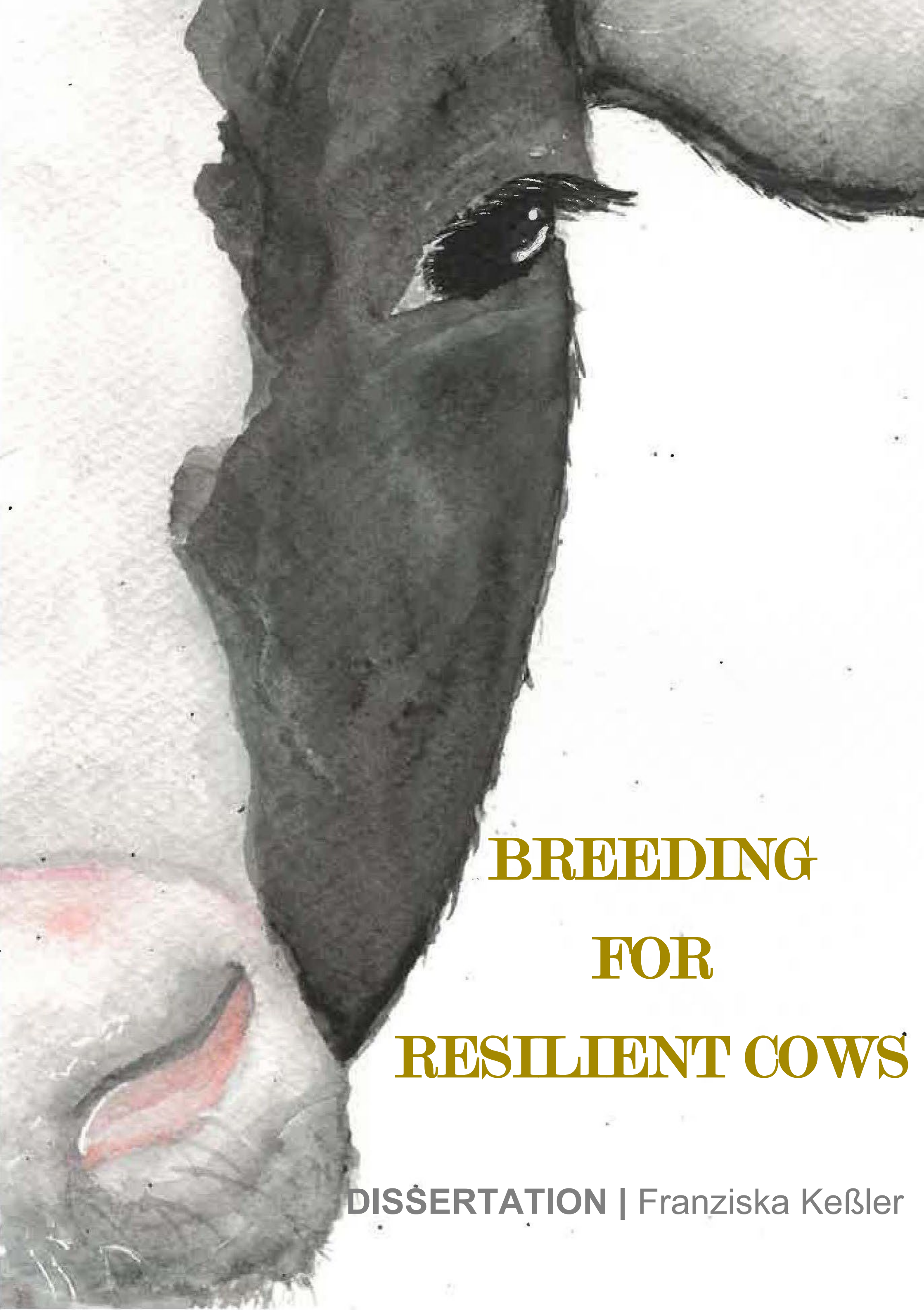


BREEDING FOR RESILIENT COWS

DISSERTATION | Franziska Keßler

The cover was designed in collaboration with © Lisa Kühn (2025).

Breeding for resilient cows

Dissertation
to obtain the doctoral degree of Agricultural Sciences (Dr. sc. agr.)

Faculty of Agricultural Sciences
University of Hohenheim
Institute of Animal Science

submitted by

Franziska Keßler

from Forst (Lausitz)
Germany

2025

Date of Oral Examination: 07.07.2025

Dean of Faculty: Prof. Dr. Ralf Vögele

Examination Committee

Chairperson of the Oral Examination: Prof. Dr. Martin Hasselmann
Supervisor and Reviewer: Prof. Dr. Jörn Bennewitz
Second Reviewer: Prof. Dr. Georg Thaller Prof.
Additional Examiner: Dr. Hans-Peter Piepho

TABLE OF CONTENTS

THE CONCEPT OF RESILIENCE

RESILIENCE INDICATOR TRAITS IN 3 DAIRY CATTLE BREEDS IN BADEN-WÜRTTEMBERG

TOWARD A RESILIENCE SELECTION INDEX WITH INDICATOR TRAITS IN GERMAN HOLSTEIN DAIRY CATTLE

MAPPING GENES FOR RESILIENT DAIRY COWS BY MEANS OF ACROSS-BREED GENOME-WIDE ASSOCIATION ANALYSIS

SUMMARY

Dairy cows are an indispensable part of modern livestock farming and make a significant contribution to human nutrition with producing a high-quality protein. At the same time, they are influenced by environmental factors and must maintain their performance, stay healthy, and remain fertile under given environmental conditions. In recent decades, we have faced an increasing number of new or suddenly emerging environmental stressors: extreme weather events, heatwaves, invasive species, and constantly changing requirements for housing conditions are just a few examples. This demands a high level of robustness and resilience from our dairy cows. While comprehensive research has been conducted on adaptation to changing environmental conditions, there is still a lack of knowledge about coping with short-term disturbances. Resilience is the ability of an individual to respond to these disturbances, recover from them, and return to its previous physiological equilibrium while maintaining the same level of performance. This study examines the concept of resilience in German dairy cattle breeds, analyzes genetic parameters, and discusses possibilities for future breeding strategies.

The **first chapter** describes interactions between organisms and the environment, as well as statistical approaches to assessing the influence of environmental gradients on livestock. The concepts of resilience and robustness were distinguished, and methods for measuring and phenotyping resilience were explored. A promising approach is the analysis of variance and autocorrelation of daily milk yields during lactation. Under the assumption that resilient animals maintain a stable performance level along a natural lactation curve, low variance and an autocorrelation close to zero indicate high resilience. The genetic parameters of these resilience indicator traits were studied in the **second chapter** for the three most important German dairy breeds: German Holstein, German Fleckvieh, and German Brown Swiss. Within each breed and across breeds, low to moderate heritabilities were observed, along with desirable phenotypic and genetic correlations with performance traits. A comparison between breeds revealed only minimal differences, with no clear trend across all resilience indicator traits studied.

Next, correlations between resilience indicator traits and functional as well as health traits were analyzed. While hardly any significant correlations were found for autocorrelation, the variance of daily milk yield correlated in a desirable direction with these traits. Resilient animals appear to be healthier and more long-lived. **Chapter three** also discusses the design of a selection index for resilience. This requires economic weighting factors, which cannot yet be determined. Therefore, optimizing the selection index resilience by maximizing breeding response in the selection index health was proposed. It was shown that breeding for resilience would lead to genetic progress in overall health. In the German Holstein breed, which was exclusively considered in this context, a selection index consisting of two different variance-based resilience indicator traits was recommended. The adaptation of the methodology to optimize a selection index to the German Fleckvieh and German Brown Swiss breeds was subsequently addressed in the **general discussion** and considered feasible.

The **fourth chapter** analyzes the genetic architecture of resilience using genome-wide association studies within the three dairy breeds. The results indicated that the resilience indicator traits are polygenic traits. SNPs that significantly influence resilience are located near to QTLs known to affect performance, fertility, or health. Additionally, population structure was examined using linkage disequilibrium analysis.

The final **general discussion** applied the methods from **chapter three** to the German Fleckvieh and German Brown Swiss breeds. Significant negative, undesirable correlations between autocorrelation and functional and health traits were found in German Fleckvieh. In contrast, variance-based resilience indicator traits correlated positively with most known traits, which is desirable. A selection index resilience was proposed for both breeds, consisting of two to three individual indicator traits, similar to the German Holstein breed. To better understand resilience, differences in breeding values were translated into milk loss per lactation, the number of disturbances an individual suffered from, and the impact on test-day results for milk ingredients. Finally, an outlook was provided on potential future research directions for resilience in livestock.

SUMMARY (GERMAN)

Milchkühe sind aus der modernen Nutztierhaltung nicht wegzudenken und leisten einen enormen Beitrag zur Ernährung der Menschheit mit hochwertigen Protein. Dabei stehen sie selbst unter dem Einfluss der Umwelt und müssen unter den gegebenen Umweltbedingungen ihre Leistung erbringen, sowie gesund und fruchtbar bleiben. In den letzten Jahrzehnten sehen wir uns einer steigenden Anzahl neuer oder plötzlich auftretender Störeinflüsse entgegen: Extremwettersituationen, Hitzewellen, invasive Arten, stetig wandelnde Anforderungen an die Haltungsbedingungen sind nur einige Beispiele. Dies fordert eine hohe Robustheit und Resilienz von unseren Milchkühen. Während bereits viel Forschungsarbeit zur Anpassung an sich wandelnde Umweltbedingungen geleistet wurde, fehlt es noch an Erkenntnissen zur Widerstandsfähigkeit gegenüber kurzfristigen Störeinflüssen. Die Resilienz ist die Fähigkeit eines Organismus, auf diese zu reagieren, sich schnell davon zu erholen und in das zuvor bestandene physiologische Gleichgewicht bei gleichem Leistungsniveau zurückzukehren. Die vorliegende Arbeit untersucht das Konzept Resilienz bei deutschen Milchkuhrassen, analysiert genetische Parameter und diskutiert Möglichkeiten einer zukünftigen züchterischen Bearbeitung.

Im **ersten Kapitel** werden Interaktionen zwischen Organismen und der Umwelt sowie statistische Ansätze zur Erfassung des Einflusses von Umweltgradienten auf Nutztiere beschrieben. Insbesondere die Konzepte Resilienz und Robustheit werden voneinander abgegrenzt und Möglichkeiten zur Messung und Phänotypisierung der Resilienz herausgearbeitet. Ein vielversprechender Ansatz ist die Analyse der Varianz und der Autokorrelation von täglichen Milchmengen während einer Laktation. Unter der Annahme, dass resiliente Tiere ein gleichbleibendes Leistungsniveau entlang einer natürlichen Laktationskurve halten, beschreibt eine geringe Varianz und eine Autokorrelation nahe null eine hohe Resilienz.

Die genetischen Parameter der Resilienzindikatoren werden im **zweiten Kapitel** in den drei wichtigsten deutschen Milchkuhrassen Deutsches Holstein, Fleckvieh und Braunvieh untersucht. Dabei zeigten sich innerhalb jeder Rasse und rasseübergreifend geringe bis moderate Heritabilitäten und wünschenswerte phänotypische und genetische Korrelationen mit Leistungsmerkmalen. Ein Vergleich zwischen den Rassen zeigte nur minimale Unterschiede, die über alle betrachteten Resilienzindikatoren hinweg keine klare Tendenz aufwiesen.

Im nächsten Schritt wurden Korrelationen zwischen Resilienzindikatoren und funktionalen

sowie Gesundheitsmerkmalen analysiert. Während für die Autokorrelation kaum signifikante Zusammenhänge gezeigt werden können, korreliert die Varianz der täglichen Milchleistung in erwünschter Richtung mit anderen Merkmalen. Resiliente Tiere scheinen gesünder und langlebiger zu sein. Außerdem wird in **Kapitel drei** die Gestaltung eines Selektionsindex Resilienz diskutiert. Hierfür bedarf es ökonomischer Gewichtungsfaktoren, die aktuell noch nicht determiniert werden können. Daher wird die Optimierung des Selektionsindex Resilienz nach einer Maximierung im Zuchtfortschritt des Selektionsindex Gesundheit vorgeschlagen. Hier zeigt sich, dass eine Zucht auf Resilienz zu einem Zuchtfortschritt in der allgemeinen Gesundheit führen würde. In der Rasse Deutsches Holstein, die hier ausschließlich betrachtet wurde, empfiehlt sich ein Selektionsindex bestehend aus zwei verschiedenen varianzbasierten Resilienzindikatoren. Die Anwendung der Methode zur Optimierung eines Selektionsindex Resilienz in den Rassen Fleckvieh und Braunvieh wird abschließend in der **Generellen Diskussion** aufgegriffen und als durchführbar eingestuft.

Im **vierten Kapitel** wird die genetische Architektur für ein tiefergehendes Verständnis analysiert. Mittels genomweiter Assoziationsstudie innerhalb der drei Milchkuhrassen zeigt sich, dass Resilienzindikatoren polygene Merkmale sind. SNP, die einen signifikanten Einfluss auf die Resilienz haben, liegen im Genom in unmittelbarer Nähe zu QTL, die bekanntermaßen einen Effekt auf die Leistung, Fruchtbarkeit oder Gesundheit nehmen. Ergänzend wird die Populationsstruktur mittels Kopplungsungleichgewicht-Analyse untersucht.

In der abschließenden **Generellen Diskussion** werden die Methoden aus **Kapitel drei** auf die Rassen Fleckvieh und Braunvieh angewandt. Hier zeigen sich signifikant negative, unerwünschte Korrelationen zwischen der Autokorrelation und den funktionalen und Gesundheitsmerkmalen beim Fleckvieh. Die varianzbasierten Resilienzindikatoren korrelieren hingegen mit den meisten bekannten Merkmalen in erwünschter, positiver Richtung. Ein Selektionsindex Resilienz wird für beide Rassen vorgeschlagen und setzt sich, ebenso wie bei der Deutschen Holstein, aus zwei bis drei Einzelmerkmalen zusammen. Für ein besseres Verständnis der Resilienz werden Unterschiede in den Zuchtwerten in Milchverlust je Laktation, die Anzahl einflussnehmender Störevents und die Auswirkung auf Testtagsergebnisse für Milchinhaltsstoffe umgerechnet. Abschließend wird ein Ausblick auf Anknüpfungspunkte für weitere Forschungen zum Thema Resilienz bei Nutztieren gegeben.

GENERAL INTRODUCTION

Climate phenomena, pathogen burden, housing condition – there are manifold environmental influences, which affect living beings, especially livestock. While producing high-quality food for human consumption, they have to cope with changing environmental conditions. In addition to normal cyclical fluctuations such as the passage of the year or life status, unpredictable changes like extreme weather conditions due to climate change (Hansen et al. 2012), new and rapidly evolving pathogens, or changes in husbandry due to increasing demands of society, politics, and economics are occurring more frequently (Schader et al. 2015; Dominik and Swan 2014; Alonso et al. 2020). Modern livestock farming is forced to perform a balancing act between food security for the world's population and sustainable resource use (Madhusoodan et al. 2019; Phocas et al. 2016). The focus is shifting towards feed-efficient, long-lived animals that achieve high productivity with low levels of climate-negative emissions (Rojas de Oliveira et al. 2024; Løvendahl et al. 2018). To meet these demands, it is necessary to optimize farm management and to adapt livestock to changing conditions by breeding. Resilient and robust livestock, which can cope with present and future requirements, is required.

In this framework, resilience is a buzzword that has gained importance in many areas of life in recent years. Started in the 1950s in human research (Holling 1973), it is analyzed in economics and industry as well as in ecosystems and organisms today. Wherever living and non-living systems are exposed to disruptive influences. There are various closely related and partly overlapping concepts such as robustness, sensitivity, plasticity and adaptability (de Goede et al. 2013; Urruty et al. 2016; Walker et al. 2004). What they have in common is their complexity and the diversity of the influences acting on them. Resilience primarily considers how an organism copes with short-term disturbances. This includes the reaction to and recovery from a disruptive influence as well as the ability to restore the original performance level in terms of basic maintenance and performance (Colditz and Hine 2016; Berghof et al. 2018; Poppe et al. 2020).

The main challenge is to determine the capacity for resilience. It is a complex process, as an external stimulus must be recognized, processed and reacted to. At each of these points, individuals can respond resiliently or non-resiliently. Scheffer et al. (2018) and Dakos et al. (2012a) used various parameters of time series analysis to predict the resilience of systems. This has been transferred and adapted to many scientific fields. In livestock, the parameters variance and autocorrelation of longitudinal measured traits have proven to be the suitable (Berghof et al. 2018; Poppe et al. 2020; Poppe et al. 2022b).

The aim of the thesis was to evaluate resilience in German dairy cattle, to study heritabilities and genetic correlations of resilience indicator traits, to gain a better understanding of their genetic architecture and to look for a way to implement them in breeding value estimation. Based on previous studies (Poppe et al. 2020; Poppe et al. 2021b; Poppe et al. 2021a), the daily milk yield was used for calculate resilience indicator traits, because dairy cows show a response in milk yield against different external factors like heat waves or changes in food quality (Poppe et al. 2021b). While so far mainly Holstein Friesian cows have been examined in resilience studies in dairy cows, we also considered Fleckvieh and Brown Swiss cattle. These are the most important dairy cow breeds in Germany.

German Holstein (HF), which accounts for more than 50 % of dairy cows in Germany, are found throughout Germany. German Fleckvieh (FV; 25 % of dairy cows) and German Brown Swiss (BS; 3.5 % of dairy cows) are mainly located in southern Germany (Bundesverband Rind und Schwein e.V. 2023). It is known that there are differences between the breeds in performance with the highest milk yield at HF (Glatz-Hoppe et al. 2019; Toledo-Alvarado et al. 2017). On the other hand, local and dual-purpose breeds such as BS and FV are supposed to have higher fertility (Toledo-Alvarado et al. 2017), better health (Bieber et al. 2019) and a better adaptation to heat events (Mylostyvyi et al. 2021). Initial studies of the resilience of different cattle breeds showed only minimal differences so far (Adriaens et al. 2023; Bonekamp et al. 2022; Bapst et al. 2022).

The background and possibilities of phenotyping and measuring resilience in livestock are presented in **chapter one**. Related concepts are described and requirements for analyzing resilience indicator traits are identified.

In **chapter two**, five different resilience indicator traits, four variance-based parameters and the autocorrelation, logarithmized and non-logarithmized, were analyzed. Moreover, heritabilities and genetic correlations between the resilience indicator traits and performance traits were estimated. The analyses were performed across breeds and separated by breed. Differences between the breeds were discussed.

Chapter three evaluates the possibility to implement resilience indicator traits in the breeding goal. Because of missing economic values for resilience, we introduced a new way to determine weighting factors of single resilience indicator traits with the aim to combine them in one selection index. This was done by maximizing the joint selection response of resilience and health. Thus, individuals with a high favorable value in a selection index for resilience were ought to be performance-stable and healthy. The analyses thereby focused only on HF breed, but can adapted to the other both breeds as well.

Moreover, due to the limited research on the genetic architecture of resilience indicator traits, we conducted genome-wide association studies of several resilience indicator traits and the selection index resilience (introduced in **chapter three**) in all breeds, described in **chapter four**. Instead of the previously used pedigree, we used imputed high-density genotypes (around 400,000 SNPs across all breeds). Additionally, population analysis within and across breeds were done.

At last, the potential of breeding for resilience in the German dairy cattle population is addressed in the **general discussion**. For the breeds FV and BS, the results of the correlation analysis of resilience indicator traits and functional and health traits as well as the optimization of a selection index resilience according to the methodology in **chapter three** are shown. To gain a better insight into resilience, EBV of resilience indicator traits are expressed as reduced milk yield per lactation, number of disturbances suffered by a cow and the effect on test day data. Finally, an outlook is given on future research questions in resilience and possible approaches are discussed.

References

Adriaens, Ines; Bonekamp, Gerbrich; Napel, Jan ten; Kamphuis, Claudia; Haas, Yvette de (2023): Differences across herds with different dairy breeds in daily milk yield based proxies for resilience. In *Front. Genet.* 14, p. 1120073. DOI: 10.3389/fgene.2023.1120073.

Alonso, Marta E.; González-Montaña, José R.; Lomillos, Juan M. (2020): Consumers' Concerns and Perceptions of Farm Animal Welfare. In *Animals* 10 (3). DOI: 10.3390/ani10030385.

Bapst, B; von Rohr, P; Seefried, F.R. (2022): Deep data recording for developing resilience traits in Swiss cattle populations: a proof of concept and an application. In *Proceedings of 12th World Congress on Genetics Applied to Livestock Production*, pp. 647–650. Available online at https://www.wageningenacademic.com/doi/epdf/10.3920/978-90-8686-940-4_149?role=tab.

Berghof, Tom V. L.; Poppe, Marieke; Mulder, Han A. (2018): Opportunities to Improve Resilience in Animal Breeding Programs. In *Front. Genet.* 9, p. 692. DOI: 10.3389/fgene.2018.00692.

Bieber, Anna; Wallenbeck, Anna; Leiber, Florian; Fuerst-Waltl, Birgit; Winckler, Christoph; Gullstrand, Patricia et al. (2019): Production level, fertility, health traits, and longevity in local and commercial dairy breeds under organic production conditions in Austria, Switzerland, Poland, and Sweden. In *J. Dairy Sci.* 102 (6), pp. 5330–5341. DOI: 10.3168/jds.2018-16147.

Bonekamp, Gerbrich; Poppe, M.; ten Napel, J.; Kamphuis, C.; de Haas, Yvette; Adriaens, I. (2022): Comparison of milk yield based resilience indicators across dairy cattle breeds. Proceedings of 12th World Congress on Genetics Applied to Livestock Production. Wageningen Academic Publishers. Wageningen, Netherlands, 2022. Available online at https://www.wageningenacademic.com/pb-assets/wagen/WCGALP2022/27_002.pdf.

Bundesverband Rind und Schwein e.V. (2023): Rinder- und Schweineproduktion in Deutschland 2022.

Colditz, Ian G.; Hine, Brad C. (2016): Resilience in farm animals: biology, management, breeding and implications for animal welfare. In *Anim. Prod. Sci.* 56 (12), pp. 1961–

1983. DOI: 10.1071/AN15297.

Dakos, Vasilis; Carpenter, Stephen R.; Brock, William A.; Ellison, Aaron M.; Guttal, Vishwesha; Ives, Anthony R. et al. (2012): Methods for detecting early warnings of critical transitions in time series illustrated using simulated ecological data. In *PloS one* 7 (7), e41010. DOI: 10.1371/journal.pone.0041010.

de Goede, D. M.; Gremmen, B.; Blom-Zandstra, M. (2013): Robust agriculture: Balancing between vulnerability and stability. In *NJAS: Wageningen Journal of Life Sciences* 64-65 (1), pp. 1–7. DOI: 10.1016/j.njas.2012.03.001.

Dominik, Sonja; Swan, Andrew A. (Eds.) (2014): Breeding Focus 2014 – Improving Resilience. Resilience, tolerance, robustness and genotype x environment interaction in Merino sheep breeding. Armidale, Australia: Animal Genetics and Breeding Unit, University of New England (International Forum "Breeding Focus 2014 - Improving Resilience"). Available online at https://www.cabdirect.org/cabdirect/abstract/20203123711.

Glatz-Hoppe, Julia; Onken, F; Eggert, Anja; Mohr, E; Losand, B (2019): Nutzung von Milchinhaltsstoffen zur Beurteilung der Versorgungssituation von Milchkühen 1. Mitteilung: Milchleistung und Inhaltsstoffe deutscher Milchrindrassen im Vergleich. In *Züchtungskunde* 91 (6), pp. 423–448. Available online at https://d-nb.info/1293661236/34#page=17.

Hansen, James; Sato, Makiko; Ruedy, Reto (2012): Perception of climate change. In *PNAS* 109 (37), E2415-23. DOI: 10.1073/pnas.1205276109.

Holling, C. S. (1973): Resilience and Stability of Ecological Systems. In *Annu. Rev. Ecol. Syst.* 4 (1), pp. 1–23. DOI: 10.1146/annurev.es.04.110173.000245.

