

## Investigating Genetic Diversity and Determining Inbreeding Rates Using Pedigree Information in Iranian Kurdish Horses

Reza Seyed Sharifi<sup>1</sup>, \* | Sajad Badbarin<sup>2</sup> | Mohammad Heydari<sup>2</sup> | Jamal Seifdavati<sup>1</sup> | Nemat Hedayat-Evrigh<sup>1</sup> | Abdolfattah Zeidan Mohammad Salem<sup>3</sup>

<sup>1</sup>Department of Animal Sciences, Faculty of Agriculture and Natural Resources  
University of Mohaghegh Ardabili, Ardabil, Iran

<sup>2</sup> Department of Animal Science Research, Kermanshah Agricultural and Natural  
Resources Research and Education Center, Kermanshah, Iran

<sup>3</sup>Department of Animal Nutrition School of Veterinary Medicine and Zootechnics  
Autonomous University of the State of Mexico Toluca, Edo de México, México

\*Corresponding Author E-mail: [reza\\_seyedsharifi@yahoo.com](mailto:reza_seyedsharifi@yahoo.com)

Submitted: 2025-09-13, Revised: 2025-10-04, Accepted: 2025-11-02

### Abstract

The present study aimed to investigate the genetic diversity and determine inbreeding rates in Iranian Kurdish horses, a vital genetic reserve for the country's equine population, utilizing pedigree information. There are over 60,000 horses in the country, of which over 20,000 horses have been counted in the fields of sports, jumping and beauty. Of these, about 4,000 horses have also been registered as Kurdish horses. For this comprehensive study, registered data for over 4,000 horses served as the basis for the analyses. The primary objective of this research was to accurately estimate key population parameters of the Kurdish horse. These parameters included genetic diversity, pedigree completeness, genetic conservation index, effective population size, effective number of founding animals, effective number of ancestors, generation interval, individual inbreeding coefficient, and average kinship coefficient. Investigating these factors represents a crucial step toward a deeper understanding of the genetic status and strategic planning for the conservation of this valuable breed. The generation interval was estimated at 7.94 years, representing the average age difference between parents and their offspring. Concurrently, average kinship was calculated to be 0.37%. The overall average inbreeding level across the study population was 0.11%, which suggests a relatively low incidence of inbreeding within this breed. Further analyses yielded an effective population size of 405.08, derived from methods tracking individual inbreeding increases and maximum generation depth. This indicates a healthy genetic diversity. The effective founder size was also examined at 150, pointing to a balanced reproductive contribution from the foundational animals. Complementing this, the effective founder number ( $f_e$ ) was 150, and the effective ancestor number ( $f_a$ ) was 136. The resulting  $f_e/f_a$  ratio of 1.10 further supports the notion of a low impact from past genetic bottlenecks. Given that diminished genetic diversity and increased homozygosity can negatively impact performance traits, it is vital to implement proactive strategies. By continuing to monitor genetic diversity and carefully managing parent-offspring pairings to avoid close relatives, this valuable breed can be safeguarded from future declines in performance and preserve its unique genetic heritage.

**Keywords:** Inbreeding Coefficient, Kurdish Horse, Population Parameters, Studbook.

## Introduction

Iranian horse breeds can be divided into four main groups according to their origin and breeding location: northern horses (such as the Caspian breed), northeastern horses (such as the Turkmen breed), western horses (such as the Kurdish breed), and southern horses (such as the Arab breed) [1]. Kurdish horses are mainly distributed in Kermanshah Province and to a lesser extent in Kurdistan, Lorestan, Ilam, West Azerbaijan, Zanjan, and Isfahan provinces. The Iranian Kurdish horse is directly related to the famous Nisa horse, which dates back to 500 BC [2]. The Kurdish horse has a thick neck and chest, a strong hindquarter, and a full mane and tail, with a prominent cheekbone. The most important and best trait of the Kurdish horse is its good temperament and trainability, which is why it is a great option for training novice riders. The Kurdish horse can be used well in various horse racing, jumping and endurance competitions [3]. The Kurdish horse is one of the famous horses in the country with many outstanding characteristics. This breed is very beautiful and has good endurance (Figure 1). The Kurdish horse has high quality in polo, jumping and beauty competitions and has won many honors in these fields [4].



