetic Research, 74, 329–340. DOI: https://doi.org/10.1017/s0016672399004152

Croatian Agency for Agriculture and Food (2020) Annual report: Pig breeding. Osijek: Croatian Agency for Agriculture and Food.

FAO (2000) Secondary guidelines for development of national farm animal genetic resources management plans: Management of small populations at risk. Rome: Food and Agriculture Organization.

FAO (2007) The state of the world's Animal genetic resources for food and agriculture. Rome: Food and Agriculture Organization.

Gourdine, F, Sorensen, A.C., Rydhmer, L. (2012) There is room for selection in a small local pig breed when using optimum contribution selection: A simulation study. Journal of Animal Science, 90, 76-84. DOI: https://doi.org/10.2527/jas.2011-3898

Groeneveld, E., Kovač, M., Mielenz, N. (2010) VCE: User's Guide and Reference Manual, version 6.0. Neustadt: Institute of Farm Animal Genetics.

Gvozdanović, K., Škorput, D., Djurkin Kušec, I., Salajpal, K., Kušec, G. (2020) Estimation of population differentiation using pedigree and molecular data in Black Slavonian pig. Acta fytotechnica et zootechnica, 23, 241-249. DOI: https://doi.org/10.15414/afz.2020.23.mi-fpap.241-249

Gourdine, J.L., Sórensen, A.C., Rydhmer, L. (2012) There is room for selection in a small local pig breed when using optimum contribution selection: A simulation study. Journal of Animal Science, 90, 76-84.

Grundy, B., Villanueva, B., Woolliams, J. (1998) Dynamic selection procedures for constrained inbreeding and their consequences for pedigree development. Genetics Research, 72,159–168. DOI: https://doi.org/10.1017/S0016672398003474

Howard, D.M., Pong-Wong, R, Knap, P.W., Kremer, V.D., Wooliams, J.A. (2019) Selective advantage of implementing optimal contributions selection and timescales for the convergence of long-term genetic contributions. Genetic Selection Evolution, 50, 24. DOI: https://doi.org/10.1186/s12711-018-0392-z

Kohl, S., Wellmann, R., Herold, P. (2020). Advanced optimum contribution selection as a tool to improve regional cattle breeds: A feasibility study for Vorderwald cattle. Animal, 14 (1),1-12. DOI: https://doi.org/10.1017/S1751731119001484

Maignel, L., Boichard, D., Verrier, E. (1996) Genetic variability of French dairy breeds estimated from pedigree information. Interbull Bullettin 14,49–54.

Luković, Z., Škorput, D. (2015) Factors influencing litter size in pigs. Cabi Reviews, 10 (6), 1-9.

Menčik, S., Klišanić, V., Špehar, M., Mahnet, Ž., Škorput, D., Luković, Z., Karolyi, D., Ekert Kabalin, A., Salajpal K. (2019) Reproductive parameters in a Banija Spotted pig breed population during breed revitalization. Veterinarski arhiv, 89 (2),183-189. DOI: https://doi.org/10.24099/vet.arhiv.0428

Meuwissen, T. (1997) Maximizing the response of selection with a predefined rate of inbreeding. Journal of Animal Science, 75, 934–940. DOI: https://doi.org/10.2527/1997.754934x

Meuwissen, T., Luo, Z. (1992) Computing inbreeding coefficients in large populations. Genetics Selection Evolution, 24, 305-313. DOI: https://doi.org/10.1186/1297-9686-24-4-305

Noguera, J.L., Ibáñez-Escriche, N., Caellas, J., Rosas, P., Varona, L. (2019) Genetic parameters and direct, maternal and heterosis effects on litter size in a diallel cross among three commercial varieties of Iberian pig. Animal, 13 (12), 2765 – 2772. DOI: https://doi.org/10.1017/S1751731119001125

Ogawa, S., Konta, A, Kimata, M, Kazuo, I., Yoshinobu, U., Satoh, M. (2018) Estimation of genetic parameters for farrowing traits in purebred Landrace and Large White pigs. Animals science journal, 90 (1), 23-28. DOI: https://doi.org/10.1111%2Fasj.13120

Paixão, G., Martins, A., Esteves, A, Payan-Carreira, R., Carolino, N. (2019) Genetic parameters for reproductive, longevity and lifetime production traits in Bísaro pigs. Livestock science, 225, 129-134. DOI: https://doi.org/10.1016/j.livsci.2019.05.010

Posta, J., Szabó, P., Komlósi, I. (2016) Pedigree analysis of Mangalica pig breeds. Annals of Animal Science, 16 (3), 701-709. DOI: https://doi.org/10.1515/aoas-2015-0075

R Core Team (2020) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. Available at: https://www.R-project.org/ [Accessed 1 April 2022].