Løvendahl, P.; Difford, G. F.; Li, B.; Chagunda, M. G. G.; Huhtanen, P.; Lidauer, M. H. et al. (2018): Review: Selecting for improved feed efficiency and reduced methane emissions in dairy cattle. In *animal* 12 (s2), s336-s349. DOI: 10.1017/S1751731118002276.

Madhusoodan, Aradotlu Parameshwarappa; Seijan, Veerasamy; Rashamol, Veettiparambil Pandarathil; Savitha, Sira Tulasiramu; Bagath, Madiajagan; Krishnan, Govindan; Bhatta, Raghavendra (2019): Resilient capacity of cattle to environmental challenges – An updated review. In *JABB* 7 (3), pp. 104–118. DOI:

10.31893/2318-1265jabb.v7n3p104-118.

Mylostyvyi, Roman; Lesnovskay, Olena; Karlova, Lina; Khmeleva, Olena; Kalinichenko, Olena; Orishchuk, Oksana et al. (2021): Brown Swiss cows are more heat resistant than Holstein cows under hot summer conditions of the continental climate of Ukraine. In *JABB* 9 (4), pp. 1–8. DOI: 10.31893/jabb.21034.

Phocas, F.; Belloc, C.; Bidanel, J.; Delaby, L.; Dourmad, J. Y.; Dumont, B. et al. (2016): Towards the agroecological management of ruminants, pigs and poultry through the development of sustainable breeding programmes: I-selection goals and criteria. 10 volumes: Animal (11). Available online at https://www.cambridge.org/core/journals/animal/article/review-towards-the-agroecological-management-of-ruminants-pigs-and-poultry-through-the-development-of-sustainable-breeding-programmes-iselection-goals-and-criteria/7284d3e0214f3a92e2e517e2b9d72a85.

Poppe, M.; Bonekamp, Gerbrich; van Pelt, M. L.; Mulder, H. A. (2021a): Genetic analysis of resilience indicators based on milk yield records in different lactations and at different lactation stages. In *J. Dairy Sci.* 104 (2), pp. 1967–1981. DOI: 10.3168/jds.2020-19245.

Poppe, M.; Mulder, H. A.; Veerkamp, Roel F. (2021b): Validation of resilience indicators by estimating genetic correlations among daughter groups and with yield responses to a heat wave and disturbances at herd level. In *J. Dairy Sci.* 104 (7), pp. 8094–8106. DOI: 10.3168/jds.2020-19817.

Poppe, M.; Veerkamp, Roel F.; van Pelt, M. L.; Mulder, H. A. (2020): Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. In *J. Dairy Sci.* 103 (2), pp. 1667–1684. DOI: 10.3168/jds.2019-17290.

Poppe, Marieke; Mulder, Han A.; van Pelt, Mathijs L.; Mullaart, Erik; Hogeveen, Henk; Veerkamp, Roel F. (2022): Development of resilience indicator traits based on daily step count data for dairy cattle breeding. In *Genet Sel Evol* 54 (1), p. 21. DOI: 10.1186/s12711-022-00713-x.

Rojas de Oliveira, Hinayah; Sweett, Hannah; Narayana, Saranya; Fleming, Allison; Shadpour, Saeed; Malchiodi, Francesca et al. (2024): Development of genomic evaluation for methane efficiency in Canadian Holsteins. In *JDS Communications* 5

(6), pp. 756–760. DOI: 10.3168/jdsc.2023-0431.

Schader, Christian; Muller, Adrian; Scialabba, Nadia El-Hage; Hecht, Judith; Isensee, Anne; Erb, Karl-Heinz et al. (2015): Impacts of feeding less food-competing feedstuffs to livestock on global food system sustainability. In *J R Soc Interface* 12 (113), p. 20150891. DOI: 10.1098/rsif.2015.0891.

Scheffer, Marten; Bolhuis, J. Elizabeth; Borsboom, Denny; Buchman, Timothy G.; Gijzel, Sanne M. W.; Goulson, Dave et al. (2018): Quantifying resilience of humans and other animals. In *Proceedings of the National Academy of Sciences of the United States of America* 115 (47), pp. 11883–11890. DOI: 10.1073/pnas.1810630115.

Toledo-Alvarado, Hugo; Cecchinato, Alessio; Bittante, Giovanni (2017): Fertility traits of Holstein, Brown Swiss, Simmental, and Alpine Grey cows are differently affected by herd productivity and milk yield of individual cows. In *J. Dairy Sci.* 100 (10), pp. 8220–8231. DOI: 10.3168/jds.2016-12442.

Urruty, Nicolas; Tailliez-Lefebvre, Delphine; Huyghe, Christian (2016): Stability, robustness, vulnerability and resilience of agricultural systems. A review. In *Agron. Sustain. Dev.* 36 (1), pp. 1–15. DOI: 10.1007/s13593-015-0347-5.

Walker, Brian; Holling, C. S.; Carpenter, Stephen R.; Kinzig, Ann P. (2004): Resilience, Adaptability and Transformability in Social-ecological Systems. In *E&S* 9 (2). DOI: 10.5751/ES-00650-090205.

CHAPTER ONE

THE CONCEPT OF RESILIENCE

Livestock and the environment

The environment is constantly changing. At this, the climate change is of particular importance as it has led to constant global warming since the end of the 19th century. Moreover, it entails new and altered environmental effects. In addition to the rise in average temperatures, this also includes the increase in extreme weather events. In Europe, the intensity and frequency of heat events and heavy precipitation is increasing, while cold events are becoming more seldom. Among other things, this leads to postponed and extended growing seasons, a loss of biodiversity and the appearance of invasive species,

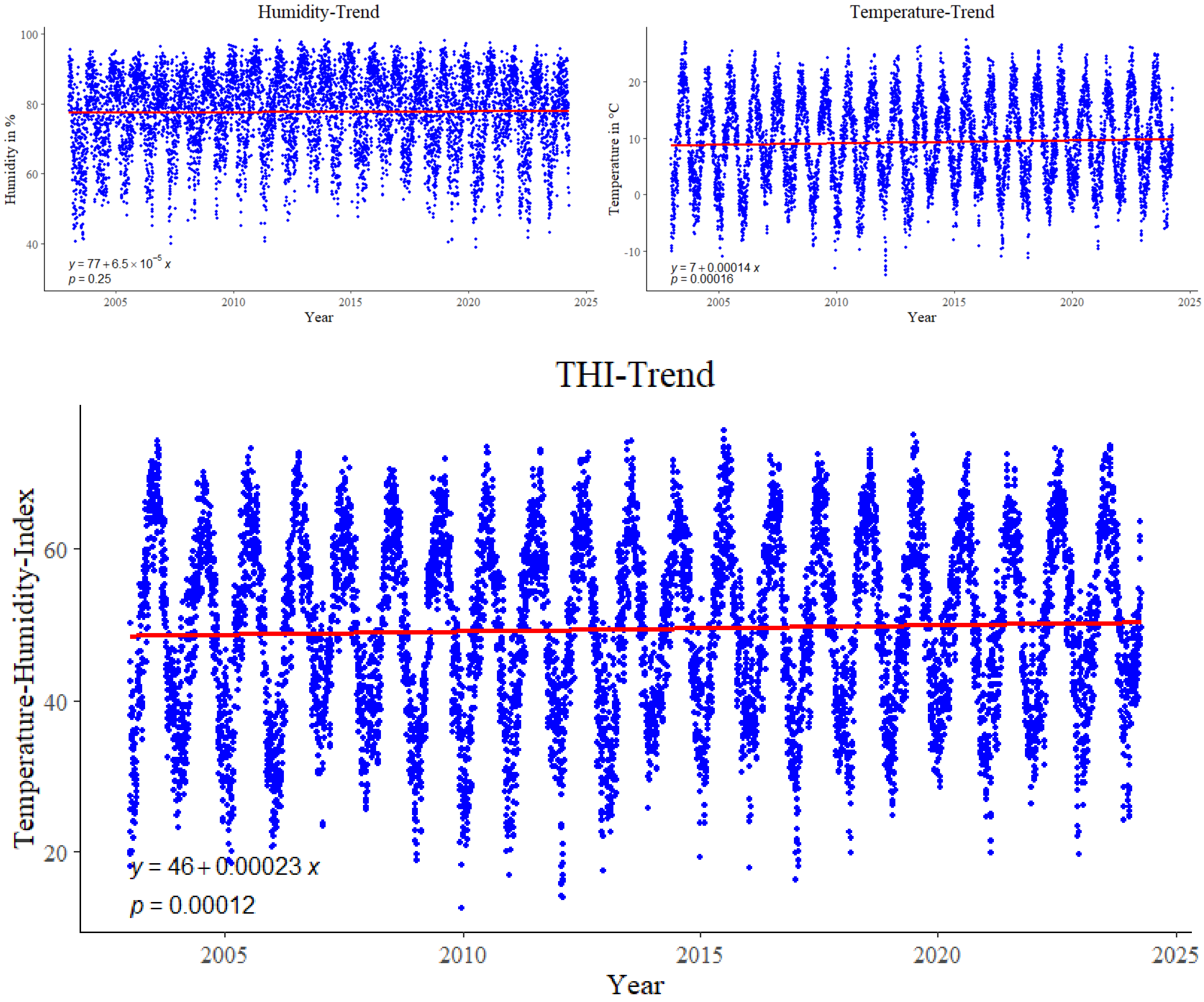


Figure 1: Trends of temperature, humidity and temperature-humidity-index (THI) from 2003 to 2024 in Baden-Württemberg considering 28 different weather stations. Regression equations and p-values are given.

which can affect the availability and quality of forage (Change 2023; Hansen et al. 2012). Another indirect effect is the emergence of new and exotic pathogens. For example, mosquitoes, which act as vectors for many viral diseases, spread more widely in the northern hemisphere as average temperatures rise (Mordecai et al. 2017; Cheng et al. 2022).

The current study is based on data from the region Baden-Württemberg, which is located in the South-West of Germany. Local weather records proof that climate change is also causing a change in this temperate climate zone. Figure 1 presents the trend of the daily mean humidity H (top left), mean temperature T (top right) and the temperature-humidity index (THI) calculated as $\mathbf{THI} = 46.3 + 0.81 * \mathbf{T} + 0.99 * \mathbf{H} * \mathbf{T} - 14.3 * \mathbf{H}$. The THI is related to the thermal stress of an organism and is a more reliable climatic environmental gradient than temperature and humidity alone (Bohmanova et al. 2007). Weather data were recorded at 28 weather stations in Baden-Württemberg near to farms participating in our study between 2003 and 2024. The regression of the daily temperatures over time shows a significant increase over the last 20 years. Depending on this and the constant humidity, the average daily THI also increased. Although the slope is low, it is therefore a locally relevant issue. Due to the joint evaluation of weather data from several stations, greater regional differences are to be expected.

The named direct (i.e., extreme weather events, high pathogen pressure) and indirect (i.e., loss of biodiversity, emergence of invasive species) environmental variables influence our livestock and can initiate a visible or invisible change in behavior, physiological traits or in the immune response (Colditz and Hine 2016; Cheng et al. 2022; Misztal 2017). The biological background is described in the resource allocation theory. According to this, each individual has a limited amount of resources that are available either through the intake of food or the mobilization of body reserves. The resources are divided among all the functions of the body, like maintenance, health or reproduction. Under the influence of a disturbance, the organism has to reallocate resources, for example to cool down the body when exposed to heat or to fight or flee in a dangerous situation. Not every individual is able to distribute and redistribute resources equally well (Friggens et al. 2017; Rauw et al. 1998). Artificial selection for certain traits can reduce an animal's ability to adapt to environmental influences. This becomes apparent when the environment is changed. For example, an animal from a good husbandry environment is less likely to fulfill its genetic potential in a poor husbandry environment and the correlation between high performance and poor survival rates increases (van der Waaij 2004; Rauw 2009).

Concepts to capture reactions to the environment

The phenotypic variance is made up of genetic and environmental variance. Known fixed effects, maternal and paternal effects, effects of repeated measurements and nowadays also microbial or epigenetic effects are taken into account in statistical models analyzing livestock breeding traits. The unexplained variance is summarized as the residual, which also includes the interaction between genotype and environment (GxE), if not properly modeled. These GxE effects can be also interpreted as environmental sensitivity (Falconer 1990). The environment can be divided into a macro-environment and a micro-environment. The former is predictable, and the trait expression of an animal can be regressed on it (Gavrilets and Hastings 1994; Wu 1997), for example, the development of the daily weight gain of a fattening pig as a function of the environmental variable feeding intensity or the development of the daily milk yield of a cow as a function of the environmental variable THI. GxE are well known and frequently studied with mixed-linear models and reaction norms in different environments (Hayes et al. 2016), e.g. by Streit et al. (2012) and Schmid et al. (2021) in dairy cattle. The micro-environment summarizes unpredictable effects. Sensitivity to it is animal-specific and leads to phenotypic differences even if genotypically identical individuals are kept in an identical environment (Gavrilets and Hastings 1994; Wu 1997). It is also called genetic heterogeneity of the residual variance and can be estimated accordingly. The residual variance from a mixed linear model of a phenotypic observation is analyzed for its genetic components, for example with a double hierarchical generalized linear model (Rönnegård et al. 2013; Strandberg et al. 2013; Rönnegård et al. 2010). A combined estimation of micro- and macro-environmental sensitivity is possible (Ehsaninia et al. 2019).

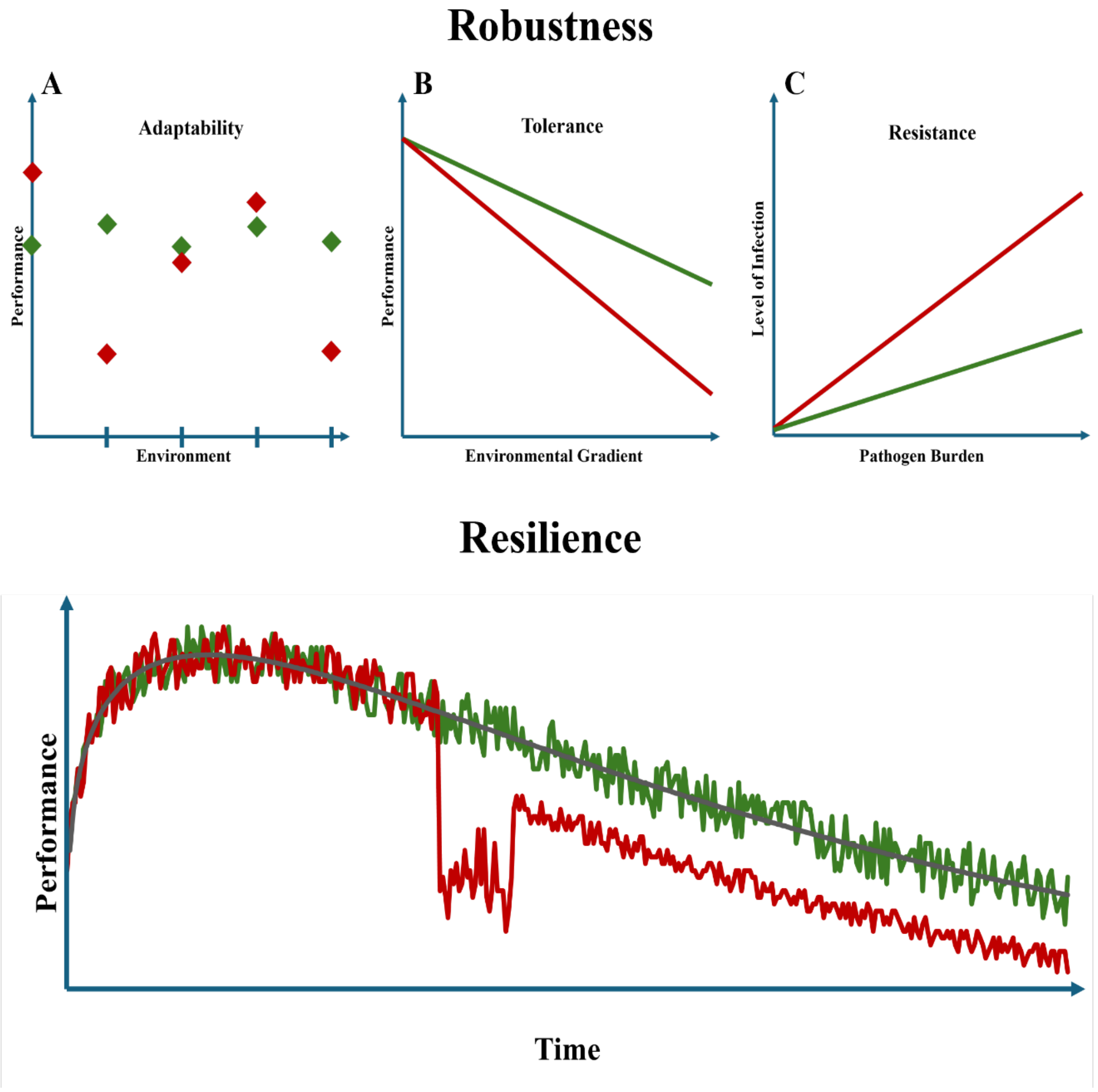


Figure 2: Overview of concepts to illustrate the low (green) and high sensitivity (red) of an organism to the environment. **Robustness**, the capacity of maintain productivity in a wide range of environments and under several environmental conditions (Colditz and Hine 2016), consisting of: **A** – Adaptability, the ability of an individual to perform within a defined environment (Prayaga and Henshall 2005), to adapt to long-term changes and show a similar performance in different environments (de Goede et al. 2013); **B** – Tolerance, the decrease in performance of an individual with increasing effect of the environmental gradient (e.g., temperature, pathogen burden)(Hermesch and Dominik 2014; Mulder 2016); **C** – resistance, the ability of an individual to take control over a pathogen and its life cycle (Mulder 2016; Bishop 2012). **Resilience**, the ability of an individual to cope with short-term disturbances, response to and recover from them with equilibrium restored (Colditz and Hine 2016; Berghof et al. 2018).

Various concepts for responding to the environment are based on sensitivity to the macro- and micro-environment. Definitions and categorization of these concepts may differ from one another; in the following, resilience and robustness in particular will be separated from one another. An overview of all the concepts mentioned can be found in Figure 2.

Robustness combines various elements, mainly resistance, tolerance and adaptability. It describes the ability to exist, perform and remain fertile and healthy in a wide range of environments and environmental conditions (Colditz and Hine 2016; Strandberg et al. 2013; Amer 2012). The upper plots A, B and C in Figure 2 each show a schematic example of the concepts associated with robustness, with a green graph reflecting desired high robustness and a red graph reflecting little robustness. Resistance (C in Figure 2) is developed towards pathogens and describes the ability of an individual to control the life cycle of pathogens and thus minimize their impact (Bishop 2012; Mulder 2016). An individual is considered resistant if its infection level, i.e. the amount of pathogens in the body, is lower than that of less resistant conspecifics under the same external pathogen pressure. This concept is complemented by tolerance (B in Figure 2), which describes the ability to maintain performance in the face of biotic (e.g. pathogens) and abiotic (e.g. heat) influences (Berghof et al. 2018; Bishop 2012; Cheruiyot et al. 2022). The change in performance, in statistical terms the slope of the performance curve, is considered along with a continuous environmental gradient. This is the classic GxE interaction depicted by reaction norms (Hayes et al. 2016). The steeper the reaction norm, i.e. the greater the change in an individual's performance, the less tolerant it is. Adaptation to a defined environment is adaptability (A in Figure 2) (Prayaga and Henshall 2005). It considers the totality of all factors in an environment, i.e. performance is compared on the basis of categorically divided environments. It belongs to the GxE interactions and can be evaluated using mixed-linear models (Hayes et al. 2016). In terms of robustness, an individual is desired that shows consistent performance across different environments. Sometimes, a specialist for one environment may be desired (e.g. for grazing at high altitudes), whereby performance in other environments would play a minor role. The concept of adaptability is often also considered at the population level, for example when deciding which breed to use in a particular environment or how to adapt the breeding goal to future conditions (Strandberg et al. 2013).

In contrast, resilience describes the ability of an animal to cope with short-term disturbances, including the response to them and the recovery of the original performance level (Berghof et al.; Friggens et al. 2022; Colditz and Hine 2016). This requires consideration of macro- and micro-environmental sensitivity. As can be seen in Figure 2, the independent variable is no longer an environmental gradient, but time. The disturbance is generally disregarded, the focus is placed on the reaction and recovery phase in the considered trait. A non-resilient individual, red line in Figure 2, shows a sharp decline due to the disturbance and cannot fully recover from it. A resilient animal (green line) is less affected and can restore equilibrium after disturbance. To differentiate between robustness and resilience, the environment should be taken into account: As far as resilience is concerned, the environment can be described as stable or changeable, and in terms of robustness, it can be described as good or bad. Both characterizations can be considered together, so that an animal can be robust and resilient, robust but not resilient, resilient but not robust or neither robust nor resilient (Friggens et al. 2022).

Possibilities to capture resilience

Resilience is complex: the individual must perceive an external stimulus, react to it and return to the original equilibrium of maintenance and performance. From a physiological perspective, there are many levels at which an individual can be resilient or non-resilient, for example in the transmission of stimuli in the central nervous system, the release of messenger substances or the activation of protective mechanisms such as the immune system. The approaches to making this measurable are correspondingly diverse.

Resilience could be expressed by using existing traits like the body condition score, longevity, or growth rate (Bengtsson et al. 2022; Calus and Veerkamp 2003; Colditz and Hine 2016; Friggens et al. 2022), as well as health traits such as number of disease cases, feed intake, fertility, and udder health (Bengtsson et al. 2022; Friggens et al. 2022). Physiological variables, e.g., body temperature and heart rate, and behavioral changes, e.g., number and duration of visits to a feeder or milking system, could also be considered as proxies for resilience (Colditz and Hine 2016; Homma et al. 2021). Single traits could combined as described in Adriaens et al. (2020), who combined the number of calvings, age by first calving, insemination index, number of treatments and the 305-day milk yield in a weighted index. The aim was to identify high-yielding individuals (high 305-day milk yield) with high fertility (low insemination index), good health (few treatments) and longevity (high number of calvings).

Another approach is the creation of novel trait resilience by using parameters from time series analysis. This can be found in various fields of science and is based on the assumption that a disturbance can be recognized by a change in a known and measured trait (Dominik and Swan 2014; Dakos et al. 2012a). The trait could characterize the behavior, the physiology, the performance or the immune system of an individual (Colditz and Hine 2016). In general, performance traits like milk yield in dairy cattle (Poppe 2022; Elgersma et al. 2018), body weight or wool growth in sheep production (Albers et al. 1987) as well as feed intake in pig production (Homma et al. 2021) are chosen. However, there are also studies, which reviewed functional traits or indirect traits like plasma concentration of non-esterified fatty acid (Barreto-Mendes et al. 2022) or daily step count (Poppe et al. 2022b). The disadvantage compared to performance traits is generally a more costly and less reliable data collection and results (Colditz and Hine 2016).

The change in the trait is determined with the help of time series analysis parameters, whereby either the total trait expression or the deviation of the expected from the observed trait expression can be used. At first, deviations has to be calculated using a data-based or a concept-based approach (Friggens et al. 2024; Taghipoor et al. 2023). The data-based calculation is the smoothing of real collected data and adjustment for outliers (Codrea et al. 2011; Poppe et al. 2020). The concept-based calculation aims to avoid underestimating disturbing influences and provides a priori assumptions of the expected performance, such as the Woods curve for milk yield (Ben Abdelkrim et al. 2021a; Adriaens et al. 2021). However, studies have shown that the choice of method has a negligible influence (Poppe et al. 2020; Chen et al. 2023a; Ghaderi Zefreh et al. 2024).

Time series analysis parameters can be dynamic indicators of resilience, as Scheffer et al. (2018) and Dakos et al. (2012a) showed by predicting responses to disturbances in ecosystems, humans and animals. While they analysed various parameters, e.g. variance, autocorrelation, skewness, standard deviation and cross correlation, the first two in particular proved promising in previous livestock studies (Dakos et al. 2012b; Berghof et al. 2018; Poppe et al. 2020).

The variance quantifies the magnitude of upward and downward fluctuations of the trait under consideration. A high variance can be interpreted as a lower resilience and vice versa (Berghof et al. 2018). However, there are two aspects to consider: persistence and the scaling effect (Elgersma et al. 2018; Poppe et al. 2020). A trait with a natural progression curve like the lactation curve of a dairy cow, leads to a higher variance for individuals with a steeper decrease in milk yield at the end of the lactation. It is therefore advisable to model an expected expression of the trait for each data collection point and to analyze the deviation between expected and observed performance using a time series.

