# Genetic Parameters of Foal Inspection Scores in the International Sporthorse Registry and Oldenburg Registry North America

Adrienne Sharda Bhatnagar

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Rebecca K. Splan, Chair
Ronald M. Lewis
David R. Notter
Christian E.M. Schacht

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**ABSTRACT**

Foal scores from the International Sporthorse Registry and Oldenburg Registry North America were used for statistical and genetic analysis. Scored traits include type and conformation (TC), athletic ability of movement (AM), overall development as related to age (OD), and total score (TS) calculated as a weighted average of TC, AM, and OD. Premium status (PS) was analyzed as a binary trait. Preliminary statistical analysis determined significant fixed effects of sex, year of birth, dam breed, and inspection period. Offspring of stallions with only one offspring in the dataset and non-warmblood sires were deleted. Non-warmblood or non-Thoroughbred dams were also removed. Variance components were estimated using ASReml methodology to obtain genetic parameters. Traits were moderately to highly heritable with heritabilities of 0.45, 0.47, 0.49, and 0.55 for TC, AM, OD, and TS, respectively. PS had a heritability of 0.32 on a binary scale and 0.51 when transformed to the normal scale. Genetic correlations between TC, AM, OD, and TS were all high and favorable, ranging from 0.80 to 0.99. Genetic correlations with PS were inestimable. Foal inspection scores are heritable and should respond to selection. Selection for improvement in one trait should result in improvement in all traits. If genetic parameters can be correlated to data obtained in older horses, incorporating foal scores in selection decisions could improve warmblood breeding programs. Utilizing foal inspection scores should be beneficial to breeding objectives of the International Sporthorse Registry and Oldenburg Registry North America.

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## ATTRIBUTIONS

My committee provided significant aid in the research and writing of this thesis. Their contributions are described here.

**Dr. Rebecca K. Splan, Ph.D.** – As committee chair, Dr. Splan was essential in the planning and execution of this project. Her connections in the sporthorse industry were responsible for the attainment of data, and her genetics knowledge was crucial in the designing and development of the research. Dr. Splan provided guidance in the creation of the database of foal scores, considerations for statistical analysis, and formation of the models for estimation. Additionally, her extensive knowledge of equine conformation and biomechanics was useful in the interpretation of results.

**Dr. Ron M. Lewis, Ph.D.** – Dr. Lewis' background in quantitative genetics was important to the execution of this project. His knowledge of the ASReml software was vital in the estimation of genetic parameters that was the main focus of the research.

**Dr. Dave R. Notter, Ph.D.** – Dr. Notter's substantial knowledge of genetics and estimation of genetic parameters contributed significantly to the implementation and interpretation of this research. He provided several considerations for the linear models involved to ensure the accuracy of the results.

**Christian Schacht** – As the breeding director for the registries involved, Herr Schacht was crucial in obtaining necessary data for the formation of the database used for analysis. His extensive knowledge of the workings of the European sporthorse industry was also very instructive for interpretation of results.

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# CHAPTER I

## Introduction

Warmblood horse registries aim to produce superior equine athletes to compete in all sporthorse disciplines. Nearly all of the past winners in dressage and show-jumping at top international competitions such as the Olympics and World Cup have come from European sporthorse registries (World Breeding Federation for Sport Horses, 2009). Over the years, registries have defined specific breeding goals and implemented selection and mating practices to increase the likelihood of producing superior horses (Clarke and Wallin, 1991). A process of inspections and performance tests allows for selection based on conformation and movement at young ages, and many European registries employ genetic evaluations of scores from these events to ensure the effectiveness of their breeding programs.

European countries, such as Germany and the Netherlands, are traditionally associated with the production of excellent sport horses, and the equine industry in Europe is of substantial economic importance. The annual turnover per horse in the European Union is estimated to be 2,200 to 2,800 EUR for direct expenditures alone with a total of about 4.4 million horses (Swedish University of Agricultural Science, 2001). Because the horse industry has such a large economic impact, analyzing breeding practices is important. Heritability of performance in competition has been shown to be low and defining a strategy to evaluate competition data is problematic (Bruns, 1981; Tavernier, 1990, 1991; Wallin et al., 2003; Ducro et al., 2007a,b, Gerber Olsson et al., 2008). Also, horses do not begin competition until at least 4 years of age, with prime competition years being much later (Wallin et al., 2003; Kearsley et al., 2008; Gerber Olsson et al., 2008). Therefore, many sporthorse breeds in Europe have developed inspections and other methods of evaluation to indirectly select for animals with potential both as future breeding stock or performance mounts.

Sporthorse breeding in North America has been expanding, though importation of European-bred horses is still common (Clarke and Wallin, 1991). In the United States, there are close to 9.3 million horses, and the horse industry has always had a large economic impact ($39 billion direct, $102 billion total effect on GDP). The sporthorse industry is growing, with showing responsible for $29 billion total effect on GDP and breeding within the showing sector responsible for $2.2 billion (American Horse Council, 2005). The International Sporthorse Registry and Oldenburg Registry North America (ISR/OLNA) was created to bring European methods to the growing sporthorse industry in the US. ISR/OLNA has adopted inspections and performance tests similar to those used in Europe in order to produce modern sporthorses that will be competitive at all levels, including international events (International Sporthorse Registry, Inc., 2010).

Inspections in both Europe and North America evaluate horses based on conformation and gait qualities that are considered necessary for success in later competitions. BLUP methodology using data from these inspections has also been implemented in many European registries for over 30 years to achieve genetic improvement. Genetic correlations between inspection scores and competition data are computed to ensure that these methods are effective at identifying superior horses that should be maintained as breeding animals or competed at the international level. However, the most useful inspections do not occur until the horses are at least 3 yr of age with performance test occurring between 4 and 6. Delaying selection decisions until 3 or 4 yr of age increases the generation interval and reduces genetic gain. If a horse does not score well, this implies the horse may be unsuitable for breeding or competition at a high level, and reflects the potential wastage of 3 or more yr of investment. Additionally, since inspections are not required for all horses, data exists for only a small percentage of the total sporthorses born each year (Preisinger et al., 1991; Hellsten et al., 2006). Inspection of young (3 to 4 yr of age) horses is well established and breed registries could now explore further ways to improve their breeding programs, particularly by inspecting a larger percentage of horses at younger ages.

Since postponing the first inspection of a sporthorse until the horse is 3 or 4 yr of age can be economically and genetically detrimental, many breed registries, including ISR/OLNA, also inspect foals born each year before they are allowed to be registered. Inspecting foals not only presents opportunities for earlier selection, but also provides more data on all offspring that can be used to evaluate the breeding merit of current sires and dams. As with the later inspections, the judges are highly qualified for evaluating conformation and gaits of horses and, therefore, their scores could be useful in early identification of potential breeding animals. Though few breed registries provide a quantitative score of foal conformation, heritability of conformation at foal age can be determined for registries that do provide these scores. If scores are deemed at least moderately heritable and can be genetically correlated with other economically important traits in older horses, then foal scores can be used to select potential breeding or performance horses at an earlier age, increase genetic gain, and prevent the investment of time and money in inferior animals. Additionally, foal scores could be incorporated into current selection practices for stallions as an early progeny test. Also, correlations between conformation and selling price should be favorable for foals if conformation and movement at foal age is correlated with later performance. Use of foal scores in the ISR/OLNA could be both genetically and economically beneficial to horse breeders in the United States.

## Objectives

The objectives of this study are:

1. to analyze a database of foal inspection scores for the International Sporthorse Registry and Oldenburg Registry North America for sire distribution, significant fixed effects, and percentage of premium foals, and
2. to estimate genetic parameters of type and conformation, athletic ability of movement, overall development as related to age, total score, and premium status of foals registered with the International Sporthorse Registry and Oldenburg Registry North America.

# CHAPTER II

## Review of Literature

### Abstract

Inspection and scoring of young warmblood horses for conformation and movement traits is widely utilized to select breeding animals and indirectly select for performance potential. Conformation and movement have been associated with superior performance and many major European registries have estimated genetic parameters of inspected traits for use in breeding programs. This chapter reviews and summarizes parameters associated with conformation and gait traits estimated for young (3 to 4 yr of age) warmblood horses. Heritability for overall conformation was generally higher than for individually measured component traits, and conformation of the legs was particularly lowly heritable. Movement was moderately heritable, with trot having a higher heritability than walk. Genetic correlations among conformation traits were generally moderate to high and favorable. The majority of correlations between movement traits were also high and favorable. Available genetic correlations between conformation and movement traits were limited, but low to moderate, favorable correlations were found. Conformation and movement in young horses was favorably correlated with dressage competition success and lower, but still favorable, correlations with show-jumping prowess. Evaluation of conformation and movement in foals is performed, but there is a deficiency in the literature concerning development of these traits and related genetic parameter estimates in foals. However, available literature shows favorable phenotypic and genetic correlations for conformation and movement traits between both foals and mature horses. Therefore, use of foal data in genetic evaluations could further benefit the sporthorse industry by providing earlier

information for selection decisions, provided more estimates are available and genetically correlated to later performance.

## I. Introduction

The ultimate goal of modern sporthorse breeding is to produce elite equine athletes for competition at the international level in events such as the Olympics and World Cup, but production of quality horses for amateur riders is also a priority. Two primary competitive disciplines are dressage and show-jumping, and most sporthorse organizations have defined breeding objectives that emphasize performance and conformation traits deemed important for success in these events (Koenen et al., 2004). In dressage, a horse and rider team is scored for the quality of performance of a memorized series of figures which become increasingly difficult as the pair moves up the levels of competition. Show-jumping requires a horse and rider team to jump a designed sequence of jumps as quickly as possible without knocking down any rails or refusing any jumps. A third discipline, eventing, combines dressage and show-jumping with a cross-country test that requires the team to complete an outdoor course of obstacles within an allotted amount of time (Fédération Equestre Internationale, 2010). Additionally, many warmbloods excel in hunter competitions where a horse and rider team jump a sequence of jumps but are judged on style and quality of movement and not speed (United States Equestrian Federation, 2010). Some registries focus on a particular discipline in their breeding goals, but a majority aim to produce superior horses in all fields of competition. Europe has long been the powerhouse for production of sporthorses, with a majority of top performers and breeding stock coming primarily from Germany and the Netherlands (World Breeding Federation for Sporthorses, 2009).

Many breed registries use competition results exclusively when making selection and mating decisions (Barrey and Langlois, 2000; Dubois and Ricard, 2006, 2007; Dubois et al., 2008). However, heritability of performance traits has generally been shown to be low and horses do not begin competition until at least 4 years of age, with prime competition years occurring much later (10 yr or older) (Huizinga et al., 1989; Koenen et al., 1995; Wallin et al., 2003; Kearsley et al., 2008; Gerber Olsson et al., 2008). Also, calculating a quantitative indicator of performance is complicated (Bruns, 1981; Tavernier, 1990, 1991). Therefore, many sporthorse breeds in Europe have developed inspections and other pre-competition evaluations to identify superior young horses with potential as future breeding or performance stock. These inspections evaluate horses based on conformation and gait qualities that are considered necessary for success in future competition. Phenotypic analysis of conformation and movement in young horses reveals that many specific traits are associated with improved scores and higher levels of competition later in life (Holmström et al., 1990; Holmström and Philipsson, 1993; Holmström, 2001, Barrey et al., 2002). Also, analysis of auction data from Germany has shown that conformation and movement traits are highly correlated with price across many ages (Schwark et al., 1988). Therefore, identification of horses with superior conformation is economically useful for breeders.

Genetic correlations between inspection scores and competition results are also computed to ensure that these methods are effective at identifying superior horses that should be maintained as breeding or high-performance animals. Many breed societies also inspect foals born each year before they are allowed to be registered. Scoring foals for conformation and movement could be useful in early identification of potential breeding animals. There is little research about changes in conformation from foal age to adult, but movement qualities at least seem to be predictable from foal to adult age (Back et al., 1995). Few breed societies provide a quantitative score of foal conformation, and even fewer have estimated genetic parameters. If these scores are deemed at least moderately heritable and can be genetically correlated with conformation at later ages, then foal scores can be used to select potential breeding or performance horses.

**II. Materials**

Data reviewed in this chapter first sets a phenotypic precedent for evaluating conformation and movement in sporthorse. Several studies investigated the phenotypic differences in conformation between elite competition and "normal" horses. There are also phenotypic studies describing movement characteristics required for success in competition. Additionally, studies analyzing changes in conformation and movement from foal to adult age are reviewed to determine if traits evaluated in foals can effectively predict adult traits.

Data reviewed for genetic parameters of conformation and movement in young warmbloods can come from a wide variety of sources. The three most common sources are inspections for studbook entry of breeding mares, inspections of potential stallions, and field or station tests evaluating animals of either sex. Studbook and stallion inspections occur when the horse is 3 yr of age, though mares can also be inspected at older ages. Station tests occur at a central location over a long period of time (70 days or higher), where management and training conditions are kept identical for all horses. Field tests are more local and generally only last one day. Field or station tests can include mare or stallion performance tests exclusive to one sex, or more broad tests open to animals of any sex, including geldings. Horses are typically between 3 and 6 yr of age when they undergo field testing. Foal inspections are also required by many registries and can occur anytime between birth and 1 year of age. Because performance in sporthorse competitions is the primary breeding goal for many registries, data from competitions are also used to estimate genetic parameters and correlated with evaluations in young horses. Genetic parameters estimated in younger horses can then be correlated to performance results to ensure these inspections support the registry's breeding goals.

Genetic parameters from 16 selected studies from 1991 to 2009 of various European registries were reviewed. Registries included Swedish Warmblood, Dutch Warmblood, Belgian Warmblood, Hanoverian, Holsteiner, Trakehner, and Hungarian Sport Horse. Data from studbook inspections of mares were found for all registries as well as initial stallion inspections for the Dutch Warmblood registry. Results of mare performance tests were analyzed by the Dutch Warmblood and Hungarian Sport Horse registries and stallion performance tests came from both Dutch and Swedish Warmbloods. Field test data came exclusively from the Swedish Warmblood registry and included the Riding Horse Quality Test of 4-year-olds and Young Horse Test of 3-year-olds. Foal inspection data came from the Holsteiner and Trakehner registries.

A majority of the studies reviewed utilized an animal model, however some older studies estimated genetic parameters used a sire model (Huizinga et al., 1990; Preisinger et al., 1991; Kühl et al., 1994). Fixed environmental effects in the linear models included sex, year of birth, evaluator, specific inspection event, and occasionally percent Thoroughbred of the sire or dam. Table 1 describes the studies reviewed in this chapter.

