

Factor analysis of evaluated and linearly scored traits in Swedish Warmblood horses

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Abstract

Assessment protocols to describe the various aspects of conformation, gait and jumping traits on a linear scale were introduced at young horse tests for Swedish Warmblood horses in 2013. The traits scored on a linear scale are assumed to be less subjective and more easily compared across populations than the traditional evaluated traits that are scored relative to the breeding goal. However, the resulting number of traits is considerable, and several of the traits are correlated. The aim of this study was to investigate the interrelationship between the different evaluated and linearly scored traits in Swedish Warmbloods using factor analysis. In total, 20,935 horses born 1996–2017 had information on evaluated traits, and 5450 of these also had linearly scored trait records assessed since 2014 when the protocol was updated. A factor analysis with varimax rotation was performed separately for evaluated and linearly scored traits using the Psych package in R. Height at withers was included in both analyses. A total of four factors for evaluated traits and 14 factors for linearly scored traits were kept for further analysis. Missing values for individual traits in horses with linearly scored trait records were imputed based on correlated traits before factor scores were calculated using factor loadings. Genetic parameters for, and correlations between, the resulting underlying factors were estimated using multiple-trait animal models in the BLUPF90 package. Heritability estimates were on a similar level as for the traits currently used in the genetic evaluation, ranging from 0.05 for the factor for linearly scored traits named L.behaviour (dominated by traits related to behaviour) to 0.59 for the factor for evaluated traits named E.size (dominated by height at withers and conformation). For both types of traits, separate factors were formed for jumping and gait traits, as well as for body size. High genetic correlations were estimated between such corresponding factors for evaluated traits and factors for linearly scored traits. In conclusion, factor analysis could be used to reduce the number of traits to be included in multiple-trait genetic evaluation or in genomic analysis for warmblood horses. It can also contribute to a better understanding of the interrelationships among the assessed traits and be useful

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to decide on subgroups of traits to be used in several multiple-trait evaluations on groups of original traits.

KEYWORDS

genetic parameters, performance test, riding horses

1 | INTRODUCTION

Traits scored by judges on a linear scale from one extreme to the other has the advantages of being less subjective and more comparable across populations than traditional evaluated traits scored with regard to the breeding goal in horses (Duensing et al., 2014). Assessments using linear scales have been implemented in several European Warmblood horse studbooks, including the Swedish Warmblood (SWB) in 2013 (Viklund & Eriksson, 2018) to provide more refined phenotyping of horses. From 2014 onwards, an updated assessment protocol has been used for linearly scored traits in SWB. The introduction of linearly scored traits markedly increased the number of traits assessed by SWB. The current genetic evaluation comprises a total of 70 traits including 59 linearly scored traits, 8 traditional evaluated traits, height at withers and 2 competition traits. Whereas the evaluated traits and height at withers are assessed at all types of tests for SWB, only 50 of the linearly scored traits are recorded at tests for 3-year-olds, and the remaining linearly scored traits exclusively at tests for older horses. Within test event, the same team of two judges visually assess the horses for both evaluated and linearly scored traits, whereas height at withers is measured in centimetres before entering the test arena.

Among the subsets of the linearly scored traits, moderate to strong correlations are expected, for example, genetic correlations ranging from -0.78 to -0.99 between the evaluated trait trot and linearly scored traits describing more refined aspects of this gait were found by Viklund and Eriksson (2018). Implementing a multiple-trait evaluation that includes this large number of linearly scored traits does not seem feasible. However, ignoring these strong correlations in genetic evaluations reduces the reliability of breeding values (Mrode, 2014). Also, not utilizing the added information from strongly correlated traits in genomic studies reduces the power of the analysis (Guo et al., 2014; Zhang et al., 2018). The linearly scored traits provide detailed information useful for horse owners when deciding on the future use of a young horse and for breeding decisions, but there are situations when more summarizing information is needed. Even though the evaluated trait scores could be seen as a form of subjective combination of different characteristics contributing to each trait, there is at present no index summarizing the

many linearly scored trait values. It would, therefore, be of interest to find a lower number of latent traits that in a meaningful way could describe the variability among conformation, gait and jumping traits assessed in SWB.