On the other hand, the initial level of the trait expression affects the informative value of the absolute deviation of the observed from the expected trait performance. The absolute deviation may be identical for two individuals, but the deviation relative to the initial level may differ. This scaling effect must be countered by correcting for the disturbance-free trait level.

The autocorrelation describes the strength of the correlation between two data points (Dakos et al. 2012a), whereas the lag-1-autocorrelation, analyzing the correlation between two consecutive data points, is used. It is calculated on the basis of the deviations between the observed and predicted daily milk yield. Without the effect of a disturbance, there should be no correlation between the performance deviations of two days, because they scatter around zero. Under the influence of a disturbance, the daily deviations increase, and it takes several days for them to return to zero. As a result, the deviations of consecutive days correlate with each other. The longer it takes an individual to reach their original performance level or for the observed performance to match the expected performance, the higher the autocorrelation. The target value of the autocorrelation is zero, which corresponds to maximum resilience (Berghof et al. 2018).

Requirements for the use of resilience indicator traits

To carry out time series analyses, a longitudinal measured trait is required. Such traits are primarily collected using precision livestock farming technologies and are mainly performance traits like the daily milk yield of dairy cows or the laying performance of hens. However, advancing digitalization is also increasing the availability of new datasets such as step counts (Poppe et al. 2022b) or feed intake through sensor-controlled feeding systems (Homma et al. 2021). To interpret the results correctly, the biological background and the pathways of the considered trait should be known (Knap and Doeschl-Wilson 2020; Friggens 2023). For example, a decrease in food intake, termed anorexia, shortly before an illness is a natural reaction of the organism, and a resulting increase in variance should not be considered negative per se (Kyriazakis and Doeschl-Wilson 2009). Or, the correlation with other trait groups needs to be known in order to exclude the possibility that it is a partial resilience (for example, a performance resilience in which the individual maintains their performance under the influence of a disturbance, but stops other functions)(Bedere et al. 2022; Ben Abdelkrim et al. 2021b).

In general, it is important that the trait can be measured frequently (Poppe et al. 2020;

Elgersma et al. 2018; Friggens et al. 2022), uniformly and animal-specific (Doekes et al. 2023) at short intervals (Berghof et al. 2024; Ghaderi Zefreh et al. 2024) in a sufficient high number of individuals (Berghof et al. 2018; Friggens et al. 2022). In addition, most individuals in the population must show a response to the trait of interest under a wide range of disturbances. A comparable period should be selected for calculating the resilience indicator traits, e.g. one lactation. The environment in which the trait is recorded must either be diverse and challenging (Berghof et al. 2018) or the trait must be collected in multiple environments and analyzed using a reaction norm model (Knap and Doeschl-Wilson 2020) to ensure as far as possible holistic resilience. Recent studies show that the intensity and duration of the disturbances and the time of onset also have an influence on the detection accuracy and the significance of the resilience indicator traits. Intensive disturbances of medium duration at the beginning of a lactation are statistically easier to detect than weak, long-lasting disturbances at the end of a lactation (Ghaderi Zefreh et al. 2024; Le et al. 2024). The current focus of research is on mapping holistic resilience, although specific resilience could also be researched in the future due to the many requirements (Friggens et al. 2024).

References

Adriaens, I.; Friggens, Nicolas C.; Ouweltjes, W.; Scott, H.; Aernouts, B.; Statham, J. (2020): Productive life span and resilience rank can be predicted from on-farm first-parity sensor time series but not using a common equation across farms. In *J. Dairy Sci.* 103 (8), pp. 7155–7171. DOI: 10.3168/jds.2019-17826.

Adriaens, I.; van den Brulle, I.; D'Anvers, L.; Statham, J. M. E.; Geerinckx, K.; Vliegher, S. de et al. (2021): Milk losses and dynamics during perturbations in dairy cows differ with parity and lactation stage. In *J. Dairy Sci.* 104 (1), pp. 405–418. DOI: 10.3168/jds.2020-19195.

Albers, G.A.A.; Gray, G. D.; Piper, L. R.; Barker, J.S.F.; Jambre, L.F.Le; Barger, I. A. (1987): The genetics of resistance and resilience to Haemonchus contortus infection in young merino sheep. In *International Journal for Parasitology* 17 (7), pp. 1355–1363. DOI: 10.1016/0020-7519(87)90103-2.

Amer, Peter R. (2012): Turning science on robust cattle into improved genetic selection decisions. In *animal* 6 (4), pp. 551–556. DOI: 10.1017/S1751731111002576.

Barreto-Mendes, L.; La Torre, A. de; Ortigues-Marty, I.; Cassar-Malek, I.; Pires, J.; Blanc, F. (2022): How to approach the resilience of livestock exposed to environmental challenges? Quantification of individual response and recovery by means of differential calculus. In *Animal - Open Space* 1 (1), p. 100008. DOI: 10.1016/j.anopes.2022.100008.

Bedere, Nicolas; Berghof, Tom V. L.; Peeters, Katrijn; Pinard-van der Laan, Marie-Hélène; Visscher, Jeroen; David, Ingrid; Mulder, Han A. (2022): Using egg production longitudinal recording to study the genetic background of resilience in purebred and crossbred laying hens. In *Genet Sel Evol* 54 (1), p. 26. DOI: 10.1186/s12711-022-00716-8.

Ben Abdelkrim, A.; Puillet, L.; Gomes, P.; Martin, O. (2021a): Lactation curve model with explicit representation of perturbations as a phenotyping tool for dairy livestock precision farming. In *animal* 15 (1), p. 100074. DOI: 10.1016/j.animal.2020.100074.

Ben Abdelkrim, A.; Tribout, T.; Martin, O.; Boichard, D.; Ducrocq, V.; Friggens, Nicolas C. (2021b): Exploring simultaneous perturbation profiles in milk yield and body weight reveals a diversity of animal responses and new opportunities to identify resilience proxies. In *J. Dairy Sci.* 104 (1), pp. 459–470. DOI: 10.3168/jds.2020-18537.

Bengtsson, C.; Thomasen, J. R.; Kargo, M.; Bouquet, A.; Slagboom, M. (2022): Emphasis on resilience in dairy cattle breeding: Possibilities and consequences. In *Journal of Dairy Science*. DOI: 10.3168/jds.2021-21049.

Berghof, Tom V. L.; Bedere, Nicolas; Peeters, Katrijn; Poppe, Marieke; Visscher, Jeroen; Mulder, Han A. (2024): The genetics of resilience and its relationships with egg production traits and antibody traits in chickens. In *Genet Sel Evol* 56 (1), p. 20. DOI: 10.1186/s12711-024-00888-5.

Berghof, Tom V. L.; Poppe, Marieke; Mulder, Han A. (2018): Opportunities to Improve Resilience in Animal Breeding Programs. In *Front. Genet.* 9, p. 692. DOI: 10.3389/fgene.2018.00692.

Bishop, Stephen C. (2012): A consideration of resistance and tolerance for ruminant nematode infections. In *Front. Genet.* 3, p. 168. DOI: 10.3389/fgene.2012.00168.

Bohmanova, J.; Misztal, I.; Cole, J. B. (2007): Temperature-humidity indices as indicators of milk production losses due to heat stress. In *Journal of Dairy Science* 90 (4), pp. 1947–1956. DOI: 10.3168/jds.2006-513.

Calus, M.P.L.; Veerkamp, Roel F. (2003): Estimation of Environmental Sensitivity of Genetic Merit for Milk Production Traits Using a Random Regression Model. In *Journal of Dairy Science* 86 (11), pp. 3756–3764. DOI: 10.3168/jds.S0022-0302(03)73982-4.

Change, Intergovernmental Panel on Climate (2023): Climate change 2021. The physical science basis : Working Group I contribution to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge: Cambridge University Press.

Chen, Shi-Yi; Boerman, Jacquelyn P.; Gloria, Leonardo S.; Pedrosa, Victor B.; Doucette, Jarrod; Brito, Luiz F. (2023): Genomic-based genetic parameters for resilience across lactations in North American Holstein cattle based on variability in daily milk yield records. In *J. Dairy Sci.* 106 (6), pp. 4133–4146. DOI: 10.3168/jds.2022-22754.

Cheng, Muxi; McCarl, Bruce; Fei, Chengcheng (2022): Climate Change and Livestock Production: A Literature Review. In *Atmosphere* 13 (1), p. 140. DOI: 10.3390/atmos13010140.

Cheruiyot, Evans K.; Haile-Mariam, Mekonnen; Cocks, Benjamin G.; Pryce, Jennie E. (2022): Improving Genomic Selection for Heat Tolerance in Dairy Cattle: Current Opportunities and Future Directions. In *Front. Genet.* 13, p. 894067. DOI: 10.3389/fgene.2022.894067.

Codrea, M. C.; Højsgaard, S.; Friggens, Nicolas C. (2011): Differential smoothing of time-series measurements to identify disturbances in performance and quantify animal response characteristics: An example using milk yield profiles in dairy cows. In *J Anim Sci* 89 (10), pp. 3089–3098. DOI: 10.2527/jas.2010-3753.

Colditz, Ian G.; Hine, Brad C. (2016): Resilience in farm animals: biology, management, breeding and implications for animal welfare. In *Anim. Prod. Sci.* 56 (12), pp. 1961–1983. DOI: 10.1071/AN15297.

Dakos, Vasilis; Carpenter, Stephen R.; Brock, William A.; Ellison, Aaron M.; Guttal, Vishwesha; Ives, Anthony R. et al. (2012a): Methods for detecting early warnings of critical transitions in time series illustrated using simulated ecological data. In *PloS one* 7 (7), e41010. DOI: 10.1371/journal.pone.0041010.

Dakos, Vasilis; van Nes, Egbert H.; D'Odorico, Paolo; Scheffer, Marten (2012b): Robustness of variance and autocorrelation as indicators of critical slowing down. In *Ecology* 93 (2), pp. 264–271. DOI: 10.1890/11-0889.1.

de Goede, D. M.; Gremmen, B.; Blom-Zandstra, M. (2013): Robust agriculture: Balancing between vulnerability and stability. In *NJAS: Wageningen Journal of Life Sciences* 64-65 (1), pp. 1–7. DOI: 10.1016/j.njas.2012.03.001.

Doekes, Harmen P.; Bovenhuis, Henk; Berghof, Tom V. L.; Peeters, Katrijn; Visscher, Jeroen; Mulder, Han A. (2023): Research Note: Genome-wide association study for natural antibodies and resilience in a purebred layer chicken line. In *Poultry Science* 102 (1), p. 102312. DOI: 10.1016/j.psj.2022.102312.

Dominik, Sonja; Swan, Andrew A. (Eds.) (2014): Breeding Focus 2014 – Improving Resilience. Resilience, tolerance, robustness and genotype x environment interaction in Merino sheep breeding. Armidale, Australia: Animal Genetics and Breeding Unit, University of New England (International Forum "Breeding Focus 2014 - Improving Resilience"). Available online at https://www.cabdirect.org/cabdirect/abstract/20203123711.

Ehsaninia, Jamshid; Ghavi Hossein-Zadeh, Navid; Shadparvar, Abdol Ahad (2019): Estimation of genetic variation for macro- and micro-environmental sensitivities of milk yield and composition in Holstein cows using double hierarchical generalized linear models. In *Journal of Dairy Research* 86 (2), pp. 145–153. DOI: 10.1017/S0022029919000293.

Elgersma, G. G.; Jong, G. de; van der Linde, R.; Mulder, H. A. (2018): Fluctuations in milk yield are heritable and can be used as a resilience indicator to breed healthy cows. In *J. Dairy Sci.* 101 (2), pp. 1240–1250. DOI: 10.3168/jds.2017-13270.

Falconer, D. S. (1990): Selection in different environments: effects on environmental sensitivity (reaction norm) and on mean performance. In *Genetics Research* 56 (1), pp. 57–70. DOI: 10.1017/S0016672300028883.

Friggens, N. C.; Ithurbide, M.; Lenoir, G. (2024): Getting to grips with resilience: Toward large-scale phenotyping of this complex trait. In *JDS Communications* 5 (6), pp. 761–766. DOI: 10.3168/jdsc.2023-0434.

Friggens, Nicolas C. (2023): Statistical Modelling of Resilience Trajectories from a Biologists Perspective. Smarter Training school. INRAE. Toulouse, 2023. Available online at https://www.smarterproject.eu/wp-content/uploads/2023/05/statistical-modelling-resilience-biologists-view.pdf.

Friggens, Nicolas C.; Adriaens, I.; Boré, R.; Cozzi, G.; Jurquet, J.; Kamphuis, C. et al. (2022): Resilience: reference measures based on longer-term consequences are needed to unlock the potential of precision livestock farming technologies for quantifying this trait. In *PIC* 2, pp. 1–16. DOI: 10.24072/pcjournal.136.

Friggens, Nicolas C.; Blanc, F.; Berry, D. P.; Puillet, L. (2017): Review: Deciphering animal robustness. A synthesis to facilitate its use in livestock breeding and management. In *animal* 11 (12), pp. 2237–2251. DOI: 10.1017/S175173111700088X.

Gavrilets, Sergey; Hastings, Alan (1994): A Quantitative-Genetic Model for Selection on Developmental Noise. In *Evolution* 48 (5), p. 1478. DOI: 10.2307/2410242.

Ghaderi Zefreh, M.; Pong-Wong, R.; Doeschl-Wilson, A. (2024): Validating statistical properties of resilience indicators derived from simulated longitudinal performance measures of farmed animals. In *animal* 18 (8), p. 101248. DOI: 10.1016/j.animal.2024.101248.

Hansen, James; Sato, Makiko; Ruedy, Reto (2012): Perception of climate change. In *PNAS* 109 (37), E2415-23. DOI: 10.1073/pnas.1205276109.

Hayes, Ben J.; Daetwyler, Hans D.; Goddard, Mike E. (2016): Models for Genome × Environment Interaction: Examples in Livestock. In *Crop Science* 56 (5), pp. 2251–2259. DOI: 10.2135/cropsci2015.07.0451.

Homma, C.; Hirose, K.; Ito, T.; Kamikawa, M.; Toma, S.; Nikaido, S. et al. (2021): Estimation of genetic parameter for feed efficiency and resilience traits in three pig breeds. In *animal* 15 (11), p. 100384. DOI: 10.1016/j.animal.2021.100384.

Knap, Pieter W.; Doeschl-Wilson, Andrea (2020): Why breed disease-resilient livestock, and how? In *Genet Sel Evol* 52 (1), p. 60. DOI: 10.1186/s12711-020-00580-4.

Kyriazakis, I.; Doeschl-Wilson, A. (2009): Anorexia during infection in mammals: variation and its sources. In David Torrallardona, Eugeni Roura (Eds.): Voluntary feed intake in pigs. “Physiological Basis of Voluntary Feed Intake in Swine. Pre and Post-Absorptive Regulation” Workshop, which was organised on 19 May 2009, to precede the XIth Symposium on Digestive Physiology of Pigs, in Montbrió del Camp, Spain on 20-22 May 2009. Wageningen: Wageningen Acad. Publ, pp. 307–321. Available online at https://brill.com/edcollchap/book/9789086866892/BP000015.xml.

Le, Vincent; Rohmer, Tom; David, Ingrid (2024): Identification and characterization of unknown disturbances in a structured population using high-throughput phenotyping data and measurement of robustness: application to growing pigs. In *Journal of animal science* 102, skae059. DOI: 10.1093/jas/skae059.

Misztal, I. (2017): BREEDING AND GENETICS SYMPOSIUM: Resilience and lessons from studies in genetics of heat stress. In *Journal of animal science* 95 (4), pp. 1780–1787. DOI: 10.2527/jas.2016.0953.

Mordecai, Erin A.; Cohen, Jeremy M.; Evans, Michelle V.; Gudapati, Prithvi; Johnson, Leah R.; Lippi, Catherine A. et al. (2017): Detecting the impact of temperature on transmission of Zika, dengue, and chikungunya using mechanistic models. In *PLoS neglected tropical diseases* 11 (4), e0005568. DOI: 10.1371/journal.pntd.0005568.

Mulder, Han A. (2016): Genomic Selection Improves Response to Selection in Resilience by Exploiting Genotype by Environment Interactions. In *Front. Genet.* 7, p. 178.

DOI: 10.3389/fgene.2016.00178.

Poppe, M.; Veerkamp, Roel F.; van Pelt, M. L.; Mulder, H. A. (2020): Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. In *J. Dairy Sci.* 103 (2), pp. 1667–1684. DOI: 10.3168/jds.2019-17290.

Poppe, Marieke (Ed.) (2022): Genetic improvement of resilience in dairy cattle using longitudinal data: Wageningen University and Research.

Poppe, Marieke; Mulder, Han A.; van Pelt, Mathijs L.; Mullaart, Erik; Hogeveen, Henk; Veerkamp, Roel F. (2022): Development of resilience indicator traits based on daily step count data for dairy cattle breeding. In *Genet Sel Evol* 54 (1), p. 21. DOI: 10.1186/s12711-022-00713-x.

Rauw, W.M; Kanis, E.; Noordhuizen-Stassen, E.N; Grommers, F.J (1998): Undesirable side effects of selection for high production efficiency in farm animals: a review. In *Livestock Production Science* 56 (1), pp. 15–33. DOI: 10.1016/S0301-6226(98)00147-X.

Rauw, Wendy Mercedes (Ed.) (2009): Resource Allocation Theory Applied to Farm Animal Production. Introduction. Department of Animal Biotechnology. Reno, USA. Available online at https://epdf.tips/resource-allocation-theory-applied-to-farm-animal-production.html.

Rönnegård, L.; Felleki, Majbritt; Fikse, W. F.; Mulder, H. A.; Strandberg, E. (2013): Variance component and breeding value estimation for genetic heterogeneity of residual variance in Swedish Holstein dairy cattle. In *J. Dairy Sci.* 96 (4), pp. 2627–2636. DOI: 10.3168/jds.2012-6198.

Rönnegård, Lars; Felleki, Majbritt; Fikse, Freddy; Mulder, Herman A.; Strandberg, Erling (2010): Genetic heterogeneity of residual variance - estimation of variance components using double hierarchical generalized linear models. In *Genet Sel Evol* 42, p. 8. DOI: 10.1186/1297-9686-42-8.

Scheffer, Marten; Bolhuis, J. Elizabeth; Borsboom, Denny; Buchman, Timothy G.; Gijzel, Sanne M. W.; Goulson, Dave et al. (2018): Quantifying resilience of humans and other animals. In *Proceedings of the National Academy of Sciences of the United States of America* 115 (47), pp. 11883–11890. DOI: 10.1073/pnas.1810630115.

Schmid, M.; Imort-Just, A.; Emmerling, Reiner; Fuerst, C.; Hamann, H.; Bennewitz, Jörn (2021): Genotype-by-environment interactions at the trait level and total merit index level for milk production and functional traits in Brown Swiss cattle. In *animal* 15 (1), p. 100052. DOI: 10.1016/j.animal.2020.100052.

Strandberg, E.; Felleki, Majbritt; Fikse, W. F.; Franzén, J.; Mulder, H. A.; Rönnegård, L. et al. (2013): Statistical tools to select for robustness and milk quality. In *Advances in Animal Biosciences* 4 (3), pp. 606–611. DOI: 10.1017/S2040470013000162.

Streit, M.; Reinhardt, F.; Thaller, G.; Bennewitz, Jörn (2012): Reaction norms and genotype-by-environment interaction in the German Holstein dairy cattle. In *Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie* 129 (5), pp. 380–389. DOI: 10.1111/j.1439-0388.2012.00999.x.

Taghipoor, M.; Pastell, M.; Martin, O.; Nguyen Ba, H.; van Milgen, J.; Doeschl-Wilson, A. et al. (2023): Animal board invited review: Quantification of resilience in farm animals. In *animal* 17 (9), p. 100925. DOI: 10.1016/j.animal.2023.100925.

van der Waaij, E. H. (2004): A resource allocation model describing consequences of artificial selection under metabolic stress. In *J Anim Sci* 82 (4), pp. 973–981. DOI: 10.2527/2004.824973x.

Wu, R. L. (1997): Genetic control of macro-and micro-environmental sensitivities in Populus. In *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik* 94 (1), pp. 104–114. DOI: 10.1007/s001220050388.

CHAPTER TWO

RESILIENCE INDICATOR TRAITS IN 3 DAIRY CATTLE BREEDS IN BADEN-WÜRTTEMBERG

F. Keßler[1]*, R. Wellmann[1], M.G.G. Chagunda[2], J. Bennewitz[1]

[1] Institute of Animal Science, University of Hohenheim, 70599 Stuttgart, Germany

[2] Institute of Agricultural Sciences in the Tropics, University of Hohenheim, 70599 Stuttgart, Germany

*Corresponding author: franziska.kessler@uni-hohenheim.de

Published in Journal of Dairy Science (2024), Volume 107 (6), pp. 3780–3793
https://doi.org/10.3168/jds.2023-24305

ABSTRACT

In recent years, research in animal breeding has increasingly focused on the topic of resilience, which is expected to continue in the future due to the need for high-yielding, healthy, and robust animals. In this con- text, an established approach is the calculation of resilience indicator traits with time series analyses. Examples are the variance and autocorrelation of daily milk yield in dairy cows. We applied this methodology to the German dairy cow population. Data from the 3 breeds (German Holstein, German Fleckvieh, and German Brown Swiss) were obtained, which included 13,949 lactations from 36 farms from the state Baden-Württemberg in Germany working with automatic milking systems. Using the milk yield data, the daily absolute milk yields, deviations between observed and expected daily milk yields, and relative proportions of daily milk yields in relation to lactation performance were calculated. We used the variance and autocorrelation of these data as phenotypes in our statistical analyses. We estimated a heritability of 0.047 for autocorrelation and heritabilities between 0.026 and 0.183 for variance-based indicator traits. Furthermore, significant breed differences could be observed, with a tendency of better resilience in Brown Swiss. The breed differences can be due to both genetic and environmental factors. A high value of a variance-based indicator trait indicates a low resilience. Performance traits were positively correlated with variance-based indicator traits calculated from absolute daily milk yields, but they were negatively correlated with variance-based indicators calculated from relative daily milk yields. Thus, they can be considered as different traits. Although variance-based indicators based on absolute daily milk yields were affected by the performance level, variance-based indica- tors based on relative daily milk yields were corrected for the performance level and also showed higher heritabilities. Thus, they seem to be more suitable for practical use. Further studies need to be conducted to calculate the correlations between resilience indicators, functional traits, and health traits.

Key words: resilience, dairy cows, variance, autocorrelation

INTRODUCTION

Modern livestock production faces the challenge of supplying the world's population with high-quality food and at the same time protecting the environment by maximizing resource efficiency (Madhusoodan et al., 2019). This requires our livestock to maintain a high, stable level of performance while staying healthy. Various environmental factors have an impact on the organism, and their effects are intensified by progressive developments such as climate change, new and evolving pathogens or changing social demands (Hansen et al., 2012; Dominik and Swan, 2014; Schader et al., 2015). To breed live- stock that meet these challenges, the sole consideration of health traits and heat tolerance may not be sufficient. Overarching traits such as resilience (the ability to respond to and recover from short-term disturbances of any kind to return to original performance levels; Colditz and Hine, 2016; Poppe et al., 2021) are becoming increasingly important (Friggens et al., 2022).

In recent years, various ideas have been proposed for defining and measuring an individual's resilience. Because the disturbance events are usually unknown, one of the most promising approaches are resilience indicators based solely on statistical time series analysis (Berghof et al., 2019). First attempts to capture disturbance effects by evaluating the changes trait expressions over time were based on test-day data (Codrea et al., 2011), but the regular use of time series analysis only occurred with the further development of precision livestock farming and the availability of longitudinal data (Berghof et al., 2019). Elgersma et al. (2018) and Putz et al. (2019) were among of the first to introduce the methodology into livestock research, studying daily milk yields of dairy cattle and daily feed intake in pigs, respectively. However, their methodology did not take into account the individual performance level. Subsequent studies analyzed the deviation of the observed performance from a predicted performance. Predicted performance was calculated either for an individual or for the entire sample, with higher accuracy for the former (Bedere et al., 2022).