**Table 1: Description of selected studies**

| Study | Registry | Source of Information[a] | Sex[b] | No. of horses | Model[c] |
|---|---|---|---|---|---|
| **Bosch et al., 2000** | Holsteiner | FI | M F | 34,359 | A |
| | | SI | F | 16,523 | |
| **Ducro et al., 2007a** | Dutch Warmblood | SI | F | 36,110 | A |
| **Ducro et al., 2007b** | Dutch Warmblood | SI | M | 2,361 | A |
| **Gelinder et al., 2002** | Swedish Warmblood | FT (3 yr) | M F | 1,819 | A |
| | | FT (4 yr) | M F | 15,398 | |
| **Huizinga et al., 1990** | Dutch Warmblood | ST | M | 2,023 | S |
| **Huizinga et al., 1991** | Dutch Warmblood | FT | F | 337 | A |
| **Koenen et al., 1995** | Dutch Warmblood | SI | F | 10,665 | A |
| **Kuhl et al., 1994** | Holsteiner | FI | M F | 6,969 | S |
| | | SI | F | 453 | |
| **Olsson et al., 2000** | Swedish Warmblood | ST | M | 378 | A |
| **Olsson et al., 2008** | Swedish Warmblood | ST | M | 801 | A |
| | | FT | M F | 14,927 | |
| **Posta et al., 2009** | Hungarian Sport Horse | FT | F | 435 | A |
| **Preisinger et al., 1991** | Trakehner | FI | M F | 9,907 | S |
| | | SI | F | 4,226 | |
| **Rustin et al., 2009** | Belgian Warmblood | SI | F | 1,215 | A |
| **Stock and Distl, 2006** | Hanoverian | SI | F | 20,768 | A |
| **Viklund et al., 2008** | Swedish Warmblood | FT (3 yr) | M F | 4,110 | A |
| | | FT (4yr) | M F | 16,504 | |
| **Wallin et al., 2003** | Swedish Warmblood | FT | M F | 3,708 | A |

[a]FI: foal inspection, FT: field test, SI: studbook inspection, ST: station test
[b]M: male, F: female
[c]A: animal model, S: sire model

Most of these registries evaluated traits on a scale of 1 to 10, with 1 indicating poor quality and 10 indicating high quality. However, some registries utilize different scales. The Dutch Warmblood registry included subjective scores measured on a scale of 40 to 100 with a higher score indicating a more ideal result. The Dutch registry also utilized linear descriptive traits that are measured on a scale of 1 to 40. The Belgian Warmblood registry used similar linear descriptive traits but on a scale of -20 to 20. In both, values of high magnitude corresponded with biological extremes for each trait. For many traits, neither extreme was preferred, but higher scores tended to be favorable.

Studbook and stallion inspections evaluate conformation and movement of horses. Horses can either receive a single score for overall conformation or multiple scores evaluating several individual components. Movement in these inspections was evaluated while the horse is led by a handler on the ground (in hand) because many of these horses are not yet trained to be ridden (under saddle). Movement in hand also allows for a more unbiased evaluation of movement quality. Generally, scores are obtained for quality of walk and trot only, and in some instances gaits were also evaluated for stride length, suppleness, and impulsion separately. Quality of walk and trot can be combined to obtain a heritability estimate for overall movement, or separate heritabilities for walk and trot traits can be determined. Field tests evaluated conformation and movement as well as other traits such as jumping ability and ridability to predict that horse's performance potential. Excluding the Young Horse Test, all performance tests also evaluate movement under rider.

## III. Traits Evaluated

### *1. Conformation*

Many equestrians desire horses that are aesthetically pleasing and many breed registries include phrases such as "a noble correct and beautiful horse" in their breeding objectives (Koenen and Aldridge, 2002). Such a description is extremely subjective and therefore not useful as a selection criterion. However, the perceived "beauty" of a horse is often related to particular conformation traits. Conformation traits were major selection criteria in the equine industry well before any formal genetic evaluations were begun. Writings from Ancient Greece describe what is considered good or bad conformation in relation to the horse's function (van Weeren and Crevier-Denoix, 2006). More recently, phenotypic data has linked conformation traits to performance and longevity. Additionally, auction data from Germany showed strong, positive correlations between overall conformation and selling price (0.48), and individual conformation traits all had positive correlations with selling price indicating that breeding conformationally superior horses is economically beneficial to the breeder (Schwark et al., 1988). Therefore, conformation is commonly included in breeding objectives and inspections of sporthorses. In a survey of 19 sporthorse registries 17 listed conformation as a breeding objective and conformation traits are considered in many inspections or performance tests (Koenen et al., 2004).

Registries score a horse's conformation on criteria that are traditionally associated with beauty or performance, and there have been several studies that attempt to quantify the phenotypic relationship between conformation and performance. Advances in technology, such as digital photography and computer assisted motion analysis, have made such analyses more feasible and accurate (van Weeren and Crevier-Denoix, 2006). Conformation itself is not an interesting trait unless it can be related to more important traits such as performance and soundness. Overall, Holmström (2000) determined that conformational traits related to balance are most important for both dressage and show-jumping performance. A well-balanced horse can move more efficiently and therefore perform more complex maneuvers without having to compensate for conformational defects (Stashak and Hill, 2002).

Very few studies have evaluated conformation in foals and its relationship to adult conformation. Therefore, it is unknown whether foal conformation can predict future performance or breeding potential in horses. There is a particular lack of literature concerning changes in conformation traits as foals age. Anderson and McIlwraith (2004) measured the longitudinal change in various conformation traits of Thoroughbreds from weanling age to 3 yr. All long bone lengths were significantly correlated across age (greater than 0.69). Denham

(2007) evaluated conformation change in warmblood foals from birth to weanling age and determined that most growth occurred before 7 wk of age. The author also found that cannon bone growth completely stopped by 7 wk. However, tibia growth was most significant between 11 and 12 wk. Anderson and McIlwraith (2004) found that shoulder angle increased over time, but shoulder angle measured externally was not very closely correlated to the true angle obtained via dissection at weaning age (0.35). Therefore, subjectively measuring the shoulder angle of foals may not be accurate. Denham (2007) also found an increase with age in shoulder angle in warmblood foals. The radiometacarpal angle also increased with age, to a very slight 'over-at-the-knees' conformation. Therefore, foals that are already "over-at-the-knees" may not be ideal for selection as this conformational flaw could worsen with age (Anderson and McIlwraith, 2004). Several interesting conformational trends were found in warmblood foals, including the observation that foals have higher hip heights than wither heights through yearling ages, which is an undesirable conformation in an adult. Foals should outgrow this flaw, and therefore the trait should not be penalized in horses less than 1 yr old. Hock and tibia angle also increased over time, which reduced a 'camped out' flaw, therefore foals that are "camped out" should not be heavily faulted as they may outgrow this trait (Denham, 2007).

*2. Movement*

Many inspections and performance tests evaluate how a horse moves without the influence of a rider to determine the horse's natural ability. In a survey of European breeding registries, 14 of 19 listed gaits as a breeding objective and 16 gave it a weight of at least 8 on a 1 to 10 scale (Koenen et al., 2004). Auction data shows that gait traits are positively correlated with price, again indicating that selecting for superior movement is economically beneficial to breeders. Trot and canter in particular have a correlation coefficient of 0.39 and 0.40, respectively, with selling price (Schwark et al., 1988). Several studies have phenotypically shown how specific characteristics of movement are related to subjective evaluations. Back et al (1994a) showed that stride (0.72 forelimb, 0.66 hindlimb) and swing duration (0.58 forelimb, 0.56 hindlimb), scapula rotation (0.66), and several angles of retraction and flexion of the limbs (0.40 to 0.60) were correlated with subjective gait scores obtained during inspection. Diagonal advanced placement in the trot (the hindlimb contacts the ground prior to the diagonal forelimb), has also been associated with a more desirable trot because it indicates the horse engages the hindquarters and achieves elevation of the forehand (Holmström et al., 1994). Horses with higher gait quality should also be able to increase speed through longer stride length and duration and not an increased stride frequency (Clayton, 2001). There have been fewer studies on relationships between movement traits and performance than for conformation, but new technology in video software make this a growing area of research (Clayton, 1989).

Further research analyzing equine movement has focused on investigating changes in movement from foal to adult age. Back et al. (1993) described the basic pattern of locomotion in Dutch Warmblood foals and found that most of the phenotypic variability between foals occurs in the flexion of the elbow, carpal, and fetlock joints. Denham (2007) found an increase in stride length and duration at the walk in warmblood foals from 3 to 39 wk. The author also found that time between lateral footfalls was much less than the time between diagonal footfalls at all ages, indicating that foals have not yet developed an even, 4-beat gait by 39 wk. Therefore, when evaluating a foal at the walk, judges should consider that the gait should become more regular as the foal ages. Back et al. (1994b) investigated development of foal kinematics in Dutch Warmbloods to determine how trot characteristics changed from 4 to 26 mo. The overall duration of stride increased as the foals aged, as well as the duration of the stance component of the stride. However, the swing duration remained constant. Authors found high correlations between swing and stride duration (0.65 and 0.83, respectively). Additionally, foals maintained consistent protraction and retraction angles of the legs in the sagittal plane. The combined pro-/retraction angle had a high correlation between 4 and 26 mo (0.50). Back et al. (1995) then incorporated joint angles and lengths of bone segments with kinematics in foals to predict movement traits in adult horses. Locomotion of adult horses was then evaluated and found to be within the range of predicted values for all stride characteristics except stance duration as a percentage of total stride of the forelimb. All stride characteristics except stance duration (both as percentage and time in seconds) demonstrated a significant correlation between foals and adults (0.63 to 0.80). Range of movement of the elbow, scapula, and carpus joints in foals were all significantly correlated with measurements in adults (0.44, 0.47, and 0.47, respectively). Additionally, a subjective score for length, suppleness, and strength of movement was given both to foals and adult horses, and there were high correlations between scores for foals and adults (0.45 to 0.70).

*3. Relationship between Conformation and Movement*

Extensive phenotypic relationships have been reported between conformation and movement. The hindquarters are responsible for impulsion in gaits, therefore proper conformation of the loin and croup is crucial (Holmström, 2001). Also, horses with withers higher than the hip shift their center of gravity back, allowing for increased impulsion and freer movement of the forequarters. Horses with body length longer than height often have coordination issues and though a short back is considered stronger, it also can increase the likelihood of interference between fore and hindlimbs (Stashak and Hill, 2002). Conformation of the limbs is also associated with movement quality. Sloping shoulder, long humerus, and long pasterns with moderate slope in the forelimbs are all associated with good movement. In the hindlimbs, a flatter pelvis, larger stifle angle, larger hock angle, and most importantly, a long, forward-sloping femur are related to improved movement (Holmström, 2001).

Holmström and Philipsson (1993) evaluated the conformation of 4-yr-old Swedish Warmbloods and investigated the relationship of conformation with traits evaluated at performance tests, specifically movement traits. The authors used both quantitative measurements and subjective scores on a typical inspection scale. Significant regression coefficients between conformation and movement included: small hip joint and femur angle with higher score for trot (-0.94 and -1.7, respectively) and total gaits (-2.80 and -5.78, respectively); smaller scapula inclination with higher scores for walk (-0.40) and total gaits (-0.74); and longer humerus and femur with higher scores in total gaits (6.12 and 3.31, respectively). Subjective conformation scores were all positively related to quantitative gait scores and accounted for 25% of the variation in gait scores. Overall, of the horses that were classified in the top third for gaits, 65% were identified as having good conformation.

*4. Relationship with Dressage and Show-Jumping*

Holmström et al. (1990) evaluated the conformation of Swedish Warmbloods that were classified as either elite or "normal" to investigate differences between these two groups. Elite dressage horses had shorter necks and tibias in relation to height compared to other groups, as well as longer fore and hind phalanges. Smaller shoulder angles, larger hock angles, and larger elbow joint angle were also associated with elite dressage horses. A sloping shoulder is traditionally considered a marker of good conformation in sport horses. Dressage horses also had larger fetlock, hip joint, and femur angles than show-jumping horses. Holmström (2001) also found that most Swedish Warmbloods have outwardly rotated hindlimbs, which may help them perform some difficult dressage maneuvers.

Fewer phenotypic relationships between conformation and show-jumping ability exist. Elite show-jumpers had larger hock angles, smaller shoulder angle in relation to the horizontal plane, as well as longer phalanges and smaller angles of the front fetlock and hip joints (Holmström et al., 1990). Holmström and Philipsson (1993) found an association between small front cannon width, short hind phalanx, and large stifle and hock angles and jumping ability (regression coefficients of -1.30, -0.60, 0.09, and 0.11, respectively). Show-jumpers were also found to have longer necks and a more sloping shoulder than dressage horses. However, conformation only explained 0 to 4% of the variation in jumping ability (Holmström, 2000).

Morales et al. (1998) compared movement in highly trained elite Spanish dressage horses considered to have "good" gaits to horses that were not trained for any purpose. Elite horses demonstrated a longer swing phase and more overlap of swing phase between different legs, indicating that elite horses have more suspension. Suspension is a common consideration when evaluating gaits of riding horses. Barrey et al. (2002) compared the walk and trot of German breeds that excel in international dressage competition to the gaits of Spanish horses that perform an older style of dressage typically only seen at traditional riding schools. German horses had a faster walk with a longer stride and quicker frequency and also showed more propulsion and vertical activity and displacement at the walk. For the trot, German horses demonstrated a faster gait and slower frequency with high regularity. Additionally, the German horses had larger dorsoventral displacement and activity. These traits indicate increased elasticity and propulsion, which is commonly evaluated at inspections.

Gait characteristics of German and Spanish dressage horses were compared to French Selle Français horses that are known primarily for their jumping ability. French horses had less propulsion and a higher stride frequency at the walk and trot. They also exhibited less dorsoventral displacement and activity at the trot than German dressage horses. Overall, gaits of the French horse did not correspond favorably with characteristics desired for a dressage horse (Barrey et al., 2002).

*5. Relationship with Longevity and Soundess*

Several studies have investigated relationships between conformation scores and longevity in Swedish Warmblood horses. Wallin et al. (2001) found that conformation scores, particularly correctness of legs, were significantly related to longevity, with risk ratios dropping from 1.20 to 0.64 with higher leg conformation scores. Horses with the lowest scores were twice as likely to be culled as horses with the best scores. Wallin et al. (2000) determined that diseases of the musculoskeletal system were the leading cause of death in Swedish Warmblood horses. Poor conformation can cause unsoundness and predispose horses to musculoskeletal diseases that lead to culling. Stashak and Hill (2002) mention numerous conformational flaws that can lead to unsoundness. Specifically, any angular conformational flaw could increase tension on various tendons in the legs causing lameness. Conformation scores from Holmström and Philipsson (1993) were also related to medical and orthopedic status evaluated by a veterinarian. A long humerus and femur, small shoulder inclination, and small shoulder joint angle were favorably related to medical status (regression coefficients of 0.11, 0.07, -0.04, and -0.03, respectively). Orthopedic status was favorably related to a long humerus, large elbow joint angle, and small scapula and femur inclination (regression coefficients of 0.19, 0.07, -0.08, and -0.10, respectively). Holmström (2000) also compared conformation of injured horses to elite sporthorses and "normal" sound horses. The author found that larger femur inclination and smaller hock joint angle were particularly related to unsoundness. Anderson et al. (2004) also found several conformational flaws to have a significant effect on incidence of injury in Thoroughbred racehorses. Offset knees and a long bottom neckline increased the risk of effusion in the fetlock and long pasterns increased the risk of fracture in the front limb. A long scapula and increased carpal angle both seemed to protect against carpal fractures. Increase in hind fetlock effusion increased with an increase in dorsal hoof angle (McIlwraith et al., 2006).

Movement is also related to health and longevity of sporthorses. Holmström and Philipsson (1993) found a significant correlation between evaluation of locomotion at the trot and orthopedic and medical status in Swedish Warmbloods (regression coefficients of 0.15 and 0.29, respectively). Wallin et al. (2001) did not find a significant difference in longevity for horses with different gait scores, but horses with higher average gait score tended to live longer than those with a lower average gait score (higher scoring horses had a risk ratio of 0.98, versus a risk ratio of 1.17 for lower scoring horses). Improper gaits can lead to unsoundness and musculoskeletal disease which, as previously mentioned, is the leading cause of culling in sporthorses (Wallin et al., 2000).

## IV. Heritability

### *1. Conformation*

Table 1 shows heritability estimates for various conformation traits evaluated in young (approximately 2 to 5 yr of age) horses. All traits were moderately heritable, though the range was often very wide. Many studies calculate total conformation as an average of component traits and estimate the heritability of that average. In some instances, conformation includes scores for gait characteristics in hand. Overall conformation has been evaluated at both studbook entry and in field tests. Heritability for type is also included in this section as it is often closely related to conformation. Type refers to how a horse conforms to the breed standard and intended riding discipline. Type also includes outward characteristics of femininity or masculinity of the animal (Thomas, 2005).