Factor analysis is a commonly used method to reduce the number of observed, and correlated, variables to a lower number of underlying factors. The method has been applied on traits scored on a linear scale in multiple studies on different species such as cattle (Kern et al., 2014), dogs (Arvelius et al., 2014) and horses (Sigurðardóttir et al., 2017). Most studies have been focused on one trait group such as conformation or behaviour traits. Moderate to strong correlations between traits in different trait groups, like conformation and gaits, have been reported for SWB (Viklund et al., 2008) and other horse populations (Koenen et al., 1995; Kristjánsson et al., 2016; Sánchez et al., 2013), and this motivates inclusion of different trait groups in the factor analysis. The breeders of SWB horses have become more specialized towards either of the disciplines show jumping and dressage in recent years, but at present, all horses shown at tests for 3-year-olds are still assessed for conformation, gait and free-jumping traits (Bonow et al., 2022). Increased knowledge about the relationship between different traits and trait groups can contribute to decision making regarding future assessments in this diverging breed.

The aims of this study were to investigate the interrelationship between the different evaluated and linearly scored traits recorded for conformation, gaits and jumping ability in SWB through factor analysis and to estimate genetic parameters for the resulting underlying factors through multiple-trait analyses.

2 | MATERIALS AND METHODS

2.1 | Animals and traits

The data provided by the Swedish Warmblood Association included records for 9722 male and 11,213 female Swedish Warmblood horses assessed at young horse tests for 3-year-olds. The studied horses were born from 1996 to 2017 and were from 1379 sires and 12,717 dams.

Height at withers in centimetres and eight evaluated traits assessed on a scale from 1 to 10 (higher values are closer to the breeding goal for those traits) were recorded

from 1999 to 2020. The eight evaluated traits were type, head–neck–body conformation, correctness of legs, walk, trot, canter, free-jumping technique and ability, and free-jumping temperament and general impression (Table S1). In addition, 50 linearly scored traits on a nine-point scale from one extreme to the other that were recorded from 2014 to 2020 were included in the data (Table S2). Each horse in the data had a complete record for evaluated traits, and most horses tested since 2014 also had a record for linearly scored traits, as both trait types were recorded at the same test events by the same team of judges. Two horses in the data were missing one sheet of the assessment protocol and were removed from the analysis of linearly scored traits. In total, 121 horses had missing values for height at withers.

2.2 | Factor analysis and imputation of missing trait values

Factor analysis was performed separately for evaluated traits and linearly scored traits using the Psych package in R (Revelle, 2022). Height at withers was included with both trait types. In each factor analysis, only horses with complete trait information were included, that is, 20,814 horses for evaluated traits together with height at withers and 4768 horses for linearly scored traits together with height at withers. The factor model used in the Psych package was $\mathbf{R} = \mathbf{F}\mathbf{F}' + \mathbf{U}^2$, where \mathbf{R} is a correlation matrix approximated by the product of a factor matrix \mathbf{F} and its transpose plus a diagonal matrix of uniqueness (proportion of variance not explained by the common factor) (Revelle, 2022). Factors were extracted using maximum likelihood and subsequently rotated by the “varimax” rotation. The varimax rotation renders factors that are easier to interpret because each original variable tends to be associated with one (or a small number) of factors and each factor represents only a small number of variables (Abdi, 2003). The optimum number of factors was determined as the number of factors with Tucker Lewis Index larger than 0.9, and root mean square of residuals (RMSR) index value of close to zero (Steiger, 1990; Tucker & Lewis, 1973), as well as number of eigenvalues above 1. Traits with factor loadings equal to or greater than an absolute value of 0.3 were considered as significant traits for that factor, and the factors were named based on the significant traits. All trait observations and factor loadings were included in prediction of factor scores, however.