The deviations from either the mean performance or the predicted performance can be used to calculate resilience indicators, for example the natural logarithm of the variance or the lag-1-autocorrelation. The variance quantifies the upward-downward fluctuation in performance, whereby resilient animals are expected to show less intense responses to disturbances, meaning that the variance indicators are small. In contrast, the lag-1-autocorrelation is expected to provide information about the time until recovery from disturbances (Berghof et al., 2019; Poppe et al., 2020; Wang et al., 2022), and a value close to zero indicates higher resilience because the deviations of the observed from the expected milk yield after a disturbance were reduced more rapidly. Less resilient animals, on the other hand, take longer to recover the initial performance level, so the deviations between observed and expected daily milk yield persist over a longer period (Dai et al., 2012; Scheffer et al., 2012). Because several studies assessed the heritability and the correlations with different functional and health traits as moderate (Poppe et al., 2020; Wang et al., 2022), the variance turned out to be the more suitable parameter to represent general resilience. However, the number and density of data points needs to be high enough to capture effects of disturbances (Mehrabbeik et al., 2021). Examples for the application of time series analysis include step counts of dairy cows (Poppe et al., 2022a), eggs laid per week in laying hens (Bedere et al., 2022), activity data and feed intake in pigs (van der Zande et al., 2020; Homma et al., 2021), and growth rates in fish (Mengistu et al., 2022).

Different breeds have individual characteristics and differ, for example, in their performance or adaptability. Therefore, it could be hypothesized that different breeds cope differently with external influences. For example, low-yielding breeds often have longer life spans, reduced length of calving intervals, smaller insemination indices, and in some cases lower milk somatic cell counts (Bieber et al., 2019). However, high-yielding breeds also differ among each other. Mylostyvyi et al. (2021) found that Brown Swiss showed a lower physiological response and lower drop in milk performance under heat stress than Holstein-Friesian, indicating better heat tolerance, whereas Toledo-Alvarado et al. (2017) reported that Fleckvieh had in general a better fertility than Brown Swiss or Holstein-Friesian. For resilience, to the best of our knowledge, only a few studies have been conducted that examined resilience indicator breed differences (Bonekamp et al., 2022; Adriaens et al., 2023).

We applied the previously mentioned resilience indicators and additional variance indicators to the German Holstein (**HF**), German Brown Swiss (**BS**) and German Fleckvieh (**FV**) breeds. Along with absolute daily milk yields, we also considered variance indicators based on relative daily milk yields to correct for individual performance levels. Thus, our objectives were (1) to define and calculate various resilience indicators based on absolute and relative daily milk yields; (2) to estimate heritabilites and genetic correlations of these resilience indicators for the German dairy cattle population; (3) to estimate genetic correlations between resilience indicators and 305-d performance for milk yield (**MY_{305}**), protein yield (**PY_{305}**), fat yield (**FPY_{305}**), and average daily milk yield (**AMY_{305}**), and (3) to compare the 3 breeds (HF, BS and FV) with respect to the resilience indicators.

MATERIALS AND METHODS

Data processing and evaluation, as well as statistical analyses, were performed in the R software (version 4.2.3; R Core Team, 2022) by using ASReml-R 4 for the genetic analyses. No human or animal subjects were used, so this analysis did not require approval by an Institutional Animal Care and Use Committee or Institutional Review Board.

Materials

The data were collected between September 30, 2017, and March 28, 2023, on 36 farms in Baden-Württemberg (Germany) that participated in the projects KlimaFit or KuhVision, or both. In total, 13,949 lactations from 6,731 cows were considered. The data included 6,352 lactations from 3,075 HF cows, 6,694 lactations from 3,150 FV cows, and 903 lactations from 506 BS cows. Data collection and processing was carried out by the Landeskontrollverband Baden-Württemberg. All farms worked with an automatic milking system, which re- corded the amount of milk per milking. Aborted milkings were removed from the data set. The milking quantities were summarized to daily milk quantities. That is, the first milking of a day was prorated to the time up until midnight of the previous day and since midnight of the current day. Days when the number of animals milked on the farm differed from the average by 3 standard deviations were removed, as well as the day before and after. In addition, the first day after and the last day before a gap in an individual's records were excluded.

Methods

Modeling Lactation Curve. A lactation curve was predicted for each lactation of each animal. Because the predicted lactation curve should ideally reflect the expected performance in the absence of disturbances, a spline interpolation with weighting of the data points was performed. Data points corresponding to days in which the cow had a temporary reduction of the milk yield were given lower weights. The spline interpolation was obtained using the package *pspline* in R (Ramsey and Ripley, 2022). The weights were calculated as follows: For each day d, all intervals shorter than 60 d were considered that include day d. Intervals whose boundaries were less than 5 d away from day d were excluded. For each interval, it was determined whether the milk yield at day d is above or below the straight line that connects the 2 milk yields at the interval boundaries. The number D of times in which the milk yield was above the line was counted, and the weighting factor w_d used in the spline interpolation was calculated as $w_d = \frac{D}{N}$, where N is the total number of N intervals. Figure 1 illustrates this. The algorithm for computing the weights is given in Appendix 1. Different orders of interpolation from 3 to 9 were tested and compared, and 5 degrees of freedom were chosen by visual assessment of the lactation curves (not shown elsewhere). For standardizing the observation period, only the period between d 10 and d 305 of each lactation was considered.

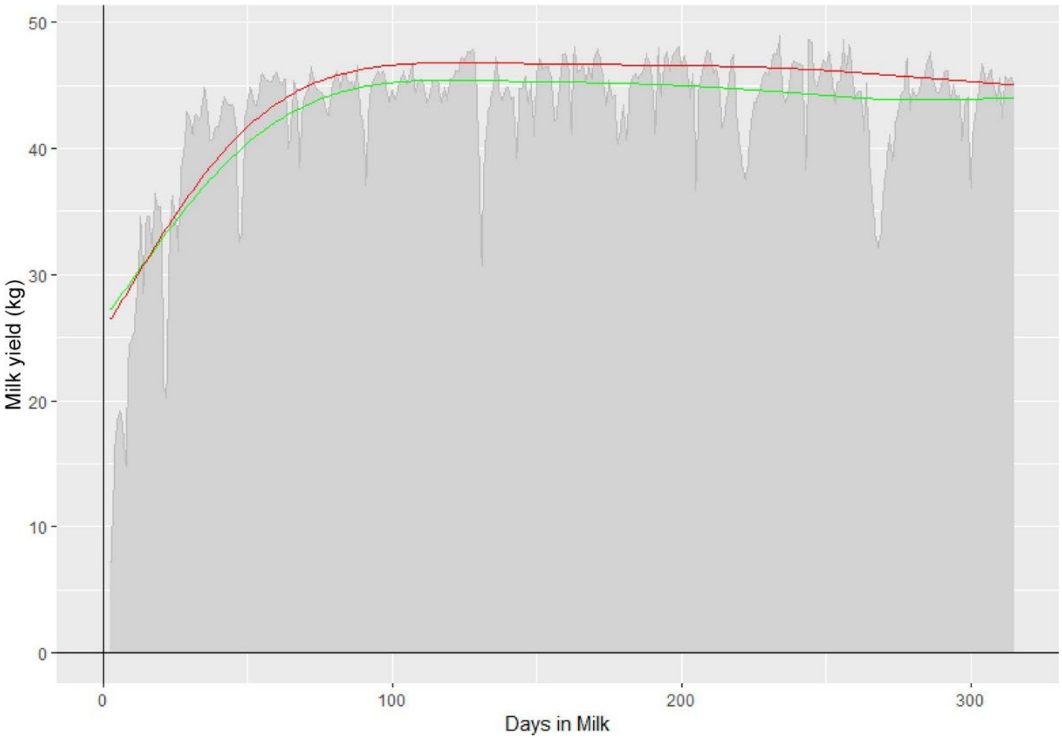


Figure 1. Modeled lactation curve with (red line) and without (green line) weighting of the daily milk yields (gray area) for a German Holstein

Calculation of Resilience Indicators. We denote with y_{il} the n-vector with milk yields of cow i in lactation l. The variance of the vector is calculated as

$$var(\boldsymbol{y}_{il}) = \frac{1}{n-1} \times \sum_{t=1}^{n} (y_{ilt} - \bar{\boldsymbol{y}}_{il})^2,$$

with t being a day and n the number of days for which daily milk yield data were available for this cow. The covariance (cov) between 2 succeeding components is calculated as

$$cov(\boldsymbol{y}_{il}) = \frac{1}{n-2} \times \sum_{t=2}^{n} (y_{ilt} - \bar{\boldsymbol{y}}_{il}) \times (y_{il,t-1} - \bar{\boldsymbol{y}}_{il}) .$$

The variance ($\mathbf{var}$) of the daily milk yields satisfies

$$var(\boldsymbol{y}_{il}) = var(\boldsymbol{y}_{il} - \bar{\boldsymbol{y}}\mathbf{1}),$$

where **1** is the vector with ones. That is, the variance quantifies the deviation of the actual milk yields from the mean milk yield. In contrast, the variance indicator ($\mathbf{var_d}$), defined as

$$var_d(\boldsymbol{y}_{il}) = var(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il}),$$

quantifies the deviation of the actual milk yields y_{ilt} from the predicted milk yields $\hat{y}_{ilt}$ obtained from spline interpolation. The variance of daily relative milk yield ($\mathbf{var_r}$) is calculated as

$$var_r(\boldsymbol{y}_{il}) = var(a_{il}\boldsymbol{y}_{il}),$$

where the scaling factor $a_{il} = 100 / \sum_{t=1}^{n} y_{ilt}$ ensures that the relative milk yield adds up to 100%. The variance of the deviations between daily relative milk yield and predicted relative daily milk yield ($\mathbf{var_{rd}}$) was calculated as

$$var_{rd}(\boldsymbol{y}_{il}) = var[a_{il}(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})].$$

Taking the natural logarithms of the parameters provides the parameters $\mathbf{ln\,var}(y_{il})$, $\mathbf{ln\,var_d}(y_{il})$, $\mathbf{ln\,var_r}(y_{il})$, and $\mathbf{ln\,var_{rd}}(y_{il})$, respectively. Finally, the lag-1-autocorrelation ($\mathbf{r_{Auto}}$) between 2 lactation days t was calculated as

$$r_{Auto}(\boldsymbol{y}_{il}) = \frac{cov(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})}{var(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})}.$$

An overview of all resilience indicators and their definitions can be found in Table 1.

Genetic Analysis. Genetic analyses were performed for both the entire data set and for each breed separately. The analysis of the entire data set is called the across breed (**AB**) evaluation. Only lactations for which at least 50% of the data were available between lactation d 10 and lactation d 305 were considered in the analysis. Univariate analysis was performed for all data sets with the following animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wpe} + \mathbf{e},$$

where $\mathbf{y}$ is the vector of observations, $\mathbf{b}$ is the vector of fixed effects described in detail later, $\mathbf{u}$ is the random vector of additive genetic effects, $\mathbf{pe}$ is the random vector of permanent environmental effects, and $\mathbf{e}$ is the vector of residuals. The matrices $\mathbf{W}$, $\mathbf{X}$, and $\mathbf{Z}$ are the corresponding incidence matrices. The vector of fixed effects $\mathbf{b}$ comprised age at first calving in month (20 levels), lactation divided in first or higher lactation (2 levels), and herd-year-season ($\mathbf{hys}$, 585 levels) for all univariate analyses. The seasons were divided into spring (March– May), summer (June–August), autumn (September–November), and winter (December–February). For AB evaluations, a breed effect was included in $\mathbf{b}$. For resilience indicators, the completeness of lactation data (divided in ≥90%, 80% to ≤ 90%, 70% to ≤ 80%, 60% to ≤ 70%, and 50% to ≤ 60%) was included. Levels of fixed effects with less than 5 individuals were excluded. The vectors of additive genetic effects $\mathbf{u}$, permanent environment effects $\mathbf{pe}$, and residuals $\mathbf{e}$ were normally distributed with $\mathbf{pe} \sim N(0, \mathbf{I_{pe}}\sigma^2_{\mathbf{pe}})$, $\mathbf{e} \sim N(0, \mathbf{I_e}\sigma^2_{\mathbf{e}})$, and $\mathbf{u} \sim N(0, \mathbf{A}\sigma^2_u)$, where $\mathbf{I_{pe}}$ and $\mathbf{I_e}$ are identity matrices, $\mathbf{A}$ is the additive genetic relationship matrix, and $\sigma^2_{\mathbf{pe}}$, $\sigma^2_{\mathbf{e}}$, and σ^2_u are variances of $\mathbf{pe}$, $\mathbf{e}$, and $\mathbf{u}$, respectively. Interbreed comparison of the average value of resilience indicators was performed as a Tukey's honestly significant difference test using the package *biometryassist* in R (Nielsen et al., 2022).

For bivariate analyses, the same model extended to 2 traits was used. The only difference was that hys was included as a random effect to facilitate convergence of the model. It was assumed to be normally distributed with $hys \sim N(0, \mathbf{I}_{hys}\sigma^2_{hys})$, whereby $\mathbf{I}_{hys}$ is an identity matrix and σ^2_{hys} is the variance of hys. Correlations were computed between resilience indicators as well as between resilience indicators and the performance traits MY_{305}, PMY_{305}, FY_{305}, and AMY_{305}.

Table 1. Overview and description of the resilience indicators

Trait	Description
var	Variance of the observed absolute daily milk yield
$\ln \mathrm{var}$	Log variance of the observed absolute daily milk yield
$\mathrm{var_d}$	Variance of deviation between observed absolute and predicted daily milk yield
$\ln \mathrm{var_d}$	Log variance of deviation between observed absolute and predicted daily milk yield
$\mathrm{r_{Auto}}$	Autocorrelation of deviation between observed absolute and predicted daily milk yield
$\mathrm{var_r}$	Variance of relative daily milk yield

$\ln \mathrm{var}_{\mathrm{r}}$	Log variance of relative daily milk yield
$\mathrm{var}_{\mathrm{rd}}$	Variance of deviation between observed relative and predicted daily milk yield
$\ln \mathrm{var}_{\mathrm{rd}}$	Log variance of deviation between observed relative and predicted daily milk yield

RESULTS

Description of Resilience Indicators

Table 2 shows the descriptive statistics of the resilience indicators across and within breeds. BS had the lowest mean values for all variance-based indicators (var, $\ln \mathrm{var}$, $\mathrm{var}_{\mathrm{d}}$, $\ln \mathrm{var}_{\mathrm{d}}$, $\mathrm{var}_{\mathrm{r}}$, and $\mathrm{var}_{\mathrm{rd}}$, except $\ln \mathrm{var}_{\mathrm{r}}$ and $\ln \mathrm{var}_{\mathrm{rd}}$). We found that FV had the lowest mean $\mathrm{r}_{\mathrm{Auto}}$ and HF showed the highest values for variances-based indicators calculated from absolute milk yields compared with BS and FV, but variance-based indicators based on relative milk yields were between the mean values of these traits in BS and FV.

Table 2. Number of lactations, mean, and SD for resilience indicators calculated from daily milk yields across breeds and subdivided by breeds[1]

Trait[2]	AB, n = 13,949		BS, n = 819		FV, n = 6,638		HF, n = 6,231	
	μ	σ	μ	σ	μ	σ	μ	σ
var	40.5	32.84	28.5	21.04	37.0	27.88	46.1	37.81
$\ln \mathrm{var}$	3. 4	0.82	3.1	0.84	3.3	0.78	3.5	0.84
$\mathrm{var}_{\mathrm{d}}$	8.7	7.37	5.3	4.99	7.3	5.79	10.6	8.55
$\ln \mathrm{var}_{\mathrm{d}}$	1.9	0.72	1.4	0.69	1.8	0.67	2.1	0.70
$\mathrm{r}_{\mathrm{Auto}}$	0.5	0.17	0. 6	0.16	0.5	0.17	0.6	0.15
$\mathrm{var}_{\mathrm{r}}$	0.7	0.72	0.5	0.60	0.8	0.78	0.6	0.67
$\ln \mathrm{var}_{\mathrm{r}}$	−14.5	0.85	−14.8	0.82	−14.4	0.80	−14.7	0.88
$\mathrm{var}_{\mathrm{rd}}$	0.2	0.18	0.1	0.13	0.2	0.2	0.2	0.18
$\ln \mathrm{var}_{\mathrm{rd}}$	−16.0	0.78	−16.4	0.77	−16.0	0.7	−16.1	0.79

[1] μ = mean; σ = SD.

[2] Description of resilience indicators can be found in Table 1.

The results from the univariate analysis using the whole data set are presented in Table 3, whereby most of the variance components were significantly different from zero. The highest heritability was estimated for $\ln \mathrm{var}_{\mathrm{r}}$ (h^2 = 0.18) and lowest for $\mathrm{var}_{\mathrm{rd}}$ (h^2 = 0.03), whereby the estimation for the additive genetic effect for $\mathrm{r}_{\mathrm{Auto}}$ and $\mathrm{var}_{\mathrm{rd}}$ was close to 0. With the exception of $\ln \mathrm{var}_{\mathrm{r}}$, the heritabilities of the variance-based indicators were higher when calculated from absolute rather than relative milk yields. Variances of the animal effects and the permanent environmental effects were similar in magnitude, with the permanent environmental effect tending to be stronger, except for var and ln var. Results of the analyses within breeds are available in Appendix 2 Table A1 with highest heritabilities for BS and lowest for FV.

Table 3. Estimation of heritability (h^2) and variance components of additive genetic (σ_u^2) and permanent environmental (σ_{pe}^2) effects for resilience indicators in the across breed analysis

Trait[1]	h^2	σ_u^2	σ_{pe}^2
var	0.16	109.35	66.98
$\ln \mathrm{var}$	0.16	0.06	0.05
$\mathrm{var}_{\mathrm{d}}$	0.11	4.35	7.52
$\ln \mathrm{var}_{\mathrm{d}}$	0.17	0.05	0.06
$\mathrm{r}_{\mathrm{Auto}}$	0.05	0.00	0.00
$\mathrm{var}_{\mathrm{r}}$	0.09	0.03	0.08
$\ln \mathrm{var}_{\mathrm{r}}$	0.18	0.08	0.08
$\mathrm{var}_{\mathrm{rd}}$	0.03	0.00	0.00
$\ln \mathrm{var}_{\mathrm{rd}}$	0.10	0.04	0.06

[1] Description of resilience indicators can be found in Table 1.

Figure 2 shows the results of the Tukey's honestly significant difference test with one plot for each trait, with significant differences marked using different letters. Indicator $\mathrm{r}_{\mathrm{Auto}}$ was significantly smaller for FV than for HF, and BS did not differ significantly from either FV or HF. Variance-based indicators calculated from absolute daily milk yields were lowest for BS but only significantly different from FV for $\ln \mathrm{var}$. In addition, HF showed significantly higher variance-based indicators based on absolute daily milk yields than BS, and for $\mathrm{var}_{\mathrm{rd}}$ and $\ln \mathrm{var}_{\mathrm{rd}}$ compared with FV. Variance-based indicators calculated from relative daily milk yields were similar in all breeds, except $\ln \mathrm{var}_{\mathrm{r}}$, with a significant difference between BS and FV. In general, BS showed the smallest values for variance-based indicators, but the largest range.

Correlations Between Resilience Indicators

Correlations between resilience indicators estimated from the whole data set are represented in Table 4, with genetic correlations shown below and phenotypic shown above the diagonal. In general, phenotypic correlations were all positive and genetic correlations between $\mathrm{r}_{\mathrm{Auto}}$ and any version of variance-based indicator were negative, but mostly with large standard errors. Variance- based indicators based on relative daily milk yields had relative smaller standard errors than variance-based indicators based on absolute milk yields.

Both genetic and phenotypic correlations between different variance-based indicators were, as expected, positive and often significant. The strongest genetic correlation was found between $\ln \mathrm{var}_{\mathrm{rd}}$ and $\mathrm{var}_{\mathrm{rd}}$($r$ = 0.95). The genetic correlations between $\ln \mathrm{var}$ and $\ln \mathrm{var}_{\mathrm{d}}$ (r = 0.43) and between $\ln \mathrm{var}_{\mathrm{r}}$ and $\ln \mathrm{var}_{\mathrm{rd}}$ (r = 0.53) were moderate, indicating that variance-based indicators calculated from observed daily milk yield can be considered as different traits compared with variance-based indicators calculated from deviations of daily milk yield. Comparing the same resilience indicators calculated from absolute and relative milk yields, the genetic correlations ranged between r = 0.75 and r = 0.84. The logarithmized traits were highly genetically correlated with their nonlogarithmized counterparts (r = 0.91–0.95). The results from the intrabreed analysis are shown in Appendix 2 Table A2. Only small deviations from the AB analysis occurred, although the standard errors were higher. We found that FV and HF were in line with the estimations in the whole data set, and stronger genetic correlations were observed for BS.

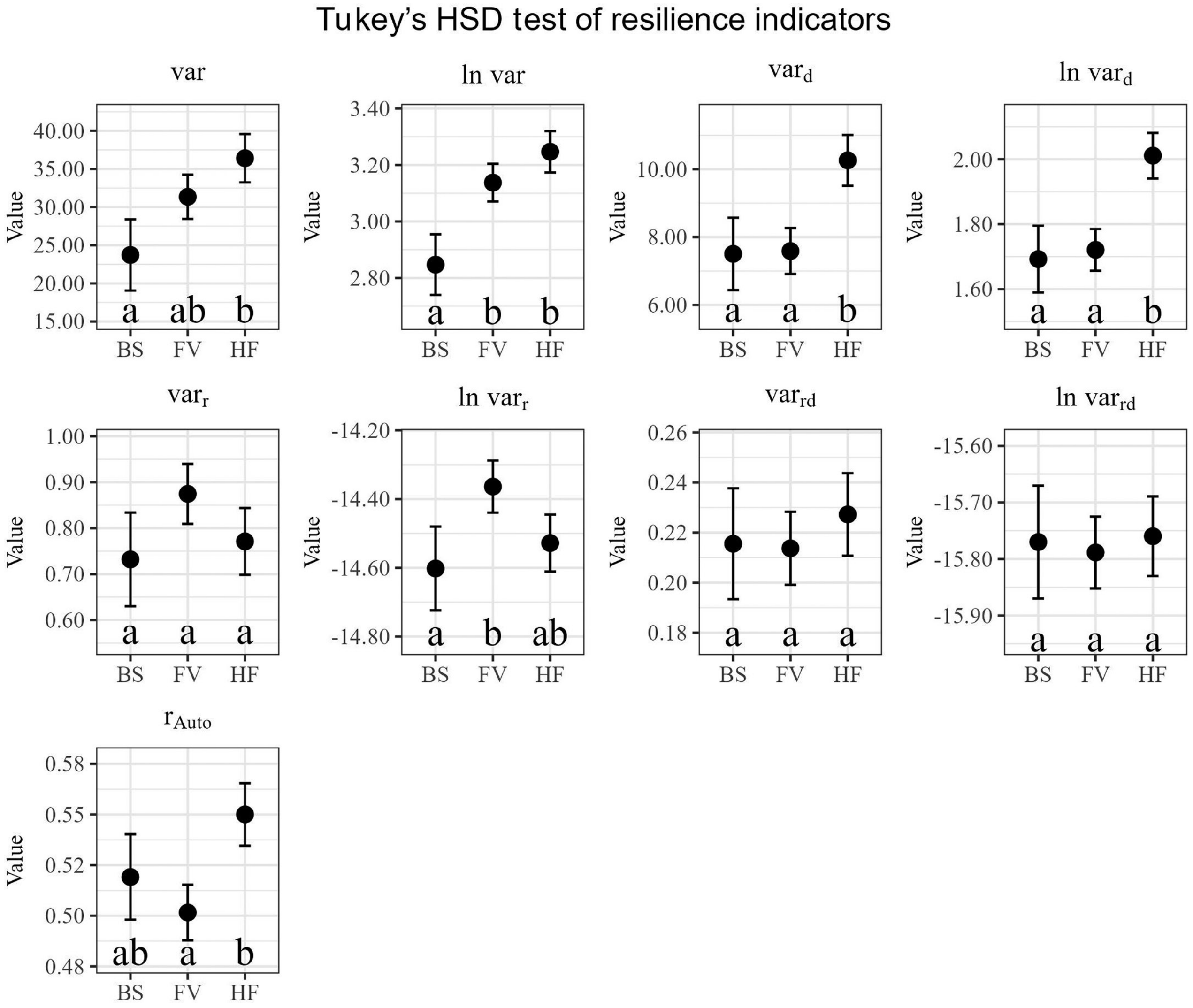


Figure 2. Tukey's honestly significant difference (HSD) test of the resilience indicators for differences between the breeds BS, FV, and HF. Plots show the mean value and the upper and lower confidence interval of the resilience indicators, with significant differences indicated by different lowercase letters (a,b). Descriptions of resilience indicators can be found in Table 1.

