



Szkoła Główna Gospodarstwa Wiejskiego

w Warszawie

Instytut Nauk o Zwierzętach

mgr inż. Weronika Klecel

**Struktura populacji  
oraz ocena pokroju i ruchu  
koni arabskich czystej krwi**

Population structure and the assessment  
of the conformation and movement  
of Purebred Arabian horses

Rozprawa doktorska

Doctoral thesis

Rozprawa doktorska wykonana pod kierunkiem  
dr hab. Elżbiety Martyniuk, prof. SGGW  
Katedra Genetyki i Ochrony Zwierząt

Promotor pomocniczy:  
dr Wioleta Drobik

Warszawa, 2024 r.

## Summary

The Purebred Arabian horse, one of the oldest and most influential breeds in history, has changed significantly from its ancient origins on the Arabian Peninsula. Initially revered as an exceptional warhorse, it has transitioned over centuries to become a cherished pet, show horse, and racehorse. Poland has maintained a special relationship with the Arabian horse since at least the 16<sup>th</sup> century, with Polish-bred Arabians playing a substantial role in shaping the modern global breeding stock. Despite experiencing several potential bottleneck events, notably during the World Wars, it has been speculated that today's population, although numerous, may suffer from a substantial loss of genetic diversity. There is a particular emphasis on preserving and continuing specific sirelines and damlines originating from renowned founders.

Modern Arabian horse breeding focuses significantly on enhancing certain conformational and kinematic features assessed in “in hand” halter shows and championships. Horses are evaluated by numerical scores in five main categories: type, head and neck, body and topline, legs, and movement. While this method is attractive to audiences and straightforward to understand, it may lack essential precision and be potentially affected by various environmental factors.

This dissertation aimed to assess the population structure and genetic diversity of modern Arabian horse populations, identify factors affecting scores at halter shows, and develop a new precision phenotyping method for evaluating conformation and movement.

To achieve the first goal, pedigree analysis was conducted on 1,498 modern Polish Arabian horses and their 11,065 ancestors dating back to the 17th century, calculating measures of pedigree quality, genetic diversity, and ancestor and founder influence. A phylogenetic meta-analysis of 896 mitochondrial DNA sequences from GenBank was performed to assess maternal interconnections among different subpopulations.

Factors hypothesized to affect halter show scoring were examined, including the relationship between scores in one category and another, and various environmental and fixed factors such as the country of origin, the country represented at the show, judges' experience and origin, coat color, and sex. A precision phenotyping method was developed using computer vision and markerless tracking systems, specifically employing the DeepLabCut software package. The model created can calculate any length and angle in the horse's body, as well as basic kinematic measurements like the duration of a single stride.

The pedigree analysis revealed that Polish Arabian horses have pedigrees of high quality and depth, with full generations equivalent reaching 11.9 – one of the highest reported in any breed. Surprisingly, no notable loss of genetic diversity was found after World War II, despite it being proposed as a bottleneck event. The total calculated loss of genetic diversity due to the bottleneck effect reached 11.8%. The inbreeding level fluctuated throughout generations, but the value for the reference population – 0.058 – is consistent with those reported for other modern populations and breeds. Moreover, the modern population was traced back to 15 sireline founders and 48 damline founders, compared to the 8 sirelines and 15 damlines listed in the Polish Breeding Program.

The phylogenetic analysis of mitochondrial DNA sequences revealed a high level of inaccuracy and potential errors in previously deposited and published mtDNA fragments. After removing inconsistent sequences, minimal genetic variation was observed among 762 sequences from various horse breeds. Distinct clusters were identified for horses of Iranian origin, including Caspian and Arabian horses, Indian Manipuri horses, Kazakh Kushum horses, Akhal-Teke horses, and North Iberian breeds. Notably, several Arabian horse sequences from Egypt, Poland, and Argentina did not cluster with the main groups, indicating potentially unique maternal lineages.

Statistical analysis of judges' scores in horse evaluations revealed very low variability among judges, with scores ranging from 14.5 to 20 despite the available 20-point scale. The “legs” category received notably lower scores (mean = 15.797) and never achieved a perfect score of 20. Stallions exhibited significantly higher variability in scores than mares in four out of six categories, and older horses showed the highest score variability overall.

Correlation analysis indicated that the total score was most strongly correlated with the scores for type ( $r = 0.907$ ) and head and neck ( $r = 0.816$ ). Scores for body and topline and movement had moderate correlations with the total score, while the “legs” category showed a weak correlation. The influence of conformation components on the score for type revealed that head and neck had a strong, highly significant impact, while body and topline and movement had significant but minimal effects; legs had no significant impact. No differences were observed between sexes and age classes in this regard.

In examining factors affecting the scores, it was found that in the junior classes, three-year-olds scored slightly higher than two-year-olds in categories of type, head and neck, and total score, with statistically significant differences. In senior horses, the greatest variability in

scores for type, head and neck, and movement was observed in those aged 4–5 years, while horses aged 11 years and older exhibited the least variability. Significant differences were found among coat colors, particularly in scores for type, head and neck, and body and topline. Judges tended to prefer grey and bay horses over chestnut and black, with bay horses receiving higher scores for body compared to other coat colors.

The analysis also revealed that the breeder's and owner's country significantly affected the scores. Horses representing the United Arab Emirates, Australia, South Africa, and Switzerland received higher average scores, especially in type, head and neck, and total score. In contrast, horses from Austria, Belgium, France, Germany, and Italy received the lowest scores. Polish horses were positioned in the middle among countries represented in the dataset, exhibiting one of the highest variabilities in all scored categories.