**Figure 1:** The Kurdish horse

Iranian horse breeds can be divided into four main groups according to their origin and

breeding location: northern horses (such as the Caspian breed), northeastern horses (such as the Turkmen breed), western horses (such as the Kurdish breed), and southern horses (such as the Arab breed) [1]. Kurdish horses are mainly distributed in Kermanshah province and to a lesser extent in Kurdistan, Lorestan, Ilam, West Azerbaijan, Zanjan, and Isfahan provinces. The Iranian Kurdish horse is directly related to the famous Nisa horse, which dates back to 500 BC [2]. The Kurdish horse has a thick neck and chest, a strong hindquarter, and a full mane and tail, with a prominent cheekbone. The most important and best trait of the Kurdish horse is its good temperament and trainability, which is why it is a great option for training novice riders. The Kurdish horse can be effectively used in various horse racing, jumping, and endurance competitions [3]. The Kurdish horse is one of the most renowned horses in the country with many outstanding characteristics. This breed is very beautiful and has good endurance (Figure 1). The Kurdish horse excels high quality in polo, jumping, and beauty competitions and has won many honors in these fields [4].

Pedigree analysis allows for the assessment of inbreeding levels and population structure. Since indigenous breeds are considered national assets and key reserves in each country, their preservation and propagation are of great value and importance. Examining the genetic diversity of breeds is one of the important issues in preserving genetic reserves, and many efforts are being made to preserve it at different levels. Usually, in populations that are under selection pressure, inbreeding of offspring increases. Crucially, a cornerstone of conservation efforts for endangered breeds lies in meticulously managing inbreeding levels. When faced with the twin challenges of selection pressure and the imperative to conserve genetic resources, certain foundational population parameters—heavily

influenced by effective management strategies—emerge as potent determinants of gradual shifts in genetic diversity. The effective population size, for instance, stands out as a pivotal metric. It not only offers a robust description of genetic diversity within animal populations, but also proven invaluable for accurately predicting future breeding values. Using this information, it is possible to predict to what extent an inappropriate mating program can lead to the destruction of genetic diversity in populations. Through pedigree analysis, it is possible to determine the level of reduction in genetic diversity in a small population and predict inbreeding coefficients and other population parameters. The country's horse population is smaller than that of domesticated livestock such as cattle and sheep, and breeders are very sensitive to the selection of stallions and mating with their mares. In these circumstances, the possibility of using a limited number of sires to form the next generation is very high, which can greatly increase the level of inbreeding in this population. In recent decades, pedigree analysis has been widely used to analyze population structure, inbreeding, and the genetic diversity of horses [5-7]. Pedigree analysis provides data that is very useful in assessing genetic diversity, especially for small populations [8]. The quality of pedigree information, the depth of the pedigree, and the degree of quality of the pedigree information affect all parameters. Native breeds in each country are key national assets and genetic reserves, and their preservation and conservation are of high value and importance. By analyzing the pedigree, it is possible to calculate to some extent the increase in homozygosity and decrease in heterozygosity for the entire genome. This method can be considered as a suitable strategy for monitoring populations to implement mating programs and manage genetic diversity. Therefore, the aim of the

present project was to investigate genetic diversity and determine inbreeding rates using pedigree information in Iranian Kurdish horses.