Table 4. Correlations (genetic: below the diagonal; phenotypic: above the diagonal) between the resilience indicators calculated from daily milk yields across breeds (SE in parentheses)

Trait[1]	var	$\ln \mathrm{var}$	$\mathrm{var}_{\mathrm{d}}$	$\ln \mathrm{var}_{\mathrm{d}}$	$\mathrm{r}_{\mathrm{Auto}}$	$\mathrm{var}_{\mathrm{r}}$	$\ln \mathrm{var}_{\mathrm{r}}$	$\mathrm{var}_{\mathrm{rd}}$	$\ln \mathrm{var}_{\mathrm{rd}}$
var		0.85 (0.003)	0.38 (0.010)	0.36 (0.011)	0.09 (0.012)	0.68 (0.006)	0.74 (0.005)	Not converged	0.31 (0.011)
$\ln \mathrm{var}$	0.94 (0.015)		0.40 (0.010)	0.44 (0.011)	0.07 (0.013)	0.65 (0.007)	0.87 (0.003)	0.32 (0.011)	0.38 (0.011)
$\mathrm{var}_{\mathrm{d}}$	0.37 (0.073)	0.37 (0.073)		0.87 (0.003)	−0.03 (0.012)	0.23 (0.011)	0.30 (0.011)	0.71 (0.005)	0.77 (0.005)
$\ln \mathrm{var}_{\mathrm{d}}$	0.34 (0.069)	0.43 (0.064)	0.91 (0.018)		−0.04 (0.014)	0.22 (0.013)	0.30 (0.012)	0.65 (0.007)	0.85 (0.004)
$\mathrm{r}_{\mathrm{Auto}}$	−0.11 (0.105)	−0.17 (0.104)	−0.21 (0.114)	−0.18 (0.104)		0.09 (0.012)	0.07 (0.013)	−0.01 (0.012)	−0.03 (0.013)
$\mathrm{var}_{\mathrm{r}}$	0.78 (0.043)	0.79 (0.044)	0.12 (0.103)	0.08 (0.097)	−0.13 (0.128)		0.77 (0.004)	0.48 (0.009)	0.41 (0.011)
$\ln \mathrm{var}_{\mathrm{r}}$	0.74 (0.035)	0.84 (0.021)	0.08 (0.080)	0.09 (0.075)	−0.30 (0.101)	0.91 (0.026)		0.44 (0.009)	0.51 (0.010)
$\mathrm{var}_{\mathrm{rd}}$	Not converged	0.44 (0.111)	0.80 (0.059)	0.75 (0.066)	−0.66 (0.167)	0.44 (0.123)	0.47 (0.101)		0.79 (0.004)
$\ln \mathrm{var}_{\mathrm{rd}}$	0.36 (0.078)	0.50 (0.070)	0.67(0.050)	0.75 (0.036)	−0.43 (0.112)	0.41 (0.090)	0.53 (0.062)	0.95 (0.034)	

[1] Description of resilience indicators can be found in Table 1.

Table 5. Number of lactations, mean, and SD of the performance traits MY_{305}, PY_{305}, FY_{305}, and AMY_{305} across breeds and subdivided by breed[1]

Trait[2]	AB, n = 8,446		BS, n = 487		FV, n = 3,275		HF, n = 4,466	
	μ	σ	μ	σ	μ	σ	μ	σ
MY_{305}	10,033	2,111.0	9,040	1,683.4	8,775	1,523	11,064	1,987.5
PY_{305}	346	66.5	321	58.1	308	50	376	62.8
FY_{305}	387	75.1	377	61.8	345	58	417	73.5
AMY_{305}	31.8	6.8	29.0	5.4	27.8	4.9	35.0	6.5

[1] μ = mean; σ = SD.

Correlations Between Resilience Indicators and 305-D Yields

Means and standard deviations of performance traits MY_{305}, FMY_{305}, PMY_{305}, and AMY_{305}, are summarized in Table 5, with highest yields in HF and lowest in FV for all traits; BS and the records of all breeds evaluated jointly ranked in between.

Correlations between performance traits and resilience indicators estimated in the whole data set are presented in Table 6. Phenotypic correlations between $\mathrm{r}_{\mathrm{Auto}}$ and performance traits were close to zero, whereas genetic correlations were all positive, but only partly significant. Performance traits were genetically and phenotypically positively correlated with variance-based indicators based on absolute daily milk yields, but negatively correlated with variance-based indicators based on relative daily milk yields. More specifically, the variance-based indicators of absolute daily milk yields (var, $\ln var$) tended to show a positive correlation with performance traits, the variance-based indicators of deviations from predicted daily milk yields (var_d, $\ln var_d$) had a moder- ate positive correlation with performance traits, whereas variance-based indicators based on relative milk yields and variance-based indicators based on deviations of relative milk yields were negatively correlated. The resilience indicators tended to show the strongest genetic correlations with MY_{305}, PY_{305}, and AMY_{305}, whereas the genetic correlations with FY_{305} were weaker. For the first 3 performance traits, the strongest positive genetic correlation was observed with $\ln \mathrm{var}_{\mathrm{d}}$, whereas FY_{305} had the strongest positive genetic correlation with var_d (r = 0.25). The strongest negative genetic correlations for MY_{305}, PY_{305}, and AMY_{305}were obtained for $\ln var_r$, and the strongest negative genetic correlation for FY_{305} was obtained for var_r. Hence, as performance increased, the variance-based indicators of relative daily milk yields decreased. Results for each breed are presented in Appendix 2 Table A3.

Table 6. Phenotypic ($corr_{phenotypic}$) and genetic ($corr_{genetic}$) correlations between the MY_{305}, PY_{305}, FY_{305}, AMY_{305}, and resilience indicators calculated from daily milk yields across breeds, with SE in parentheses (n = 8,846 lactations)

Trait[2]	MY_{305}		PY_{305}		FY_{305}		AMY_{305}	
	$corr_{phenotypic}$	$corr_{genetic}$	$corr_{phenotypic}$	$corr_{genetic}$	$corr_{phenotypic}$	$corr_{genetic}$	$corr_{phenotypic}$	$corr_{genetic}$
var	0.12 (0.013)	0.11 (0.085)	0.07 (0.014)	0.03 (0.091)	0.08 (0.013)	0.10 (0.063)	0.10 (0.014)	0.07 (0.087)
$\ln \mathrm{var}$	0.14 (0.014)	0.11 (0.080)	0.09 (0.014)	−0.01 (0.087)	0.09 (0.014)	0.09 (0.087)	0.12 (0.014)	0.07 (0.082)
$\mathrm{var}_{\mathrm{d}}$	0.19 (0.013)	0.58 (0.072)	0.14 (0.013)	0.33 (0.088)	0.10 (0.013)	0.25 (0.092)	0.13 (0.014)	0.52 (0.078)
$\ln \mathrm{var}_{\mathrm{d}}$	0.26 (0.014)	0.65 (0.058)	0.21 (0.014)	0.38 (0.076)	0.15 (0.014)	0.21 (0.084)	0.22 (0.014)	0.62 (0.063)
$\mathrm{r}_{\mathrm{Auto}}$	−0.02 (0.014)	0.23 (0.122)	−0.04 (0.015)	0.32 (0.129)	−0.01 (0.014)	0.06 (0.126)	0.01 (0.015)	0.27 (0.124)
$\mathrm{var}_{\mathrm{r}}$	−0.27 (0.012)	−0.48 (0.084)	−0.30 (0.012)	−0.50 (0.087)	−0.24 (0.012)	−0.32 (0.100)	−0.32 (0.012)	−0.50 (0.083)
$\ln \mathrm{var}_{\mathrm{r}}$	−0.33 (0.012)	−0.50 (0.059)	−0.36 (0.013)	−0.51 (0.063)	−0.26 (0.013)	−0.18 (0.079)	−0.38 (0.012)	−0.52 (0.058)
$\mathrm{var}_{\mathrm{rd}}$	−0.20 (0.013)	−0.05 (0.110)	−0.23 (0.013)	−0.23 (0.112)	−0.20 (0.013)	−0.09 (0.119)	−0.30 (0.013)	−0.10 (0.108)
$\ln \mathrm{var}_{\mathrm{rd}}$	−0.25 (0.013)	−0.09 (0.092)	−0.27 (0.014)	−0.30 (0.092)	−0.24 (0.013)	−0.10 (0.100)	−0.31 (0.013)	−0.11 (0.092)

[1] Description of resilience indicators can be found in Table 1.

DISCUSSION

Modelling of the Lactation Curve

Different existing and newly developed approaches exist for modeling lactation curves, which have been tested in the context of resilience research in dairy cattle. The choice of the modeling method has only a minor influence on the estimated values of resilience indicators in variance component and correlation analyses, as shown in a previous study, which compared resilience indica- tors calculated on the basis of different lactation curves (Poppe et al., 2020; Chen et al., 2023). Basically, it has been argued that a separate curve should be predicted for each lactation of each individual for a more accurate estimation (Elgersma et al., 2018), and it should smooth out atypical lactation patterns as good as possible (Wang et al., 2022). We decided to use a spline interpolation similar as in Codrea et al. (2011), but we used penalized splines instead of B-splines to best represent the data and preserve the variability of the function (Ramsay et al., 1997). Spline interpolation has the advantage over polynomial regression functions that it creates individual polynomial functions for different sections and finally merges them, instead of using one function over the entire time (Codrea et al., 2011).

Considering all dairy milk yields equally for modeling, would result in an incorrect expected lactation curve because milk yields under the influence of a disturbance would also be included in the estimation. Therefore, very low milk yields should not be weighted at all or should be given less weight to obtain good predictions of the lactation curves that would be expected in the absence of disturbances. Known approaches are the removal of daily values that reflect large deviations between observed and expected values on the basis of absolute values (Wang et al., 2022) or the residuals (Adriaens et al., 2020). The weighting we use preserves more data points and captures performance declines more sensitively.

Interpretation of Resilience Indicators

Using time series analysis of daily milk yields for mapping resilience simplifies genetic analyses compared with traditional health and well-being traits (Elgersma et al., 2018) because the raw data are in continuous rather than binary form, data collection is less subject to error, and the accuracy of statistical analyses is higher (Pitkänen et al., 2012; Sitkowska et al., 2020).

Heritability for $\ln var$ was slightly higher than in Elgersma et al. (2018) and lower than in Poppe et al. (2020), as well as for $\ln var_d$, except for BS. Our results were in line with estimated genetic parameters in studies of African (Oloo et al., 2023) and North American dairy cattle (Chen et al., 2023). Across all species and traits examined in recent studies, the heritability of the logarithmized variance of the deviation of an observed to an expected trait expression ranged from 0.1 to 0.4 (Homma et al., 2021; Mengistu et al., 2022; Bedere et al., 2022), and thus our results fall right in between. Under the assumption that a resilient individual shows low fluctuations in performance, low variance means higher resilience (Berghof et al., 2019; Poppe et al., 2020).

Considering $\mathrm{r}_{\mathrm{Auto}}$, our results of the variance component analysis were similar to previous studies (Poppe et al., 2020; Wang et al., 2022; Chen et al., 2023). Only the heritability of BS was significantly higher than in the literature, whereby we are the first to study this trait in another breed than Holstein-Friesian. As described above, a value of $\mathrm{r}_{\mathrm{Auto}}$ close to zero indicates a shorter recovery time after a disturbance and a higher resilience.

Variance and autocorrelation of longitudinal measured traits are used to predict system collapses in various scientific fields (Scheffer et al., 2012), where an increase in the indicator value is associated with an increasing probability of a collapse (Wichers and Groot 2016). Both parameters are used simultaneously, as they are similarly robust (Dakos et al. 2012a,b; Mehrabbeik et al., 2021). In livestock research, variance was found to be more appropriate because it was more heritable and more strongly correlated with health traits (Bedere et al., 2022; Poppe et al. 2022b). This is consistent with our results, which also showed higher heritabilities.

Negative correlations between $\mathrm{r}_{\mathrm{Auto}}$ and the variance-based indicators denote that with an increasing variance of the performance, the duration of the recovery phase after a disturbance decreases (Poppe et al., 2020; Bedere et al., 2022). Another explanation could be that a larger baseline fluctuation of the milk yield tends to reduce the autocorrelation, but increases the variance of the performance.

To our knowledge, few studies have been conducted on the correlation between resilience indicators and performance traits. Correlations between resilience indicators and average daily milk yield were in line with literature reports (Poppe et al., 2020), whereas the correlations with lactation milk yield were lower than in previous studies (Wang et al., 2022; Chen et al., 2023). As the resilience indicators and milk performance traits MY_{305} and AMY_{305} are based on the same raw data, it could be that they are partly influenced by the same genes. Our results only partially support this hypothesis, as only some of the resilience indicators showed highly significant correlations with MY_{305} and

AMY_{305}. In addition, the genetic correlation between milk yield and milk protein yield is stronger than between milk yield and milk fat yield, as shown in previous studies (e.g., Soyeurt et al., 2007). This could explain why milk protein yield correlates more strongly with resilience indicators than milk fat yield.

Comparison of Variance-Based Indicators

We considered 8 different variance-based indicators. Logarithmization provides a better normal distribution of the data and genetic as well as phenotypic correlations with performance traits were slightly stronger and standard errors were smaller than for nonlogarithmized indicators. Because a normal distribution of a resilience indicator is desirable for the computation of breeding values, the use of logarithmized variance-based indicators can be recommended.

The variance-based indicator of absolute daily milk yield var and $\ln var$, respectively, was calculated as in Elgersma et al. (2018). It is influenced by the milk performance and the persistence over the lactation of an individual. This would result in different variances of different individuals even under the assumption of disturbance-free lactations (Elgersma et al., 2018; Wang et al., 2022). To exclude persistence, we considered the variation of daily milk yield around the predicted lactation curve with var_d and $\ln var_d$, respectively, as described in previous studies as *LnVar* (Berghof et al., 2019; Poppe et al., 2020; Bedere et al., 2022).

Additionally, the effect of the performance level on the magnitude of performance decrease under disturbance in absolute and relative terms should be noted (Berghof et al., 2019; Poppe et al., 2020; Oloo et al., 2023), because when comparing a high- and a low-performing individual with the same absolute decrease in milk yield, the relative decrease is lower for the high-performing cow. This scaling effect already occurred in analyses of environmental sensitivity in livestock (Rönnegård et al., 2013) and in general time series analysis (Dai et al., 2012). Variance- based indicators derived from absolute and relative milk yields are different traits, with correlations ranging from 0.75 to 0.84 and opposite correlations with performance traits. Variance-based indicators of absolute daily milk yield gave similar results as shown in previous studies, i.e., the higher the performance, the higher the value of the variance-based indicator, which indicates a lower resilience of the animal (Poppe et al., 2020). Variance-based indicators based on relative milk yields indicate the opposite, i.e., the higher the yield, the lower the value of the variance-based indicator, which indicates a greater resilience. This can be explained mainly by 4 reasons.

First, in favor of a sufficiently large data set, all individuals were included in analyses with the distinction between primiparous and multiparous as a fixed effect, because Poppe et al. (2021) and Chen et al. (2023) found that resilience indicators are highly correlated across lactations from the second lactation upwards. However, milk yield increases with number of lactations (Ray et al., 1992), and cows in a high lactation are inherently more resilient, as they have not already left the farm due to disease or underperformance.

Second, resilient individuals can keep their milk yield stable, which in turn favors high milk yield. Third, the physiological response to a disturbance differs among individuals. According to the resource allocation theory (Rauw, 2009), an individual does not have to respond to disturbances with a decrease in performance, but may have impaired health or fertility (Llonch et al., 2020). However, our resilience indicators based on daily milk yields can only reflect performance resilience (Ben Abdelkrim et al., 2021; Bedere et al., 2022; Poppe et al., 2022a).

Fourth, a background fluctuation of the daily milk yield occurs even in the absence of disturbances. The magnitude of the fluctuation could be higher in high- performing cows, indicating that variance-based indica- tors based on absolute milk yields tend to be larger in high-performing cows even if their larger values are not reflected by lower resilience.

Evaluation of Resilience Across and Within Different Breeds

In addition to the consideration of the whole data set including 3 breeds, all analyses were also performed within breeds, with approximately equal data sets for HF and FV, but smaller for BS. The level of performance traits was, as expected, significantly higher for HF than for the other 2 breeds, which differed significantly only in milk fat yield and milk protein yield with an absolutely higher level for BS. This difference in performance from HF to BS and FV is well known (LKV, 2022).

The variance-based indicators showed breed differences, with BS being the most resilient across all. However, differences between breeds were small and care must be taken that different breeds tend to be kept in different environments, and thus significant breed differences do not necessarily reflect heritable differences in the resilience of the breeds. In addition, FV showed the lowest autocorrelation and thus shortest recovery period, although this may be due to a higher baseline fluctuation of daily milk yields due to environment-specific peculiarities. This higher baseline fluctuation increased the values of the variance-based indicators but decreased the autocorrelation.

CONCLUSIONS

Livestock resilience can be represented using the indicator traits variance and autocorrelation of daily milk yield, with the former resulting in higher hertiabilities in our study. To address the problem of scaling effects during performance declines, it is recommended to calculate variance-based indicators using relative rather than absolute daily milk yields. In this regard, $\ln var_r$ (the log variance of relative daily milk yields) showed the highest heritabilities and strongest favorable correlations with performance traits. In addition to the AB analysis, we performed uni- and bivariate analyses for HF, FV, and BS. The lower autocorrelation of FV indicates a shorter recovery time after disturbances compared with HF and BS, whereas lower variance-based indicators of HF and BS indicate that the latter are less susceptible to disturbances. An alternative explanation could be that FV has a higher baseline fluctuation of daily milk yields. Further studies are needed to analyze the interrelationship with health and fertility traits, to assess the suitability of the indicator traits to be included in the breeding goal.

REFERENCES

Adriaens, I., G. Bonekamp, J. ten Napel, C. Kamphuis, and Y. de Haas. 2023. Differences across herds with different dairy breeds in daily milk yield based proxies for resilience. Front. Genet. 14:1120073. https://doi.org/10.3389/fgene.2023.1120073.

Adriaens, I., N. C. Friggens, W. Ouweltjes, H. Scott, B. Aernouts, and J. Statham. 2020. Productive life span and resilience rank can be predicted from on-farm first-parity sensor time series but not using a common equation across farms. J. Dairy Sci. 103:7155–7171. https://doi.org/10.3168/jds.2019-17826.

Bedere, N., T. V. L. Berghof, K. Peeters, M.-H. Pinard-van der Laan, J. Visscher, I. David, and H. A. Mulder. 2022. Using egg production longitudinal recording to study the genetic background of resilience in purebred and crossbred laying hens. Genet. Sel. Evol. 54:26. https://doi.org/10.1186/s12711-022-00716-8.

Ben Abdelkrim, A., T. Tribout, O. Martin, D. Boichard, V. Ducrocq, and N. C. Friggens. 2021. Exploring simultaneous perturbation profiles in milk yield and body weight reveals a diversity of animal responses and new opportunities to identify resilience proxies. J. Dairy Sci. 104:459–470. https://doi.org/10.3168/jds.2020-18537.

Berghof, T. V. L., M. Poppe, and H. A. Mulder. 2019. Opportunities to improve resilience in animal breeding programs. Front. Genet. 9:692. https://doi.org/10.3389/fgene.2018.00692.

Bieber, A., A. Wallenbeck, F. Leiber, B. Fuerst-Waltl, C. Winckler, P. Gullstrand, J. Walczak, P. Wójcik, and A. S. Neff. 2019. Production level, fertility, health traits, and longevity in local and commercial dairy breeds under organic production conditions in Austria, Swit- zerland, Poland, and Sweden. J. Dairy Sci. 102:5330–5341. https:// doi.org/10.3168/jds.2018-16147.

Bonekamp, G., M. Poppe, J. ten Napel, C. Kamphuis, Y. de Haas, and I. Adriaens. 2022. Comparison of milk yield based resilience indi- cators across dairy cattle breeds. Pages 402–405 in Proceedings of 12th World Congress on Genetics Applied to Livestock Production. Wageningen Academic Publishers. Wageningen, Netherlands.

Chen, S.-Y., J. P. Boerman, L. S. Gloria, V. B. Pedrosa, J. Doucette, and L. F. Brito. 2023. Genomic-based genetic parameters for resilience across lactations in North American Holstein cattle based on vari- ability in daily milk yield records.

J. Dairy Sci. 106:4133–4146. https://doi.org/10.3168/jds.2022-22754.

Codrea, M. C., S. Højsgaard, and N. C. Friggens. 2011. Differential smoothing of time-series measurements to identify disturbances in performance and quantify animal response characteristics: An example using milk yield profiles in dairy cows. J. Anim. Sci. 89:3089–3098. https://doi.org/10.2527/jas.2010-3753.

Colditz, I. G., and B. C. Hine. 2016. Resilience in farm animals: Biology, management, breeding and implications for animal welfare. Anim. Prod. Sci. 56:1961–1983. https://doi.org/10.1071/AN15297.

Dai, L., D. Vorselen, K. S. Korolev, and J. Gore. 2012. Generic indica- tors for loss of resilience before a tipping point leading to population collapse. Science 336:1175–1177. https://doi.org/10.1126/science.1219805.

Dakos, V., S. R. Carpenter, W. A. Brock, A. M. Ellison, V. Guttal, A. R. Ives, S. Kéfi, V. Livina, D. A. Seekell, E. H. van Nes, and M. Scheffer. 2012a. Methods for detecting early warnings of critical transitions in time series illustrated using simulated ecological data. PLoS One 7:e41010. https://doi.org/10.1371/journal.pone.0041010.

Dakos, V., E. H. van Nes, P. D'Odorico, and M. Scheffer. 2012b. Robust- ness of variance and autocorrelation as indicators of critical slowing down. Ecology 93:264–271. https://doi.org/10.1890/11-0889.1.

Dominik, S., and A. A. Swan. 2014. Resilience, tolerance, robustness and genotype x environment interaction in Merino sheep breeding. Pages 115–128 in Breeding Focus 2014—Improving Resilience. S. Hermesch and S. Dominik, ed. Animal Genetics and Breeding Unit, University of New England, Armidale, Australia.

Elgersma, G. G., G. de Jong, R. van der Linde, and H. A. Mulder. 2018. Fluctuations in milk yield are heritable and can be used as a resil- ience indicator to breed healthy cows. J. Dairy Sci. 101:1240–1250. https://doi.org/10.3168/jds.2017-13270.

Friggens, N. C., I. Adriaens, R. Boré, G. Cozzi, J. Jurquet, C. Kamphuis, F. Leiber, I. Lora, T. Sakowski, J. Statham, and Y. de Haas. 2022. Resilience: Reference measures based on longer-term consequences are needed to unlock the potential of precision livestock farming technologies for quantifying this trait. Peer Community J. 2:e38. https://doi.org/10.24072/pcjournal.136.

Hansen, J., M. Sato, and R. Ruedy. 2012. Perception of climate change. Proc. Natl. Acad. Sci. USA 109:E2415–E2423. https://doi.org/10.1073/pnas.1205276109.

Homma, C., K. Hirose, T. Ito, M. Kamikawa, S. Toma, S. Nikaido, M. Satoh, and Y. Uemoto. 2021. Estimation of genetic parameter for feed efficiency and resilience traits in three pig breeds. Animal 15:100384 https://doi.org/10.1016/j.animal.2021.100384.

Landesverband Baden-Württemberg für Leistungs- und Qualitätsprüfungen in der Tierzucht e.V. (LKV). 2022. Ergebnisse des Prüfung- sjahres 2021. Pages 54–56. Jahresbericht 2021. LKV Beratungs- und Service GmbH. Stuttgart, Germany.