**Table 2: Heritabilities of various conformation traits in young warmblood horses**

| | | *Heritability* | | |
|---|---|---|---|---|
| *Trait* | **N** | **Mean** | **Min** | **Max** |
| Overall Conformation | 11 | 0.34 | 0.17 | 0.58 |
| Type | 9 | 0.37 | 0.28 | 0.46 |
| Head | 3 | 0.46 | 0.42 | 0.50 |
| Neck | 8 | 0.24 | 0.12 | 0.31 |
| Shoulder/Withers | 8 | 0.24 | 0.16 | 0.34 |
| Body | 15 | 0.29 | 0.15 | 0.55 |
| Hindquarters | 6 | 0.28 | 0.15 | 0.47 |
| Legs | 31 | 0.20 | 0.06 | 0.46 |

Overall conformation was found to be moderately heritable in both studbook inspections and field tests of young horses (Gerber Olsson et al., 2000; Gelinder et al., 2002; Wallin et al., 2003; Stock and Distl, 2006; Ducro et al., 2007a; Gerber Olsson et al., 2008). The lowest heritability was from an older study of studbook entry for mares in the Trakehner registry (Preisinger et al., 1991). One study found high heritabilities of 0.55 and 0.58 for 2 different field tests of the Swedish Warmblood registry (Viklund et al., 2008). Type was also found to be moderately heritable, with the Swedish Warmblood field test again having the highest estimate (Preisinger et al., 1991; Gelinder et al., 2002; Stock and Distl, 2006; Viklund et al., 2008; Posta et al., 2009).

Head and neck connection was more highly genetically correlated to conformation of the neck, and therefore were included in that category in Table 1 (Koenen et al., 1995; Rustin et al., 2009). Genetic correlations will be discussed in more detail later. Conformation of the head was the most highly heritable trait with the smallest range among estimates. However, it did have the fewest number of estimates (Stock and Distl, 2006; Posta et al., 2009; Rustin et al., 2009). Height and length of the withers and position and length of the shoulder were only evaluated in 2 studies of linear traits with 8 total estimates. These traits were evaluated separately but had similar heritabilities and are usually considered closely connected, therefore ranges were combined in Table 1. Heritabilities for both traits were higher in the Belgian Warmblood registry than the Dutch Warmblood registry (Koenen et al., 1995; Rustin et al., 2009).

Conformation of the body had the widest range of heritabilities (along with leg conformation) and this is most likely because it is comprised of several different traits. Individual traits such as saddle region, frame, and conformation of the back were included in this category in Table 1. There were no clear trends, and heritabilities varied widely between registries (Koenen et al., 1995; Gelinder et al., 2002; Stock and Distl, 2006; Posta et al., 2009; Rustin et al., 2009). Conformation of the hindquarters included the haunches, croup, and loin. Estimates were available from the Belgian and Dutch Warmblood registries, and the Belgian registry reported much higher heritabilities for similar traits than the Dutch registry (Koenen et al., 1995; Rustin et al., 2009).

Overall, conformation of the legs had the lowest heritability, but also the largest range. However, the high heritabilities came exclusively from the Hungarian Sport Horse and Belgian Warmblood registries (Posta et al., 2009; Rustin et al., 2009). All other registries reported low to moderate heritabilities for conformation of the legs (Kühl et al., 1994; Koenen et al., 1995; Gelinder et al., 2002; Stock and Distl, 2006; Posta et al., 2009; Rustin et al., 2009). Conformation of the legs encompasses many individual traits and some registries evaluate different aspects of leg conformation separately. The numerous possible leg conformation flaws could account for the wide range of reported heritabilities.

Estimates for foal scores differ substantially from most estimates for young horses, and were therefore not included in Table 1. In the Trakehner registry, conformation of foals had a heritability on the lower end of the range (0.18) (Preisinger et al., 1991). Heritability of type in a study on Holsteiner foals was lower than any of the estimates in Table 1 (0.20) (Kühl et al., 1994). However, a more recent study in Holsteiner foals found a higher heritability of 0.42 for type (Bösch et al., 2000).

*2. Movement*

Table 2 shows heritabilities for movement traits in young horses. Heritabilities for overall movement were moderate to high with the lowest estimate coming from foals in the Holsteiner registry and the highest from field tests in the Swedish Warmblood registry (Kühl et al., 1994; Viklund et al., 2008). When movement was divided into separate components for correctness and impulsion, correctness had a much lower heritability (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000; Posta et al., 2009). Additionally the highest heritability for correctness came from the Hungarian Sport Horse registry and was somewhat of an outlier as the next highest estimate was 0.19.

**Table 3: Heritabilities of various movement traits in young warmblood horses.**

| | | *Heritability* | | |
|---|---|---|---|---|
| *Trait* | **N** | **Mean** | **Min** | **Max** |
| Overall Movement | 3 | 0.38 | 0.27 | 0.53 |
| Movement (Correctness) | 5 | 0.17 | 0.09 | 0.32 |
| Movement (Impulsion) | 4 | 0.30 | 0.23 | 0.43 |
| Overall Walk | 7 | 0.32 | 0.26 | 0.37 |
| Walk (Correctness) | 2 | 0.23 | 0.21 | 0.25 |
| Walk (Elasticity) | 4 | 0.31 | 0.14 | 0.52 |
| Walk (Stride Length) | 3 | 0.22 | 0.12 | 0.38 |
| Overall Trot | 6 | 0.41 | 0.31 | 0.50 |
| Trot (Impulsion) | 8 | 0.30 | 0.20 | 0.36 |
| Trot (Stride Length) | 3 | 0.34 | 0.22 | 0.47 |

Heritability of quality of walk in hand was moderate and had a fairly small range (Gelinder et al., 2002; Stock and Distl, 2006; Ducro et al., 2007b; Viklund et al., 2008). Heritabilities for correctness of the walk and stride length of walk were lower than those for elasticity (Koenen et al., 1995; Stock and Distl, 2006; Ducro et al., 2007a). However, elasticity was only measured in the Dutch and Belgian Warmblood registries, and heritability in the Belgian Warmblood registry was much higher than the Dutch, which is indicated in the large range (Koenen et al., 1995; Ducro et al., 2007a; Rustin et al., 2009).

Heritability for evaluation of overall trot was high (Gelinder et al., 2002; Ducro et al., 2007b; Viklund et al., 2008). Occasionally components of the trot such as stride length, impulsion, and elasticity were evaluated. Elasticity and impulsion had similar average heritabilities and ranges and were combined in Table 2 (Koenen et al., 1995; Stock and Distl, 2006; Ducro et al., 2007a; Rustin et al., 2009). Impulsion of the trot had a moderate heritability. Stride length also had a moderate heritability, though slightly higher than impulsion (Koenen et al., 1995; Ducro et al., 2007a; Rustin et al., 2009).

Heritability of movement in foals was consistently lower than estimates found in young horses (Preisinger et al., 1991; Kühl et al., 1994). The study by Bösch et al. (2000) was an exception; heritability of movement was higher than the overall average shown in Table 2. In Trakehner foals, regularity or correctness of gaits was much less heritable than impulsion of movement (0.17 compared to 0.31) (Preisinger et al., 1991).

## V. Genetic Correlations

### *1. Conformation Traits*

Few studies estimated genetic correlations among overall conformation and component traits of conformation. Viklund et al. (2008) found a high correlation of 0.81 between overall conformation and body conformation and a lower correlation of 0.47 with leg conformation. Genetic correlations between type and overall conformation, as well as other conformation components are reported in Table 3. Type is highly and favorably correlated with both overall conformation and conformation of the body. However, type is less highly correlated with conformation of the legs, though the genetic correlation is still favorable (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000; Viklund et al., 2008; Posta et al., 2009).

**Table 4: Genetic correlations between type and various conformation traits**

| | | *Type* | | |
|---|---|---|---|---|
| *Trait* | **N** | **Mean** | **Min** | **Max** |
| Overall Conformation | 2 | 0.83 | 0.83 | 0.83 |
| Body | 6 | 0.84 | 0.74 | 0.94 |
| Legs | 8 | 0.52 | 0.28 | 0.83 |

Genetic correlations between various linearly scored conformation traits were numerous and covered a wide range. Conformation of the withers was strongly related to conformation of the shoulder (0.66 to 0.80) with high and long withers being associated with a long, sloping shoulder. A long, sloping croup was also genetically correlated to muscular haunches (0.52 to 0.70). Low to moderate correlations were found between various leg conformation traits (Koenen et al., 1995).

*2. Movement Traits*

Genetic correlations between correctness and impulsion of overall movement ranged from 0.72 to 0.82 (Preisinger et al., 1991; Kühl et al., 1994; Posta et al., 2009). The genetic correlation estimated in foals was much lower than in young horses (0.57) (Preisinger et al., 1991). Genetic correlations between the components traits of the walk and overall movement are generally high (0.67 and 0.82 for stride length and elasticity, respectively) with the exception of correctness of walk (-0.06) (Ducro et al., 2007a). Stride length and suppleness of walk were highly genetically related, showing a correlation of 0.90, but correctness of walk was lowly correlated with both stride length and suppleness (0.03 and 0.15, respectively) (Koenen et al., 1995). Components of the trot were all highly and favorably genetically correlated with overall movement with correlations ranging from 0.93 to 0.97 (Ducro et al., 2007a). Estimates of genetic correlations between component traits of the trot were also extremely favorable, ranging from 0.80 to 0.98 (Koenen et al., 1995).

*3. Walk and Trot*

The genetic correlation between quality of walk and trot ranged from 0.63 to 0.86 (Ducro et al., 2007b; Viklund et al., 2008). In the Belgian Warmblood registry, genetic correlations were all above 0.40 between linearly scored walk and trot traits, with a majority being above 0.60 (Rustin et al., 2009). In the linear system used by the Dutch Warmblood registry, genetic correlations among walk and trot traits ranged from 0.55 to 0.74 with the exception of the correlations between trot traits and correctness of walk, which ranged from -0.01 to 0.05 (Koenen et al., 1995).

*4. Conformation and Movement*

Tables 4 and 5 summarize a few of the important genetic correlations between conformation and movement traits evaluated in young warmbloods. There was only one available estimate between overall movement and overall conformation, but it was very high and favorable (Ducro et al., 2007a). Genetic correlations between various conformation and movement traits are numerous, therefore only those with multiple estimates from different studies will be discussed.

**Table 5: Genetic correlations between movement, overall conformation, and type traits in young warmblood horses**

| | *Conformation* | | | | *Type* | | | |
|---|---|---|---|---|---|---|---|---|
| *Trait* | **N** | **Mean** | **Min** | **Max** | **N** | **Mean** | **Min** | **Max** |
| **Movement** | 1 | 0.82 | - | - | 3 | 0.80 | 0.69 | 0.93 |
| **Correctness** | 2 | 0.75 | 0.65 | 0.84 | 4 | 0.60 | 0.24 | 0.93 |
| **Impulsion** | 2 | 0.72 | 0.71 | 0.72 | 5 | 0.60 | 0.38 | 0.69 |
| **Walk** | 4 | 0.52 | -0.04 | 0.77 | 2 | 0.34 | 0.32 | 0.36 |
| **Trot** | 4 | 0.78 | 0.71 | 0.90 | 2 | 0.60 | 0.57 | 0.62 |

**Table 6: Genetic correlations between movement traits and conformation of body and legs**

| | *Body* | | | | *Legs* | | | |
|---|---|---|---|---|---|---|---|---|
| *Trait* | **N** | $\bar{r}_g$ | **Min** | **Max** | **N** | $\bar{r}_g$ | **Min** | **Max** |
| **Movement** | 1 | 0.83 | - | - | 3 | 0.67 | 0.57 | 0.88 |
| **Correctness** | 3 | 0.49 | 0.10 | 0.83 | 4 | 0.58 | 0.20 | 0.99 |
| **Impulsion** | 4 | 0.43 | 0.18 | 0.66 | 5 | 0.46 | 0.19 | 0.84 |
| **Walk** | 2 | 0.24 | 0.20 | 0.28 | 2 | 0.14 | 0.09 | 0.19 |
| **Trot** | 2 | 0.58 | 0.53 | 0.62 | 2 | 0.24 | 0.22 | 0.26 |

Overall conformation showed high and favorable genetic correlations with all movement traits, though correlations with walk traits were lowest. Walk traits did have the largest range, and an unfavorable genetic correlation of -0.04 was reported between overall conformation and correctness of the walk (Ducro et al. 2007a). If that correlation was excluded, then the average genetic correlation would be 0.71 (Ducro et al., 2007a; Viklund et al., 2008). Genetic correlations between overall movement and type were favorable but lower than analogous correlations between overall movement and overall conformation. Walk again had the lowest correlations with type, but was still favorable (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000; Viklund et al., 2008; Posta et al., 2009).

The single genetic correlation between overall movement and body conformation was high and favorable (Bösch et al., 2000). However, genetic correlations with all other movement traits were much lower, but favorable, though correctness of movement had a wide range (Kühl et al., 1994; Bösch et al., 2000; Posta et al., 2009). Quality of trot seemed to have higher and more favorable genetic correlations with body conformation than quality of walk (Viklund et al., 2008). Genetic correlations between movement traits and conformation of the legs were generally the lowest, particularly between leg conformation and individual gaits, with quality of walk having a lower genetic correlation than trot. Regardless, all correlations were favorable (Kühl et al., 1994; Bösch et al., 2000; Viklund et al., 2008; Posta et al., 2009).

Genetic correlations between conformation traits and movement in foals were also high and favorable. Conformation had the highest correlations with movement traits in foals, with genetic correlations of 0.71 and 0.84 for impulsion and regularity, respectively (Preisinger et al., 1991). Correlations between type and movement ranged from 0.53 to 0.69 (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000).

*5. Later Inspections and Performance Testing*

Conformation evaluated in young horses has been genetically correlated to traits in performance tests. Horses undergoing the Riding Horse Quality Test had a genetic correlation of 0.18 with gaits under rider evaluated in the Stallion Performance Test (Gerber Olsson et al., 2008). Within the Riding Horse Quality Test, genetic correlations between conformation traits and gaits under rider were moderate to high, ranging from 0.23 to 0.55, except for a low correlation of 0.09 between correctness of legs and walk under rider (Viklund et al., 2008).

Walk in hand and trot in hand were very highly correlated with the same gait under rider (0.98 and 0.89, for walk and trot, respectively). The correlations between each gait in hand and the opposite gait under rider were also favorable. The correlation between walk in hand and trot under rider was 0.55 and the correlation between trot in hand and walk under rider was 0.58. Walk and trot in hand were both also favorably correlated at 0.69 with the canter under rider (Viklund et al., 2008).

Genetic correlation between jumping traits and conformation are generally low, but still positive. Genetic correlations ranged from 0.11 to 0.27 (Ducro et al., 2007a; Viklund et al., 2008). Type and jumping ability showed genetic correlations ranging from 0.02 to 0.23 (Viklund et al., 2008). Type in Holsteiner foals showed a genetic correlation of 0.29 with free jumping at mare performance testing (Bösch et al., 2000). Genetic correlations between movement and jumping ability are also low with overall movement and jumping ability exhibiting a genetic correlation of 0.02 (Ducro et al., 2007a). Genetic correlations between walk in hand and jumping ability ranged from -0.05 and 0.17, while correlations with trot in hand ranged from 0.03 and 0.25 (Viklund et al., 2008).