## Materials and Methods

### *Collection of Forest Tree Leaf Waste*

This study was conducted using data from the Kurdish Horse Pedigree Book [3] and data from the National Animal Science Research Institute. According to statistics presented by the former head of the National Livestock Breeding Center at the Second National Horse Industry Conference, there are over 60,000 horses in the country, of which over 20,000 horses have been registered in the fields of sports, jumping, and beauty. Of these, about 4,000 horses have also been registered as Kurdish horses. Therefore, the total population studied with registered data exceeds 4,000. These horses are mostly bred in the provinces of Kermanshah, Kurdistan, Lorestan, and West Azerbaijan. The information used included the animal number, sire number, dam number, gender, and date of birth of each horse. The aim of the present study was to estimate the population parameters of Kurdish horses including: genetic diversity, pedigree completeness, genetic conservation index, effective population size, effective number of founders, effective number of ancestors, generation interval, individual inbreeding coefficient, and average relatedness coefficient. First, the level of pedigree evolution was examined. For this purpose, the percentage of animals with known parents in the pedigree file was estimated. Then, the pedigree evolution index was calculated for all animals in the pedigree file using Equation 1.

$$PCI_{\text{animal}} = (C_{\text{sire}} \times C_{\text{dam}}) / (C_{\text{sire}} + C_{\text{dam}}) \quad (1)$$

Where,  $C_{\text{sire}}$  and  $C_{\text{dam}}$  are the linear contributions of the animal's parents, respectively, and are estimated by Equation 2.

$$C = 1/d(\sum a_i) \quad (2)$$

Where,  $a_i$  is the proportion of known ancestors in generation  $i$  and  $d$  is the number of generations considered. Also, to check the level of completeness of the pedigree, animals with both known parents are counted and expressed as a percentage of the total animals in the pedigree. The genetic conservation index for each individual is determined by the genetic contributions of all founder animals and is calculated using Equation 3 [9].

$$GCI = 1/\sum P_i^2 \quad (3)$$

Where,  $P_i$  is the proportion of genes from each founder animal in the pedigree of this animal. The generation interval is defined as the average age of parents at the time of birth of their offspring and is calculated for the four paths father-son, father-daughter, mother-son and mother-daughter (Equation 4).

$$L = (L_{mm} + L_{mf} + L_{fm} + L_{ff})/4 \quad (4)$$

The effective population size is the number of individuals in an ideal genetic population that can have a genetic drift rate similar to the population under study. One method of estimating the effective population size is to use the inbreeding rate between animals and their direct parents. In this method, two groups of animals are considered in generations  $t$  and  $t-1$ , and the inbreeding rate and effective population size are calculated using Equations 5 and 6, respectively.

$$\Delta F_p = (F_t - F_{t-1})/1 - F_{t-1} \quad (5)$$

$$N_e = 1/2\Delta F \quad (6)$$

The founding animals of the population were identified by going back through the pedigree. The expected contribution of each

founder animal to the establishment of the reference population ( $P_i$ ) was calculated. To examine the balance of genetic contributions of the founder animals to the establishment of the current population, the effective number of founder animals was estimated using Equation 7 [10].

$$E_e = 1/\sum P_i^2 \quad (7)$$

The inbreeding coefficient ( $F$ ) can be calculated based on the size of the population or pedigree information (Equation 8). The inbreeding coefficient is defined as the probability that two genes at a given locus are identical. This means that these genes are copies of the same gene and have a common origin. The inbreeding coefficient of the animals in the pedigree be calculated using the method of Meuwissen and Luo [11].

$$F_{(x)} = \sum[(\frac{1}{2})^{n+1}](1 + F_{(a)}) \quad (8)$$

Where,  $n$  is the number of paths connecting the parents of individual  $x$  and  $F_{(a)}$  is the degree of inbreeding of the common ancestor. ENDOG software is a population genetics software that uses pedigree information to examine the evolution of genetic diversity in populations. This software is capable of performing several demographic and genetic analyses on pedigree information in a user-friendly environment and helps researchers monitor changes in genetic diversity and population structure. In this study, CFC software be used to estimate the inbreeding coefficient, PDIGREE software be used to complete the pedigree and correct its defects, and ENDOG software be used for other pedigree analyses.

## Results and Discussion

### Descriptive Statistics of the Pedigree

Descriptive statistics of the Kurdish horse population data are shown in Table 1.

