Deciphering cattle temperament measures derived from a four-platform standing scale using genetic factor analytic modeling

Haipeng Yu[1], Gota Morota[1*], Elfren F. Celestino, Jr.[2], Carl R. Dahlen[2], Sarah A. Wagner[2], David G. Riley[3], and Lauren L. Hulsman Hanna[2*]

[1]Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061
[2]Department of Animal Sciences, North Dakota State University, Fargo, ND 58108
[3]Department of Animal Science, Texas A&M University, College Station, Texas 77843, USA

Running title: Cattle temperament in four-platform standing scale

ORCID: 0000-0002-8923-9733 (HY) 0000-0002-3567-6911 (GM)

* Corresponding authors:

*Lauren L. Hulsman Hanna
Department of Animal Sciences
North Dakota State University
DEPT 7630, P.O. Box 6050
Fargo, North Dakota 58108 USA.
Email: lauren.hanna@ndsu.edu

*Gota Morota
Department of Animal and Poultry Sciences
Virginia Polytechnic Institute and State University
175 West Campus Drive
Blacksburg, Virginia 24061 USA.
E-mail: morota@vt.edu

Abstract

Background: The animal's reaction to human handling, also known as temperament, is critical for work safety, productivity, and welfare. Subjective phenotyping methods, such as docility score, have been traditionally used in cattle production as a means for improving the safety, productivity, and welfare of animals. Even so, subjective scales rely on the evaluator's knowledge and interpretation of temperament, which may require substantial experience. With that being said, selection based on such subjective scores may not precisely impact temperament preferences in cattle.

Results: We investigated the statistical relationships among subjective methods including docility score (DS), temperament score (TS), 12 qualitative behavior assessment (QBA) attributes along with a movement-based objective method (four-platform standing scale, FPSS) including the standard deviation of total weight on FPSS over time (SSD) and coefficient of variation of SSD (CVSSD) using 1,528 calves at weaning age. An exploratory factor analysis (EFA) identified two underlying latent variables contribute to TS and 12 QBA attributes that were named *difficult* and *easy* according to their characteristics. As DS is evaluated under constraint and other measures are not, inclusion of DS in EFA of subjective methods was not a good fit. A Bayesian confirmatory factor analysis inferred the factor scores of *difficult* and *easy* using the latent structure discovered in EFA. This was followed by fitting a pedigree-based Bayesian multi-trait model using *difficult*, *easy*, DS, SSD, and CVSSD to characterize the genetic interrelationships between subjective and FPSS measures. The estimates of heritability range from 0.17 to 0.4 with the posterior standard deviation averaging 0.06. The factors of *difficult* and *easy* exhibited a large negative genetic correlation of -0.92. DS displayed a moderate genetic correlation with *difficult* (0.36), *easy* (-0.31), SSD (0.42), and CVSSD (0.34). FPSS and DS were found to have a moderate genetic correlation with *difficult* (0.35 to 0.41) and *easy* (-0.39 to -0.31), indicating selection could be performed with either and have similar outcomes.

Conclusions: The application of genetic factor analytic model for temperament measures provided a new approach to unravel the complexity of animal behaviors. In summary, we contend that FPSS measures could increase the efficiency of genetic selection by providing automatic, objective, and consistent phenotyping measures with a lower cost, and may potentially become an alternative of DS which has been widely used in beef production.

Keywords: cattle temperament, factor analysis, four-platform standing scale, precision agriculture

Background

Temperament in cattle traditionally refers to the animal's behavior in the bail [1] or the reaction of animal to human handling [2]. Previous studies have revealed cattle temperament has a significant relationship with production, reproduction, immunity, and carcass traits [3–5], therefore genetic selection on temperament provides an opportunity to improve production and efficiency in the beef industry. Temperament is a complex trait that comprises various behavioral characteristics such as shyness-boldness, exploration avoidance, activity, sociability, and aggressiveness [6]. A set of subjective methods were first proposed to phenotype temperament, such as temperament scoring of cattle handled in a crush with head bail [1], flight distance [7], docility test [8], chute test [9], and qualitative behavior assessment (QBA) [10]. These subjective methods are able to integrate the various aspects of temperament into a single score and create a standardized test by taking advantage of the experience and interpretation of the human evaluator on cattle. This is advantageous for typical production operations due to ease of capturing data. Even so, closely working with cattle may cause potential danger for evaluators during scoring. Furthermore, there is a concern with evaluation bias in subjective methods, which makes comparison of temperament scoring methods across experiments difficult. Due to this, measurements without human interpretation, such as exit velocity [11], movement-measuring-device [12, 13], strain gauges [14], and objective chute score [15], have been tested to provide objective and quantifiable temperament measurements. Understanding how these objective measures relate to behavioral attributes is of interest, where most studies have only compared a few common subjective methods with objective methods using a standard multi-trait model [11–13, 15]. Computational limitations have also hindered further research in understanding relationship between objective and subjective methods of temperament. Therefore, this study introduces a novel, potentially cost effective objective method using a four-platform standing scale (FPSS) and investigates its relationship with subjective methods of docility score (DS), temperament score (TS), and qualitative behavior assessment (QBA) attributes. The objective of this study is to validate FPSS as measures of cattle temperament and decipher underlying genetic interrelationships by joint analyses with subjective measurements using genetic factor analytic modeling. We employed new statistical approaches, explanatory factor analysis (EFA) and confirmatory factor analysis (CFA), to overcome the computational challenges due to a large number of correlated subjective measure-

ments. To our knowledge, this is the first study to investigate the novel objective measurement FPSS using EFA and CFA for the genetic analysis of cattle temperament.

Materials and methods

Animals

From 2014 to 2017, data were collected at weaning time (late September to late October) at North Dakota State University Central Grasslands Research Extension Center (CGREC) near Streeter, North Dakota. Calves ($n = 1,528$), including 749 heifers and 779 steers were scored at the weaning age (average age was 161.0 +/- 17.0 d), were included for analysis. Calves were either sired by Angus bulls (all 4 yr) or by Hereford bulls (3 yr) and were from Angus-influenced (all 4 yr) or Hereford by Angus-influenced (2 yr) dams. Calves were assigned to one of two primary breeds (50% or greater) based on known breed percentages, which resulted in 1,346 Angus- and 182 Hereford-based calves. A pedigree including 109,703 animals was formed using the information of dams and records of complete ancestry for registered bulls provided by the American Angus Association and American Hereford Association. All procedures involved in data collection were reviewed and approved by the Institutional Animal Care and Use Committee of North Dakota State University.