Bösch et al. (2000) showed that foal inspection scores were genetically correlated to traits evaluated in later inspections and performance tests. Genetic correlations between type at foal age and various conformation traits at studbook inspection ranged from 0.59 to 0.88. Correlations between movement in foals and conformation at studbook inspection were slightly lower, ranging from 0.51 to 0.69. Genetic correlations ranged from 0.65 to 0.87 between type and movement evaluated in foals and movement traits evaluated at studbook inspections. Genetic correlations between type in foals and traits evaluated at mare performance tests ranged from 0.20 to 0.35. Movement in foals and mare performance traits showed genetic correlations ranging from 0.31 to 0.52. All of these genetic correlations were favorable (Bösch et al., 2000). A genetic correlation of 0.40 was also found between movement in Holsteiner foals and free jumping in mare performance testing (Bösch et al., 2000).

*6. Dressage and Show-Jumping*

In the literature, correlations between conformation measured in young horses and dressage results ranged from 0.42 to 0.67 (Wallin et al., 2003; Ducro et al., 2007a; Gerber Olsson et al., 2008). When conformation is divided into linear component traits, specific genetic correlations between certain aspects of conformation and dressage ability can be observed. Length of neck, length of shoulder, and position of shoulder were moderately to highly genetically correlated with dressage: -0.32, -0.27, and -0.40, respectively. These correlations indicate that young horses with a long neck and long, sloping shoulder are good prospects for dressage performance. A long, sloping croup and muscled haunches are also favorable; genetic correlations between dressage and length of croup, position of croup, and muscularity of haunches were -0.25, -0.49, and -0.29, respectively (Koenen et al., 1995).

Ducro et al. (2007a) estimated a correlation of 0.69 between overall movement in young horses and dressage performance. In the first stallion inspection of the Dutch Warmblood registry, walk and dressage performance had a genetic correlation of 0.72, while trot showed a correlation of 0.58 (Ducro et al., 2007b). When quality of gaits is broken down into component traits, dressage performance is associated with young horses that have a longer stride and more elastic walk (genetic correlations of 0.53 and 0.50, respectively). Correlations between dressage performance and stride, elasticity, impulsion, and carriage of the trot (0.65, 0.67, 0.59, and 0.65, respectively) are also favorable traits to evaluate in young horses that are potentially headed for dressage careers. Performance in dressage is associated with a longer stride, more elasticity, greater impulsion, and improve carriage of the trot measured at studbook entry (Ducro et al., 2007a). Estimates of genetic correlations by Koenen et al. (1995) agree with these results, though the magnitudes of the correlations are smaller.

Estimates of genetic correlations between conformation of young horses and future show-jumping results were 0.29 and 0.42 for the Dutch and Swedish Warmblood registry, respectively (Wallin et al., 2003; Ducro et al., 2007a). Specific conformational traits evaluated in young horses that are favorably genetically correlated with show-jumping performance include a strongly muscled neck, a sloping croup, and strongly muscled haunches, with correlations of -0.25, -0.24, and -0.28, respectively between each trait and show-jumping competition results. Genetic correlations between show-jumping performance and all other traits were not significantly different from zero (Koenen et al., 1995).

Overall movement measured in young horses showed a genetic correlation of 0.23 with show-jumping performance; and correlations between show-jumping performance and walk and trot were unfavorable at -0.45 and -0.36, respectively (Ducro et al., 2007a,b). Components of the walk showed low or no correlations with show-jumping results, ranging from -0.12 to 0.14. Stride length, elasticity, impulsion and carriage of the trot were also not good predictors of show-jumping potential in young horses, with genetic correlations ranging from 0.02 to 0.14 (Koenen et al., 1995; Ducro et al., 2007a).

**VI. Discussion**

Phenotypic data show that relationships between performance in competition and conformation and movement exist. Therefore, traits evaluated in young warmbloods are useful for predicting potential performance ability. Several trends in conformational change from foal age to adult exist and should be examined further to determine if conformation at foal age is relevant to adult conformation. Movement characteristics of foals seem to remain consistent as foals age and can be used to predict movement in adult horses.

The studies evaluated here included a wide variety of fixed effects in the linear models used to estimate genetic parameters. These fixed effects account for environmental factors in order to better estimate what impact genetics has on conformation and movement traits. In studies involving inspections that included both sexes, sex was always included as a fixed effect

(Preisinger et al., 1991; Huizinga et al., 1991; Kühl et al., 1994; Bösch et al., 2000; Viklund et al., 2008). Sex can often have a large effect on conformation traits, especially traits such as type. Even though these studies generally covered a small age range, year of birth is also commonly included in genetic analyses to account for differences in development at different ages (Preisinger et al., 1991; Kühl et al., 1994; Koenen et al., 1995; Bösch et al., 2000, Gerber Olsson et al., 2000; Ducro et al., 2007a; Gerber Olsson et al., 2008; Rustin et al., 2009). Additionally, the evaluator or specific inspection event was often included to account for differences in scoring between inspections and potential evaluator bias (Huizinga et al., 1990; Preisinger et al., 1991; Gerber Olsson et al., 2000; Gelinder et al., 2002; Wallin et al., 2003; Stock et al., 2006; Ducro et al., 2007a,b; Viklund et al., 2008, Rustin et al., 2009). Occasionally, the percentage of Thoroughbred in the pedigree was calculated for sires and dams to account for what effect Thoroughbred genes have on the conformation and movement of sporthorses (Huizinga et al., 1990, 1991; Kühl et al., 1994, Koenen et al., 1995; Ducro et al., 2007b).

Heritability estimates for overall conformation in young horses were low to high indicating there is potential for genetic improvement in overall conformation through selection. Overall conformation was generally more heritable than component traits evaluated in the same population. In general, leg conformation traits were much less heritable than all other conformation traits from the same population. This may be partially due to the fact that there are numerous possible conformational flaws of the legs making accurate and consistent evaluation difficult. Additionally, a slight shift in a horse’s stance can somewhat disguise some limb conformation flaws. The Dutch Warmblood registry evaluates 7 different limb conformation traits and the Belgian Warmblood registry evaluates 11. Heritabilities for these traits ranged from 0.16 to 0.46, therefore attempting to accurately evaluate leg conformation as a single trait would be difficult (Koenen et al., 1995; Rustin et al., 2009). Heritabilities indicate that genetic progress in conformation scores for young warmbloods should be realized.

The heritability of overall movement is moderate, with the heritability of impulsion being higher than for correctness of gaits. Walk and trot are both at least moderately heritable, with the trot consistently having a higher heritability. The overall quality of the walk is moderately heritable, but component traits of the walk evaluated separately had lower heritabilities. There are inconsistencies among estimates regarding which components of the walk are more heritable.

Because heritability of conformation and movement in young (3 to 4 yr of age) horses is fairly well established, investigation of heritability in foals provides a source of novel information. At foal age, early studies indicated that heritability of conformation was lower than similar traits measured in young horses, but a more recent study found a high heritability (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000). Heritability of movement traits at foal age was also low to moderate in older studies, but within the same range as young horses in a more recent study (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000). Regardless, heritabilities are high enough to indicate that improvement can be made through selective breeding.

Linear scored conformation and movement traits are extremely useful for breeders making mating decision, because they provide extensive information about specific component traits. This can allow breeders to find stallions that should ideally complement their mare's strengths and weaknesses. However, it is possible that the amount of traits measured could be too numerous for breeders to analyze. Genetic correlations were high among some linearly scored conformation traits and this may indicate where these traits can be combined to reduce the number of measurements, which may alter heritability estimates. This could increase the somewhat low heritabilities found for linearly scored conformation traits and improve genetic gain, as well as simplifying the process for breeders. However, for foals, analyzing linear traits may not be beneficial due to the variation in conformation with age. Correlations between component traits and overall conformation were high in young horses therefore, selection for overall conformation in foals may provide better results. Regardless, improvement in overall conformation score should be associated with an improvement in individual conformation traits.

Genetic correlations among movement traits were all high and favorable. Favorable genetic correlations among correctness and impulsion were also found in foals. Genetic correlations between components of the walk were mostly high and favorable, so improvement in one aspect of the walk should yield improvement in other characteristics. Correctness of walk does seem to be poorly correlated with other walk characteristics, however the correlation was still favorable; therefore, selecting for other components should have a minimal effect on correctness. Additionally, walk traits were highly and favorably correlated with overall walk and overall movement, therefore these broader traits may be more efficient for selection. Components of the trot are also highly and favorably correlated, therefore selection for improvement in any trot characteristic should improve the overall quality of the trot in young horses. Because the component traits are so highly correlated to each other and to the overall trot and overall movement scores, the trot can most likely be evaluated as a single trait, without losing genetic improvement. Genetic correlations between walk and trot characteristics are generally high, indicating that improving one gait will be associated with an improvement in the other gait.

Overall, genetic correlations between conformation and movement are high and positive, indicating that selection for improvement in either trait will allow for improvement in the other.

The walk is moderately correlated with conformation traits in young horses, excluding correctness of legs. The trot was moderately to highly correlated with conformation traits; however, the genetic correlation between trot and correctness of legs is lower than other correlations. Overall, correlations between conformation and trot are higher than correlations between conformation and walk. Again, a positive correlation between trot and conformation indicates a favorable relationship.

In foals, genetic correlations between conformation and movement were again high and favorable (Kühl et al., 1994; Bösch et al., 2000). Regularity or correctness of gaits was found to be more highly correlated with type and conformation, which is interesting since phenotypic data determined that foals have not established an even four-beat walk by 39 wk of age (Preisinger et al., 1991; Denham, 2007). However, Back et al. (1994, 1995) did find that foals developed distinctive gait characteristics at an early age. Correctness of gaits may be determined more by a foal's inherent abilities while impulsion can be improved through training.

Genetic correlations between conformation and movement with inspections at older ages were moderate to high and favorable. Conformation and movement in young horses were both correlated with gaits under rider evaluated at field tests as well as at stallion licensing inspections. Correlations between movement traits and gaits under rider were more favorable than with conformation. Conformation and movement scores do not seem genetically correlated with free-jumping traits evaluated at these inspections; therefore, other methods for early evaluation of jumping ability is necessary, or a better understanding of what conformation or movement qualities are important for jumping ability. Overall, inspection scores in young horses can be used to select potential breeding horses at an earlier age.

Conformation and movement at the walk and trot in young horses were both favorably correlated with later dressage performance. Therefore, using these criteria for indirect selection of future equine competitors, as well as breeding animals, is feasible. Using linear based scoring systems may allow for a better indication of which specific conformation traits are related to performance. Regardless of scoring methods, selection for improved conformation and movement should result in offspring that are better able to meet the demands of dressage competition.

Conformation and movement of the walk and trot evaluated in young horses was not highly genetically correlated with show-jumping performance and in some cases unfavorable correlations were found. Show-jumpers do not walk or trot during competition, and though conformation is important to determine if they have the athletic ability to clear the fences, aesthetics included in conformation scores are also unimportant. Canter and free-jumping traits are commonly evaluated in young horses, but not in foals and therefore were not included in this review, but they have the most favorable genetic correlations with show-jumping performance (0.28 to 0.33 for canter and 0.52 to 0.88 for free-jumping) (Ducro et al., 2007a). Often, these traits are only evaluated at performance tests where horses have been pre-selected for dressage or show-jumping competition and undergone some degree of training. Therefore, conformation and movement at the walk and trot in young horses may not be an ideal way to evaluate show-jumping ability.

Only one study estimated genetic correlations between traits evaluated at foal inspections and studbook inspections, as well as at mare performance testing, and therefore cannot be considered conclusive. No studies have investigated correlations between foal scores and performance in either dressage or show-jumping competitions. Correlations between conformation traits in foals and all traits evaluated at studbook inspection were high and favorable, indicating that selection for conformation in foals should improve conformation of breeding mares in future generations. Genetic correlations between foal conformation and movement at studbook inspection were also favorable. Genetic correlations between movement at foal inspections and studbook inspections were also very high and favorable, and while correlations between foal movement and conformation at studbook inspection were lower, they were still favorable. Finally, foal conformation had moderate, but favorable correlations with traits evaluated in the mare performance test; and foal movement was moderate to highly, and favorably, correlated with mare performance test results.

**VII. Conclusions**

Genetic parameters of conformation and movement in young warmblood horses indicate that genetic progress in these traits can be achieved. Genetic correlations show that these traits are correlated with evaluated performance traits as well as competition results, at least in dressage. However, there are a limited number of studies that estimated genetic correlations between traits at separate events and therefore more work is necessary to ensure that traits inspected in young horses are genetically related to the actual breeding goals of warmblood registries. Conformation and movement seem particularly unrelated to show-jumping ability and alternate selection methods may be necessary. Parameter estimates at foal inspections are also scarce, especially genetic correlations between foal inspection traits and later inspections or competition results. If foal scores can be accurately correlated with later inspections, they can be utilized for earlier selection as well as progeny testing for approved stallions. However, the lack of research concerning development of foal conformation as well as few parameter estimates makes these applications unlikely at present. Further research in genetic parameters of conformation and movement in young horses, as well as foals, should strengthen breeding programs of warmblood horses and allow for earlier selection of superior progeny.

## Chapter III

## Summary of Foal Inspection Data for Two North American Sporthorse Registries

**A.S. Bhatnagar[1], R.M. Lewis[1], D.R. Notter[1], C. Schacht[2], and R.K. Splan[1]**

[1]Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA

[2]International Sporthorse Registry, Inc., Sycamore, IL

### Abstract

Foal inspection scores from the International Sporthorse Registry and Oldenburg Registry North America from 1999 to 2009 were analyzed to provide implications for more complex analyses. Traits evaluated were type and conformation, athletic ability of movement, overall development, total score, and premium status. Population distribution, change in scores over time, as well as the effect of sex, year of birth, year of birth by sex interaction, inspection period (1999 to 2005; 2006 to 2009), and breed of dam and sire on scores were calculated. Offspring distribution indicates that a large number of sires produced only one offspring in the years included and therefore do not contribute much information to further analyses. Female foals exhibited significantly higher scores for all traits excluding movement. All traits increased over time, with the most significant increase occurring from 1999 to 2003. Scores were significantly higher in inspection period 2 than period 1. Offspring of warmblood dams had consistently higher scores and offspring of Thoroughbred dams generally had higher scores than offspring of miscellaneous or unknown dams, though not always significantly so. However, sire breed and the year of birth and sex interaction were relatively unimportant in explaining variation in the scores. Percentage of foals named premium was very high.

## Introduction

The International Sporthorse Registry and Oldenburg Registry North America (ISR/OLNA) was created in 1983 to bring European methods to independent breeders in North America and produce excellent sporthorses from North American stock. The breeding goal for both registries is to produce modern sporthorses that can compete with those bred in Europe in dressage, jumper, eventing, and hunter disciplines. The methods of ISR/OLNA are adopted from the Oldenburg registry in Germany, but neither registry is formally associated with this or any other European registry. It operates on an open book policy that allows for the registration of horses from all warmblood breeds as well as Thoroughbreds and other breeds based on the individual quality of the horse itself. Foals are required to be inspected prior to registration and ISR/OLNA publishes foal inspection scores every year. Though both registries are overseen by the same administrative personnel, they are essentially two separate registries with different criteria for registration. The main distinction between ISR and OLNA involves criteria for approval of mares for breeding. The OLNA manages premium and main mare studbooks which enforce stricter pedigree standards. Foals can only be registered with OLNA if their dam is in one of the OLNA mare books, provided the foals own inspection scores meet the appropriate standards. ISR maintains the mare book and pre-mare book which primarily allows for the approval of mares other than warmbloods, Thoroughbreds, and Arabians. Offspring of mares in the mare book and pre-mare book can only be registered with ISR. Approved stallions overlap both registries, providing enough genetic connections that the two registries can be considered a single genetic population (International Sporthorse Registry, Inc., 2010).