Llonch, P., G. Hoffmann, R. Bodas, D. Mirbach, C. Verwer, and M. J. Haskell. 2020. Opinion paper: Measuring livestock robustness and resilience—Are we on the right track? Animal 14:667–669. https:// doi.org/10.1017/S1751731119003306.

Madhusoodan, A. P., V. Seijan, V. P. Rashamol, S. T. Savitha, M. Bagath, G. Krishnan, and R. Bhatta. 2019. Resilient capacity of cattle to environmental challenges—An updated review. J. Anim. Behav. Biometeorol. 7:104–118. https://doi.org/10.31893/2318-1265jabb.v7n3p104-118.

Mehrabbeik, M., R. Ramamoorthy, K. Rajagopal, F. Nazarimehr, S. Jafari, and I. Hussain. 2021. Critical slowing down indicators in synchronous period-doubling for salamander flicker vision. Eur. Phys. J. Spec. Top. 230:3291–3298. https://doi.org/10.1140/epjs/ s11734-021-00113-0.

Mengistu, S. B., H. A. Mulder, J. W. Bastiaansen, J. A. Benzie, H. L. Khaw, T. Q. Trinh, and H. Komen. 2022. Fluctuations in growth are heritable and a potential indicator of resilience in Nile tilapia (*Oreochromis niloticus*). Aquaculture 560:738481. https://doi.org/10.1016/j.aquaculture.2022.738481.

Mylostyvyi, R., O. Lesnovskay, L. Karlova, O. Khmeleva, O. Kalin- ichenko, O. Orishchuk, S. Tsap, N. Begma, N. Cherniy, B. Gutyj, and O. Izhboldina. 2021. Brown Swiss cows are more heat resistant than Holstein cows under hot summer conditions of the continental climate of Ukraine. J. Anim. Behav. Biometeorol. 9:1–8. https://doi.org/10.31893/jabb.21034.

Nielsen, S., S. Rogers, and A. Conway. 2022. Functions to assist design and analysis of agronomic experiments [R package biometryassist version 1.1.2]. Accessed Oct. 09, 2023. https://cran.r-project.org/ web/packages/biometryassist/index.html.

Oloo, R. D., R. Mrode, J. Bennewitz, C. Ekine-Dzivenu, J. M. Ojango, G. Gebreyohanes, O. A. Mwai, and M. Chagunda. 2023. Potential for quantifying general environmental resilience of dairy cattle in sub-Saharan Africa using deviations in milk yield. Front. Genet. 14:1208158. https://doi.org/10.3389/fgene.2023.1208158.

Pitkänen, T., E. Mäntysaari, G. Aamand, M. Lidauer, P. Madsen, and U. Nielsen. 2012. Measurement error variance of test-day observations from automatic milking systems. Interbull Bull. 46:103–108.

Poppe, M., G. Bonekamp, M. L. van Pelt, and H. A. Mulder. 2021. Ge- netic analysis of resilience indicators based on milk yield records in different lactations and at different lactation stages. J. Dairy Sci. 104:1967–1981. https://doi.org/10.3168/jds.2020-19245.

Poppe, M., H. A. Mulder, M. L. van Pelt, E. Mullaart, H. Hogeveen, and R. F. Veerkamp. 2022a. Development of resilience indicator traits based on daily step count data for dairy cattle breeding. Genet. Sel. Evol. 54:21. https://doi.org/10.1186/s12711-022-00713-x.

Poppe, M., R. F. Veerkamp, H. A. Mulder, and H. Hogeveen. 2022b. Observational study on associations between resilience indicators based on daily milk yield in first lactation and lifetime profitability. J. Dairy Sci. 105:8158–8176. https://doi.org/10.3168/jds.2021-21532.

Poppe, M., R. F. Veerkamp, M. L. van Pelt, and H. A. Mulder. 2020. Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. J. Dairy Sci. 103:1667–1684. https://doi.org/10.3168/jds.2019-17290.

Putz, A. M., J. C. S. Harding, M. K. Dyck, F. Fortin, G. S. Plastow, and J.C. M. Dekkers. 2019. Novel resilience phenotypes using feed intake data from a natural disease challenge model in wean-to-finish pigs. Front. Genet. 9:660. https://doi.org/10.3389/fgene.2018.00660.

R Core Team. 2022. R: A language and environment for statistical com- puting. Accessed Oct. 9, 2023. https://www.R-project.org/.

Ramsay, J. O., N. Heckman, and B. W. Silverman. 1997. Spline smooth- ing with model-based penalties. Behav. Res. Methods Instrum. Com- put. 29:99–106. https://doi.org/10.3758/BF03200573.

Ramsey, J., and B. Ripley. 2022. pspline: Penalized Smoothing Splines. Version 1.0-

19. Accessed Nov. 29, 2023. https://cran.r-project.org/web/packages/pspline/pspline.pdf.

Rauw, W. M. 2009. Introduction. Pages 1–21 in Resource Allocation Theory Applied to Farm Animal Production. CABI, Wallingford, UK.

Ray, D. E., T. J. Halbach, and D. V. Armstrong. 1992. Season and lactation number effects on milk production and reproduction of dairy cattle in Arizona. J. Dairy Sci. 75:2976–2983. https://doi.org/10.3168/jds.S0022-0302(92)78061-8.

Rönnegård, L., M. Felleki, W. F. Fikse, H. A. Mulder, and E. Strandberg. 2013. Variance component and breeding value estimation for genetic heterogeneity of residual variance in Swedish Holstein dairy cattle.

J. Dairy Sci. 96:2627–2636. https://doi.org/10.3168/jds.2012-6198. Schader, C., A. Muller, N. E.-H. Scialabba, J. Hecht, A. Isensee, K.-H.

Erb, P. Smith, H. P. S. Makkar, P. Klocke, F. Leiber, P. Schwegler, M. Stolze, and U. Niggli. 2015. Impacts of feeding less food-competing feedstuffs to livestock on global food system sustainability. J. R. Soc. Interface 12:20150891. https://doi.org/10.1098/rsif.2015.0891. Scheffer, M., S. R. Carpenter, T. M. Lenton, J. Bascompte, W. Brock, V. Dakos, J. van de Koppel, I. A. van de Leemput, S. A. Levin, E. H. van Nes, M. Pascual, and J. Vandermeer. 2012. Anticipating critical transitions. Science 338:344–348. https://doi.org/10.1126/science.1225244.

Sitkowska, B., M. Kolenda, and D. Piwczyński. 2020. Comparison of the fit of automatic milking system and test-day records with the use of lactation curves. Asian-Australas. J. Anim. Sci. 33:408–415. https://doi.org/10.5713/ajas.19.0190.

Soyeurt, H., A. Gillon, S. Vanderick, P. Mayeres, C. Bertozzi, and N. Gengler. 2007. Estimation of heritability and genetic correlations for the major fatty acids in bovine milk. J. Dairy Sci. 90:4435–4442. https://doi.org/10.3168/jds.2007-0054.

Toledo-Alvarado, H., A. Cecchinato, and G. Bittante. 2017. Fertility traits of Holstein, Brown Swiss, Simmental, and Alpine Grey cows are differently affected by herd productivity and milk yield of indi- vidual cows. J. Dairy Sci. 100:8220–8231. https://doi.org/10.3168/ jds.2016-12442.

van der Zande, L. E., J. R. Dunkelberger, T. B. Rodenburg, J. E. Bolhuis, P. K. Mathur, W. J. Cairns, M. C. Keyes, J. M. Eggert, E. A. Little, S. A. Dee, and E. F. Knol. 2020. Quantifying individual response to PRRSV using dynamic indicators of resilience based on activity. Front. Vet. Sci. 7:325. https://doi.org/10.3389/fvets.2020.00325.

Wang, A., L. F. Brito, H. Zhang, R. Shi, L. Zhu, D. Liu, G. Guo, and Y. Wang. 2022. Exploring milk loss and variability during environmental perturbations across lactation stages as resilience indicators in Holstein cattle. Front. Genet. 13:1031557. https://doi.org/10.3389/ fgene.2022.1031557.

Wichers, M., and P. C. Groot. 2016. Critical slowing down as a personalized early warning signal for depression. Psychother. Psychosom. 85:114–116. https://doi.org/10.1159/000441458

SUPPLEMENTARY MATERIAL

APPENDIX 1 of *Resilience indicator traits in 3 dairy cattle breeds in Baden-Württemberg*

APPENDIX 2 of *Resilience indicator traits in 3 dairy cattle breeds in Baden-Württemberg*

APPENDIX 1

The following algorithm was used to compute the vector weight of weights for spline interpolation, where **y** is the vector with length nDays = length(y) containing the daily milk yields. The vectors **nAbove** and **nTotal** have the same length and contain initially zeros. When the algorithm terminates, vector **nAbove** contains for each day the number of times the milk yield was above a connecting line, and vector **nTotal** contains the total number of connecting lines that were taken into consideration. The connecting lines were determined as follows: For each day d = i + j, all lines were considered that connected two milk yields that were gained before and after day d, respectively. The first milk yield was gained at day i, which was more than margin = 5 days before day d. The other milk yield was gained at day i + k − 1, which was more than margin days after day d. Both days were less than maxLength=60 days apart.

```
for(k in (3+2*margin):maxLength){ for(i in 1:(nDays-k+1)){
for(j  in  (1+margin):(k-margin-2)){
if(!is.na(y[i]) & !is.na(y[i+j]) & !is.na(y[i+k-1])){  nTotal[i+j] <- nTotal[i+j] + 1
Est <- y[i]+ j*(y[i+k-1]-y[i])/(k-1) if(y[i+j] >= Est){
nAbove[i+j]  <-  nAbove[i+j]+1
}
}
}
}
}
weight  <-  nAbove/nTotal
```

APPENDIX 2

Table A1. Estimation of heritability (h^2) and variance components of the additive genetic effect (σ_u^2), the permanent environmental effect (σ_{pe}^2), and the residuum (σ_e^2) (SE given) for resilience indicators calculated from daily milk yields, subdivided by breed

Breed[1]	Trait[2]	h^2	SE	σ_u^2	SE	σ_{pe}^2	SE	σ_e^2	SE
AB	var	0.16	0.017	109.35	12.303	66.98	11.260	507.57	8.152
	$\ln \mathrm{var}$	0.16	0.018	0.06	0.007	0.05	0.006	0.25	0.004
	$\mathrm{var_d}$	0.11	0.016	4.35	0.651	7.52	0.680	26.92	0.448
	$\ln \mathrm{var_d}$	0.16	0.019	0.05	0.006	0.06	0.006	0.21	0.003
	$\mathrm{r_{Auto}}$	0.05	0.013	0.00	0.000	0.00	0.000	0.02	0.000
	$\mathrm{var_r}$	0.09	0.015	0.03	0.006	0.08	0.007	0.27	0.005
	$\ln \mathrm{var_r}$	0.18	0.019	0.08	0.009	0.08	0.008	0.28	0.005
	$\mathrm{var_{rd}}$	0.03	0.011	0.00	0.000	0.00	0.000	0.02	0.000
	$\ln \mathrm{var_{rd}}$	0.10	0.016	0.03	0.006	0.06	0.006	0.26	0.004
BS	var	0.26	0.079	67.74	22.448	0.41	19.822	196.40	14.123
	$\ln \mathrm{var}$	0.37	0.092	0.13	0.038	0.01	0.031	0.22	0.017
	$\mathrm{var_d}$	0.18	0.077	3.70	1.598	0.00	Inestimable	16.30	1.143
	$\ln \mathrm{var_d}$	0.31	0.082	0.10	0.030	0.00	Inestimable	0.23	0.017
	$\mathrm{r_{Auto}}$	0.19	0.086	0.00	0.002	0.00	0.002	0.02	0.001
	$\mathrm{var_r}$	0.13	0.084	0.04	0.024	0.07	0.025	0.17	0.013
	$\ln \mathrm{var_r}$	0.46	0.103	0.21	0.056	0.04	0.043	0.21	0.016
	$\mathrm{var_{rd}}$	0.16	0.078	0.00	0.001	0.00	0.001	0.01	0.001
	$\ln \mathrm{var_{rd}}$	0.27	0.080	0.10	0.033	0.00	Inestimable	0.28	0.020
FV	var	0.16	0.025	81.82	13.579	64.05	12.496	371.74	8.603

	$\ln \mathrm{var}$	0.14	0.025	0.05	0.009	0.06	0.009	0.24	0.006
	$\mathrm{var}_{\mathrm{d}}$	0.08	0.022	1.92	0.558	6.02	0.645	17.53	0.423
	$\ln \mathrm{var}_{\mathrm{d}}$	0.13	0.027	0.04	0.008	0.06	0.008	0.20	0.005
	$\mathrm{r}_{\mathrm{Auto}}$	0.03	0.016	0.00	0.000	0.00	0.000	0.02	0.000
	$\mathrm{var}_{\mathrm{r}}$	0.10	0.024	0.05	0.011	0.12	0.012	0.29	0.007
	$\ln \mathrm{var}_{\mathrm{r}}$	0.15	0.027	0.06	0.011	0.09	0.011	0.26	0.006
	$\mathrm{var}_{\mathrm{rd}}$	0.01	0.011	0.00	0.000	0.00	0.000	0.02	0.000
	$\ln \mathrm{var}_{\mathrm{rd}}$	0.07	0.021	0.02	0.007	0.07	0.008	0.25	0.006
HF	var	0.14	0.026	126.84	23.823	87.28	22.351	685.37	16.451
	$\ln \mathrm{var}$	0.15	0.026	0.06	0.010	0.04	0.009	0.27	0.007
	$\mathrm{var}_{\mathrm{d}}$	0.13	0.025	7.00	1.400	9.54	1.423	37.94	0.944
	$\ln \mathrm{var}_{\mathrm{d}}$	0.18	0.028	0.06	0.010	0.06	0.009	0.21	0.005
	$\mathrm{r}_{\mathrm{Auto}}$	0.05	0.020	0.00	0.000	0.00	0.000	0.01	0.000
	$\mathrm{var}_{\mathrm{r}}$	0.07	0.022	0.02	0.007	0.05	0.008	0.25	0.006
	$\ln \mathrm{var}_{\mathrm{r}}$	0.18	0.028	0.08	0.013	0.06	0.012	0.30	0.008
	$\mathrm{var}_{\mathrm{rd}}$	0.05	0.020	0.00	0.000	0.00	0.001	0.02	0.000
	$\ln \mathrm{var}_{\mathrm{rd}}$	0.10	0.024	0.04	0.009	0.06	0.009	0.27	0.007

[1] AB = across breeds; BS = German Brown Swiss; FV = German Fleckvieh; HF = German Holstein.

[2] Description of resilience indicators can be found in Table 1.

Table A2. Correlations (genetic: below the diagonal; phenotypic: above the diagonal) between the resilience indicators calculated from daily milk yields across breeds (SE in parentheses)

Breed[1]	Trait[2]	var	ln var	var_{d}	$\ln \text{var}_{d}$	r_{Auto}	var_{r}	$\ln \text{var}_{r}$	var_{rd}	$\ln \text{var}_{rd}$
BS	var		not converged	not converged	not converged	0.05 (0.036)	not converged	not converged	not converged	not converged
	ln var	not converged		0.36 (0.034)	0.41 (0.036)	0.04 (0.038)	0.63 (0.023)	0.89 (0.009)	not converged	0.39 (0.034)
	var_{d}	not converged	0.62 (0.195)		not converged	0.13 (0.036)	not converged	0.27 (0.038)	0.78 (0.015)	not converged
	$\ln \text{var}_{d}$	not converged	0.69 (0.144)	not converged		0.07 (0.038)	0.20 (0.038)	0.26 (0.042)	not converged	0.86 (0.011)
	r_{Auto}	0.12 (0.251)	0.01 (0.234)	-0.05 (0.270)	-0.25 (0.243)		0.09 (0.036)	0.03 (0.038)	0.11 (0.036)	0.07 (0.037)
	var_{r}	not converged	0.83 (0.124)	not converged	0.24 (0.295)	-0.11 (0.350)		0.74 (0.017)	0.50 (0.027)	0.39 (0.032)
	$\ln \text{var}_{r}$	not converged	0.95 (0.028)	0.47 (0.217)	0.48 (0.181)	-0.15 (0.235)	0.84 (0.123)		0.45 (0.031)	0.48 (0.032)
	var_{rd}	not converged	not converged	0.98 (0.168)	not converged	-0.06 (0.411)	0.84 (0.391)	0.92 (0.316)		0.79 (0.013)
	$\ln \text{var}_{rd}$	not converged	0.87 (0.129)	not converged	0.92 (0.055)	-0.31 (0.265)	0.38 (0.287)	0.78 (0.125)	not converged	
FV	var		not converged	0.33 (0.014)	not converged	0.10 (0.017)	0.68 (0.009)	0.75 (0.007)	0.22 (0.015)	0.26 (0.016)
	ln var	not converged		0.34 (0.015)	0.38 (0.016)	0.09 (0.018)	0.65 (0.010)	0.86 (0.005)	0.27(0.015)	0.30 (0.016)
	var_{d}	0.19 (0.131)	0.16 (0.141)		0.88 (0.003)	-0.04 (0.018)	0.18 (0.017)	0.24 (0.016)	0.71 (0.008)	0.77 (0.007)
	$\ln \text{var}_{d}$	not converged	0.18 (0.127)	0.98 (0.014)		-0.06 (0.020)	0.17 (0.019)	0.24 (0.017)	0.64 (0.010)	0.85 (0.005)
	r_{Auto}	-0.06 (0.191)	-0.16 (0.201)	-0.33 (0.219)	-0.22 (0.196)		0.10 (0.019)	0.10 (0.018)	0.02 (0.018)	-0.03 (0.020)
	var_{r}	0.90 (0.044)	0.90 (0.048)	0.09 (0.161)	0.08 (0.146)	0.06 (0.209)		0.80 (0.006)	0.46 (0.014)	0.38 (0.016)
	$\ln \text{var}_{r}$	0.75 (0.054)	0.86 (0.033)	-0.10 (0.144)	-0.11 (0.130)	-0.28 (0.190)	0.96 (0.027)		0.41 (0.014)	0.46 (0.014)
	var_{rd}	0.31 (0.254)	0.36 (0.254)	0.93 (0.112)	0.94 (0.106)	-0.99 (0.513)	0.49 (0.237)	0.360 (0.231)		0.78 (0.006)
	$\ln \text{var}_{rd}$	0.12 (0.139)	0.25 (0.140)	0.75 (0.074)	0.80 (0.053)	-0.47 (0.211)	0.32 (0.145)	0.29 (0.128)	0.10 (0.309)	
HF	var		0.85 (0.005)	0.41 (0.014)	not converged	0.10 (0.017)	0.73 (0.007)	not converged	not converged	0.36 (0.016)
	ln var	0.95 (0.022)		not converged	0.52 (0.015)	0.08 (0.019)	0.65 (0.010)	0.88 (0.004)	0.38 (0.016)	0.46 (0.016)

var_d	0.44 (0.105)	not converged		0.88 (0.004)	-0.04 (0.019)	0.30 (0.016)	not converged	0.74 (0.008)	0.79 (0.007)
$\ln \mathrm{var}_d$	not converged	0.55 (0.084)	0.90 (0.025)		-0.03 (0.020)	0.29 (0.017)	0.38 (0.018)	0.66 (0.010)	0.86 (0.005)
r_{Auto}	-0.36 (0.147)	-0.33 (0.141)	-0.26 (0.144)	-0.23 (0.133)		0.07 (0.017)	0.05 (0.019)	-0.05 (0.018)	-0.05 (0.019)
var_r	0.84 (0.054)	0.80 (0.066)	0.18 (0.149)	0.13 (0.142)	-0.46 (0.189)		0.77 (0.006)	0.51 (0.012)	0.46 (0.014)
$\ln \mathrm{var}_r$	not converged	0.79 (0.037)	not converged	0.13 (0.105)	-0.42 (0.135)	0.98 (0.026)		0.49 (0.014)	0.58 (0.013)
var_{rd}	not converged	0.44 (0.133)	0.76 (0.070)	0.65(0.087)	-0.55 (0.172)	0.49 (0.147)	0.52 (0.114)		0.80 (0.006)
$\ln \mathrm{var}_{rd}$	0.52 (0.106)	0.57 (0.092)	0.64 (0.072)	0.69 (0.056)	-0.45 (0.143)	0.60 (0.114)	0.64 (0.075)	0.91 (0.044)	

[1] AB = across breeds; BS = German Brown Swiss; FV = German Fleckvieh; HF = German Holstein.

[2] Description of resilience indicators can be found in Table 1.

Table 6. Phenotypic ($corr_{phenotypic}$) and genetic ($corr_{genetic}$) correlations between the MY_{305}, PY_{305}, FY_{305}, AMY_{305}, and resilience indicators calculated from daily milk yields across breeds, with SE in parentheses (n = 8,846 lactations)

Breed, n	Trait²	MY_{305}		PY_{305}		FY_{305}		AMY_{305}	
		$corr_{phenotypic}$	$corr_{genetic}$	$corr_{phenotypic}$	$corr_{genetic}$	$corr_{phenotypic}$	$corr_{genetic}$	$corr_{phenotypic}$	$corr_{genetic}$
BS, n = 579	var	Not converged	Not converged	-0.04 (0.052)	-0.15 (0.338)	Not converged	Not converged	Not converged	Not converged
	$\ln \mathrm{var}$	Not converged	Not converged	-0.03 (0.054)	-0.26 (0.179)	Not converged	Not converged	0.01 0.054)	-0.29 (0.283)
	$\mathrm{var}_{\mathrm{d}}$	0.20 (0.045)	0.20 (0.045)	0.13 (0.047)	0.19 (0.447)	0.15 (0.046)	0.15 (0.047)	0.13 (0.014)	0.52 (0.078)
	$\ln \mathrm{var}_{\mathrm{d}}$	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged
	$\mathrm{r}_{\mathrm{Auto}}$	-0.01 (0.048)	-0.05 (0.449)	0.00 0.047)	0.41 0.535)	0.04 (0.047)	0.50 (0.440)	0.01 0.048)	0.07 0.493)
	$\mathrm{var}_{\mathrm{r}}$	-0.32 (0.043)	-0.29 (0.440)	-0.35 (0.042)	-0.20 (0.459)	-0.28 (0.043)	-0.38 (0.379)	-0.37 (0.041)	-0.37 (0.404)
	$\ln \mathrm{var}_{\mathrm{r}}$	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged
	$\mathrm{var}_{\mathrm{rd}}$	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged	Not converged
	$\ln \mathrm{var}_{\mathrm{rd}}$	Not converged	Not converged	-0.21 (0.050)	-0.26 (0.341)	Not converged	Not converged	Not converged	Not converged
FV, n = 3,635	var	0.15 (0.021)	0.10 (0.177)	0.09 0.022)	-0.13 (0.194)	0.10 0.021)	0.04 0.190)	0.13 0.021)	0.09 0.178)
	$\ln \mathrm{var}$	0.17 0.021)	0.02 0.176)	0.11 0.022)	-0.20 (0.187)	Not converged	Not converged		0.15 (0.022)
	$\mathrm{var}_{\mathrm{d}}$	0.21 0.020)	0.72 0.151)	0.17 0.021)	0.42 0.187)	0.15 0.020)	0.20 0.196)	0.15 0.021)	0.71 0.158)
	$\ln \mathrm{var}_{\mathrm{d}}$	0.26 0.021)	0.74 0.107)	0.21 0.023)	0.50 0.144)	0.19 0.022)	0.24 0.162)	0.21 0.022)	0.73 0.113)
	$\mathrm{r}_{\mathrm{Auto}}$	-0.07 (0.023)	0.27 (0.271)	-0.10 (0.024)	0.33 (0.278)	-0.06 (0.023)	-0.07 (0.271)	-0.04 (0.024)	0.25 (0.272)
	$\mathrm{var}_{\mathrm{r}}$	-0.29 (0.019)	-0.40 (0.144)	-0.32 (0.019)	-0.56 (0.137)	-0.28 (0.019)	-0.33 (0.160)	-0.34 (0.019)	-0.38 (0.142)
	$\ln \mathrm{var}_{\mathrm{r}}$	-0.33 (0.019)	-0.58 (0.118)	-0.36 (0.019)	-0.67 (0.115)	-0.29 (0.019)	-0.33 (0.151)	-0.37 (0.019)	-0.55 (0.118)
	$\mathrm{var}_{\mathrm{rd}}$	-0.23 (0.020)	0.03 (0.229)	-0.25 (0.020)	-0.20 (0.221)	-0.22 (0.019)	-0.14 (0.231)	-0.30 (0.019)	0.04 (0.228)
	$\ln \mathrm{var}_{\mathrm{rd}}$	-0.27 (0.021)	0.12 (0.210)	-0.29 (0.022)	-0.10 (0.212)	-0.25 (0.021)	-0.09 (0.218)	-0.34 (0.021)	0.14 (0.211)
HF, n = 4,632	var	0.11 0.018)	0.07 0.107)	0.07 0.019)	0.03 0.114)	0.07 0.019)	0.07 0.117)	0.05 (0.015)	0.05 (0.111)

ln var	0.13 (0.019)	0.14 (0.100)	0.08 (0.020)	0.04 (0.107)	0.08 (0.020)	0.10 (0.110)	0.10 (0.020)	0.08 (0.104)
$\mathrm{var_d}$	0.18 (0.019)	0.55 (0.091)	0.13 (0.019)	0.33 (0.108)	0.07 (0.019)	0.27 (0.115)	0.11 (0.020)	0.48 (0.098)
$\ln \mathrm{var_d}$	0.25 (0.019)	0.64 (0.074)	0.19 (0.020)	0.37 (0.097)	0.10 (0.020)	0.20 (0.108)	0.20 (0.020)	0.60 (0.081)
$\mathrm{r_{Auto}}$	0.02 (0.019)	0.17 (0.133)	0.00 (0.019)	0.23 (0.140)	0.02 (0.019)	-0.02 (0.141)	0.06 (0.019)	0.22 (0.136)
$\mathrm{var_r}$	-0.27 (0.016)	-0.62 (0.112)	-0.28 (0.016)	-0.54 (0.117)	-0.21 (0.017)	-0.33 (0.146)	-0.32 (0.016)	-0.65 (0.109)
$\ln \mathrm{var_r}$	-0.33 (0.017)	-0.52 (0.073)	-0.35 (0.018)	-0.50 (0.078)	-0.24 (0.018)	-0.14 (0.099)	-0.38 (0.017)	-0.56 (0.070)
$\mathrm{var_{rd}}$	-0.20(0.018)	-0.11 (0.128)	-0.21 (0.014)	-0.25 (0.131)	-0.19 (0.018)	-0.02 (0.142)	-0.28 (0.018)	-0.17 (0.124)
$\ln \mathrm{var_{rd}}$	-0.25 (0.019)	-0.19 (0.110)	-0.28 (0.019)	-0.39 (0.110)	-0.26 (0.019)	-0.11 (0.123)	-0.32 (0.019)	-0.22 (0.109)

[1] HF = German Holstein; BS = German Brown Swiss; FV = German Fleckvieh.