**Table 1:** Data structure and genealogical information of Kurdish horse

Results resume	Amount
Number of animals	3,084
Mean inbreeding (%)	0.11
Mean average relatedness (%)	0.37
Mean maximum generations	1.36
Base population (one or more unknown parents)	1723
Actual base population (one unknown parent = half founder)	1,300
Effective population size of founders	346.57
Expected inbreeding by unbalancing of founder's contribution (%)	0.14
Number of animals in the reference population	1,361
Number of ancestors contributing to the reference population	682
Effective number of founders/Ancestors for the reference population	150/136
N <sup>o</sup> of ancestors explaining 50%	69

The total number of horses, stallions, and mares surveyed was 3,084, 1,184, and 1,900, respectively. The number of horses with known parents was 1,361, which is about 44% of the population. Of the total number of horses surveyed, 296 stallions and 786 mares had offspring. The number of founders was calculated by the mean inbreeding coefficient. The total number of horses included in the analysis was 3,084 and the number of foundation stock with one or both unknown parents was 1,723. The actual foundation population with only one unknown parent was 1,300. The effective population size of the foundation stock was 346.57 and the expected inbreeding coefficient with unbalanced participation of the foundation stock was 0.14%. The number of founders, equivalent founders and ancestors was calculated to be 758, 657, and 682, respectively. The effective number of founders and ancestors for the reference population was also calculated to be 150 and 136, respectively (Figure 2).

#### *Pedigree Completeness: Understanding the Foundation*

A key indicator of pedigree completeness is the proportion of animals with identified parents. In this study, a notable 44% of the horses had both parents recorded, providing a

solid, though not exhaustive, foundation for the genetic analyses. As illustrated in Figure 3, this metric reflects the overall development of the pedigree for both the total and reference populations. It is crucial to understand that the depth of pedigree information directly influences the accuracy of estimated inbreeding coefficients. In summary, a more complete pedigree generally leads to more reliable inbreeding calculations. In this study, an average level of pedigree development was observed. Consequently, it is prudent to exercise caution when interpreting these coefficients. This means that mating strategies should be carefully considered, with a greater emphasis placed on understanding the probabilities of inbreeding. This observation aligns with previous research, which consistently shows that incomplete pedigrees tend to result in an underestimation of true inbreeding levels.

#### *Generational Interval*

Table 2 shows the mean generational interval and the mean total generational interval in the four genetic paths of father-son, father-daughter, mother-son and mother-daughter for all animals and animals involved in reproduction. The mean total generational interval was estimated to be 7.94 years.