To avoid removing horses from the subsequent factor score calculation due to missing values for a few of the linearly scored traits, we imputed those missing values based on information on correlated traits. From 2014 onwards, all included traits were recorded for between 97% and 100% of the horses with linearly scored trait records. The

average number of missing traits per horse was 0.25 (ranging from 0 to 19). Close to 13% of the horses were missing at least one trait observation. Imputation was thus done for the 50 linearly scored traits, and for height at withers, using the Mice package (Van Buuren & Groothuis-Oudshoorn, 2011) in R (R Core Team, 2019), by applying five multiple imputations with a maximum number of iterations of 50, using predictive mean matching (pmm) method for numeric values. After imputation, 20,935 records on height at withers and the 8 evaluated traits, and 5450 records on 50 linearly scored traits remained for factor score calculations. To calculate factor scores, we used the factor loadings, the inverse of the data covariance matrix and the trait data after imputation, and we applied the Thurstone, or regression, method (Thurstone, 1935).

2.3 | Variance component estimation

(Co)variances (genetic and residual) for the factors were estimated using the Airemlf90 software in the BLUPF90 package (Aguilar et al., 2018; Misztal et al., 2002), by average restricted maximum likelihood method (AIREML) with multiple-trait animal model including all factors for evaluated traits and one factor for linearly scored traits at a time. The same fixed effects of sex (male or female) and event (548 different place–date combinations) as described by Viklund and Eriksson (2018) were included for all traits in the model:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e}$$

where \mathbf{y} is a vector with observations for the five factor traits (one factor for linearly scored traits and four factors for evaluated traits), \mathbf{X} and \mathbf{Z} are incidence matrices relating the observations to fixed and random effects, respectively, vector \mathbf{b} contains the fixed effects, \mathbf{a} is a vector of additive genetic effects of the animals and \mathbf{e} is a vector of random residuals. The (co)variance structures of random effect were assumed to be $\mathbf{a} \sim N(0, \mathbf{G}_a \otimes \mathbf{A})$ and $\mathbf{e} \sim N(0, \mathbf{R}_0 \otimes \mathbf{I})$, where \mathbf{A} is the additive genetic relationship matrix, \mathbf{G}_a is the variance–covariance matrix of genetic effects, \mathbf{I} is an identity matrix and \mathbf{R}_0 is the residual variance–covariance matrix. The pedigree used included seven generations and in total 51,177 animals.

3 | RESULTS

3.1 | Factors for evaluated traits

The factor analysis resulted in four factors for evaluated traits (Figure 1 and Table S3) that together explained 50%

of the total variance. For the first factor for the evaluated traits, E.jump, the traits with highest factor loadings were free-jumping technique and ability and free-jumping temperament and general impression. The factor E.gaits was dominated by walk, trot and canter. The significant traits for the factor E.size were height at withers, type and head-neck-body. For the factor E.conf, the conformation traits type and head-neck-body were the most important traits.

Among the evaluated traits, the free-jumping traits were best described by the formed factors (88% of the variance explained for technique and ability and 77% for temperament and general impression at free jumping). In contrast, for correctness of legs only 6%, and for walk 24% of the variance was explained by the formed factors (Table S3).

3.2 | Factors for linearly scored traits

The factor analysis of linearly scored traits resulted in 14 factors, together explaining 42% of the total variance (Figure 2 and Table S4). There were two factors for linearly scored traits mainly related to free jumping. The factor L.jump explained more than 6% of the total variance and was dominated by 11 traits describing various aspects of jumping technique. For the factor L.quick that explained less (2%) of the variance, take-off quickness and quickness of reactivity at jumping were the most important traits. In addition, the factor L.behaviour included as significant traits both approach to assignment (focused-unfocused) and distance estimation (secure-insecure) at free jumping, but also more general behaviour (relaxed-tense).