Though foal inspection scores are published for use by members of the registry, no formal analyses of these data has been conducted. Breeders often consider these foal scores when making mating decisions to determine which stallions may produce superior foals when crossed with their mares. Therefore, formal analyses of foal scores would allow for more educated mating decisions. Further, although many sires are approved for breeding, the distribution of offspring by sires is unavailable to breeders. Such a distribution would allow breeders to identify sires that are over or under represented in the registry. Genetic evaluations of these foal inspection scores would also assist breeders in their decisions, and analysis would provide important considerations for genetic parameter estimations including identification of significant fixed effects. Because ISR/OLNA is an open book registry, non-warmblood sires may be used and many different dam breeds produce foals. Sex of foals may also have a significant effect on scores as well as year of birth. Before any genetic parameter estimation can be performed for foal inspection scores, the potential influence of effects other than genetics must be determined in order to design an appropriate analytical model.

## Materials and Methods

A database of foal inspection (n=5505) scores from the ISR/OLNA was created for the years 1999 to 2009. This database included sire, dam, sex, birth year, inspection period, breed of sire, breed of dam, scores for evaluated traits, and premium status. Traits evaluated were type and conformation (TC), athletic ability of movement (AM), overall development as related to age (OD), and total score (TS). Foals received subjective scores ranging from 1 to 10 for TC, AM, and OD with 10 indicating a perfect score. From 1999 to 2000, scores were evaluated by 0.5 intervals; from 2001 on, scores were evaluated by 0.1 intervals. TS was calculated as 0.4(TC) + 0.4(AM) + 0.2(OD). From 1999 to 2007, premium status (PS) was awarded to foals with TS higher than 8.0; from 2008 onward, only those foals with scores of 8.0 or higher for all 4 traits received premium status. Each criterion was then applied to all years to investigate the effect the criteria change had on PS. There were 2 inspection periods (1999-2005; 2006-2009) which coincided with a change in breeding director for the organization in 2006. Breeding directors are responsible for inspecting the majority of foals each year, therefore inspection period includes an evaluator effect. Sires were grouped into 3 breed categories: warmblood, pony, and miscellaneous. Dams were grouped into 4 breed categories: warmblood, thoroughbred, miscellaneous, and unknown.

Statistics describing the dataset were obtained using SAS 9.2 (SAS Inst., Cary, NC). The Frequency procedure was used to determine number of offspring per sire and number of premium foals per year and sex. Analysis of variance tests were run using the Mixed Model procedure to obtain least squares means for each trait and test for significance of sex, year of birth nested within inspection period, year of birth by sex interaction, inspection period, dam breed, and sire breed. Sire was included as a random effect. Significance was set at $P \leq 0.05$ for all tests.

**Results**

Distributions of offspring by sire are shown in Figures 1 and 2. The database included offspring of 500 sires, with an average of 11.01 foals per sire. However, 26.6% sires had only one offspring in the database, and 73.6% had less than 10 offspring. No significant difference in number of foals per year was found. The overall mean, standard deviation, and range for each trait are shown in Table 1. There were no significant differences among all traits for overall mean. Figure 11 shows the change in percentage of PS foals each year. Overall, 42.1% of foals were awarded PS with 38.8% of all males and 45.2% of all females being named premium foals (Figure 11). There were significantly more premium females than males from 1999 to 2003. The drop in all premium numbers at 2008 coincides with the change in the definition of PS.

However, percent premium increased again in 2009. Figure 12 shows the percentage of foals awarded PS for both criteria across all years. The overall percentage of PS foals was 42.1% Criteria 2 resulted in a lower percentage for all years. When the second criteria were applied to all years, the overall percentage of premium foals was 29.1%.

The influences of the fixed effects included in the model are shown in Figures 7 through 10. Sex, year of birth, inspection period, and dam breed were all found to be significant while sire breed and year of birth by sex interaction were not significant. Female foals had higher scores for all traits except AM. There were also significantly more female foals awarded PS. Figures 7 through 10 illustrate the change in each trait over time as well as years when sexes were significantly different Scores for all traits increased over time, though the increase was greater in early years (1999 to 2003). TC scores did not change from 2004 to 2008, while AM showed a steady increase across all years. OD did not change from 2004 to 2005 and then increased in 2006 and remained unchanged from 2007 to 2009. TS increased from 2004 on, but less dramatically than the increase prior to that year. Foals born in inspection period 2 also had significantly higher scores for all 4 traits. There were also significantly more foals awarded PS in inspection period 2.

The majority of dams with offspring in the registry were warmbloods or Thoroughbreds. Warmblood dams produced significantly higher scoring foals for all 4 traits, while offspring of Thoroughbreds and other miscellaneous breeds were similar. Offspring of Thoroughbred dams were not significantly different from offspring of dams of unknown breeds for TC, and were not significantly different from the miscellaneous dam breed category for AM and OD. With the exception of TC, mares of unknown breed had offspring with lowest scores. The effects of dam breed on PS closely mirrored scored traits, with warmblood dams producing significantly more premium foals. Thoroughbred dams produced more premium foals than dams of unknown breed, but were not significantly different from the miscellaneous dam breed category. Miscellaneous dams did not produce significantly more premium foals than dams of unknown breed.

Although sex by year of birth interaction was not significant across the overall time period, females were significantly higher for TC, OD, and TS in early years (Figures 7 through 10). There were no significant differences due to sex in scores for AM at any year. There were few significant differences between scores for each sire breed category. However, there were far more warmblood sires represented in the database than any other breed category. Offspring of pony sires had significantly higher scores than warmbloods, but were not different from the miscellaneous category of sire breeds. Offspring of warmblood sires were also not significantly different from offspring of miscellaneous sires. The effect of sire breed on PS was identical to its effect on scored traits.

## Discussion

The information gained from evaluation of large datasets provides important considerations for further work including genetic analysis. First, the overall means indicate that a majority of foals are being scored quite high. The range also shows that the entire available scale is not being utilized making it difficult to determine if foals are truly superior or inferior. The reduced scale may also limit the amount of variation captured between each foal and could create issues in separating variance components in genetic analysis. However, since the change in scale in 2001, foals are being measured on an approximately 30 point scale, which should be sufficient.

The analysis of PS provided several interesting results. PS is intended to reward breeders of truly superior foals, but the percentage is quite high, indicating it may not be an adequate indication of better quality. Percent PS closer to 20% would be more ideal to indicate foals that are likely to succeed at the upper levels of performance or become quality breeding stock. If the second criteria had been in place early, then the percentage PS would have been close to 20% until 2003. Interestingly, if the second criteria had been in place prior to 2008 the reduction in percent PS seen in 2008 would not have been significant. However, if the criteria had not been changed, percentage of foals awarded PS would have increased to 68.6% in 2009. The definition of premium status may need to be reevaluated in order to better enhance the ISR/OLNA breeding program. Increasing the cutoff scores would not necessarily be ideal since the current cutoff level is 8.0 for each trait, which is very high on the 1 to 10 scale. It may be more beneficial to encourage evaluators to utilize the entire 1 to 10 scale and leave the current criteria for premium status. This will reduce the percentage of premium foals along with increasing the general variance of foal scores to better determine differences. An alternative would be to award PS to the top 20% of foals after the completion of all inspections.

Distribution of offspring by sire identifies if certain stallions are over or under represented in the dataset. A large number of sires only produced one foal in the years recorded, and 73.6% had less than 10 foals in the database. Though all animals are probably connected through their pedigrees, sires with only one foal do not provide significant genetic information because there are no full or paternal half-siblings with which to compare inspection scores, therefore these records will only complicate calculations (Mrode, 2005). Therefore, for the purposes of genetic evaluation, the records of these foals can be excluded without losing much accuracy. At the other extreme, there were 7 sires with more than 100 offspring in the registry.

With these sires, there are many half-siblings and probably several full-siblings with inspection scores, so these high numbers provide connectedness as well as stronger relationships amongst records and should improve accuracy of results from genetic analysis (Falconer and Mackay, 1996; Mrode, 2005; Kuehn et al., 2007).

Analysis of variance of mixed linear models is used to determine which factors have a significant effect. Sex was consistently a significant effect in all 4 traits, with the exception of AM. Sex is almost always a significant effect in sporthorse inspection data that includes both sexes (Preisinger et al., 1991; Huizinga et al., 1991; Kühl et al., 1994; Bösch et al., 2000; Viklund et al., 2008). It is possible that male foals are scored more rigorously than females because selection of potential future stallions is more intense than for future mares, or there may be some evaluator bias toward female foals. Additionally, the type component of TC can refer to the femininity or masculinity of the foal, which is traditionally more important for females (Strickland, 1992). The significant effect of year of birth and the increase for all traits across years could be an indication of genetic improvement. Year of birth or age is also typically significant for sporthorse inspection data from other registries (Preisinger et al., 1991; Kühl et al., 1994; Koenen et al., 1995; Bösch et al., 2000, Gerber Olsson et al., 2000; Ducro et al., 2007a; Gerber Olsson et al., 2008; Rustin et al., 2009). The difference between inspection periods is somewhat confounded with year of birth, but since the breeding director is responsible for inspecting a majority of the foals, it could indicate slightly different preferences. The breeding director also has a substantial influence on the breeding goals for the registry, and any differences between goals of the director in each period may be reflected in foal scores. Therefore, period should be included as a fixed effect to account for that potential bias. Many other registries include an evaluator effect or specific inspection event effect (Huizinga et al., 1990; Preisinger et al., 1991; Gerber Olsson et al., 2000; Gelinder et al., 2002; Wallin et al., 2003; Stock et al., 2006; Ducro et al., 2007a,b; Viklund et al., 2008, Rustin et al., 2009), but the ability to measure such effects was limited in the current study. Additionally, any significant differences between sexes were unobserved in period 2, so this may be an effective way to account for the year and sex interaction that was insignificant overall. Since the sex and year of birth interaction was insignificant, it should not be included as a fixed effect in any further analyses.

Breed of sire had no significant effect overall on any score; however, there were very few offspring from non-warmblood sires. The higher scores from offspring of pony sires may have been more pronounced with more numbers. Similarly, warmblood sires may prove to produce offspring with significantly higher scores than miscellaneous sires. However, since warmbloods are traditionally more suited to the breeding objective of this registry, it is unlikely that substantially more offspring of miscellaneous sires will be inspected in the future. Sire breed is generally not included in analyses performed by other registries, though often percent Thoroughbred in the pedigree of the sire is calculated (Huizinga et al., 1990, 1991; Kühl et al., 1994, Ducro et al., 2007b). Due to the small numbers, records of offspring from non-warmblood sires can be eliminated for the purposes of genetic analysis. If those records are removed, then there will only be one sire breed category, and therefore sire breed does not need to be included as a fixed effect in the linear model.

Dam breed was much more important and showed consistent trends. Again, the comparatively low numbers of offspring from dams of miscellaneous and unknown breeds may affect significance. Also, many of the dams of unknown breed generally have unknown pedigrees and therefore do not contribute additional information to a genetic analysis. For further analyses, records from offspring from miscellaneous or unknown dam breed can be eliminated, primarily to eliminate dams with incomplete pedigree information. It seems certain that offspring of warmblood dams score higher than those of all other breeds for all 4 traits. However, the use of Thoroughbred mares requires further consideration. Utilization of Thoroughbreds in sporthorse breeding is widespread, accounting for 35% of the genes in the Hanoverian warmblood (Hamann and Distl, 2008). Thoroughbreds were originally incorporated to lighten the coarseness of warmbloods, thereby improving type (Wilkens, 2005; Reed, 2008). However, breeders later became more selective when including Thoroughbreds due to conformational disadvantages (Hamann and Distl, 2008; Reed, 2008). Therefore, use of Thoroughbred dams should positively affect the type component of TC, while potentially having a negative effect on the conformation component. Thoroughbred genes can have both a beneficial and detrimental effect on AM. Thoroughbreds are primarily bred for speed over a flat course and are not necessarily suitably designed for the demands of dressage and jumping (Clayton, 2001; Reed, 2008). However, their speed and athleticism can provide positive gains to movement and seem particularly useful in eventing competitors (Clayton, 2001; World Breeding Federation for Sporthorses, 2009). Few other registries have incorporated dam breed into their analyses, though occasionally percentage Thoroughbred is calculated (Koenen et al, 1995). Overall, including dam breed as fixed effect may be beneficial, particularly for registries that include many non-warmblood dams.

Preliminary analysis of data and evaluation of the significance of fixed effects should precede any more elaborate analyses including genetic parameter estimation. Including insignificant fixed effects in a linear model can over-parameterize the model and affect the accuracy of the results (Verbeke, 2000). Evaluating the distribution of offspring can also provide indications of how strong genetic relationships will be and if the data contains sufficient genetic connections to obtain accurate results (Mrode, 2005). Also, eliminating unnecessary records will simplify calculations and reduce noise. The analyses done here indicate that records from single offspring of a sire, offspring of pony and miscellaneous sire breeds, and offspring of miscellaneous and unknown dam breed can be eliminated. Analyses also conclude that sire breed and sex by year of birth interaction should not be included as fixed effects. Identifying those fixed effects that explain significant variation in foal inspection scores will aid in the design of appropriate linear models and ensure the ease and accuracy of any future and more complex analyses. Also, knowing the effects of sex, breed, and inspection period on foal inspection data can provide important considerations to breed organizations and facilitate improvements in their breeding program.

| *Trait* | Mean | St Dev | Min | Max |
|---|---|---|---|---|
| TC | 7.87 | 0.34 | 6.4 | 9.5 |
| AM | 7.89 | 0.36 | 6.8 | 9.5 |
| OD | 7.89 | 0.32 | 6.4 | 9.5 |
| TS | 7.88 | 0.31 | 6.5 | 9.3 |
| PS | 0.42 | 0.49 | 0 | 1 |