Experiment procedure

The details of temperament evaluation procedure during the first year data collection was previously described by Hanna et al. [16]. All years of data collection followed the same procedure described except blood draw grouping was not continued as it was found to have minimal effect on temperament scoring [16]. Briefly, calves were moved through the working pens to the evaluation areas and then sorted to different holding pens for management. Four evaluators were randomly assigned two of three subjective scoring methods (DS, TS, and QBA) prior to evaluation and retained those methods each year of participation in the study. Some evaluators were not able to return for all years of the study, which resulted in a total of 11 evaluators over the 4 yr period. Averages for each subjective method that had at least three evaluator scores were used in this study. DS is a six point scale where one and six refer to calm and aggressive, respectively [17]. The evaluation of DS was done at the silencer chute with the head of the calf caught and each calf was evaluated less than one minute. Following the evaluation of DS, weaning weight of the calf was recorded when its

body was squeezed. Upon released from silencer chute, the calf then entered FPSS (Pacific Industrial Scale, British Columbia, Canada) to collect the weight shifts on each quadrant. Following FPSS, TS and 12 QBA attributes were evaluated in the outside testing area, while a single human handler calmly interacted with the calf. The presence of this human handler was intended to facilitate evaluation of the different aspects of these subjective methods. Following Sant'Anna et al. [10], TS is a five point scale, with a neutral scale three removed, where one indicates calm and five indicates wild or aggressive. The 12 attributes of QBA consists active, agitated, apathetic, attentive, calm, curious, distressed, fearful, happy, irritated, positive, and relaxed [10], which can be grouped into groups of positive and negative behaviors. Each attributes was scored on a 136 mm line indicating the extent of expression, where the far left and far right refer to no expression and complete expression of the attribute, respectively. Each calf was measured less than three minutes and then sorted into a holding pen for management purposes. The average scoring of all evaluators was used for the downstream analysis for DS, TS and 12 QBA attributes.

FPSS Measurements

The FPSS provides a novel method of quantifying cattle temperament while also weighing the animal (Figure S1 in Additional File 1). The FPSS was connected to a computer controlled by a worker. Prior to the calf entering the scale, the worker first enters the tag number of the calf. Once the calf is on the scale, the worker starts recording weights on the four-platform for at least 45 seconds. The FPSS is able to record approximately 15 records per second. The worker also keeps a log of any issues encountered with the calf, large movements, and where those issues fall in the records. Following data collection, FPSS records of each animal were reviewed for quality before used in subsequent analyses. To do this, the ideal start point for a given animal's scale records (i.e., when the animal is considered as completely standing on the scale) was identified following Figure 1. Once the start point was identified, that point and subsequent 499 records following were used to calculate the mean and standard deviation of the total weight. The standard deviation of FPSS measurements (SSD) and the coefficient of variation of the SSD (CVSSD = SSD divided by mean) were used as temperament scores for subsequent analyses. The CVSSD was calculated as there was concern the actual weight of animal would bias the SSD as larger animals may naturally have larger standard deviations in records.

Exploratory factor analysis

We fitted EFA using subjective measurements including TS and 12 QBA attributes (t = 13). The logic of using EFA is to discover the underlying latent variables or factors (q) to represent observed measurements. Thereby, a network structure between latent variables and phenotypes was first explored and further used for the downstream analysis. An EFA model is given as a function of latent factor scores

$$\mathbf{T} = \mathbf{\Lambda F} + \boldsymbol{\epsilon}, \tag{1}$$

where $\mathbf{T}$ is a $t \times n$ phenotypic matrix, $\mathbf{\Lambda}$ is the $t \times q$ factor loading matrix, $\mathbf{F}$ is the $q \times n$ latent factor scores, and $\boldsymbol{\epsilon}$ is the $t \times n$ matrix of specific effects. The variance-covariance structure of $\mathbf{T}$ is

$$var(\mathbf{T}) = \mathbf{\Lambda \Phi \Lambda'} + \mathbf{\Psi}, \tag{2}$$

where $\mathbf{\Phi}$ is the variance of factor scores and $\mathbf{\Psi}$ is the variance of specific effects. With the assumption of $\mathbf{F} \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$, a vector of phenotypes follows a multivariate Gaussian distribution $\mathbf{t}_i \overset{iid}{\sim} \mathcal{N}(\mathbf{0}, \mathbf{\Sigma})$, where i refers to ith individual and $\mathbf{\Sigma} = \mathbf{\Lambda \Lambda'} + \mathbf{\Psi}$. The log-likelihood of the factor analysis model is

$$\mathcal{L}(\mathbf{\Lambda}, \mathbf{\Psi}|\mathbf{T}) = -\frac{nq}{2} log 2\pi - \frac{n}{2} log(\mathbf{\Sigma}) - \frac{n}{2} log(\mathbf{T'\Sigma^{-1}T}).$$

The number of underlying latent variables q was determined using a parallel analysis [18]. In brief, the eigenvalues of the observed data and simulated data conditioned on the observed data were computed to extract latent variables until the observed data had a smaller eigenvalue than the simulated data. Parameters $\mathbf{\Lambda}$ and $\mathbf{\Psi}$ were estimated by maximizing the log-likelihood of $\mathcal{L}(\mathbf{\Lambda}, \mathbf{\Psi}|\mathbf{T})$ using an iteration method. We used the R package psych [19] to fit EFA. We posited that DS may not align with other subjective measures since it is collected in a confined setting, whereas other subjective measures used in this study were in a pen with free movement. An additional EFA was fitted including DS to confirm this assumption.