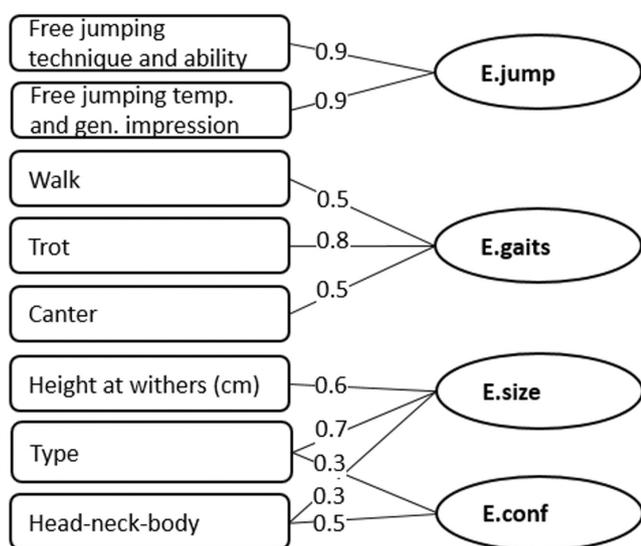


FIGURE 1 Factor loadings ≥ 0.3 for evaluated traits assessed at young horse tests for Swedish Warmbloods on four orthogonally rotated factors.

One factor was formed for each of the gaits walk (L.walk) and canter (L.canter). Trot traits loaded significantly on two factors that both explained the same amount (3%) of the total variance: L.trot and L.trot.hind, but whereas trot front leg activity and stride length were most important for the former, the traits describing position and activity of hind legs in trot loaded strongly on the latter. The factor L.direction was related to both conformation and gaits, in that it was dominated by traits describing direction of body as well as of movements and by canter balance. Also related to movements and conformation, the factor L.correct included correctness in movements and forelegs (toed-in-toed-out) as significant traits.

There were several factors for morphology: L.neck, covering shape and position of neck and shoulders, as well as L.height and L.length that were dominated by traits related to length and height of different body parts, respectively. Another factor related to body size was L.type for which type (refined-heavy) and height at withers loaded significantly. Front and hind pastern conformation (upright-weak) were the only traits that loaded strongly on the factor L.pastern.

There were large differences in the percentages of variation explained by the formed factors for different linearly scored traits, ranging from 2% to 83% (Table S4). In general, linearly scored traits related to body size and proportions, certain aspects of gaits, jumping technique and behaviour were among the best explained traits ($>60\%$) by the formed factors. Several leg and hoof conformation traits together with traits related to the backline conformation, as well as walk suppleness, had the lowest percentages of variance explained ($<10\%$).

3.3 | Heritability and correlations

Overall, heritability estimates for factors for evaluated traits were moderate to high, ranging from 0.29 for E.conf to 0.59 for E.size. For factors for linearly scored traits, heritability estimates ranged from 0.05 for L.behaviour to 0.54 for L.height (Table 1).

Genetic (r_g) and residual (r_e) correlations between factors for evaluated traits and factors for linearly scored traits, estimated using linear models, are presented in Table 2 and Table S5, respectively. The correlations were in most cases weak, with some exceptions; the strongest genetic correlations were estimated between E.jump and L.jump ($r_g = -0.96$, $r_e = -0.62$), between E.size and L.height ($r_g = -0.92$, $r_e = -0.46$) and between E.gaits and L.trot ($r_g = -0.88$, $r_e = -0.40$). All factors for evaluated traits had a strong genetic correlation with at least one factor for linearly scored traits. However, some factors for linearly scored traits, like L.length, L.correct and L.pastern,