Judges' nationality and level of experience had a significant impact on scoring. Judges from Argentina and Australia tended to award higher average scores, while those from Austria gave lower scores. Judges from the B list awarded generally higher scores with less variability, whereas judges from non-ECAHO (European Conference of Arab Horse Organizations) countries exhibited the greatest variability in scoring. These findings suggest that both the origin and experience level of judges influence the evaluation of phenotypic traits in horses.

An analysis of variance revealed a significant paternal influence on all judged traits and a significant maternal influence on all traits except legs. Estimated heritability coefficients were high for type, head and neck, and legs; moderate for the total score; and low for body and topline and movement. In predicting future show scores based on catalog information, the Random Forest model achieved the lowest mean squared error and highest  $R^2$  values, slightly outperforming the XGBoost model. All models predicted scores for type, head and neck, and movement with good accuracy but showed poor predictive performance for body and topline and legs. The most informative predictors – more informative than the identity of the assessed horse itself – were the name of the judge, judge's country of origin, and show year; surprisingly, the lowest weights were assigned to handler, sex, and show category.

The evaluation of the trained neural network for precision phenotyping of Arabian horses demonstrated high accuracy, with a mean Euclidean error of 7.8 pixels (0.601%) in landmark detection. Analysis of scaled Euclidean lengths revealed minimal variability in the lengths of the pasterns, the shortest measured segments. The largest lengths—four to five times greater than the reference humerus length—were observed in total body lengths measured from the

shoulder or atlanto-occipital joint to the sacrum. Most body measurements were moderately positively correlated, with the strongest correlations among lengths comprising the horse's topline.

Significant differences between sexes were found in most scaled body lengths; mares exhibited significantly higher proportions relative to humerus length in the body region. Age-related differences were notable in limb proportions: yearlings had significantly longer pasterns and limb segments relative to the humerus compared to older horses. Conversely, older horses showed increased proportional lengths of the scapula and the segment from the 12th thoracic vertebra to the humerus. Principal component analysis identified five components explaining 74.35% of the total variability, revealing key patterns among body measurements.

Joint angle analysis showed that the femorotibial and hip joints exhibited the smallest measures of central tendency and the lowest maximum angulation values, indicating limited variability and specific functional constraints in these joints. Conversely, the fetlock joints showed the highest mean and maximum angle values, reflecting their essential role in providing a greater range of motion necessary for efficient locomotion. The angle representing the horse's topline – formed by the withers, the twelfth thoracic vertebra, and the sacral tuberosity – averaged around 180 degrees, aligning with ideal conformation standards, although individual variations were notable.

Correlation analysis uncovered significant relationships among joint angles. The lumbosacral joint angle had negative correlations with adjacent joints, specifically the sacroiliac joint and the hip joint, as well as with the scapulohumeral joint in the forelimb. Positive correlations were observed between the hip and femorotibial joints and between the femorotibial and hock joints, suggesting coordinated movement patterns within the hind limb. The scapulohumeral joint also showed positive correlations with hind limb joints, indicating interconnected biomechanical relationships between the forelimb and hind limb.

Significant differences were identified between sexes and age groups. Mares exhibited different mean angle values in the atlanto-occipital joint, withers, back line, croup line, scapulohumeral joint, and sacroiliac joint compared to stallions. Age-related changes included a decrease in the mean angle of neck set and back line with advancing age, as well as slight decreases in angulation of the scapulohumeral, elbow, carpal, and hock joints. The range of motion in certain joints, such as the elbow and hock, varied with age and sex, with older stallions exhibiting a reduced range in the hock joint.

In conclusion, the modern Polish Arabian horse population maintains high genetic diversity and pedigree depth, suggesting that effective historical breeding practices have mitigated the impact of occurred bottleneck events. The mitochondrial control region points more to the existence of multi-breed cluster rather than to the uniqueness of specific Arabian maternal lines, but separate branches identified in the consensus tree need further investigation. Halter show scores are significantly influenced by non-genetic factors such as judges' nationality and experience, coat color, and country of origin, indicating potential biases in the evaluation system. High heritability in key traits like type, head and neck, and legs suggests that these characteristics can be effectively selected for in breeding programs to improve desired qualities. The developed computer vision-based method provides accurate, objective measurements of conformation and movement, offering a valuable tool to complement traditional scoring.

For the future, it is recommended to implement regular genetic monitoring using both pedigree and molecular data to ensure the preservation of genetic diversity and health within the population. Incorporating precision phenotyping into standard evaluation practices can reduce subjective biases and enhance the accuracy of conformation and movement assessments. Developing and enforcing standardized guidelines and training for judges can minimize variability and biases linked to nationality and experience. Acknowledging and addressing environmental factors influencing show scores, such as preferences for certain coat colors or origins, can foster fairness in evaluations. Providing resources and training to breeders and owners on the importance of genetic diversity, objective assessment methods, and the impact of non-genetic factors on performance is essential. Encouraging further research into the genetic basis of conformation and movement traits, utilizing technologies like genomics and advanced computer vision, will inform and improve breeding decisions. By adopting these recommendations, the Arabian horse breeding community can enhance genetic diversity, improve evaluation accuracy, and ensure the breed's continued excellence and legacy.