Bayesian confirmatory factor analysis

Using results from the EFA as a prior, a confirmatory factor analysis (CFA) under the Bayesian framework was fitted following the procedure described in Yu et al. [20] to obtain factor scores. We assigned the following priors for equations (1) and (2).

$$\boldsymbol{\Lambda} \sim \mathcal{N}(0, 0.01)$$

$$\boldsymbol{\Phi} \sim \mathcal{W}^{-1}(\mathbf{I_{22}}, 3)$$

$$\boldsymbol{\Psi} \sim \Gamma^{-1}(1, 0.5).$$

The blavaan R package [21] coupled with the rstan R package [22] were applied to solve the Bayesian CFA model. A Markov chain Monte Carlo (MCMC) with 6,000 samples and 3,000 burn-in was adapted to infer the model parameters and in total three MCMC chains were sampled. The model convergence was validated using the combination of trace plots and a potential scale reduction factor (PSRF) less than 1.2 [23]. A PSRF compares the estimated variances across chains and within the chain, where a large difference indicates additional Gibbs samplings may be required. This was followed by calculating the factor scores ($\mathbf{F}$) of latent variables using the Gibbs samples. When factor scores are considered missing, the $\mathbf{F}$ is sampled from a conditional distribution of $p(\mathbf{F}|\boldsymbol{\theta}, \mathbf{T})$ [24] using a data augmentation [25], where $\boldsymbol{\theta}$ refers to the unknown parameters $\boldsymbol{\Lambda}$, $\boldsymbol{\Phi}$, and $\boldsymbol{\Psi}$. The factor scores of latent variables were summarized from the posterior mean of $\mathbf{F}$ and considered as new phenotypes in the downstream analysis.

Bayesian multivariate best linear unbiased prediction

We used a pedigree-based Bayesian multivariate best linear unbiased prediction model to perform genetic analysis of SSD, CVSSD, DS, and latent variables.

$$\mathbf{Y} = \boldsymbol{\mu} + \mathbf{Xb} + \mathbf{Zu} + \boldsymbol{\epsilon},$$

where $\mathbf{Y}$ is a vector of factor scores with individuals ordered within traits, $\mathbf{X}$ is the incidence matrix of fixed effects, $\mathbf{Z}$ is the incidence matrix relating individuals with additive genetic effects, $\boldsymbol{\mu}$ is the vector of intercept, $\mathbf{b}$ is the vector of fixed effects, $\mathbf{u}$ is the vector of additive genetic effects, and $\boldsymbol{\epsilon}$ is the vector of residuals. The incidence matrix $\mathbf{X}$ included primary breed and sex following Hanna et al. [16]. The joint distribution of $\mathbf{u}$ and $\boldsymbol{\epsilon}$ follows a multivariate normal

$$\begin{pmatrix} \mathbf{u} \\ \boldsymbol{\epsilon} \end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix} \mathbf{0} \\ \mathbf{0} \end{pmatrix}, \begin{pmatrix} \boldsymbol{\Sigma}_{\boldsymbol{u}} \otimes \mathbf{A} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\Sigma}_{\boldsymbol{\epsilon}} \otimes \mathbf{I} \end{pmatrix}\right],$$

where $\mathbf{A}$ refers to the numerator relationship matrix, $\mathbf{I}$ is an identity matrix, $\boldsymbol{\Sigma}_{\boldsymbol{u}}$ and $\boldsymbol{\Sigma}_{\boldsymbol{\epsilon}}$ are genetic and residual variance-covariance matrices, respectively. Flat priors were assigned to $\boldsymbol{\mu}$ and $\mathbf{b}$. Inverse Wishart distributions with identity scale matrix and 5 degrees of freedom were assigned for $\boldsymbol{\Sigma}_{\boldsymbol{u}}$ and $\boldsymbol{\Sigma}_{\boldsymbol{e}}$. The MTM R package (https://github.com/QuantGen/MTM) was employed to infer the parameters in the Bayesian multi-trait linear mixed model and obtain the posterior distribution of these parameters. This was followed by estimating genetic correlations and heritabilities using posterior mean estimates from 10,000 Gibbs samples with 3,000 burn-in and a thinning rate of 5. The model convergence was checked using the trace plots.

Results

Phenotypic correlation

The phenotypic correlations between all subjective and objective measurements are displayed in Figure 2. The subjective measurement TS showed a large positive correlation with active, fearful, agitated, irritated, and distressed, whereas, a large negative correlation with relaxed, calm, and apathetic was found. Among 12 QBA attributes, we observed large positive correlations between similar attributes of temperament (e.g., relaxed and calm) and large negative correlations for opposite aspects of temperament (e.g., fearful and calm).

Latent structure

The parallel analysis scree plot discovered the first two factors as latent groups (Figure S2 in Additional File 1). The EFA loadings in Figure 3 further identified these two latent groups can be interpreted as *difficult* (factor 1) and *easy* (factor 2) due to loading values. The descriptors *difficult* and *easy* were identified because we observed factor 1 has higher loadings for negative temperament attributes (i.e., TS, active, fearful, agitated, irritated, and distressed) and factor 2 has higher loadings for positive temperament attributes (i.e., relaxed, calm, attentive, positive, curious, apathetic, and happy). According to Figure 3, we retained the largest positive loadings for each latent variable (> 0.5). The final latent structure between factors and phenotypes is shown in Figure 4. The EFA factor loadings including DS is displayed in Figure S3 in Additional File 1. As expected, we found that both factors 1 and 2 have low loadings for DS.

The standardized factor loading coefficients and their posterior standard deviations from CFA assuming latent structure shown in Figure 4 are presented in Table 1. The standardized factor loading coefficients can be interpreted as regression coefficients. Overall, we found two factors have strong contributions to 13 subjective measurements. The factor *difficult* presented a positive strong loading to TS (0.861), active (0.820), fearful (0.840), agitated (0.937), irritated (0.844), and distressed (0.607), suggesting difficult is a comprehensive representation of undesirable aspects of temperament. The factor *easy* showed a positive

strong loading to relaxed (0.968), calm (0.982), positive (0.636), curious (0.514), apathetic (0.761), and happy (0.730), indicating an increase of *easy* can result in more desirable temperament.