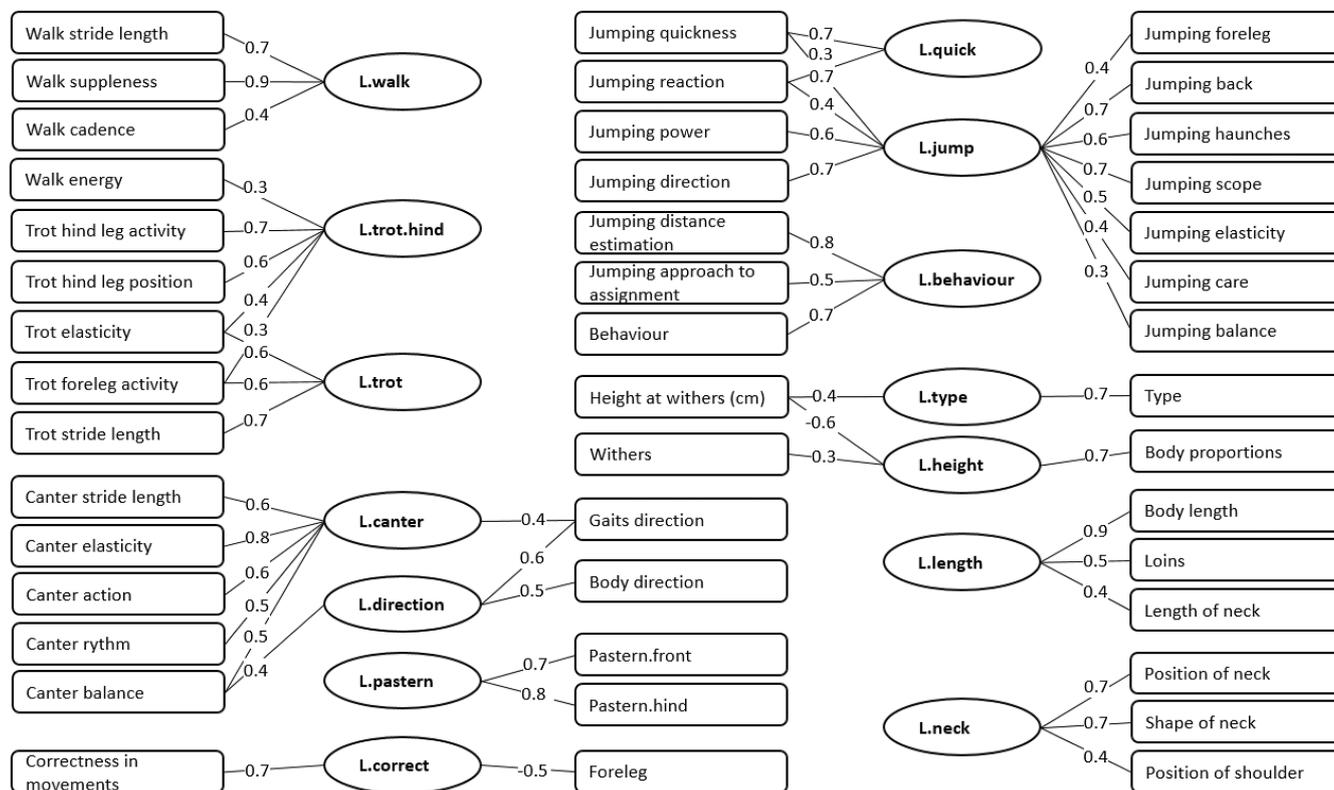


FIGURE 2 Factor loadings with absolute values ≥ 0.3 for linearly scored traits assessed at young horse tests for Swedish Warmbloods on 14 orthogonally rotated factors.

did not have a strong correlation with any of the factors for evaluated traits.

4 | DISCUSSION

Several benefits of linearly scored traits compared with the traditional evaluated trait scores have been suggested, including the potential use in future international genetic evaluations (Sperrle et al., 2016) and in the development of genomic selection of warmbloods (Wobbe et al., 2021). The linearly scored traits are also assumed to be less subjectively scored and to describe the horse in more detail, which may be especially important for optimum traits such as correctness of legs on a scale from toed-in to toed-out (Duensing et al., 2014; Viklund & Eriksson, 2018). For SWB horses, both evaluated and linearly scored traits are subjectively assessed through visual inspection by trained judges. However, whereas the intent is to evaluate the quality of the horse relative to a set goal in the former assessment, the purpose of the latter is to provide a more neutral description that could be used also if the desired characteristics of horses would change. Linearly scored scores from the same assessment can thus be used to select horses for different purposes such as dressage or show jumping. Knowledge about the optimal scores on the

linear assessment scale is then needed, as these may differ between traits, disciplines and populations.