**Table 1.** Mean, standard deviation, and range for each inspected trait

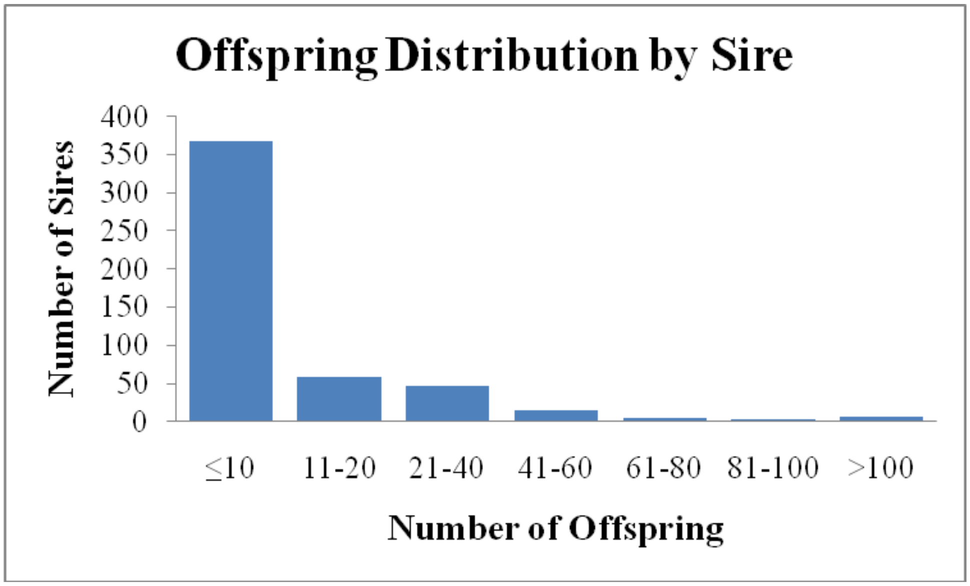


**Figure 1.** Distribution of offspring by sires in database

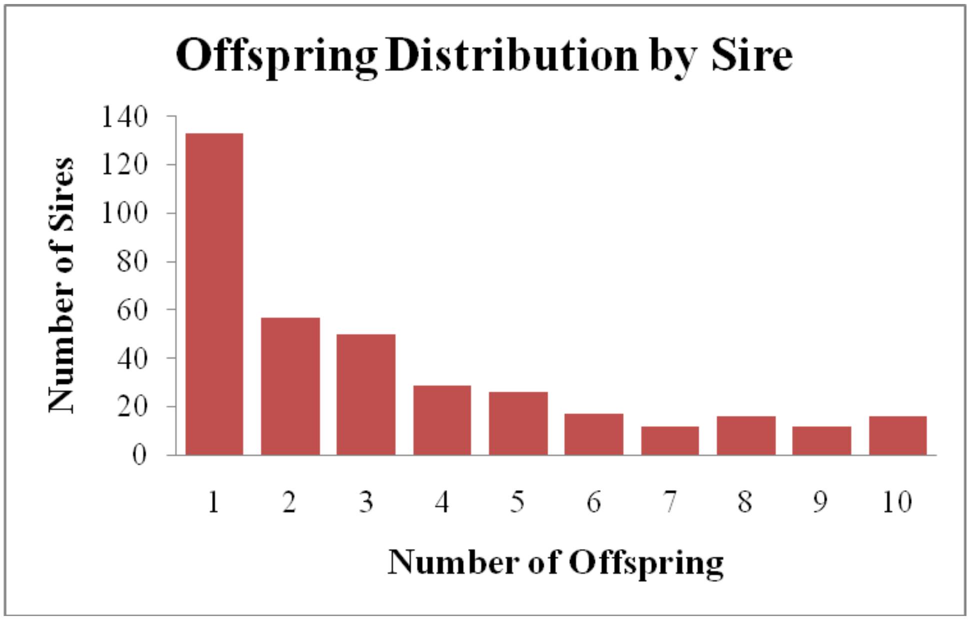


**Figure 2.** Distribution of offspring for sires with less than 10 total offspring in database

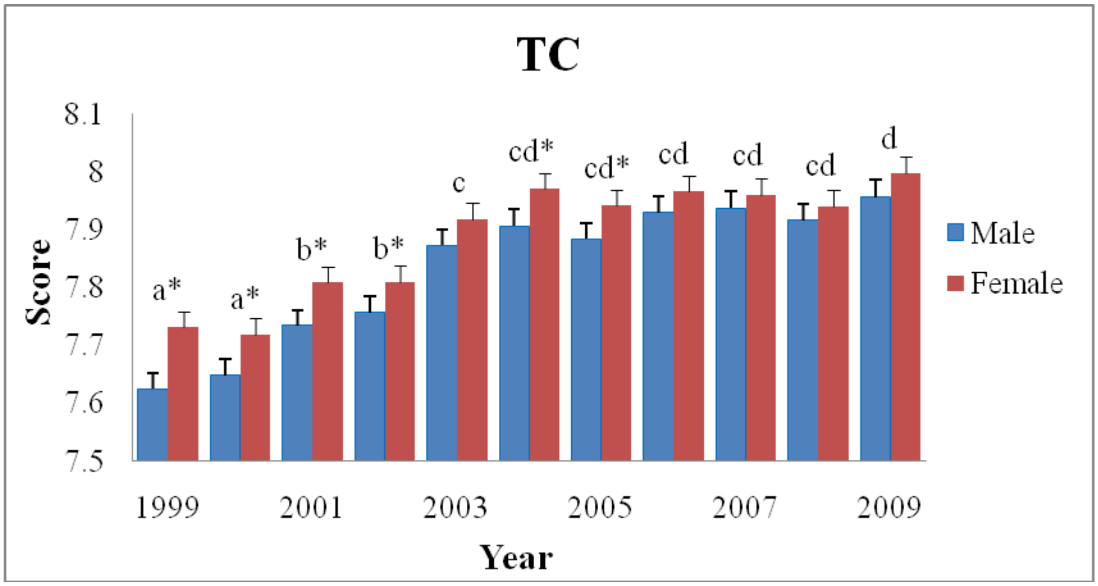


**Figure 3.** Change in TC (type and conformation) over time; year means with same letter are not significantly different; asterisk indicates significant difference between sexes (P ≤ 0.05)

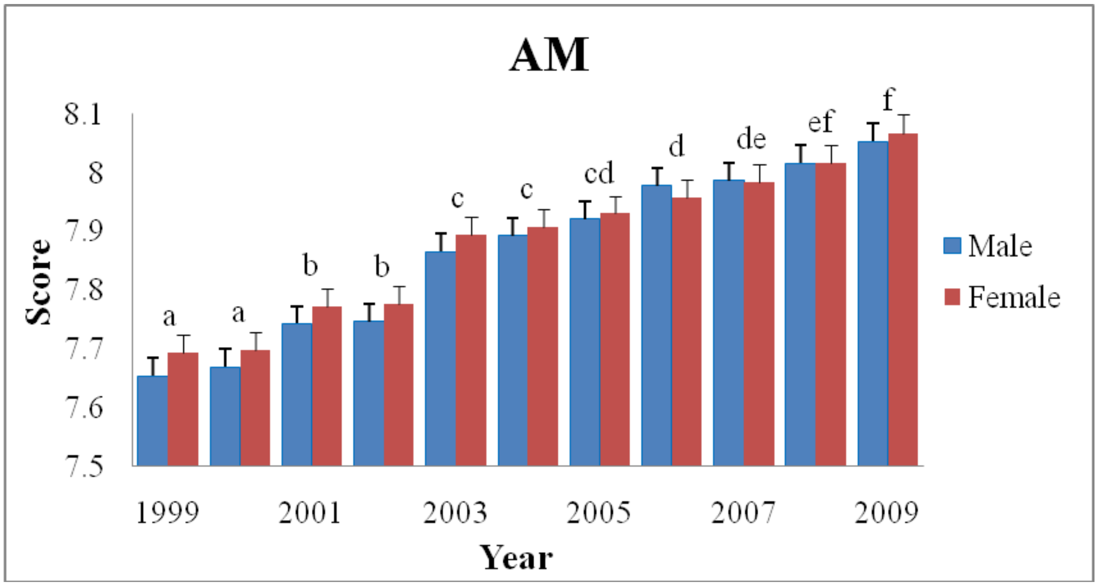


**Figure 4.** Change in AM (athletic ability of movement) over time; year means with same letter are not significantly different; asterisk indicates significant difference between sexes ($P \leq 0.05$)

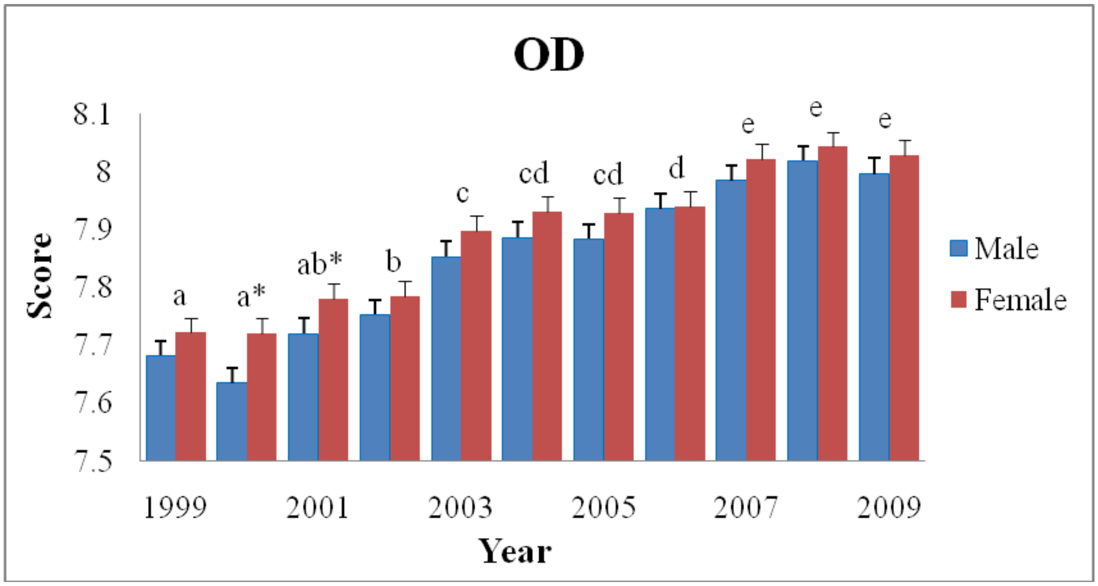


**Figure 5.** Change in OD (overall development) over time; year means with same letter are not significantly different; asterisk indicates significant difference between sexes ($P \leq 0.05$)

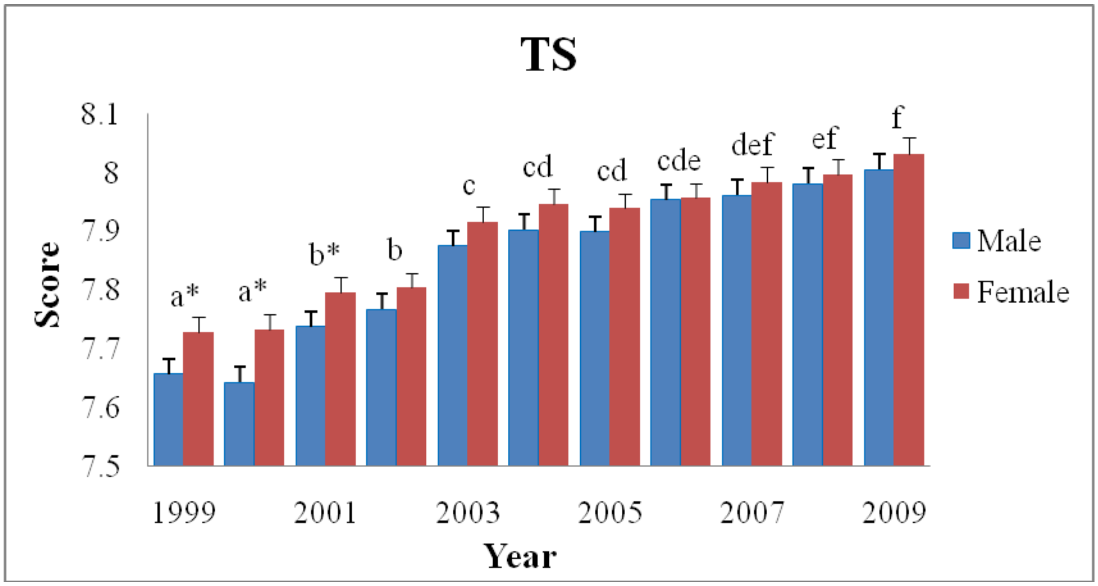


**Figure 6.** Change in TS (total score) over time; year means with same letter are not significantly different; asterisk indicates significant difference between sexes (P ≤ 0.05)