Genetic relationships among temperament measurements

The estimates of heritability (diagonals) and genetic correlation coefficients (off-diagonals) among SSD, CVSSD, DS, and two factors are shown in Figure 5. The largest negative genetic correlation was observed between *difficult* and *easy* with a posterior standard deviation of 0.02. In reference to DS, SSD, and CVSSD, *difficult* and *easy* moderate genetic correlations with a posterior standard deviation of 0.16. Intuitively, *difficult* had positive genetic correlations (Figure 5) with DS, SSD, and CVSSD indicating difficulty of handling increased with increasing values of those variables, respectively. Likewise, *easy* had negative genetic correlations with all three variables. The subjective measure of DS showed a positive genetic correlation with objective measures SSD and CVSSD, along with a posterior standard deviation of 0.16 and 0.17, respectively. Thus, a selection on DS measurement may also increase SSD and CVSSD measurements. The two objective measurements SSD and CVSSD showed the largest positive genetic correlation with a posterior standard deviation of 0.06. Among all five measurements, we found *difficult* and *easy* showed the largest heritability estimates. The subjective measure DS showed larger heritability estimates than SSD and CVSSD. Heritability estimates of SSD and CVSSD were similar. All heritability estimates had a posterior standard deviation of about 0.06.

Discussion

Temperament measurements

Previous studies reported the estimate of chute score heritability, similar with DS in this study, ranged from 0.11 to 0.34 [8, 26–28]. Burrow and Corbet [29] suggested the objective methods have higher heritabilities than subjective methods. However, our findings show FPSS measures have slightly lower heritabilities than subjective methods (Figure 5). Haskell et al. [5] reviewed the studies using objective method of flight speed (exit velocity) and found it has a heritability ranges from 0.05 to 0.70. As suggested by previous studies, the estimate of heritability varied with studies based on the population's phenotypic variation, which could be caused by the evaluation bias across experiments, different measurement protocols, and breed differences.

Most subjective measures have been found to have positive genetic correlations in previous studies. Grandin [30] reported a positive correlation between docility test and chute test using Limousin cattle. A positive genetic correlation between race score and crush score (0.530) was detected by Turner et al. [31] in *Bos taurus* cattle. Sant'Anna and da Costa [10] discovered a positive genetic correlation between flight speed and temperament index (0.49), which is the first principle component derived from QBA attributes in principle component analysis. An analogous correlation has been detected in this study, where DS showed a positive genetic correlation with *difficult* (0.36), and a negative genetic correlation with *easy* (-0.31) as shown in Figure 5. *Difficult* and *easy* exhibited a large negative genetic correlation (-0.92) which is expected based on the pattern of the temperament measures they loaded to. In this study, subjective methods of DS and *difficult* displayed a moderate positive genetic correlation with objective measurements of SSD (0.42 and 0.41) and CVSSD (0.34 and 0.35). Turner et al. [31] reported the flight speed has a positive genetic correlation with race score (0.210) and crush score (0.321). Parham et al. [32] found the exit score and exit velocity capture the same temperament behavior based on a high genetic correlation (0.81). A moderate genetic correlation between flight speed and chute test score has been reported by previous studies [28, 33]. These genetic correlations may vary with the differences in breeds, beef production system, evaluator design, and/or the number of traits included in a multi-trait analysis. However, genetic correlations found in this study are consistent with previous studies. DS used in this study, which is also known as chute score [30],

has been widely used in the cattle industry due to its convenience. However, the application of DS is still relying on the human evaluator, which suggests a lack of automation and consistency [34, 35]. Furthermore, DS is the only measurement of temperament with the animal under a restrained condition in contrast with other measurements. A poor loading from two factors in Figure S3 in Additional File 1 suggested DS measures different aspects of temperament than other subjective methods. Therefore, we did not combine DS with other subjective methods. Because DS and the two FPSS measures showed similar correlations with *difficult* and *easy* latent variables, the use of FPSS over DS is preferred. This is because the FPSS measures provide automatic, objective, accurate, and consistent measures of temperament. It is unlikely, however, that replacement of current scales in cattle production will occur soon due to this. However, the theory of using movement-based scores for temperament has been supported by Sebastian et al. [13] and Bruno et al. [15], indicating that replacement of DS with a cost-effective movement-based measure is feasible for genetic selection purposes. Even though DS and FPSS measures identify similar selection on *difficult* and *easy* attributes based on pedigree, it is unclear if similar biological pathways or systems are being selected on. Expanding this work to include molecular data is needed to clarify these relationships further.

Factor analytic model

Phenotypes are often correlated at the genetic level due to the pleiotropic effect or the linkage disequilibrium among quantitative trait loci. The multivariate modeling has been widely used to model correlated structure by taking the advantage of the genetic or environmental covariance between phenotypes [36, 37]. The standard multi-trait approach has been proven to be useful for a trait with low heritability or having scarce records [38]. However, it faces a computational challenge when the number of phenotypes included is large. Thus, dimensional reduction methods play an important role in handling high-dimensional phenotypes.

One commonly used approach to study temperament measures is principal component analysis (PCA). This approach calculates principal components (PCs) from a linear combination of observed phenotypes by maximizing the total variance. Napolitano et al. [39] and Fleming et al. [40] applied PCA to analyze QBA with the aim of studying dairy buffalo behavior and horse behavior during endurance ride, respectively. Sant'Anna and da Costa [10] extracted the first principal component from QBA and used it as a new phenotype to study cattle temperament. These studies all suggested traits associated with calm and agitated have a large

contribution to the first principle component, which are two extreme characteristics of temperament. The validity of PCs derived from PCA in capturing animal behaviors of both calm and agitated have been supported by the significant correlations with other temperament methods in several studies [10, 41]. One of the favorable features of QBA is its comprehensive description of temperament by measuring different behaviors. However, the integration of all QBA attributes using PCs with extremely opposite measures (e.g., calm and agitated) may not be desirable because PCA maximizes the total variance, not the variance due to the common signal among measurements. Consequently, selection for temperament based on PCs may be accompanied by substantial risk. Thus, we employed factor analytic modeling for the first time to study temperament measures, which provides a novel approach to investigate multi-phenotypes. The idea behind factor analytic modeling is to represent the observed phenotypes using the unobserved latent variables or factors by maximizing the common variance between correlated phenotypes. When the number of underlying factors are unknown, it is possible to estimate from the data. For instance, de los Campos et al. [42] performed multi-trait analysis using a factor structure under the Bayesian framework. Alternatively, we can apply a CFA model, when the latent structure is assumed to be known. Penãgaricano et al. [43] investigated the interrelationships of five latent variables extracted from 19 traits in swine using CFA. Similarly, a Bayesian CFA combined with Bayesian Network was employed to characterize the wide spectrum of 48 rice phenotypes in Yu et al. [20]. These studies determined the latent structure by leveraging the prior biological knowledge between factors and phenotypes. Although the factor analytic model has been applied in animal and plant breeding, there is still paucity of its application to a temperament research.