Breeding values for linearly scored traits have been warmly welcomed by SWB breeders, who appreciate the detailed and reliable description of the linearly scored trait indices, presented in graphs (Swedish Warmblood Association, 2022). Such information is useful when matching stallion and mare, taking different strengths and weaknesses into account. However, to rank and select breeding animals efficiently based on over 50 different breeding values is not an easy task. Complementing summarizing information based also on linearly scored trait records and not only on the traditional evaluated records would be useful. The large number of traits currently evaluated for SWB, many of which are strongly correlated, which is not considered in the current single-trait genetic evaluation, calls for some means of reducing the number of traits. Benefits of utilizing correlations between traits were exemplified in a study of conformational measurements of Icelandic horses by Kristjansson et al. (2016). They showed a greater value of combinations of conformational parameters as indicators for performance, compared with single measurements.

The possibility to reduce the number of strongly correlated linearly scored traits assessed in horses was

TABLE 1 Description of factors, estimated heritability (h^2) and standard errors (SE) as subscripts, for factors for evaluated^a traits and factors for linearly scored traits for Swedish Warmblood horses.

Trait type	Factor	Higher values correspond to	h^2	
Evaluated	E.jump	Better jumping ability	0.32	0.018
	E.gaits	Better gait quality	0.53	0.018
	E.size	Taller with better conformation	0.59	0.020
	E.conf	Better conformation	0.29	0.017
Linearly scored	L.jump	Weaker, slower, more forward directed takeoff, less bent forelegs, less rounded back, tighter haunches, less scope, stiffer, less careful, slower reaction, less balanced, less secure distance estimation	0.33	0.025
	L.quick	Slower take-off and reaction	0.07	0.021
	L.behaviour	More tense and unfocused, less secure distance estimation	0.05	0.018
	L.walk	Stiffer, more uneven walk with shorter stride length	0.24	0.033
	L.trot	Less elastic trot with shorter stride length and foreleg activity	0.27	0.027
	L.trot.hind	Less elastic trot with less active hind legs positioned more behind the body	0.21	0.028
	L.canter	Less even, less balanced, flatter and less elastic canter with shorter stride length and more downhill direction of movements	0.32	0.030
	L.direction	More downhill body and gaits direction, less balanced canter	0.14	0.025
	L.correct	Less toed-out or more toed-in forelegs with more paddling or less winging movements	0.17	0.032
	L.pastern	Less upright or more weak pasterns	0.18	0.033
	L.height	Lower height at withers, more short legged, lower withers	0.54	0.031
	L.length	Shorter body, neck and loins	0.23	0.034
	L.type	Taller and heavier body type	0.35	0.040
	L.neck	Steeper shoulder, more horizontal position of neck and straighter neck shape	0.32	0.035

^aAverage heritability values and SE from the different multiple-trait analyses are presented.

TABLE 2 Genetic correlations, with standard errors as subscripts, estimated between factors for linearly scored traits and factors for evaluated traits for Swedish Warmblood horses.

Factor	Genetic correlation							
	E.jump		E.gaits		E.size		E.conf	
L.jump	-0.96	0.013	-0.21	0.041	-0.08	0.047	-0.35	0.049
L.quick	-0.43	0.122	0.05	0.109	0.31	0.119	-0.14	0.129
L.behaviour	-0.39	0.126	-0.06	0.121	-0.01	0.137	-0.22	0.153
L.walk	0.03	0.070	-0.49	0.055	0.01	0.069	0.02	0.077
L.trot	-0.19	0.054	-0.88	0.028	-0.34	0.056	-0.64	0.056
L.trot.hind	-0.01	0.071	-0.64	0.053	-0.12	0.071	-0.42	0.074
L.canter	-0.35	0.050	-0.73	0.034	-0.58	0.046	-0.55	0.054
L.direction	0.19	0.082	-0.38	0.077	-0.48	0.082	-0.43	0.089
L.correct	-0.06	0.075	0.16	0.068	0.17	0.069	-0.03	0.083
L.pastern	0.02	0.084	0.09	0.076	-0.04	0.083	0.00	0.093
L.height	-0.13	0.045	-0.24	0.038	-0.92	0.014	-0.19	0.049
L.length	-0.06	0.086	-0.07	0.079	-0.31	0.084	-0.01	0.096
L.type	0.08	0.064	-0.03	0.057	0.43	0.053	-0.18	0.068
L.neck	0.06	0.064	-0.32	0.055	-0.33	0.059	-0.64	0.052