[2] Description of resilience indicators can be found in Table 1.

CHAPTER THREE

TOWARD A RESILIENCE SELECTION INDEX WITH INDICATOR TRAITS IN GERMAN HOLSTEIN DAIRY CATTLE

F. Keßler[1]*, R. Wellmann[1], M.G.G. Chagunda[2], J. Bennewitz[1]

[1] Institute of Animal Science, University of Hohenheim, 70599 Stuttgart, Germany

[2] Centre of Tropical Livestock Genetics and Health (CTLGH), Roslin Institute/ILRI, Edinburgh, United Kingdom EH25 9RG

*Corresponding author: franziska.kessler@uni-hohenheim.de

Published in Journal of Dairy Science (2025), Volume 108 (1), pp. 726–734
https://doi.org/10.3168/jds.2024-25323

ABSTRACT

Resilience expresses the ability of an individual to cope with short-term disturbances and to recover quickly by returning to the original level of performance. It can be measured by variance-based parameters and by the autocorrelation of daily milk yields in dairy cows. The design of resilience indicator traits and their heritabilities and genetic correlations have been studied in detail in recent years. There is a need to combine different resilience indicators in an index. The relevance of resilience indicator traits for incorporation into selection indices arises from their correlations with health traits and longevity. The correlations of diverse resilience indicator traits with health traits and longevity were analyzed. The resilience indicator traits were identified that would lead to the highest correlated selection response in the German selection index for health, and appropriate weights of the resilience indicator traits in a selection index for resilience were derived. Certain variance-based indica- tors were significantly positively correlated with most of the established health and functional traits, whereas the autocorrelation had a negligible correlation with these traits. A resilience selection index composed of 2 different variance-based resilience indicator traits was most likely to be recommended. Its correlation with overall performance was positive but moderately small. Incorporating more than 2 resilience indicator traits into the index improved the correlated response in health traits only slightly.

Key words: variance, autocorrelation, resilience index, dairy cattle, resilience

INTRODUCTION

Resilience traits measure the ability of an animal to cope with short-term disturbances and to recover quickly from them (Colditz and Hine, 2016; Poppe et al., 2020). They have become interesting traits in livestock science in recent years and can be considered as higher-order indicator traits for health and robustness. However, defining and measuring resilience indicator traits poses a challenge. One promising approach is to analyze the variance and the autocorrelation of a longitudinal recorded trait (Poppe et al., 2020). For example, the longitudinal trait could be the daily milk yield of dairy cows (Poppe et al., 2020; Wang et al., 2022), the egg production of laying hens (Bedere et al., 2022), or the feed intake of pigs (Homma et al., 2021). The underlying assumption is that an animal responds to a disturbance with a change of the longitudinal trait. As it is generally not known when a disturbance begins, when it ends, and whether it exists at all, it is not the direct response to a specific disturbance which is analyzed, but the change of the longitudinal trait over a certain period of time. The variance quantifies the fluctuation in the trait over a certain period of time, whereby a low variance implies a high resilience. It is often assumed that the autocorrelation indicates how quickly an individual recovers from a disturbance, with an autocorrelation close to zero suggesting a high level of resilience (Berghof et al., 2019; Poppe et al., 2020; Friggens et al., 2022). Most resilience indicators are calculated from the deviation of the observed trait expression from the expected trait expression. For dairy cows, for example, the expected lactation curve can be modeled and compared with the observed daily milk yields (Poppe et al., 2020). This approach also takes into account the different persistence of individuals (Elgersma et al., 2018). In addition, it can be appropriate to correct for the performance level because high-yielding individuals show higher absolute reactions to disturbances than low-yielding individuals. This can be done by computing the resilience indicator traits not from absolute daily milk yields but from relative daily milk yields (Keßler et al., 2024a).

First attempts were made to include resilience indicator traits in routine breeding value estimation (Meijer et al., 2024). However, no gold standard is established for how to decide which resilience indicator traits should be included in the total merit index. This is because the underlying disturbance is usually not known, making the derivation of economic weights difficult. One approach is to analyze genetic correlations of resilience indicator traits with health traits, length of productive life, or overall performance. Some previous studies have done this by studying the correlation with existing selection indices (Elgersma et al., 2018; Poppe et al., 2020) or their correlations to disease prevalence (e.g., reproductive disorders; Wang et al., 2022), in Holstein Friesian cows. Those studies showed that resilient animals tend to be healthier. However, the correlations between resilience indicators and certain diseases have been little researched to date. The different sensitivity of different resilience indicator traits can be seen by the example of mastitis. Although the variance of daily milk yield tended to be higher in diseased individuals, as expected, the autocorrelation was lower (Kok et al., 2021).

The present study suggests a way to establish a selection index for resilience in practice with the data and knowledge available today. For this purpose, we derived an optimum resilience selection index that maximizes the expected correlated response in the German Holstein selection index for overall health. Based on its calculation from the daily milk yield, it should stabilize the daily milk yields on the one hand and increase the health of the animals on the other. Therefore, in addition, correlations between resilience indicators and EBV for health traits were estimated.

MATERIALS AND METHODS

Data processing and evaluation as well as statistical analyses were performed in software R (version 4.2.2; R Core Team), by using ASReml-R 4 for genetic analysis.

We considered 3,919 German Holstein Friesian (**HF**) cows. The number of lactations per cow varied from one to 6. In total 7,623 lactations were considered. The data were collected between October 2017 and 2023 by the Landeskontrollverband Baden-Württemberg (Stuttgart, Germany) on 48 farms in the state of Baden-Württemberg, Germany. The farms were registered as members of the breeding organization Rinderunion Baden-Württemberg e.V. (Herbertingen, Germany) in the herd book and used automatic milking systems. The first milking of a day was prorated to the time up to midnight of the previous day and since midnight of the current day. Days on which the number of animals milked on the farm differed from the average by 3 SD or more were removed, as well as the day before and after. The first day after and last day before a gap in an individual's records were also excluded.

The EBV for functional and health traits were estimated using genomic information and were provided by Vereinigte Informationssysteme Tierhaltung w.V. (Verden, Germany). We considered selection indices and trait EBV, described in detail in vit (2023). The most relevant index for our study is the selection index for health ($\mathbf{SI_{health}}$). It includes all currently collected traits of udder health, claw health, metabolism health, and fertility health. Estimation of EBV was conducted in August 2023. A high EBV was desirable for all traits.

Calculation of Resilience Indicators

Daily milk yields were used to predict a lactation curve using cubic penalized spline interpolation. The smoothing splines were computed with *pspline* in R (Ramsey and Ripley 2022), with the degrees of freedom set to 5 after a visual comparison of the modeled lactation curves with different degrees of freedom. Data points corresponding to days in which the cow had a temporary reduction of the milk yield were given lower weights. To do this, we used a function that checks how often the milk yield of a day was below the linear connection of 2 interval limits at intervals of 5 to 60 d from the observation day. The weighting factor was calculated from the proportion of times below the line in all tested intervals (Keßler et al., 2024a). The lactations under consideration were limited to the period of 10 to 305 DIM, and lactations with less than 50% of data points were excluded. The modeling of the lactation curve, the weighting of disturbed days, and the calculation of resilience indicators are detailed in Keßler et al. (2024a) and are described briefly in the following.

Variance-based parameters and the lag-1 autocorrelation were used as resilience indicators and calculated for each lactation of each individual. Multiple lactations of an individual were included in the study. Let $\mathbf{y}$ denote the vector with daily milk yields of a cow in a certain lactation, let $\mathbf{1}$ denote the vector with ones, $\hat{\mathrm{y}}$ denote the vector with interpolated milk yields, $\widehat{var}$ denote the sample variance, and $\ln$ denote the natural logarithm. The variance-based indicators were calculated from the deviations between

- the daily milk yields and the average daily milk yield:

$$v(\mathbf{y}) = -\ln[\widehat{var}(\mathbf{y} - \bar{\mathrm{y}}\mathbf{1})],$$

- the daily milk yields and the predicted daily milk yields:

$$v_d(\mathbf{y}) = -\ln[\widehat{var}(\mathbf{y} - \hat{\mathbf{y}})],$$

- the relative daily milk yields and their average value:

$$v_r(\mathbf{y}) = -\ln\{\widehat{var}[a_y(\mathbf{y} - \bar{\mathrm{y}}\mathbf{1})]\}, \text{ with}$$

$$a_y = 100/\textstyle\sum_{t=1}^{n} y_t,$$

- the relative daily milk yields and the predicted relative daily milk yields:

$$v_{rd}(\mathbf{y}) = -\ln\{\widehat{var}[a_y(\mathbf{y} - \hat{\mathbf{y}})]\}.$$

The trait autocorrelation was calculated as

$$r_{Auto}(\mathbf{y}) = -\frac{\widehat{cov}(\mathbf{y}-\hat{\mathbf{y}})}{\widehat{var}(\mathbf{y}-\hat{\mathbf{y}})},$$

with $\widehat{cov}$ the covariance and $\widehat{var}$ the variance of the deviations between observed and predicted absolute daily milk yields ($\mathbf{y} - \hat{y}$). The resilience indicators were defined so that high values are desirable.

Genetic Analysis

Univariate analyses of the resilience indicators were performed with an animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wpe} + \mathbf{e},$$

where $\mathbf{y}$ is the vector of observations; $\mathbf{b}$ is the vector of fixed effects; $\mathbf{u}$ is the vector of additive genetic effects; $\mathbf{pe}$ is the vector of permanent environmental effects; $\mathbf{e}$ is the vector of residuals; and $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{W}$ are incidence matrices. The vector of fixed effects, $\mathbf{b}$, comprises age at first calving in month, lactation (divided into first or higher lactation), herd-year-season effect (divided into spring [March to May], summer [June to August], autumn [September to November], and winter [December to February]) and completeness of lactation data (divided into ≥90%, 80% to ≤90%, 70% to ≤80%, 60% to ≤70%, and 50% to ≤60% availability of daily milk yields in a lactation between d 10 and 305), whereby levels of fixed effects with less than 5 individuals were excluded. For the vectors $\mathbf{u}$, $\mathbf{pe}$, and $\mathbf{e}$, normal distributions were assumed with $\mathbf{u} \sim N(0, \mathbf{A}\sigma_{\mathbf{u}}^2)$, $\mathbf{pe} \sim N(0, \mathbf{I_{pe}}\sigma_{\mathbf{pe}}^2)$, and $\mathbf{e} \sim N(0, \mathbf{I_e}\sigma_{\mathbf{e}}^2)$, whereby $\mathbf{I_{pe}}$ and $\mathbf{I_e}$ are identity matrices and $\mathbf{A}$ is the pedigree-based additive genetic relationship matrix. Heritability was calculated as the proportion of additive genetic to phenotypic variance and tested for significance using the chi-squared test.

The EBV for resilience indicators were derived from this univariate model. They were standardized to a mean of 100 and a genetic SD of 12, as it is common practice in dairy cattle breeding value estimation in Germany. A high EBV of a resilience trait is synonymous with a low variance or an autocorrelation close to zero and thus points to a high resilience. For further analysis, individuals with an EBV reliability smaller than 15% in one of the resilience indicators were excluded. This filtering left 2,206 individuals in the dataset for the development of the resilience selection index.

Development of a Selection Index

Correlations between EBV of resilience indicators and functional and health traits, respectively, were estimated using Pearson's method. The resilience selection index was defined as a weighted mean of the 5 resilience indicator traits. The weights were determined by the limited-memory Broyden–Fletcher–Goldfarb–Shanno algorithm using the package *optim* in R (Byrd et al., 1995), which is an optimization algorithm in the family of quasi-Newton methods. The weights were chosen to achieve a maximum correlated selection response in the selection index for overall health ($\mathbf{SI_{health}}$) in the hypothetical case that the population is phenotypically selected on the resilience selection index. This is an alternative approach to determining the weighting factors of the resilience indicators integrated in the selection index ($\mathbf{SI_{resilience}}$), as no economic weights are available. The health selection index $\mathrm{SI_{health}}$, which is used for optimization, consists of EBV of 13 single health traits for udder and claw health as well as resistance against metabolism and reproduction diseases. The composition of $\mathrm{SI_{health}}$ is based on the genetic correlations between the single health traits (vit, 2023).

The formula used to estimate the selection response *R* was adopted from selection index theory (e.g., Mrode, 2005) and was as follows:

$$R = \sqrt{\mathrm{h}^2_{SI_{resilience}}} \times r_{I_{resilience}SI_{health}},$$

where $\mathrm{h}^2_{SI_{resilience}}$ is the heritability of the resilience selection index and the genetic correlation $r_{SI_{resilience}SI_{health}}$ is estimated as the Pearson correlation between the resilience selection index $\mathrm{SI_{resilience}}$ and the election index health $\mathrm{SI_{health}}$. The heritability $\mathrm{h}^2_{SI_{resilience}}$ as calculated from the additive variance V_A and the phenotypic variance V_P as follows:

$$\mathrm{h}^2_{SI} = \frac{V_A}{V_P} = \frac{\mathbf{w}^T \mathbf{\Omega_A} \mathbf{w}}{\mathbf{w}^T \mathbf{\Omega_P} \mathbf{w}} = \frac{\sum_{i,j} \mathbf{w}_i \mathbf{w}_j \mathrm{cov}(TBV_i, TBV_j)}{\sum_{i,j} \mathbf{w}_i \mathbf{w}_j \mathrm{cov}(y_i, y_{\boldsymbol{j}})},$$

where $\mathbf{w}$ is the vector with index weights, $\mathbf{\Omega_A}$ is the variance-covariance matrix of the true breeding values, and $\mathbf{\Omega_P}$ is the variance-covariance matrix of phenotypes, which were derived from the quantitative-genetic and phenotypic correlation analyses between the resilience indicators using mixed linear models as described in our previous study (Keßler et al., 2024a).

RESULTS

Descriptive statistics and results of the variance component analysis of resilience indicator traits and the reliabilities of their EBV are shown in Table 1. The highest heritability was estimated for v_r (0.21) and the smallest for r_{Auto} (0.05). All heritabilities were significantly different from zero. The mean reliability of EBV for resilience indicators was higher for variance-based indicator traits, with the highest reliability for v_r (0.45) and the lowest for r_{Auto} (0.20), with the SD being smaller for the latter.

Correlations between EBV for resilience indicators and $\mathrm{SI_{health}}$ and single health traits are shown in Figure 1, with stronger colors indicating stronger correlations. Only significant correlations are shown (*P* < 0.05). The EBV for r_{Auto} had the lowest correlation with the Metritis trait (−0.14) and the highest with Late Mastitis (0.08). Variance-based indicator traits showed mainly significant positive correlations with other traits, except v_d with Milk Yield. In particular, strong positive correlations were found with udder health traits, Late Mastitis and Early Mastitis, and $\mathrm{SI}_{\mathrm{health}}$, as well as Longevity. The strongest correlations with fertility health traits were found for v_d, whereas v_r showed the highest correlation with traits of metabolism, except Ketosis. Claw health correlated most strongly with v, and for udder health, the highest correlation coefficients were found with v_{rd} and v_{rd}. Correlations with further selection indices of breeding value estimation in HF are shown in Supplemental Figure S3 (see Notes; Keßler et al., 2024b).

Table 1. Descriptive statistics showing the means ($\bar{\mathrm{x}}_{\mathrm{RI}}$) and SD ($\mathrm{SD}_{\mathrm{RI}}$) of resilience indicator traits, their heritabilities (h^2) with SE, and the means ($\bar{\mathrm{x}}_{rel}$) and SD ($\mathrm{SD}_{\mathrm{rel}}$) of the reliabilities of the EBV

Variable[1]	$\bar{\mathrm{x}}_{\mathrm{RI}}$	$\mathrm{SD}_{\mathrm{RI}}$	h^2	$\mathrm{SE\ h}^2$	$\bar{\mathrm{x}}_{\mathrm{rel}}$	$\mathrm{SD}_{\mathrm{rel}}$
v	3.37	0.874	0.18	0.024	0.42	0.054
v_d	1.92	0.655	0.19	0.027	0.43	0.051
r_{Auto}	0.58	0.173	0.05	0.017	0.20	0.037
v_r	−14.74	0.867	0.21	0.026	0.45	0.052
v_{rd}	−16.19	0.716	0.11	0.021	0.32	0.046

[1] v = variance of absolute daily milk yield; v_d = variance of deviations between observed and predicted absolute daily milk yield; r_{Auto} = autocorrelation of deviations between observed and predicted absolute daily milk yield; v_r = variance of relative daily milk yield; v_{rd} = variance of deviations between observed and predicted relative daily milk yield.

Results of selection index optimization for indices consisting of 2 to 5 resilience indicators can be seen in Table 2. As expected, the highest breeding response of 0.222 was detected for a resilience index comprising all 5 resilience indicators. A positive joint selection response denotes a proportional increase in EBV of $\mathrm{SI}_{\mathrm{health}}$ when selecting for a higher EBV of $\mathrm{SI}_{\mathrm{resilience}}$. Indices consisting of less than 5 resilience indicators showed

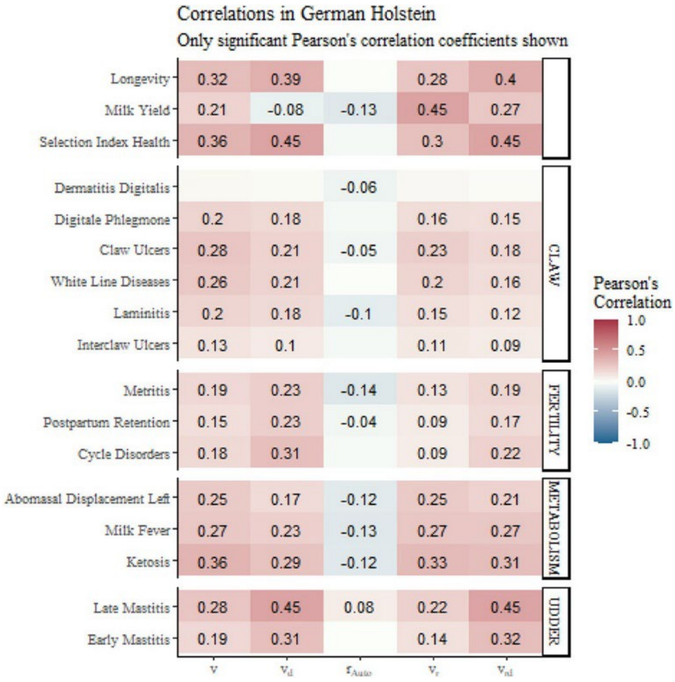


Figure 1. Correlations between selection indices and EBV of different functional and health traits and variance of absolute (v) and relative (v_r) daily milk yield, variance of deviations between observed and predicted absolute (v_d) and relative (v_{rd}) daily milk yield and autocorrelation of deviations between observed and predicted absolute daily milk yield (r_{Auto}).

only slightly smaller breeding responses. This indicates that there is no pronounced maximum. An index containing only v_d and v_r had similar selection response (0.218), heritability (0.196) and correlation with $\mathrm{SI}_{\mathrm{health}}$ (0.492) as the index consisting of all 5 resilience indicators.

Figure 2 represents the correlations between the optimum resilience selection index of 2, 3, 4, or 5 resilience indicators and $\mathrm{SI}_{\mathrm{health}}$ (taken from Table 2) and single trait EBV for health. All considered resilience selection indices performed similar. The correlation coefficients differed by less than 0.06. Resilience selection indices containing fewer resilience indicator traits partly showed stronger favorable correlations with other traits than a resilience selection index containing more resilience indicators. For example, the correlation between the resilience index containing 2 resilience indicators and Late Mastitis was 0.45, whereas the correlation between Late Mastitis and a resilience index of 5 resilience indicators was 0.41. All correlations were positive and significant. We also studied correlations between resilience selection indices and other selection indices used in HF breeding, which showed similar results and are given in Supplemental Figure S4 (see Notes; Keßler et al., 2024b).

Table 2. Different resilience selection indices with the weighting factor of each considered resilience indicator,[1] heritability (h^2) of the resilience selection index $\mathrm{SI}_{\mathrm{resilience}}$, correlation coefficient (r) for correlation between resilience selection index $\mathrm{SI}_{\mathrm{resilience}}$ and health selection index $\mathrm{SI}_{\mathrm{health}}$, and breeding response (R) in $\mathrm{SI}_{\mathrm{health}}$[2]

Resilience selection index consisting of							
v	v_d	r_{Auto}	v_r	v_{rd}	$\mathrm{h}^2\mathrm{SI}_{\mathrm{resilience}}$	r	$\mathrm{R}_{SI_{health}}$
−1.377	1.925	−0.076	1.809	−1.281	0.227	0.467	0.222
−1.219	1.730		1.624	−1.135	0.224	0.468	0.221
−0.344	0.785	−0.034	0.593		0.202	0.490	0.220
−0.319	0.753		0.566		0.201	0.491	0.220
	0.685	−0.042	0.357		0.196	0.492	0.218
	0.654		0.346		0.196	0.492	0.218
	0.903		0.429	−0.333	0.206	0.476	0.216
	0.959	−0.075	0.449	−0.333	0.204	0.478	0.216
0.350	0.761	−0.111			0.183	0.477	0.204
0.323	0.677				0.183	0.477	0.204
	0.891	−0.140		0.249	0.180	0.467	0.198
	0.768			0.232	0.178	0.466	0.197
	1.25.2	−0.252			0.191	0.449	0.196
0.364	0.559	−0.053		0.130	0.163	0.486	0.196
0.347	0.529			0.124	0.163	0.486	0.196
0.619		0.035	−0.209	0.555	0.148	0.481	0.185
0.641			−0.212	0.571	0.147	0.481	0.184
			0.286	0.714	0.171	0.444	0.184
0.426		0.043		0.530	0.152	0.471	0.184
0.448				0.552	0.151	0.471	0.183
		0.058	0.344	0.598	0.139	0.437	0.163
0.900			0.100		0.181	0.362	0.154
0.890		0.013	0.098		0.181	0.362	0.154
1.026		−0.026			0.179	0.364	0.154
		−0.006		1.006	0.109	0.446	0.147
		0.053	0.947		0.208	0.305	0.139

[1] v = variance of absolute daily milk yield; v_d = variance of deviations between observed and predicted absolute daily milk yield; r_{Auto} = autocorrelation of deviations between observed and predicted absolute daily milk yield; v_r = variance of relative daily milk yield; v_{rd} = variance of deviations between observed and predicted relative daily milk yield.