In this study, we leveraged the combination of EFA and CFA models to identify the mapping between underlying factors and temperament measures, and performed genetic analysis of inferred factors scores. The EFA model aims at estimating the degree of the contributions of factor to phenotypes, while cross-loading (multiple factors contribute to the same phenotype) is allowed. Using the factor loading coefficients, we inferred the latent structure by removing cross-loading. The combination of EFA and CFA modeling relied on a data-driven method to detect the mapping between factors and phenotypes, which is a common case in practice when prior biological knowledge is not available. In this study, we identified two factors *difficult* and *easy* from TS and 12 QBA. This corroborates the findings from previous studies using PCA, where the first principle component has been heavily influenced by both calm and agitated related traits [10, 39, 40].

Conclusions

In conclusion, this study showed the validity of a novel cost-effective objective temperament measurement of FPSS. FPSS and DS capture the same direction of behaviors with *difficult*, and opposite direction with *easy*. We presented a combination of the factor analytic model and multivariate analysis that allows us to decipher the interrelationships among temperament measurements. We contend that the multivariate factor analytic model applied to the current cattle temperament study provides a new avenue to unravel the complexity of animal behaviors.

Availability of data and materials

The datasets used in the current study are available from the co-corresponding author Lauren L. Hulsman Hanna: auren.hanna@ndsu.edu

Abbreviations

CFA: Confirmatory Factor Analysis

CGREC: Central Grasslands Research Extension Center

CVSSD: Coefficient of Variation of SSD

DS: Docility Score

EFA: Exploratory Factor Analysis

FPSS: Four-platform Standing Scale

MCMC: Markov chain Monte Carlo

PCA: Principal Component Analysis

PCs: Principal Components

PSRF: Potential Scale Reduction Factor

QBA: qualitative behavior assessment

SSD: standard deviation of total weight on FPSS

TS: Temperament Score

Acknowledgements

The authors wish to express their gratitude to the Central Grasslands Research Extension Center director and staff for their assistance with this project, specifically Bryan Neville, Kevin Sedivec, Stephanie Becker, Jessalyn Bachler, Cody Molle, and Rodney Schmidt. Additionally, data collection for this manuscript would not have been possible without the assistance of Kelsey Amborn, Friederike Baumgaertner, Nayan Bhowmik, Dani Black, Justin Crosswhite, Mellissa Crosswhite, Sarah Cushing, Erin Gaugler, Ashley Giedd, Michael Gonda, Lauren Goetze, Jordan Hieber, Alexis Hoelmer, Logan Hulst, Leah Maertens, Kacie McCarthy, Mikayla Miller, Nicolas Negrin, Blaine Novack, William Ogdahl, Nathan Olson, Felipe da Silva, Andrea Strong, Xin Sun, and Sarah Underdahl.

Funding

This work was supported by the North Dakota Agricultural Experiment Station funds to LLHH.

Author Information

Authors' contributions

This temperament study was conceived and implemented by LLHH, CRD, SAW, and DGR. EFC performed data entry and audit of raw temperament data and pedigree. HY and GM conceptualized applying factor analytic modeling. HY performed the statistical analysis, initial interpretations of results, and drafted the manuscript. HY, GM, EFC, CRD, SAW, DGR, and LLHH revised the manuscript. All authors read and approved the final manuscript.

Ethics approval and consent to participate

All procedures were reviewed and approved by the Institutional Animal Care and Use Committee of North Dakota State University (protocols A15015 and A18005).

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Table

Table 1: Standardized factor loading and corresponding posterior standard deviation from the Bayesian confirmatory factor analysis.

Latent Variable	Observed Phenotype	Loading	Posterior standard deviation
Difficult	TS	0.861	0.007
Difficult	Active	0.820	0.010
Difficult	Fearful	0.840	0.008
Difficult	Agitated	0.937	0.004
Difficult	Irritated	0.844	0.009
Difficult	Distressed	0.607	0.016
Easy	Relaxed	0.968	0.002
Easy	Calm	0.982	0.002
Easy	Attentive	0.079	0.025
Easy	Positive	0.636	0.015
Easy	Curious	0.514	0.019
Easy	Apathetic	0.761	0.011
Easy	Happy	0.730	0.012