proposed already by Samoré et al. (1997). Also, Rustin et al. (2009) suggested the possibility to use principal component analysis to reduce the information into a limited number of factors, or to construct indices based

on the traits, to avoid difficulties for breeders to interpret information about a very large number of traits. The use of factor analytical models was suggested by de Oliveira Bussiman et al. (2022) to be even more useful

than principal component models to reduce the number of morphometric traits in Campolina horses for breeding purposes. Findings from factor analysis could be applied in case of conducting several multiple-trait evaluations of groups of traits to consider genetic correlations among traits.

The loading of traits assessed in young horse tests for SWB on different factors in this study appears to follow a logical pattern. For example, several linearly scored traits related to jumping ability loaded significantly on one factor. This agrees with previously reported strong correlations between evaluated free-jumping traits and linearly scored jumping traits (Ducro et al., 2007; Viklund & Eriksson, 2018) and between linearly scored jumping traits and show-jumping performance recorded later in life (Ducro et al., 2007). Similarly, separate factors dominated by linearly scored traits related to specific gaits could be expected based on previously reported correlations with evaluated gait traits, as well as with dressage performance (Ducro et al., 2007; Viklund & Eriksson, 2018).

In a previous multiple-trait analysis of linearly scored traits related to gaits and conformation in warmbloods by Rustin et al. (2009), stride length in walk, suppleness in walk and impulsion in walk were more strongly correlated with each other than, for example, stride length in walk and stride length in trot were. Also in SWB horses, certain aspects of the gaits are assessed separately for the different gaits (e.g., walk stride length, trot stride length and canter stride length; trot elasticity and canter elasticity). Aspects such as elasticity likely share a common biological background across gaits, for example, relating to properties of connective tissue structures like tendons (Clayton & Hobbs, 2019; Verkade et al., 2020). We note that no such aspects formed factors of their own in the present study, such as a factor for stride length and another factor for elasticity. Instead, they were grouped together with other aspects of the gait into gait-specific factors.

The division into two different factors for linearly scored traits for trot was not seen for the other two gaits. Hind leg position and hind leg activity that were important for the second trot factor (L.trot.hind) are not assessed for walk or canter, which may explain the difference. For the fewer and less specific evaluated traits, a factor was formed including all three gaits, most strongly correlated (r_g of -0.49 to -0.88) with the factors for linearly scored traits dominated by gaits. The summarizing nature of the evaluated traits and the complexity behind the factors for evaluated traits are supported by the result that factors for linearly scored traits L.trot and L.canter showed moderate genetic correlations with the factors for evaluated traits dominated by size and conformation (E.size and E.conf).

It is possible that some traits are difficult to separate clearly at the assessment, even for trained judges, which may also contribute to the correlations between traits and the formation of factors. To assess several different traits related to technique at jumping may be challenging as the time span is short, for example, at the take-off. All the 11 linearly scored traits that loaded significantly on the factor L.jump were jumping traits. On the other hand, the factor L.behaviour collected traits related both to jumping and also to more general behaviour during the test. This suggests that information from free-jumping part of the evaluation may be of value for the assessment of behaviour also for horses not intended for show jumping.

The factors for linearly scored traits found in this study appear to cover similar aspects as the traditional evaluated traits, but also add aspects through factors such as body length (L.length), quickness in reaction and take-off at jumping (L.quick) and two different factors for trot (L.trot and L.trot.hind). Still, neither the factors for evaluated traits nor the factors for linearly scored traits explained more than half the variation among the traits. Linearly scored traits describing certain aspects of the conformation related to backline and leg conformation, as well as to hoof size, did not load significantly on any of the factors. This should be considered in any practical application of the results. Some traits that are not well explained by the factors may still be of importance and thus still need to be assessed and evaluated.