Salajpal, K., Menčik, S., Šalamon, D., Karolyi, D., Klišanić,V., Mahnet, Ž., Škorput, D., Z. Luković (2017) Revitalizacija uzgoja banijske šare svinje. Zagreb: University of Zagreb, Faculty of Agriculture.

Sargolzaei, M., Iwaisaki, H., Colleau, J.J. (2006) CFC: A tool for monitoring genetic diversity. 8th World Congress on Genetics Applied to Livestock Production. Belo Horizonte, Brazil.

Škorput, D., Gorjanc, G., Đikić, M., Luković, Z. (2014) Genetic parameters for litter size in Black Slavonian pigs. Spanish Journal of Agricultural Research, 12 (1), 89-97. DOI: http://dx.doi.org/10.5424/sjar/2014121-4299

Škorput, D., Gvozdanović, K., Klišanić, V., Menčik, S., Karolyi, D., Margeta, P., Kušec, G., Djurkin-Kušec, I., Luković, Z., Salajpal, K. (2018) Genetic diversity in Banija spotted pig: pedigree and microsatellite analyses. Journal of Central European Agriculture, 19 (4), 871-876. DOI: https://doi.org/10.5513/JCEA01/19.4.2335

Škorput, D., Torček, I., Menčik, S., Mahnet, Ž., Klišanić, V., Karolyi, D., Luković, Z., Salajpal, K. (2020) Čimbenici plodnosti krmača banijske šare svinje. In: Mioč, B., Širić, I., eds. Zbornik radova 55. hrvatskog i 15. međunarodnog simpozija agronoma, Vodice, Croatia, 16-21 February, University of Zagreb Faculty of Agriculutre, 389-393.

Vandenberghe, L. (2010) The CVXOPT linear and quadratic cone program solvers. Available at: http://abel.ee.ucla.edu/cvxopt/documentation/coneprog.pdf [Accessed 1 April 2022]

Wellmann, R. (2019) Optimum contribution selection for animal breeding and conservation: the R package optiSel. BMC Bioinformatics 20, 25. DOI: https://doi.org/10.1186/s12859-018-2450-5

Woolliams, J.A., Meuwissen, T.H.E. (1993) Decision rules and variance of response in breeding schemes. Animal Production, 56, 179–186. DOI: https://doi.org/10.1017/S0003356100021231

Woolliams, J.A., Thompson, R. (1993) A theory of genetic contributions. Proceedigs of 5th World Congress on Genetics Applied in Livestock Production, University of Guelph, 25, 127–134.

Wooliams, J,A,, Bijma, P., Villanueva, B. (1999) Expected genetic contributions and their impact on gene flow and genetic gain. Genetics, 153 (2),1009-1020. DOI: https://doi.org/10.1093%2Fgenetics%2F153.2.1009

Zhao, Q., Huiming, L, Qadri, Q.R., Wang, Q., Pan, Y., Guosheng, S. (2021) Long-term impact of conventional and optimal contribution conservation methods on genetic diversity and genetic gain in local pig breeds. Heredity, 127, 546-553. DOI: https://doi.org/10.1038/s41437-021-00484-z

Zorc, M., Škorput, D., Gvozdanović, K., Margeta, P., Karolyi, D., Luković, Z., Salajpal, K., Savić, R., Muñoz, M., Bovo, S., Djurkin-Kušec, I., Radović, Č., Kušec, G., Čandek-Potokar, M., Dovč, P. (2022) Genetic diversity and population structure of six autochthonous pig breeds from Croatia, Serbia, and Slovenia. Genetics Selection Evolution, 54, 30. DOI: https://doi.org/10.1186/s12711-022-00718-6