Figures

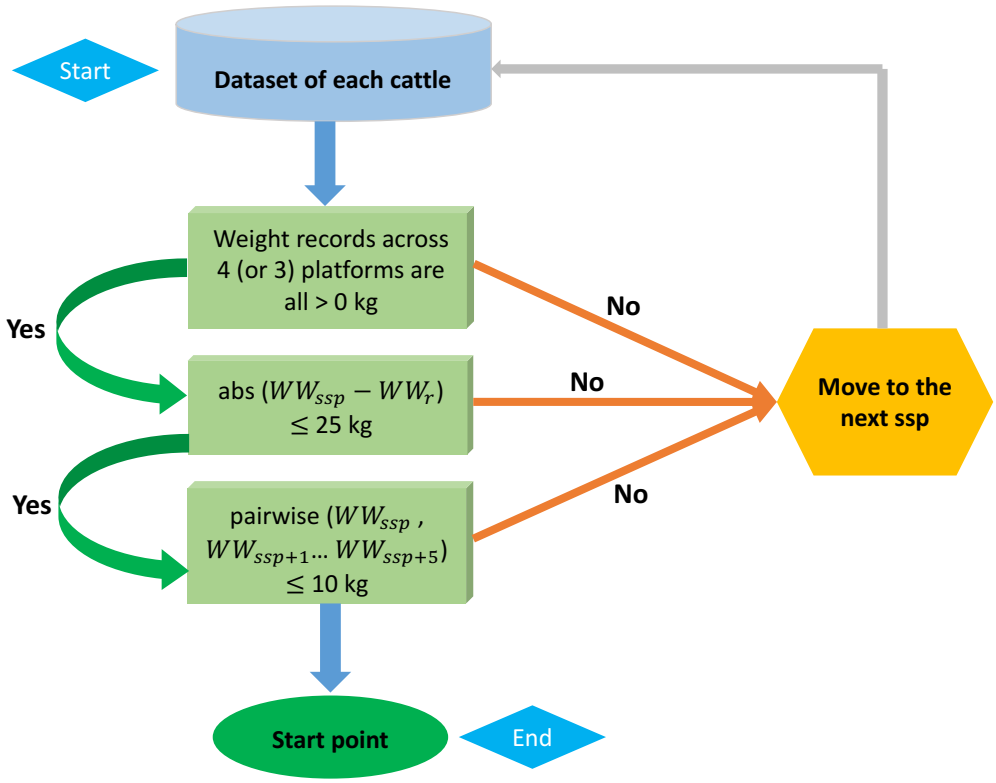

Figure 1: A flow of criteria to identify the start point of four-platform standing scale measurement. The abs and pairwise refer to the absolute difference and pairwise absolute difference, respectively. WW_{ssp} denotes the weaning weight at current suspected start point (ssp) and WW_{ssp+i} is the weaning weight at the following ith point of ssp, where $i = 1$ to 5. WW_r is weaning weight recorded in chute system.

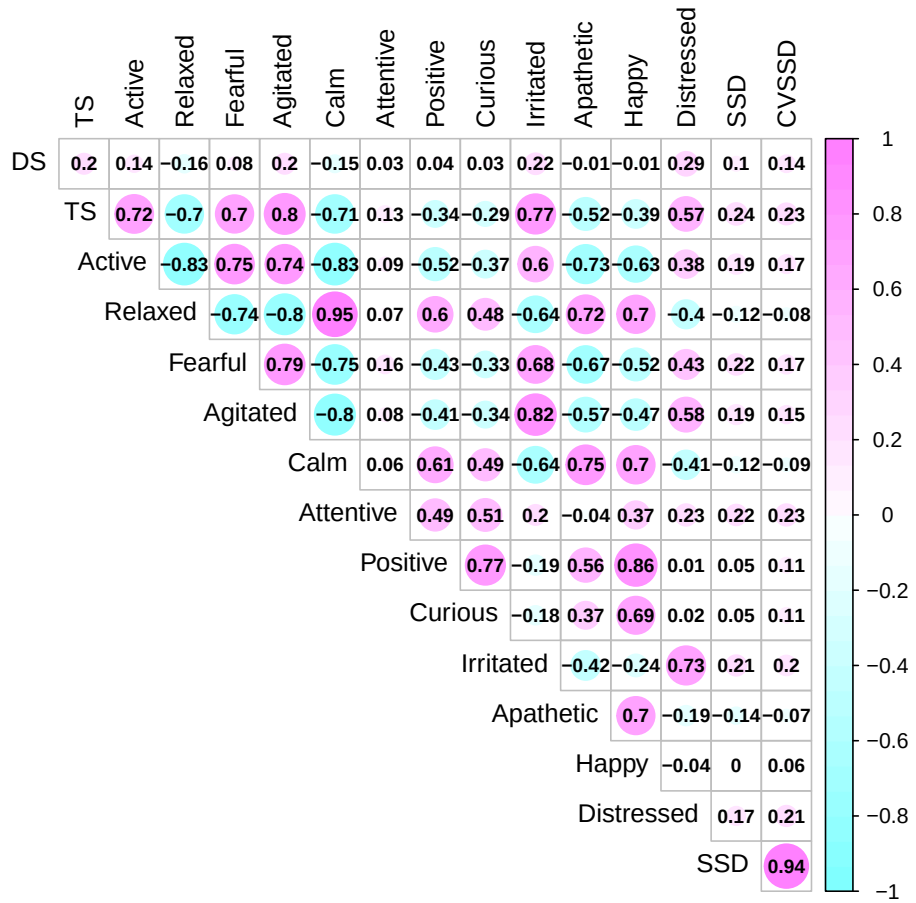

Figure 2: Phenotypic Pearson correlation coefficients between temperament measurements including temperament score (TS), docility score (DS), 12 qualitative behavior assessment attributes, and movement-based scores using four-platform standing scale standard deviation (SSD) and its coefficient of variation (CVSSD).

	Factor1	Factor2
TS	0.83	−0.14
Active	0.76	−0.42
Relaxed	−0.79	0.52
Fearful	0.79	−0.28
Agitated	0.89	−0.21
Calm	−0.80	0.52
Attentive	0.28	0.55
Positive	−0.22	0.88
Curious	−0.16	0.74
Irritated	0.88	0.05
Apathetic	−0.57	0.54
Happy	−0.32	0.88
Distressed	0.69	0.22

Figure 3: Factor loadings between factors and phenotypes derived from the explanatory factor analysis using temperament score (TS) and 12 qualitative behavior assessment attributes.

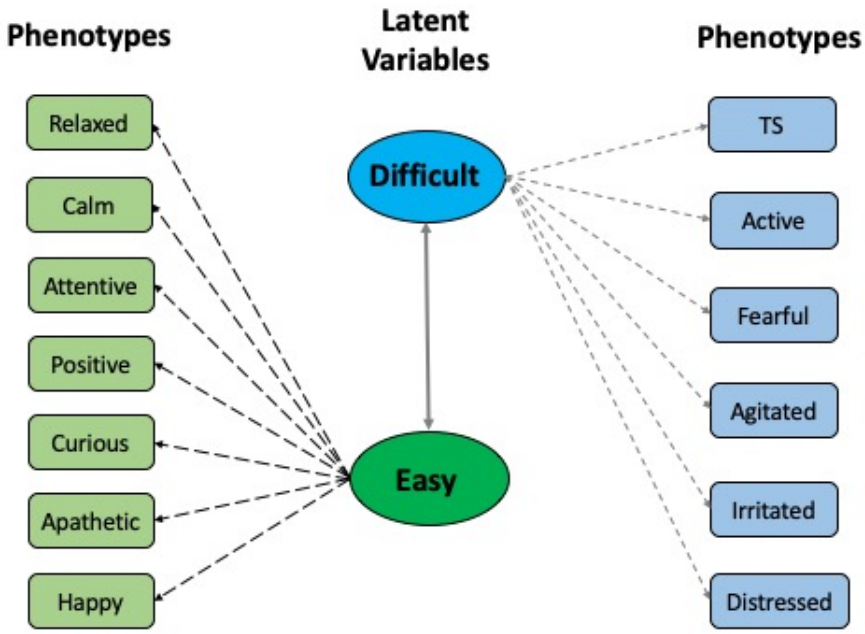

Figure 4: The latent structure between two factors and 12 qualitative behavior assessment attributes.