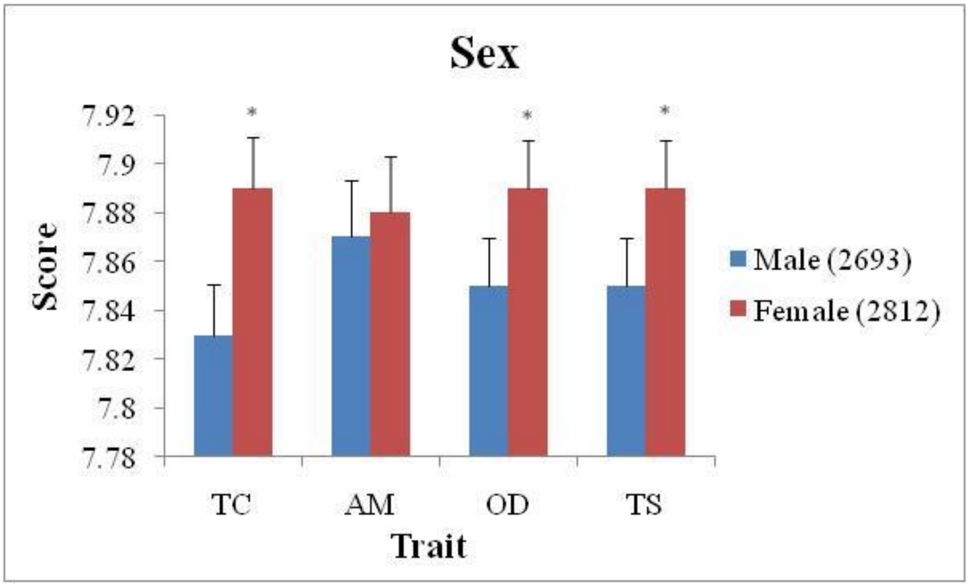


**Figure 7.** Effect of sex on scores for each trait; asterisk indicates significant difference ($P \leq 0.05$).

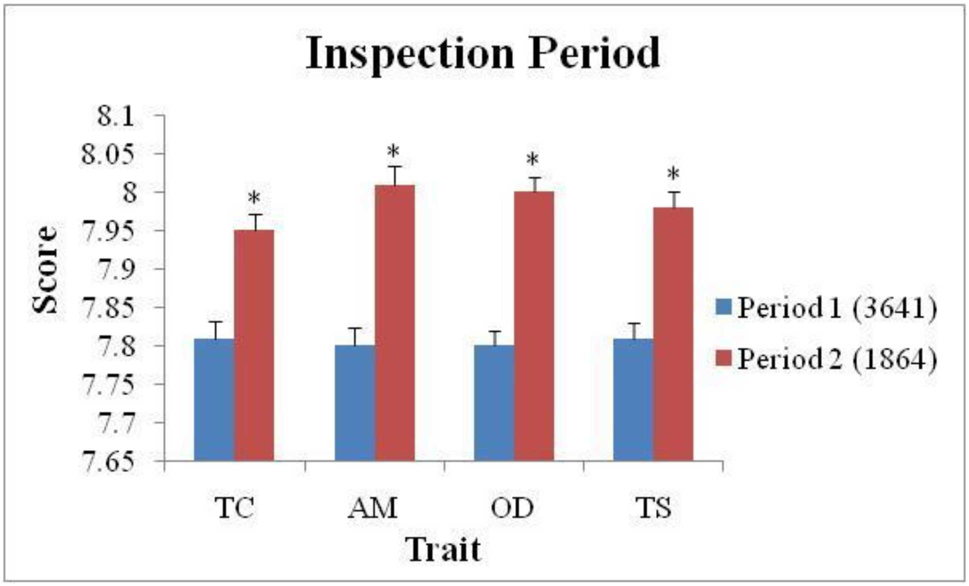


**Figure 8.** Effect of inspection period on scores; asterisk indicates significant effect (P ≤ 0.05).

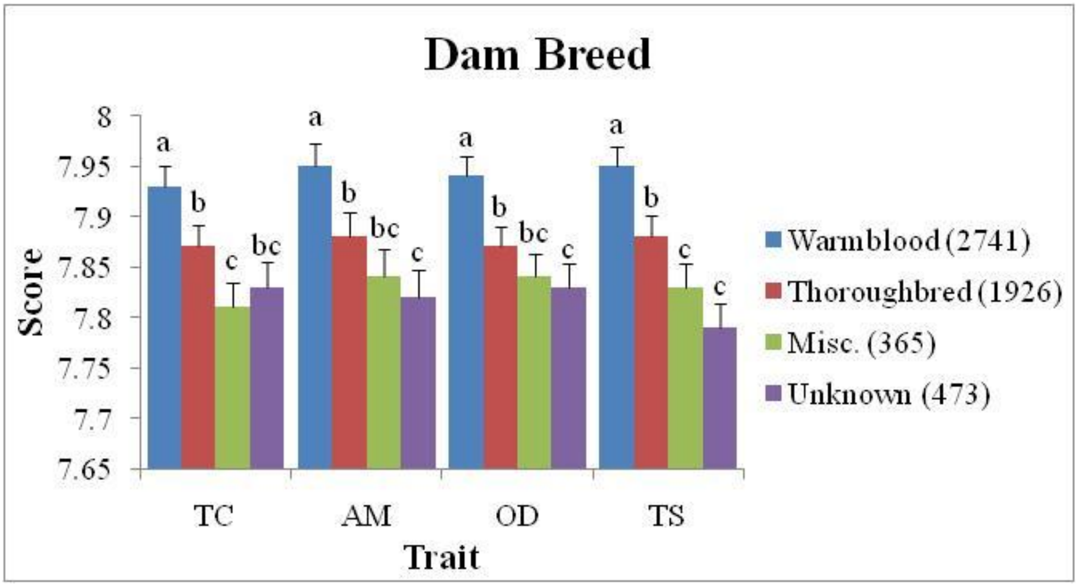


**Figure 9.** Effect of dam breed on scores; bars with same letter are not significantly different (P ≤ 0.05)

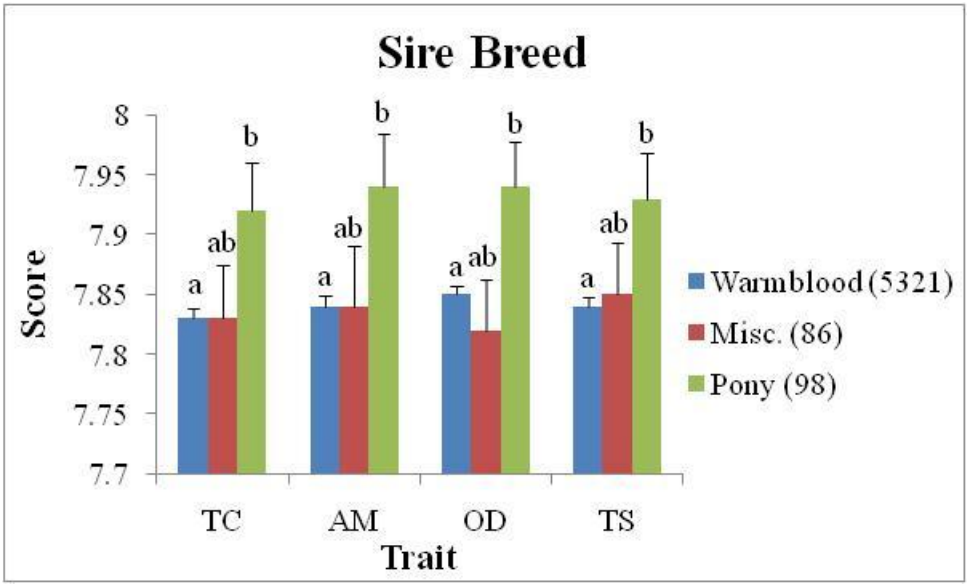


**Figure 10.** Effect of sire breed on scores; bars with same letter are not significantly different (P ≤ 0.05)

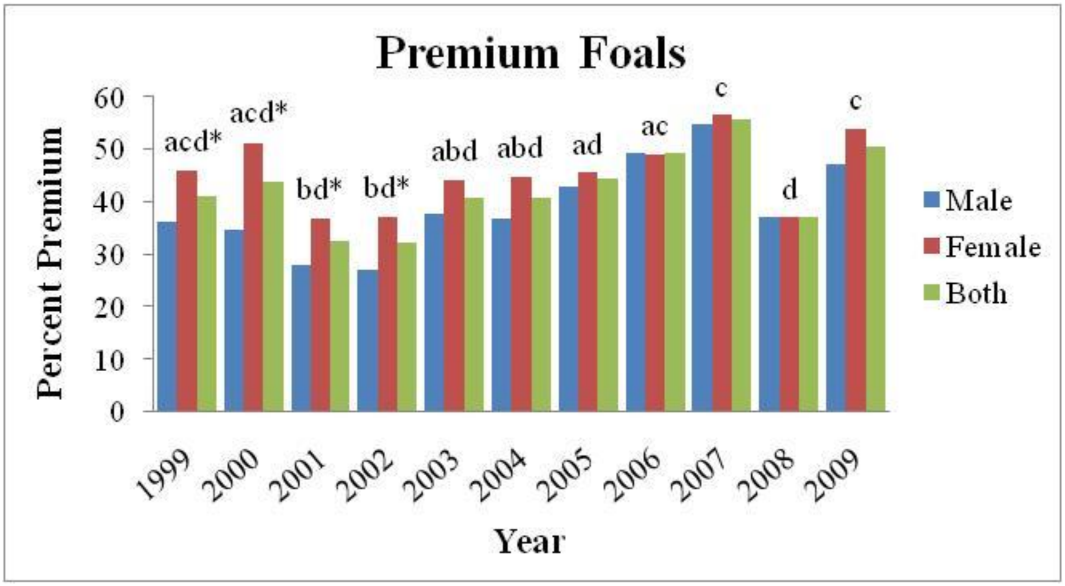


**Figure 11.** Percentage of foals awarded PS (premium status) by year; asterisk indicates significant difference between sexes; bars with same letter are not significantly different across years ($P \leq 0.05$)

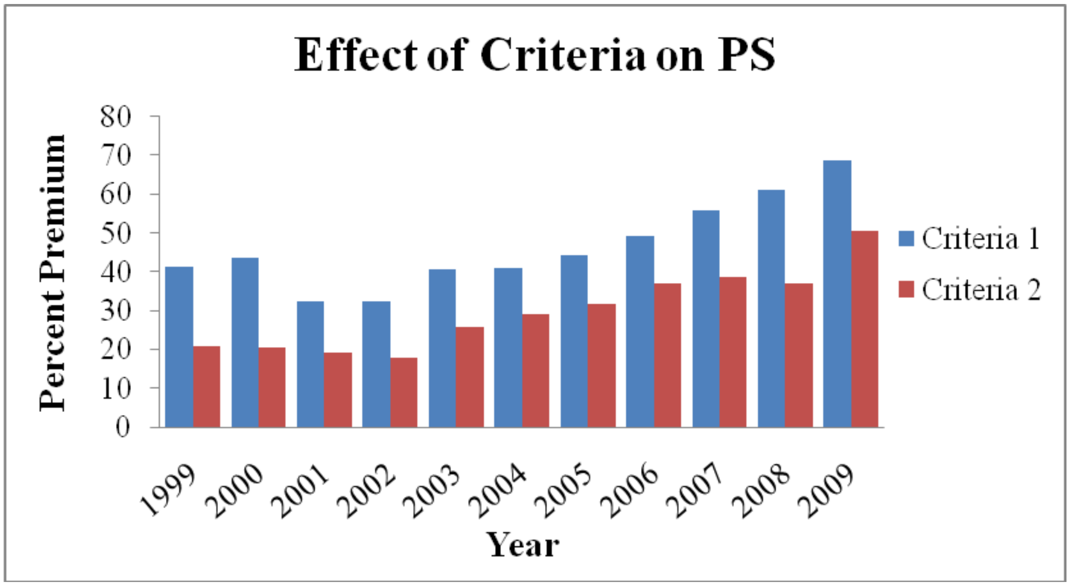


**Figure 12.** Percent of foals theoretically awarded PS each year for both criteria (criteria 1: TS ≥ 8.0; criteria 2: TC, AM, OD, and TS all ≥ 8.0)

## Chapter IV

# Genetic Parameters of Foal Inspection Scores for Two North American Sporthorse Registries

**A.S. Bhatnagar[1], R.M. Lewis[1], D.R. Notter[1], C. Schacht[2], and R.K. Splan[1]**

[1]Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA

[2]International Sporthorse Registry, Inc., Sycamore, IL

## Abstract

Genetic parameters of foal inspection traits were estimated for the International Sporthorse Registry and Oldenburg Registry North America. Estimates were obtained using an animal model for the scored traits type and conformation, athletic ability of movement, overall development, total score, and the binary trait premium status. Heritabilities were estimated to be 0.45 ± 0.05, 0.47 ± 0.05, 0.49 ± 0.05, 0.55 ± 0.05, and 0.32 ± 0.04 for each trait, respectively. Heritability of premium status was 0.51 when transformed to the underlying normal scale. Genetic correlations among all scored traits were extremely high and favorable (0.80 to 0.99). Correlations with premium status were inestimable due to extremely high genetic and residual covariances. Selection for scored traits should result in genetic progress, as heritabilities were high and genetic correlations indicate no antagonistic relationships. However, parameters may be under or overestimated due to evaluator bias, abbreviated use of scoring scale, and limitations in obtaining relevant fixed effects. Overall, it seems that foal inspection scores can be used to strengthen the breeding program of these sporthorse registries provided they are favorably correlated with performance results in adult horses.

## Introduction

Many sporthorse registries require inspections of young horses in order to evaluate their potential as performance animals, with implications for future use as breeding stock. These inspections also provide information relative to breeding merit of parents. Most registries have also estimated genetic parameters for traits evaluated at these inspections in order to improve the accuracy of their breeding programs and potential for improvement. Traits evaluated at inspections are also genetically correlated with results from dressage and show-jumping competitions since performance in these fields are the primary breeding objective of most sporthorse registries (Koenen et al., 2004).

Most sporthorse registries require foals to be inspected before they can be registered to ensure breeders are meeting registry breeding objectives. However, few registries score foals quantitatively due to high variability in foal conformation with age and growth stage. In the literature, only 3 studies reporting estimates of genetic parameters of foal scores have been produced (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000). These studies found low to moderate heritabilities for conformation and movement in foals with the exception of Bösch et al. (2000), who found high heritabilities. Additionally, Bösch et al. (2000) found that foal scores were genetically correlated with mare inspection and mare performance test scores. Furthermore, movement characteristics seem to be established at a very young age in horses (Back et al., 1995). Therefore, it seems that foal scores can be utilized to improve sporthorse breeding programs, although more estimates of genetic parameters are necessary to determine if selection will be genetically beneficial. The objective of this study was to estimate genetic parameters of foal inspection scores obtained by the International Sporthorse Registry and Oldenburg Registry North America (ISR/OLNA) to add to the body of knowledge concerning foal scores of warmblood horses.

## Materials and Methods

Foal inspection scores of 5505 foals from ISR/OLNA from 1999 to 2009 were obtained and entered into a database. Each record included sire and dam of the foal, sex, year of birth, inspection period, sire and dam breed, scores for 4 inspected traits, as well as a binary measure classifying achievement of premium status. Inspected traits could be scored 1 to 10, with 10 indicating a perfect score, although observed scores ranged from 6 to 10. From 1999 to 2000, traits were scored by 0.5 increments, and after 2001, traits were scored by 0.1 increments. The 4 scored traits were type and conformation (TC), athletic ability of movement (AM), overall development as related to age (OD), and a weighted mean of the 3 previous traits (0.4TC + 0.4AM + 0.2OD) designated as the total score (TS). Premium status (PS) is intended to identify foals of a superior quality and was awarded to foals with TS of 8.0 or higher from 1999 to 2007, and to foals with scores of 8.0 or higher for each individual trait from 2008 to 2009. To account for evaluator differences, foals were divided into two inspection periods coinciding with a change in breeding director, who is responsible for scoring the majority of foals. The first period was from 1999 to 2005 and the second from 2006 to 2009.

Before beginning genetic analysis, several edits were made to the database based on previous statistical analysis using SAS 9.2 (SAS Inst., Cary, NC). First, scores from 1999 to 2000 (n=1046) were removed due to the difference in the scoring scale. Records from non-warmblood and non-Thoroughbred dams were also removed, again because there were few records and this also eliminated dams with unknown pedigrees (n=534). Records of foals from non-warmblood sires were also removed as this only accounted for a small portion of records (n=117). Finally, there were a substantial number of sires with only one foal representative in the database (n=113), and these records were removed as they do not provide much genetic information. The final dataset included 3695 foals representing 286 sires with an average of 12.92 foals per sire. Pedigree data was expanded to include 3 generations of relatives on the sire side and 2 generations on the dams side (when possible) and included 13,227 total animals.

Variance component estimates were obtained using ASReml (Gilmour et al., 2009). The model used for all traits was as follows:

$$Y_{ijklm} = \mu + sex_i + period_j + year(period)_k + dam\ breed_l + animal_m + e_{ijklm}$$

Where $Y_{ijklm}$ is the recorded outcome for each inspection trait (TC, AM, OD, TS, and PS) of the *m*th animal; μ is the population mean; $sex_i$ is fixed effect of sex (male or female); $period_j$ is the fixed effect of the inspection period (1 = 2001 to 2005; 2 = 2006 to 2009); $year(period)_k$ is the fixed effect of year of birth (2001 to 2009) nested within inspection period; dam $breed_l$ is the fixed effect of the breed of the dam (1 = warmblood; 2 = Thoroughbred); $animal_m$ is the random additive effect of the *m*th animal; and $e_{ijklm}$ is the random residual. Univariate models were run to obtain heritabilities for the 4 scored inspected traits and a univariate binomial model with a logit function was used to estimate the heritability of PS. Heritability of PS was then transformed to the normal scale (Dempster and Lerner, 1950; Van Vleck, 1972). Bivariate models were used to estimate genetic correlations among the 4 scored inspection traits.

**Results**

Table 1 shows the genetic parameter estimates for the 4 scored inspection traits (TC, AM, OD, and TS). Heritabilities were high for all traits, particularly the weighted mean TS. The other 3 traits had similar heritabilities, with OD having the highest heritability estimate. PS had a heritability estimated of 0.32 ± 0.04 on a binary scale and 0.51 when transformed to the normal scale.

Genetic correlations among all scored inspection traits were very high. Correlations between TS and other traits were highest, ranging from 0.93 to 0.99. The genetic correlation between OD and TC was also extremely high (0.98). Genetic correlations with AM were the lowest: 0.80 with TC, 0.88 with OD, and 0.93 with TS. The covariances between the binomial trait PS and the scored traits could not be estimated because residual and genetic covariances were at the upper boundary of the parameter space and therefore genetic correlations were not available. Phenotypic correlations were also high, but slightly lower than genetic correlations. Similar to genetic correlations, TS showed the highest phenotypic correlations (0.83 to 0.87) and the phenotypic correlation between TC and OD was also high at 0.86. Lower phenotypic correlations were again found among AM and other traits.

## Discussion

Traits inspected at foal inspections are estimated to be highly heritable, and therefore appropriate selection should yield genetic gain. TS had a particularly high heritability and may prove to be the most useful selection criteria. There are very few published studies on genetic parameters of foal scores, and available studies are from European populations, so direct comparison is somewhat problematic. However, since they represent the only estimates available, comparison is necessary to determine how estimates here differ from other obtained estimates. Preisinger et al. (1991) estimated genetic parameters for foals in the Trakehner population. Traits evaluated were type, conformation, regularity of gaits, and impulsion of movement. Two studies on Holsteiner foals estimated genetic parameters for type and movement (Kühl et al., 1994; Bösch et al., 2000). Kühl et al. (1994) also estimated heritability and genetic correlation of premium status with other foal traits. No studies evaluated traits similar to OD in foals and OD is not clearly defined by the registry. A more straightforward definition of what OD encompasses would be beneficial to breeders as well as for determining if it is genetically correlated to specific traits in adult horses.