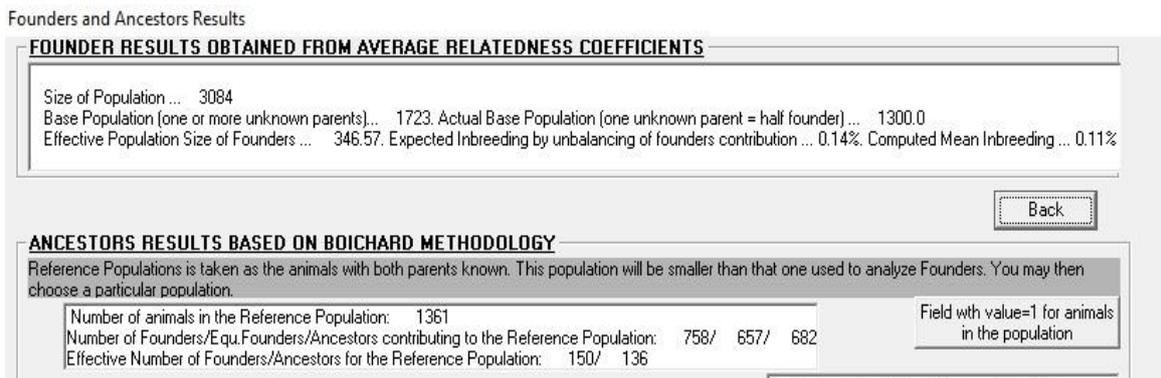


Figure 2: Founders and ancestors results

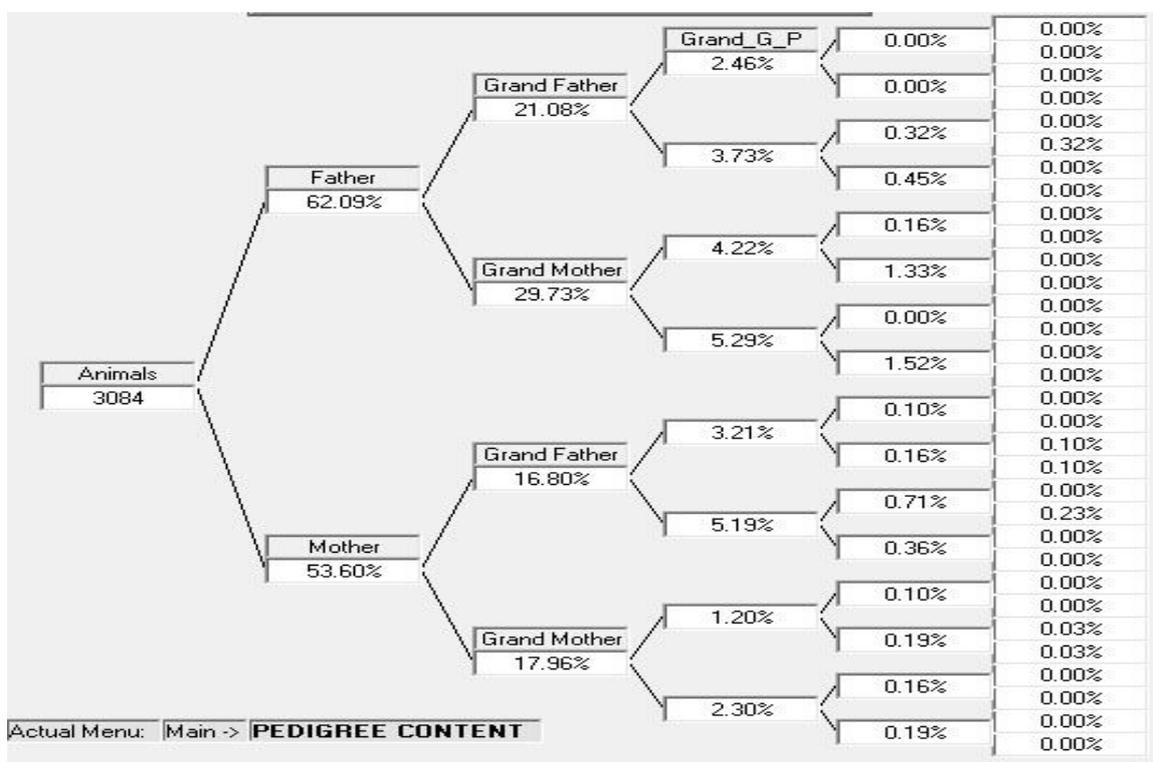


Figure 3: Percentage of pedigree evolution in the total population and the reference population of Kurdish horses studied

Table 2: Generation interval

	N	Interval	Standard deviation	Standard error of mean
Father-Son	91	8.07	4.75	± 0.50
Father-Daughter	264	8.43	5.34	± 0.33
Mother-Son	96	8.22	5.41	± 0.55
Mother-Daughter	236	7.24	4.48	± 0.29
Total	687	7.94	5.01	± 0.19

The mean generational interval in the different selection paths including father-son, father-daughter, mother-son and mother-daughter was estimated to be 8.07, 8.43, 8.22,

and 7.24 years, respectively. The highest mean generational interval was in the father-daughter lineage, which was equal to 8.43, while the lowest mean generational interval

was in the mother-daughter lineage, which was equal to 7.24 years. The generational interval is the time required for one generation to be replaced by the next. The generational interval depends on the selection, mating methods, as well as the average age of the parents at the time of the birth of their offspring in the population. Therefore, the age at which rams and ewes are first used for mating, as well as the age at which they are removed and replaced with younger animals, are important factors affecting the generation gap. The management of the population's age distribution and the age at which animals are replaced can be controlled to some extent by a breeding program, but other factors such as the age of sexual maturity and economic policy in determining the age at which mating occurs and the best age at which replacement occurs are also factors that affect the generation gap.