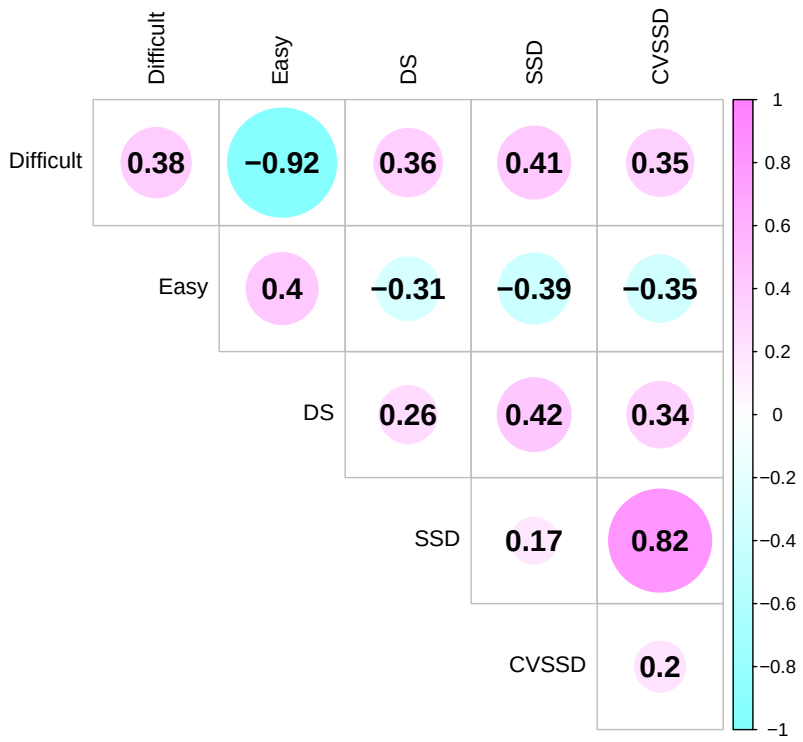

Figure 5: Genetic correlation estimates between latent variables (*Difficult* and *Easy*) and temperament measurements including docility score (DS), standard deviation of total weight on scale over time (SSD), and coefficient of variation of SSD (CVSSD). The diagonal elements are the heritability estimates.

Author details

References

1. Tulloh, N.: Behaviour of cattle in yards. ii. a study of temperament. Animal Behaviour **9**(1-2), 25–30 (1961)
2. Burrow, H., Dillon, R.: Relationships between temperament and growth in a feedlot and commercial carcass traits of bos indicus crossbreds. Australian Journal of Experimental Agriculture **37**(4), 407–411 (1997)
3. King, D., Pfeiffer, C.S., Randel, R., Welsh Jr, T., Oliphint, R., Baird, B., Curley Jr, K., Vann, R., Hale, D., Savell, J.: Influence of animal temperament and stress responsiveness on the carcass quality and beef tenderness of feedlot cattle. Meat Science **74**(3), 546–556 (2006)
4. Burdick, N., Randel, R., Carroll, J., Welsh, T.: Interactions between temperament, stress, and immune function in cattle. International Journal of Zoology **2011** (2011)
5. Haskell, M.J., Simm, G., Turner, S.P.: Genetic selection for temperament traits in dairy and beef cattle. Frontiers in Genetics **5**, 368 (2014)
6. Réale, D., Reader, S.M., Sol, D., McDougall, P.T., Dingemanse, N.J.: Integrating animal temperament within ecology and evolution. Biological Reviews **82**(2), 291–318 (2007)
7. Fordyce, G., Goddard, M., Seifert, G.: The measurement of temperament in cattle and the effect of experience and genotype. In: Proceedings of the Australian Society of Animal Production, vol. 14, pp. 329–32 (1982)
8. Le Neindre, P., Trillat, G., Sapa, J., Ménissier, F., Bonnet, J., Chupin, J.: Individual differences in docility in limousin cattle. Journal of Animal Science **73**(8), 2249–2253 (1995)
9. Tier, B., Henshall, J., McSweeny, J.: Potential for improving the docility of limousin cattle in australia. In: Proceedings of the Association for the Advancement of Animal Breeding and Genetics, vol. 14, pp. 345–347 (2001)
10. Sant'Anna, A.C., da Costa, M.J.P.: Validity and feasibility of qualitative behavior assessment for the evaluation of nellore cattle temperament. Livestock Science **157**(1), 254–262 (2013)
11. Burrow, H., Seifert, G., Corbet, N.: A new technique for measuring temperament in cattle. In: Proceedings of the Australian Society of Animal Production, vol. 17, pp. 154–157 (1988)
12. Stookey, J., Nickel, T., Hanson, J., Vandenbosch, S.: A movement-measuring-device for objectively measuring temperament in beef cattle and for use in determining factors that influence handling. Journal of Animal Science **72**(Suppl 1), 207 (1994)
13. Sebastian, T., Watts, J., Stookey, J., Buchanan, F., Waldner, C.: Temperament in beef cattle: Methods of measurement and their relationship to production. Canadian Journal of Animal Science **91**(4), 557–565 (2011)
14. Schwartzkopf-Genswein, K., Stookey, J., Welford, R.: Behavior of cattle during hot-iron and freeze branding and the effects on subsequent handling ease. Journal of Animal Science **75**(8), 2064–2072 (1997)
15. Bruno, K., Vanzant, E., Vanzant, K., Altman, A., Kudupoje, M., McLeod, K.: Relationship between quantitative measures of temperament and other observed behaviors in growing cattle. Applied Animal Behaviour Science **199**, 59–66 (2018)
16. Hanna, L.L.H., Hieber, J.K., Yu, H., Celestino Jr, E.F., Dahlen, C.R., Wagner, S.A., Riley, D.G.: Blood collection has negligible impact on scoring temperament in angus-based weaned calves. Livestock Science, 103835 (2019)
17. Federation, B.I.: Uniform guidelines for beef improvement programs. Beef improvement federation, 9th edition. revised 2018 (2018)
18. Horn, J.L.: A rationale and test for the number of factors in factor analysis. Psychometrika **30**(2), 179–185 (1965)
19. Revelle, W.: Psych: Procedures for Psychological, Psychometric, and Personality Research. Northwestern University, Evanston, Illinois (2018). Northwestern University. R package version 1.8.12. https://CRAN.R-project.org/package=psych
20. Yu, H., Campbell, M.T., Zhang, Q., Walia, H., Morota, G.: Genomic bayesian confirmatory factor analysis and bayesian network to characterize a wide spectrum of rice phenotypes. G3: Genes, Genomes, Genetics **9**(6), 1975–1986 (2019)
21. Merkle, E., Rosseel, Y.: blavaan: Bayesian structural equation models via parameter expansion. Journal of Statistical Software, Articles **85**(4), 1–30 (2018). doi:10.18637/jss.v085.i04
22. Carpenter, B., Gelman, A., Hoffman, M.D., Lee, D., Goodrich, B., Betancourt, M., Brubaker, M., Guo, J., Li, P., Riddell, A.: Stan: A probabilistic programming language. Journal of Statistical Software **76**(1) (2017)
23. Brooks, S.P., Gelman, A.: General methods for monitoring convergence of iterative simulations. Journal of Computational and Graphical Statistics