In previous studies, heritability of type was 0.20 to 0.32 and conformation was 0.18 (Preisinger et al., 1991; Kühl et al., 1994). These estimates are all much lower than heritability of TC estimated in this study. However, in the later study by Bösch et al. (2000), type had a heritability of 0.42, which is more similar to the estimate found here. This study also utilized the animal model, as opposed to the sire model used in previous studies. Type and conformation are both commonly evaluated in young sporthorses when they are entered in the breeding studbook or at performance tests to evaluate whether they will positively contribute to the registries breeding objectives, as well as potential for future performance (Gelinder et al., 2002; Stock and Distl, 2006; Viklund et al., 2008). Type is difficult to define, but generally refers to whether the horse fits the breed standards, is suitable for performance in a sporthorse discipline, and also has an appropriately feminine or masculine appearance (Thomas, 2005). Conformation refers to how the horse is put together including bone structure, musculature, and body proportions. Many European breed registries give conformation and type strong consideration in their breeding objectives (Koenen et al., 2004). However, conformation in foals is not well studied but seems to vary substantially with age, making evaluation difficult (Denham, 2007). Foals also exhibit many conformational flaws that usually diminish with maturity (Anderson and McIlwraith, 2004; Denham, 2007). Combining TC is also problematic because it is impossible to tell whether type or conformation has a larger effect. Preisinger et al. (1991) found a genetic correlation of 0.78 between type and conformation in foals, so though the two traits are highly related, they are not identical, and it may be more precise to evaluate each trait separately. Though TC evaluated here is highly heritable, these factors may affect the validity of evaluating such traits in foals.

Heritability of movement traits in previous studies ranged from 0.17 to 0.31, which is lower than estimates for AM found in the current study (Preisinger et al., 1991; Kühl et al., 1994). The heritability estimate of 0.31 was for impulsion of movement in Trakehner foals which may be more similar to AM (defined as athletic ability of movement) than regularity of gaits, which had a heritability estimate of 0.17 (Preisinger et al., 1991). Bösch et al (2000) estimated heritability of movement to be 0.40, which is much closer to the estimate obtained here. Movement in foals has been more thoroughly researched than conformation, though the data available is still not comprehensive. Similar to foal conformation, many gait characteristics are extremely variable in foals, particularly flexion of the elbow, carpal, and fetlock joints (Back et al., 1993). Denham (2007) found that foals' walk is more lateral and does not conform to the desired even 4-beat gait by 39 wk. However, Leach and Cymbaluk (1986) showed that characteristics such as stride length, stride frequency, and speed at gait transition are similar to the same characteristics measured in adults. Back et al (1994b) also found that foals maintain consistent swing duration as well as protraction and retraction angles of the legs in the sagittal plane from 4 to 26 mo of age. Additionally, diagrams of joint angles were remarkably similar at 4 and 26 mo, indicating that intralimb coordination patterns are established at foal age. Back et al (1995) also found that most kinematic characteristics recorded in foals could accurately predict the same characteristic in adult horses. In the same study, the authors found that subjective scores similar to foal inspection scores given to foals in ISR/OLNA were also highly correlated with subjective scores given to adult horses. Therefore, even though some aspects of foal movement are still variable, enough consistencies between foal and adult movement exist to justify evaluating foals for their movement.

No other registries calculate a trait similar to TS. The current weighting in the calculation of TS seems somewhat arbitrary and could perhaps be more effective if revised using selection index theory. TC should probably be weighted less than AM because conformation is so variable in foals and it is uncertain if type or conformation has a larger effect on TC. AM could potentially have a higher weighting since research discussed previously has shown that movement in adults can be predicted to a certain degree at foal age (Back et al., 1995). OD should remain with a lower weighting since the definition of OD is unclear and its potential to predict future traits in adult horses is unknown. For example, if TC, AM, and OD were given weightings of 2, 4, and 1, respectively, the resulting index coefficients would be 1.73, 2.03, and 0.13. Using an actual selection index would result in TS being inconsistent with the 1 to 10 scale and therefore may require reeducation of the breeders. The most useful selection index would use performance results or scores in older horses as goal traits in the aggregate genotype and foal scores as the index criteria. However, this is not possible since covariances between these traits do not exist for this registry.

PS as a binary trait was found to be moderately heritable, and less heritable than the 4 scored traits. However, when transformed to the underlying normal scale, heritability of PS was high and similar to the other scored traits, particularly TS. Because PS is directly determined from TS, the heritabilities should be expected to be similar. The estimated heritability of PS found here was much higher than 0.09 estimated in a previous study in Holsteiner foals, which could be due to difference in breeding goals of the Holsteiner registry (Kühl et al., 1994). Authors found that premium status was more dependent on type in this registry and the primary breeding goal of the Holsteiner registry is production of show-jumpers; therefore, type is less important than movement and breeders may be less focused on selecting for type. PS is often more important to breeders than the individual scored traits as a premium foal can perhaps be expected to have a higher selling price. As such, evaluators may subjectively decide premium status first and then determine scores for all other traits. This procedure may affect the accuracy of variance component estimation for the scored traits, which is why the heritability of PS was also estimated. The heritability of PS may be a more useful parameter for breeders making selection and mating decisions. Unfortunately, genetic correlations between PS and the scored traits were inestimable, so it was not possible to determine how closely PS was related to the other traits.

Genetic correlations were very high and favorable among all scored traits and were similar to results from previous studies. Correlations between type and gaits were 0.69 and 0.77 for Holsteiner foals (Kühl et al., 1994; Bösch et al., 2000). In Trakehner foals, the correlation between type was 0.63 and 0.58 for regularity and impulsion of movement, respectively (Preisinger et al., 1991). Regularity of gaits showed a higher genetic correlation with type than impulsion of movement. Genetic correlations between conformation and movement were 0.84 and 0.71 for regularity and impulsion, respectively (Preisinger et al., 1991). The trait AM is probably more similar to impulsion than regularity. Again, it is unknown if type or conformation has a larger effect on TC score. However, the genetic correlation between TC and AM found here was higher than any previous estimates. OD was very highly and positively correlated to TC, suggesting that these two traits are very highly related and may be evaluating the same qualities. AM had a lower correlation with OD, but was still quite high and favorable. TC, AM, and OD all had extremely high correlations with TS, which is expected since TS is a weighted average of the other three scores. However, OD had a nearly perfect correlation with TS even though it was the lowest weighted trait in the calculation. TC was also more highly correlated with TS than AM. Regardless of these differences, genetic correlations imply that these traits are all favorably related and selection for improvement in one trait should result in improvement in all traits. Because all traits are so highly correlated with TS, it may be considered a basic selection index on which selection decisions could be based. Although, as discussed previously, its usefulness in this regard requires further exploration.

With only 3 comparable studies, it is difficult to make definite conclusions, but since results here match the most recent study, it seems that foal traits have a high heritability. However, there are several other potential issues with comparisons among the current study and other works. First, previous studies come from European registries and may therefore be completely separate populations. Comparing estimates across population may not be accurate because there are environmental factors to consider. However, given the open nature of warmblood studbooks, frequent use of artificial insemination, and importation of both mares and stallions, it is likely that there is sufficient genetic connectedness to facilitate better comparisons (Kuehn et al., 2007; Hellsten et al., 2009). Also, there may be a large difference in breeding goals between all registries involved. The Trakehner registry's breeding objectives are more concerned with creating ideal dressage horses and the Holsteiner registry aims to create exceptional show-jumpers (Koenen et al., 2004). Many qualities important for either goal have antagonistic genetic correlations (Huizinga et al., 1990; Ducro et al., 2007a,b). ISR/OLNA aims to produce foals that will excel in either discipline. Overall, the availability of additional estimates of genetic parameters of foal traits is necessary to determine accurate parameters across many populations.

Genetic parameters from this study may be either over or underestimated and there are several factors that could lead to any discrepancies. The pedigree file used in this study was quite small compared to other studies, especially from other livestock species. More pedigree data would establish more genetic connections which would most likely increase estimates. If similarly scoring foals are found to be more related than estimated here, the additive genetic variance would be increased, therefore heritability would increase. However, if extending the pedigree does not strengthen relationships between any foals, heritability should remain unchanged. Additionally, there is also the possibility of some amount of bias occurring due to the evaluators' knowledge of the foals' pedigree at inspection. Evaluators would know the performance records of the foals' relatives and may subconsciously alter their scores by a small degree accordingly. Preisinger et al. (1991) and Huizinga et al. (1990, 1991) suggested that such bias is possible, and blinding the evaluators to the pedigree of the inspected animal may lower genetic parameter estimations. Finally, evaluators should be encouraged to utilize the entire 1 to 10 scale when scoring foals to better capture the amount of variation between poor and excellent foals. Abbreviated use of the available scoring scale seems common in inspections, and authors of other studies have also suggested that evaluators utilize the entire range available (Preisinger et al., 1991; Stock and Distl, 2006; Viklund et al., 2008).

There are also several useful fixed effects that were unavailable in the data that could have been used to create contemporary groups and better explain the variance in scores. Location of inspection would have accounted for foals that happened to be scored in a higher quality group than those from another location. Also, though creating inspection periods was an attempt to establish an evaluator effect, knowledge the specific evaluator for each foal could also explain some of the variation in scores. All previously discussed studies included an evaluator effect or some method of accounting for a specific inspection in their models (Preisinger et al., 1991; Kühl et al., 1994; Bösch et al., 2000). Age at inspection in months would also be very useful as foals can be inspected as early as 2 months to almost 1 year. Foals would undergo a substantial amount of development in that time period and grouping them all by year of birth alone may not accurately account for that variation. Bösch et al. (2000) included age of foal in days in their fixed effects. Additionally, the quality of the mare would be a useful effect since ISR/OLNA utilizes 4 mare books to separate mares by their perceived breeding class.

Though more research regarding foal scores of warmblood horses would be useful, results here indicate that they are moderate to highly heritable traits and can be selected for with high expectations of improvement. Genetic correlations also indicate highly favorable relationships between all traits. However, because the extreme variance in foal conformation with age and limited research concerning conformational development in foals, direct selection on foal inspection scores may not be the most ideal use of this data. Instead, it may be best to use scores to reflect the value of the foals' parents as a type of progeny testing. Overall, foal inspection scores may be a useful addition to sporthorse breeding programs because it will increase the accuracy of genetic analyses and reduce the generation interval for the breeding population. Both of these factors will increase the amount of genetic gain that can be achieved. Further research should involve estimation of genetic correlations between foal scores and traits evaluated in mature horses, including studbook inspection, performance test, and competition data.

| *Trait* | TC | AM | OD | TS |
|---|---|---|---|---|
| $\sigma_p^2$ | 0.12 | 0.13 | 0.10 | 0.10 |
| TC | **0.45** ± 0.05 | 0.80 ± 0.05 | 0.98 ± 0.01 | 0.96 ± 0.01 |
| AM | 0.51 ± 0.01 | **0.47** ± 0.05 | 0.88 ± 0.03 | 0.93 ± 0.02 |
| OD | 0.86 ± 0.00 | 0.72 ± 0.01 | **0.49** ± 0.05 | 0.99 ± 0.01 |
| TS | 0.87 ± 0.00 | 0.83 ± 0.01 | 0.87 ± 0.01 | **0.55** ± 0.05 |

**Table 1.** Estimates genetic parameters of 4 foal inspection scores; heritabilities are in bold on the diagonal, genetic correlations are above the diagonal, and phenotypic correlations are below the diagonal

# Chapter V

## Conclusions and Implications

Foal inspection scores from ISR/OLNA were shown to be moderately to highly heritable and have high, favorable genetic correlations. Sex, dam breed, year of birth, and inspection period were found to explain significant variation in the scores when testing models to estimate variance components. Analysis of the database also found that there were many sires with only one representative offspring and those records should be removed from the dataset for genetic analysis since those animals would not be strongly related to any others. Also, there were very few non-warmblood sires and few non-warmblood or non-Thoroughbred dams. Therefore, offspring of those parents should be removed to simplify the model as well as to eliminate dams with no pedigree data. The high percentage of premium foals may also require further analysis to determine if the criteria for premium status should be revised.

The heritability estimates obtained indicate that selection for improvement in foal scores should yield genetic gains. Genetic correlations also show that there are no antagonistic relationships between any pairs of traits. Total score had the highest heritability and correlations between that trait and all other traits were close to one, therefore selecting for total score alone may be the most efficient way to select for improvement in foal conformation and movement. However, genetic parameters may have been under or overestimated due to limited pedigree data, restricted ability to obtain fixed effects, and reduced range in the scoring scale.

However, if these estimates are accurate and shown to be correlated with later performance, foal scores could be a useful addition to a selection program in warmblood horses. Bösch et al. (2000) obtained similar genetic parameter estimates and also found foal parameters were highly and favorably correlated with studbook inspection scores, and moderate but favorably correlated to performance testing. If more studies can confirm these correlations, and perhaps estimate correlations with competition performance, it would help substantiate that foals scores are related to the actual breeding objectives of warmblood registries. Currently, the paucity of literature concerning development of conformation and movement from foal age to adult and lack of parameter estimates hinders utilization of foal scores in breeding programs.

Increased use of foal scores for early selection of warmblood horses would be both economically and genetically beneficial to breeding registries such as ISR/OLNA. Foal inspections require all animals to be evaluated in order to be registered, therefore basing selection decisions in some part on foal scores would therefore reduce the effects of any pre-selection that could occur before studbook inspections or performance tests, as well as provide additional quantitative data on relatives of breeding horses that might not be obtained otherwise. A study on the Trakehner horses estimated that 65% of the population would not be evaluated for conformation without foal inspections (Preisinger et al., 1991). A study by Hellsten et al. (2006) estimated that only 10 to 28% of horses born were tested at young horse inspections in 5 European countries with France and Sweden having a higher percentage of tested horses (45 and 43%, respectively). Since all foals are required to undergo inspection in order to be registered, data on all animals would be available and the effects of pre-selection would be avoided.

Additionally, early selection will reduce the long generation interval in horses which currently is between 8 and 12 years, with females having shorter generation intervals (Ström and Philipsson, 1978; Árnason and Van Vleck, 2000). Long generation intervals reduce the amount of genetic gain that can be obtained for a trait. Using young horse inspection data and performance testing reduces generation interval by 3 or 4 years and incorporating foal data should further reduce generation interval (Philipsson et al., 1990). Including foal data as type of progeny testing for current breeding will also help reduce the generation interval and may be a more useful and accurate approach to including foal inspection scores.

The horse industry has a substantial economic impact in both Europe and North America, and therefore improvement of breeding programs should translate to increased economic gains (Swedish University of Agricultural Science, 2001; American Horse Council, 2005). From an economical standpoint, accurate evaluation of conformation and movement in foals will reduce investment of time and money in horses that are not genetically predisposed to becoming elite breeding or performance animals. Accurate parameters will also support increased selling prices of foals with higher scores or premium status.

Evaluations and subsequent genetic analyses of young horses are extensive, especially in Europe, but there is ample room for improvement of breeding programs in North America. Genetic parameters of conformation and movement in foals are largely unstudied, but results here indicated that it may be beneficial for warmblood registries to include foal scores in breeding programs. However, more registries must include scores in their foal inspections and more parameter estimations are required, including correlations with traits in mature horses. Also, a better understanding of conformation and movement in foals is necessary in order to ensure traits evaluated in foals are related to important traits in adult horses. With further research, adding foal inspection scores to the current breeding strategies should improve genetic gains and strengthen the breeding program of ISR/OLNA.

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