*Inbreeding*

The average inbreeding coefficient in the population was calculated to be 0.11 percent and the average kinship was calculated to be 0.37 percent. The inbreeding coefficient indicates the probability of two pairs of genes from an individual having a common origin. Two genes from an individual have the same origin when those genes are copies of a gene inherited from a common ancestor of that individual's parents. The inbreeding coefficient is the probability of the proportion

of genes from one individual having the same origin as the genes of another individual. One of the main steps in a breeding program is calculating breeding values. To estimate these values, it is very important to know the inbreeding coefficients and kinship relationships. These coefficients are entered into the inverse of the kinship relationship matrix and will directly affect the accuracy of the assessments. The number of individuals with the maximum inbreeding coefficient was calculated to be 21. The maximum inbreeding coefficient indicates the crossing of individuals with very close kinship. This crossing leads to the production of very closely inbred individuals and should be specifically prevented. Examination of inbreeding over different generations using the maximum number of generations and the number of complete generations showed that there was an increasing trend in the studied Kurdish horse population (Table 3).

*Increasing Inbreeding Rate*

The increase in inbreeding rate and effective population size in three different cases including maximum generation, full generation and full generation equivalent are shown in Table 4. One of the valid algorithms for examining the effective population size is the effective population size calculated based on the algorithm of increasing inbreeding rate over a certain period of time.

**Table 3:** Population statistics on average inbreeding

Generation	N Animals	Mean F (%)	Inbred (%)	Average F for inbred (%)	Mean Aver. relat. (%)	Effective population size
0	877	0.00	-	-	0.09	-
1	797	0.00	-	-	0.39	-
2	936	0.13	0.75	17.86	0.53	374.4
3	381	0.36	2.62	13.75	0.55	219.6
4	72	0.95	5.56	17.19	0.60	83.8
5	18	0.00	-	-	0.52	-
6	3	0.00	-	-	0.54	-

**Table 4:** Increase in inbreeding rate, mean inbreeding and effective population size for maximum generations, complete generations and equivalent generations

	Mean maximum generation	Mean complete generation	Mean equivalent generation
Increase in inbreeding (%)	0.12	0.24	0.24
Mean inbreeding	1.36	0.47	0.83
Effective population size	405.58	207.93	209.76

The inbreeding rate per generation in the maximum generation, full generation, and generation equivalent cases was calculated to be 1.36%, 0.47%, and 0.83% percent, respectively (Table 3).

### Conclusion

The level of inbreeding achieved for the offspring is high, so it is necessary that new stallions with excellent characteristics, which can transmit this quality to their offspring are introduced into the population of interest at a more distant relationship than other populations to reduce the harmful effects of inbreeding. On the other hand, considering the high levels of inbreeding coefficient, it seems that matings should be planned more carefully to prevent further increases in this coefficient; otherwise, the crossing between related individuals may reach a high level, which will lead to undesirable effects in the population.

### Acknowledgments

The authors would like to acknowledge the staffs and management of the Department of Animal Sciences, Faculty of Agriculture and Natural Resources, University of Mohaghegh Ardabili, Ardabil, Iran.

### Conflict of Interest

No competing interests were declared by the authors in this study.

### Authors' Contributions

Reza Seyedsharifi and Sajad Badbarin conceived and designed the study; Reza

Seyedsharifi, Sajad Badbarin, Mohammad Heydari, Jamal Seifdavati, Nemat Hedayat, Abdolfattah Zeidan Mohammad Salem, the study and prepared the manuscript. Reza Seyedsharifi, Sajad Badbarin contributed data or analysis tools. All authors approved the manuscript.