7(4), 434–455 (1998)

24. Lee, S.-Y., Song, X.-Y.: Basic and Advanced Bayesian Structural Equation Modeling: With Applications in the Medical and Behavioral Sciences. John Wiley & Sons, Hoboken, New Jersey (2012)
25. Tanner, M.A., Wong, W.H.: The calculation of posterior distributions by data augmentation. Journal of the American Statistical Association **82**(398), 528–540 (1987)
26. Kadel, M.J., Johnston, D.J., Burrow, H.M., Graser, H.-U., Ferguson, D.M.: Genetics of flight time and other measures of temperament and their value as selection criteria for improving meat quality traits in tropically adapted breeds of beef cattle. Australian Journal of Agricultural Research **57**(9), 1029–1035 (2006)
27. Beckman, D., Enns, R., Speidel, S., Brigham, B., Garrick, D.: Maternal effects on docility in limousin cattle. Journal of Animal Science **85**(3), 650–657 (2007)
28. Hoppe, S., Brandt, H., König, S., Erhardt, G., Gauly, M.: Temperament traits of beef calves measured under field conditions and their relationships to performance. Journal of Animal Science **88**(6), 1982–1989 (2010)
29. Burrow, H., Corbet, N.: Genetic and environmental factors affecting temperament of zebu and zebu-derived beef cattle grazed at pasture in the tropics. Australian Journal of Agricultural Research **51**(1), 155–162 (2000)
30. Grandin, T.: Behavioral agitation during handling of cattle is persistent over time. Applied Animal Behaviour Science **36**(1), 1–9 (1993)
31. Turner, S., Navajas, E., Hyslop, J., Ross, D., Richardson, R., Prieto, N., Bell, M., Jack, M., Roehe, R.: Associations between response to handling and growth and meat quality in frequently handled bos taurus beef cattle. Journal of Animal Science **89**(12), 4239–4248 (2011)
32. Parham, J.T., Tanner, A.E., Barkley, K., Pullen, L., Wahlberg, M.L., Swecker Jr, W.S., Lewis, R.M.: Temperamental cattle acclimate more substantially to repeated handling. Applied Animal Behaviour Science **212**, 36–43 (2019)
33. Cafe, L., Robinson, D.L., Ferguson, D., McIntyre, B.L., Geesink, G., Greenwood, P.: Cattle temperament: persistence of assessments and associations with productivity, efficiency, carcass and meat quality traits. Journal of Animal Science **89**(5), 1452–1465 (2011)
34. Hieber, J.: Temperament evaluation in beef cattle: Understanding evaluator bias within subjective measurements of docility score, temperament score, and qualitative behavior assessment. PhD thesis, North Dakota State University (2016)
35. Celestino, J. Elfren F, Hieber, J.K., Dahlen, C.R., Riley, D.G., Wagner, S.A., Hulsman Hanna, L.L.: Differences in evaluators and genetic parameter estimations using subjective measurements of beef cattle temperament. Translational Animal Science **3**(Supplement_1), 1769–1773 (2019). doi:10.1093/tas/txz084
36. Henderson, C., Quaas, R.: Multiple trait evaluation using relatives' records. Journal of Animal Science **43**(6), 1188–1197 (1976)
37. Campbell, M.T., Yu, H., Momen, M., Morota, G.: Examining the relationships between phenotypic plasticity and local environments with genomic structural equation models. bioRxiv (2019)
38. Mrode, R.A.: Linear Models for the Prediction of Animal Breeding Values. Cabi, Wallingford, Oxfordshire (2014)
39. Napolitano, F., De Rosa, G., Grasso, F., Wemelsfelder, F.: Qualitative behaviour assessment of dairy buffaloes (bubalus bubalis). Applied Animal Behaviour Science **141**(3-4), 91–100 (2012)
40. Fleming, P.A., Paisley, C.L., Barnes, A.L., Wemelsfelder, F.: Application of qualitative behavioural assessment to horses during an endurance ride. Applied Animal Behaviour Science **144**(1-2), 80–88 (2013)
41. Petherick, J.C., Holroyd, R., Doogan, V., Venus, B.: Productivity, carcass and meat quality of lot-fed bos indicus cross steers grouped according to temperament. Australian Journal of Experimental Agriculture **42**(4), 389–398 (2002)
42. de Los Campos, G., Gianola, D.: Factor analysis models for structuring covariance matrices of additive genetic effects: a bayesian implementation. Genetics Selection Evolution **39**(5), 481 (2007)
43. Peñagaricano, F., Valente, B., Steibel, J., Bates, R., Ernst, C., Khatib, H., Rosa, G.: Searching for causal networks involving latent variables in complex traits: Application to growth, carcass, and meat quality traits in pigs. Journal of Animal Science **93**(10), 4617–4623 (2015)