In the present study, especially traits related to leg and hoof conformation were poorly explained by the factors both for linearly scored and evaluated traits. Even though such traits tend to have low heritability values, they have been shown to be of importance for the health status of horses (Jönsson et al., 2014). Leg conformation traits typically have optimum values in the middle of the linearly scored scale, and more extreme values are seen as deviations from the “normal,” functional conformation. Horses with extreme leg conformation are less likely to enter a young horse test, and the more extreme values are rarely or never given for linearly scored hoof and leg conformation traits by the judges. As a consequence, relatively low standard deviations were seen for such traits in this study (Table S2). In addition, leg conformation has been shown to be weakly correlated with other conformation, gait and jumping traits in young SWB horses (Viklund et al., 2008), which may explain why leg conformation traits were not well explained by the factors in this study. In a practical situation, certain traits such as those related to back or leg conformation may thus need to be included in a genetic analysis in addition to the factors.

The level of heritability estimates for most factors was similar as those for the evaluated traits presented from

the genetic evaluation of SWB (Viklund et al., 2011). The low (<0.20) heritability estimates for factors describing behaviour and correctness of legs and movements could be expected based on previous estimates for similar traits in different horse breeds, for example, by Van Bergen and Van Arendonk (1993) and Samoré et al. (1997), and in SWB (Viklund & Eriksson, 2018).

To avoid losing factor score information for horses with one or a few missing traits, we chose to use imputation. However, the performance of the imputation depends on the correlations with other traits. In our study, certain traits such as those related to jumping technique were strongly correlated with several similar traits. For other traits for which less supporting trait information is recorded, such as those related to behaviour, the performance of the imputation can be expected to be weaker. This should be considered if implemented for estimation of breeding values, for example, by giving less weight to factor traits that are considerably influenced by imputed traits. The adopted imputation method may have influenced the results in the present study, and it should be noted that there are alternative methods for imputation that could be used, such as the principal component method presented by Josse and Husson (2016). In situations when values are not missing at random, the choice of imputation method is especially important. In the present study, we were not aware of any systematic cause of missing values, except for in the first year of recording of linearly scored traits that was omitted from the analysis.

Besides benefits for genetic evaluation and ranking of horses, knowledge about interrelationships between traits and reduction of trait number can also facilitate genomic analyses of linearly scored traits. Previous genome-wide association studies used principal component analysis or factor analysis to reduce the number of linearly scored temperament or body measurements traits in Tennessee Walking horses (Staiger, Al Abri, et al., 2016; Staiger, Albright, & Brooks, 2016) or number of accelerometer gait traits in young sport horses (Ricard et al., 2020). Furthermore, genome-wide association studies in other species such as goats and cattle could find plausible candidate region(s) or genes(s) associated with principal components or factor traits (Miles et al., 2021; Nazari-Ghadikolaei et al., 2018). This can warrant the use of our results for further studies also on genomic level such as genome-wide association studies or potentially in future application of single-step genomic selection in warmblood horses.

5 | CONCLUSIONS

Factor analysis can reduce the number of traits, especially linearly scored traits, to be included in genetic analysis in

SWB horses. Information about formed factors could help interpretation of the current estimated breeding values and enable implementation of multiple-trait evaluations as well as increase power of genomic studies. Additionally, factors obtained from the evaluated and linearly scored traits could contribute to a better understanding of interrelationships among the traits assessed in SWB horses. Some traits, such as optimum traits that are not well represented by the factors, would need to be considered separately, however.

AUTHOR CONTRIBUTIONS

S. Eriksson and W.F. Fikse designed and supervised the study. Å. Gelinder Viklund provided pre-edited data and trait information. A. Nazari-Ghadikolaei carried out the data analysis with contributions from W.F. Fikse. S. Eriksson drafted the manuscript with contributions from A. Nazari-Ghadikolaei. All authors read, edited and approved the final manuscript.

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FUNDING INFORMATION

None.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

Restrictions apply to the availability of these data, which were used under license for this study. Data are available from the authors with the permission of the Swedish Warmblood Association.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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