### Funding

This research was funded by University of Mohaghegh Ardabili, Ardabil, and Kermanshah Agricultural and Natural Resources Research and Education Center, Iran.

### Availability of Data and Materials

All data and materials are available.

### ORCID

Reza Seyed Sharifi

<https://orcid.org/0000-0003-4593-2058>

Sajjad Badbarin

<https://orcid.org/0000-0001-6640-8883>

Mohammad Heydari

<https://orcid.org/0000-0003-2783-4710>

Jamal Seifdavati

<https://orcid.org/0000-0001-6794-4450>

Nemat Hedayat

<https://orcid.org/0000-0002-6802-6739>

Abdolfattah Zeidan Mohammad Salem

<https://orcid.org/0000-0001-7418-4170>

### References

- [1] Saghi, D., Mobaraki, A., [Estimation of inbreeding and survey of the pedigree structure of iranian](#)

- turkmen horses population. *Research on Animal Production*, **2018**, 9(22), 131-137.
- [2] Amjadi, M.A., Yeganeh, H.M., Sadeghi, M., Raza, S.H.A., Yang, J., Najafabadi, H.A., Batoool, U., Shoorei, H., Abdelnour, S.A., Ahmed, J.Z., [Microsatellite analysis of genetic diversity and population structure of the iranian kurdish horse](#). *Journal of Equine Veterinary Science*, **2021**, 98, 103358.
- [3] Gharegozlou ML., [Pedigree Book](#). *Equestrian Federation and Agricultural Jihad Publications, Iran*, **2016**.
- [4] Badbarin, S., [Genetic structure and assignment tests of kurdish horse based on microsatellite markers](#). *Journal of Modern Genetics*, **2020**, 14 (4), 337-344.
- [5] Barsi, B., Oláh, J., Posta, J., [Analysis of population structure in hungarian coldblood horses based on pedigree information](#). *Animals*, **2025**, 15(10), 1406.
- [6] Bussiman, F.d.O., Perez, B., Ventura, R.V., Peixoto, M., Curi, R., Balieiro, J.C.d.C., [Pedigree analysis and inbreeding effects over morphological traits in campolina horse population](#). *Animal*, **2018**, 12(11), 2246-2255.
- [7] Próchniak, T., Kasperek, K., Knaga, S., Rozempolska-Rucińska, I., Batkowska, J., Drabik, K., Zięba, G., [Pedigree analysis of warmblood horses participating in competitions for young horses](#). *Frontiers in genetics*, **2021**, 12, 658403.
- [8] Rogic, B., Strbac, L., Preradovic, S., Vazic, B., [Pedigree analysis of the lipizzan horse populations from bosnia and herzegovina and serbia: Structure, inbreeding and genetic variability](#). *Czech Journal of Animal Science*. 2022, 67(12), 483-492.
- [9] Alderson, G., [A system to maximize the maintenance of genetic variability in small populations](#). *CABI Databases, Book*, **1992**.
- [10] Lacy, R.C., [Analysis of founder representation in pedigrees: Founder equivalents and founder genome equivalents](#). *Zoo Biology*, **1989**, 8(2), 111-123.
- [11] Luo, Z., [Computing inbreeding coefficients in large populations](#). *Genetics Selection Evolution*, **1992**, 24(4), 305-313.

**How to cite this article:**

R. Seyed Sharifi, S. Badbarin, M. Heydari, J. Seifdavati, N. Hedayat, A.Z.M. Salem. Investigating Genetic Diversity and Determining Inbreeding Rates Using Pedigree Information in Iranian Kurdish Horses. *International Journal of Advanced Biological and Biomedical Research*, 2026, 14(2), 191-199.

DOI: <https://doi.org/10.48309/ijabbr.2026.2071531.1657>

Link: [https://www.ijabbr.com/article\\_731664.html](https://www.ijabbr.com/article_731664.html)

Copyright © 2026 by authors and SPC (Sami Publishing Company) + is an open access article distributed under the Creative Commons Attribution License(CC BY) license (<https://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.