[2] An empty cell is equivalent to a weighting of 0.

DISCUSSION

Variance and autocorrelation are indicator traits of resilience that have been applied in livestock research in different species and several longitudinal measured traits (Poppe et al., 2020; Mengistu et al., 2022; Oloo et al., 2023). In dairy cattle, resilience indicators calculated from daily milk yield are of particular interest because the data are available without additional effort through automatic milking systems. Descriptive statistics and estimated heritabilities (Table 1) were within the range of a previous analysis in Keßler et al. (2024a) and in line with similar studies (Poppe et al., 2020; Wang et al., 2022). Accuracies for EBV of resilience indicator traits were relatively low in our study, as only a sample of the reference population was available due to the geographical limitation of the project, and because pedigree data were used instead of genomic data. Due to the limited size of the dataset, the effect of lactation was considered in 2 stages in the univariate model, i.e., only divided into first lactation or multi-lactation. This may have negatively influenced the accuracy, but studies by Poppe et al. (2021a) and Chen et al. (2023) showed that the genetic correlation of resilience indicators between second and third lactation was high (>0.95).

Correlation Analysis

Individuals with a more stable milk yield, i.e., less variance, have in general higher EBV for health and fertility traits, which means that resilient animals are healthier and more fertile than their contemporaries. These desirable correlations with the selection indices for health and longevity and the overall breeding value have also been shown in previous studies (Elgersma et al., 2018; Poppe et al., 2020). The correlation coefficients were weaker than in our study, but comparability is limited because the composition of selection indices differs between breeding organizations. It is notable that different resilience indicators are the best predictors for certain disease groups (Figure 1). Claw diseases tended to correlate more strongly with v, reproduction diseases with v_d, metabolic diseases with v_r, and udder diseases with v_{rd}. Furthermore, the strength of the correlation varied between disease groups. These differences could be due to different external stressors. For example, a stressor negatively influencing milk yield and udder health may have a smaller or no effect on claw health (e.g., heat stress leads to a decrease in milk yield and an increase in SCS, but has no influence of claw health). On the other hand, poor claw health may cause a cow to visit the milking robot less frequently, which increases the variance of the absolute milk yield and thus contributes to a high correlation with v. For all diseases, significant correlations were found. Thus, the applied resilience indicators are able to capture the effect of external stressors on each disease group. Also notable are the different directional correlations of the variance-based indicators with the Milk Yield trait. Animals with a high v_r seem to be more stable in performance and produce more milk than animals with a low v_r. This is probably because animals with high v_r less frequently have health problems that would cause a reduction in performance. In contrast, v_d is negatively correlated with the Milk Yield trait because animals with high performance usually reduce their absolute daily milk yield in the event of disturbance more than animals with low performance.

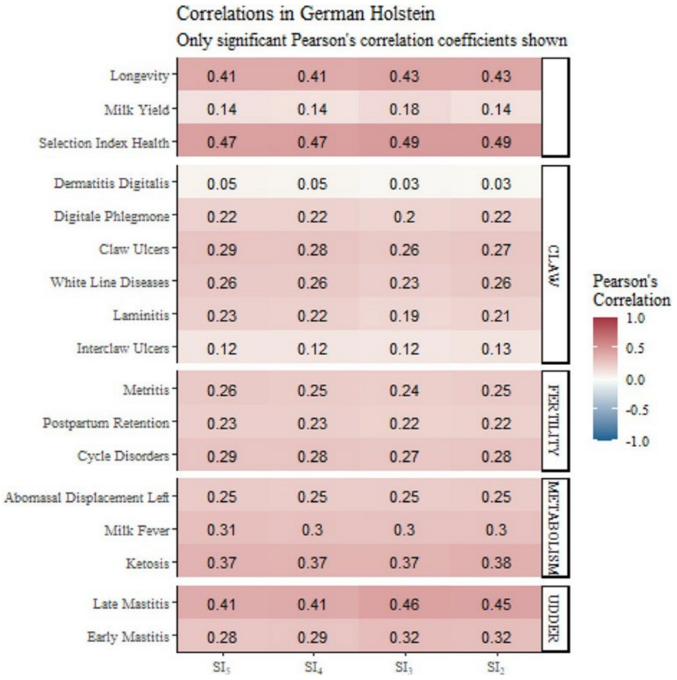


Figure 2. Comparison of resilience selection indices consisting of 5 (SI_5), 4 (SI_4), 3 (SI_3), or 2 (SI_2) resilience indicators based on the correlation to selection indices and EBV for functional and health traits. SI_5 consists of v, v_d, r_{Auto}, v_r, and v_{rd}; SI_4 consists of v, v_d, v_r, and v_{rd}; SI_3 consists of v, v_d, and v_r; SI_2 consists of v_d and v_r. v = variance of absolute daily milk yield; v_d = variance of deviations between observed and predicted absolute daily milk yield; r_{Auto} = autocorrelation of deviations between observed and predicted absolute daily milk yield; v_r = variance of relative daily milk yield; v_{rd} = variance of deviations between observed and predicted relative daily milk yield.

The trait autocorrelation seems to depend strongly on the selected approach to modeling the lactation curve. As a result, the direction and strength of the correlations with other traits can be influenced. Although our study showed few significant, slightly negative (i.e., undesirable) correlations with existing traits, Poppe et al. (2020) described desirable correlations. However, the EBV they used for health traits were estimated based on the disease prevalence of the animals. Opposite to r_{Auto}, their EBV for health contained no information about duration of an illness. Thus, prevalence and duration are 2 different aspects, which could explain why less significant correlation between r_{Auto} and health traits can be observed. The negative correlation with Milk Yield could, as with v_d, be explained by the stronger absolute drop in performance of high-yielding animals.

The differences in the strength of the correlation coefficients between various $\mathrm{SI}_{\mathrm{resilience}}$ and the EBV for single health traits suggest that it is more important to include the relevant resilience indicators than to include all of them. In $\mathrm{SI}_{\mathrm{resilience}}$ based on 5 resilience indicators, some information was redundant and negative weighting factors arises, but this is avoided in $\mathrm{SI}_{\mathrm{resilience}}$ with a smaller number of integrated resilience indicators.

Resilience Selection Index

The integration of a resilience indicator trait into the breeding value estimation can lead to a reduction in the impairment of the animal by a disturbance, the improvement of health traits, and the extension of longevity (Berghof et al., 2019). Bengtsson et al. (2022) used a simulation study to demonstrate that the resilience indicators can be used to map real resilience, and Poppe et al. (2021b) showed that effects of external influences such as heat waves are captured. As of today, there is no gold standard for the use of a trait resilience in breeding. A first step was taken by the Dutch breeding organization CRV (Arnhem, the Netherlands) with the publication of a breeding value for stability, based on v_d, and recovery, based on r_{Auto}, as well as an index of both based on approximate average genetic correlations of resilience indicators across all health traits (Meijer et al., 2024). For the development of a putative resilience selection goal, we analyzed the joint selection response with $\mathrm{SI}_{\mathrm{health}}$. This showed that selection response in health traits is increased by combining several resilience indicators in an index compared with using single resilience indicators.

The optimization did not reveal a pronounced maximum. The assumed superiority of v_{rd}, which was designed to capture relative variation in milk yield and correct for performance level, could not be confirmed. Instead, the combination of v_d and v_r showed a higher heritability as well as a larger joint selection response and a stronger correlation with $\mathrm{SI}_{\mathrm{health}}$ than v_{rd}. The index of these 2 resilience indicators is comparable to an index of all 5 indicators, which is why we recommend its use in practical breeding value estimation. This would reduce the calculation effort and increase comprehensibility compared with a 5-trait index. Contrary to the recommendation of previous studies, we exclude r_{Auto} at this point because according to our optimization, this resilience indicator does not provide enough additional information. The variance-based indicators also seem to be more stable in the case of missing daily milk yield data due to the separation of an animal from the herd by the farmer in response to a disturbance, e.g., separate milking during and after an incidence of mastitis (Kok et al., 2021; Weinans et al., 2021). We decided to maximize the joint breeding response with $\mathrm{SI}_{\mathrm{health}}$ instead of Longevity, for example, to map the most comprehensive resilience possible. The $\mathrm{SI}_{\mathrm{health}}$is made up of the prevalence of 13 different diseases, whereas Longevity represents solely the survival of the animal (vit, 2023).

By maximizing the performance of the resilience selection index according to $\mathrm{SI}_{\mathrm{health}}$, breeding is optimized for performance stability and health. In addition to recorded information such as disease incidence, a resilience selection index captures previously unmeasurable reactions of an individual to external influences such as heat waves (Poppe et al., 2021b). Furthermore, selection on animals with a high EBV in health traits shows over generations a decrease in average EBV of yield traits and vice versa (Heringstad and Larsgard, 2010; Heringstad et al., 2007), due to antagonistic correlation between performance and health traits (Schneider et al., 2023). As the resilience selection index is positively correlated with both health and performance, this index could provide additional information to the farmer, which sires pass both, good health and good performance, to their offspring.

Our results showed that resilient cows tend to be healthier, more productive and have a greater length of productive life. Resilience, therefore, also has an economic aspect. Further studies on the influence of resilience showed that the variance of the deviations between observed and predicted daily milk yields correlates significantly negatively with lifetime profitability and revenues from milk production, i.e., the lower the variance, the higher the profitability and revenues (Chen et al., 2023; Poppe et al., 2022). This is likely to be strengthened in the future due to steadily rising wages (Wilczyński and Kołoszycz, 2021), increasing number of cows per farm (Nieberg and Forstner, 2019), and higher labor costs with increasing farm size for nonresilient animals (Berghof et al., 2019). The relevance of selecting for resilience increases, as already today on many German farms, less than 60% of the cows are profitable, i.e., they generate a higher revenue than costs for the farm during their lifetime (Hoischen-Taubner et al., 2021). At the farm level, a resilient and homogeneous herd leads to easier management, e.g., through a simpler calculation of the total mixed ration or a lower incidence of disease, and a secure income through consistent milk yields (Ehsaninia et al., 2019).

In the future, further approaches to measuring resilience should be validated. In particular, the resilience indicators should be applied to other traits, such as activity data (van Dixhoorn et al., 2023), and a resilience index should be further developed. Initially, a resilience selection index calculated from daily milk yields that maximizes correlated selection response in overall health would be a solid breeding tool which, in addition to the existing breeding values, provides the breeder with information for selecting for individuals, which can cope with external stressors.

It is noteworthy that other breeds or populations for which less health recording data are available may profit even more from the introduction of a selection index for resilience.

CONCLUSIONS

Resilience indicators are correlated with EBV of health and reproduction. Breeding for resilience would result in yield-stable cows with good health and longevity. Our analysis showed that integration of a resilience selection index in breeding value estimation would be more effective than using a single resilience indicator. The selection response of indices consisting of a different number of resilience indicators varied only slightly. Thus, from the resilience indicators investigated in this study, an index of the 2 traits v_d and v_r seems to be sufficient.

REFERENCES

Bedere, N., T. V. Berghof, K. Peeters, M.-H. Pinard-van der Laan, J. Visscher, I. David, and H. A. Mulder. 2022. Using egg production longitudinal recording to study the genetic background of resilience in purebred and crossbred laying hens. Genet. Sel. Evol. 54:26. https://doi.org/10.1186/s12711-022-00716-8.

Bengtsson, C., J. R. Thomasen, M. Kargo, A. Bouquet, and M. Slagboom. 2022. Emphasis on resilience in dairy cattle breeding: Possibilities and consequences. J. Dairy Sci. 105:7588–7599. https://doi.org/10.3168/jds.2021-21049.

Berghof, T. V., M. Poppe, and H. A. Mulder. 2019. Opportunities to im- prove resilience in animal breeding programs. Front. Genet. 9:692. https://doi.org/10.3389/fgene.2018.00692.

Byrd, R. H., P. Lu, J. Nocedal, and C. Zhu. 1995. A limited memory algorithm for bound constrained optimization. SIAM J. Sci. Comput. 16:1190–1208. https://doi.org/10.1137/0916069.

Chen, S.-Y., J. P. Boerman, L. S. Gloria, V. B. Pedrosa, J. Doucette, and L. F. Brito. 2023. Genomic-based genetic parameters for resilience across lactations in North American Holstein cattle based on variability in daily milk yield records. J. Dairy Sci. 106:4133–4146. https://doi.org/10.3168/jds.2022-22754.

Colditz, I. G., and B. C. Hine. 2016. Resilience in farm animals: Biology, management, breeding and implications for animal welfare. Anim. Prod. Sci. 56:1961–1983. https://doi.org/10.1071/AN15297.

Ehsaninia, J., N. Ghavi Hossein-Zadeh, and A. A. Shadparvar. 2019. Estimation of genetic variation for macro- and micro-environmental sensitivities of milk yield and composition in Holstein cows using double hierarchical generalized linear models. J. Dairy Res. 86:145–153. https://doi.org/10.1017/S0022029919000293.

Elgersma, G. G., G. de Jong, R. van der Linde, and H. A. Mulder. 2018. Fluctuations in milk yield are heritable and can be used as a resilience indicator to breed healthy cows. J. Dairy Sci. 101:1240–1250. https://doi.org/10.3168/jds.2017-13270.

Friggens, N. C., I. Adriaens, R. Boré, G. Cozzi, J. Jurquet, C. Kamphuis, F. Leiber, I. Lora, T. Sakowski, J. Statham, and Y. de Haas. 2022. Resilience: Reference measures based on longer-term consequences are needed to unlock the potential of precision livestock farming technologies for quantifying this trait.

Peer Community J. 2:e38. https://doi.org/10.24072/pcjournal.136.

Heringstad, B., G. Klemetsdal, and T. Steine. 2007. Selection responses for disease resistance in two selection experiments with Norwegian red cows. J. Dairy Sci. 90:2419–2426. https://doi.org/10.3168/jds.2006-805.

Heringstad, B., and A. G. Larsgard. 2010. Correlated selection responses for female fertility after selection for high protein yield or low mas- titis frequency in Norwegian Red cows. J. Dairy Sci. 93:5970–5976. https://doi.org/10.3168/jds.2010-3399.

Hoischen-Taubner, S., J. Habel, V. Uhlig, E.-M. Schwabenbauer, T. Rumphorst, L. Ebert, D. Möller, and A. Sundrum. 2021. The whole and the parts—A New perspective on production diseases and economic sustainability in dairy farming. Sustainability (Basel) 13:9044. https://doi.org/10.3390/su13169044.

Homma, C., K. Hirose, T. Ito, M. Kamikawa, S. Toma, S. Nikaido, M. Satoh, and Y. Uemoto. 2021. Estimation of genetic parameter for feed efficiency and resilience traits in three pig breeds. Animal 15:100384. https://doi.org/10.1016/j.animal.2021.100384.

Keßler, F., R. Wellmann, M. G. Chagunda, and J. Bennewitz. 2024a. Resilience indicator traits in 3 dairy cattle breeds in Baden-Württemberg. J. Dairy Sci. 107:3780–3793. https://doi.org/10.3168/jds.2023-24305.

Keßler, F., R. Wellmann, M. G. Chagunda, and J. Bennewitz. 2024b. Supplementary JDS 25323. FigShare. https://doi.org/10.6084/m9.figshare.27231744.v1.

Kok, A., G. Tsousis, G. Niozas, B. Kemp, M. Kaske, and A. T. M. van Knegsel. 2021. Short communication: Variance and autocorrelation of deviations in daily milk yield are related with clinical mastitis in dairy cows. Animal 15:100363. https://doi.org/10.1016/j.animal.2021.100363.

Meijer, N., J. Bouwmeester-Vosman, M. van Pelt, and G. de Jong. 2024. Breeding for resilience in the Netherlands and Flanders. Interbull Bulletin 60:103–107. https://journal.interbull.org/index.php/ib/ article/download/1926/1935.

Mengistu, S. B., H. A. Mulder, J. W. Bastiaansen, J. A. Benzie, H. L. Khaw, T. Q. Trinh, and H. Komen. 2022. Fluctuations in growth are heritable and a potential indicator of resilience in Nile tilapia (Oreochromis niloticus). Aquaculture 560:738481. https://doi.org/10.1016/j.aquaculture.2022.738481.

Mrode, R. 2005. Genetic evaluation with different sources of records. Pages 1–25 Linear Models for the Prediction of Animal Breeding Values. 2nd ed. CABI

Publishing.

Nieberg, H., and B. Forstner. 2019. Agrarstrukturentwicklung-Bestimmende Faktoren und Perspektiven. Landentwicklung Aktuell 24:65–67.

Oloo, R. D., J. M. Ojango, C. C. Ekine-Dzivenu, G. Gebreyohanes, R. Mrode, O. A. Mwai, and M. G. Chagunda. 2023. Enhancing individual animal resilience to environmental disturbances to address low productivity in dairy cattle performing in sub-Saharan Africa. Front. Anim. Sci. 4:1254877. https://doi.org/10.3389/fanim.2023.1254877.

Poppe, M., G. Bonekamp, M. L. van Pelt, and H. A. Mulder. 2021a. Genetic analysis of resilience indicators based on milk yield records in different lactations and at different lactation stages. J. Dairy Sci. 104:1967–1981. https://doi.org/10.3168/jds.2020-19245.

Poppe, M., H. A. Mulder, and R. F. Veerkamp. 2021b. Validation of resilience indicators by estimating genetic correlations among daughter groups and with yield responses to a heat wave and disturbances at herd level. J. Dairy Sci. 104:8094–8106. https://doi.org/10.3168/jds.2020-19817.

Poppe, M., R. F. Veerkamp, H. A. Mulder, and H. Hogeveen. 2022. Observational study on associations between resilience indicators based on daily milk yield in first lactation and lifetime profitability. J. Dairy Sci. 105:8158–8176. https://doi.org/10.3168/jds.2021-21532.

Poppe, M., R. F. Veerkamp, M. L. van Pelt, and H. A. Mulder. 2020. Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. J. Dairy Sci. 103:1667–1684. https://doi.org/10.3168/jds.2019-17290.

Ramsey, J., and B. Ripley. 2022. pspline: Penalized Smoothing Splines. Version R package 528 version 1.0-19. Accessed Jun. 1, 2024. https://cran.r-project.org/web/packages/pspline/pspline.pdf.

Schneider, H., D. Segelke, J. Tetens, G. Thaller, and J. Bennewitz. 2023. A genomic assessment of the correlation between milk production traits and claw and udder health traits in Holstein dairy cattle. J. Dairy Sci. 106:1190–1205. https://doi.org/10.3168/jds.2022-22312.

van Dixhoorn, I. D. E., R. M. de Mol, S. K. Schnabel, J. van der Werf, S. van Mourik, J. E. Bolhuis, J. Rebel, and C. G. van Reenen. 2023. Behavioral patterns as indicators of resilience after parturition in dairy cows. J. Dairy Sci. 106:6444–

6463. https://doi.org/10.3168/ jds.2022-22891.

vit. 2023. zuletzt aktualisiert am 17.05.2023, zuletzt geprüft am 17.05.2023. Accessed Jun. 1, 2024. https://www.vit.de/fileadmin/ DE/Zuchtwertschaetzung/Zws_Bes_eng.pdf.

Wang, A., L. F. Brito, H. Zhang, R. Shi, L. Zhu, D. Liu, G. Guo, and Y. Wang. 2022. Exploring milk loss and variability during environmental perturbations across lactation stages as resilience indicators in Holstein cattle. Front. Genet. 13:1031557. https://doi.org/10.3389/ fgene.2022.1031557.

Weinans, E., R. Quax, and E. H. van Nes., and I. A. van Leemput. 2021. Evaluating the performance of multivariate indicators of resilience loss. Sci. Rep. 11:9148. https://doi.org/10.1038/s41598-021-87839-y.

Wilczyński, A., and E. Kołoszycz. 2021. Economic resilience of EU dairy farms: An evaluation of economic viability. Agriculture11:510. https://doi.org/10.3390/agriculture11060510.

SUPPLEMENTARY MATERIAL

The online version contains supplementary material available at https://doi.org/10.6084/m9.figshare.27231744.v1

APPENDIX 1 of *Toward a resilience selection index with indicator traits in German Holstein dairy cattle*

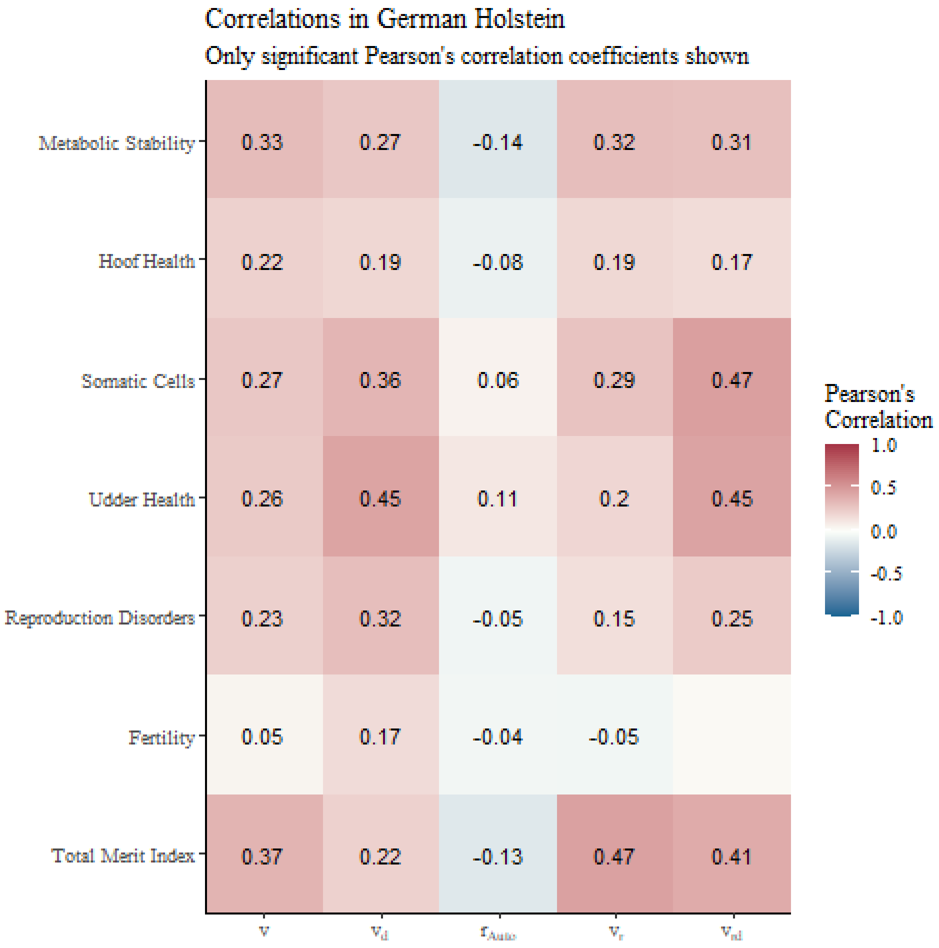


Figure 3. Correlations between selection indices for health and reproduction and variance of absolute (v) and relative (v_r) daily milk yield, variance of deviations between observed and predicted absolute (v_d) and relative (v_{rd}) daily milk yield and autocorrelation of deviations between observed and predicted absolute daily milk yield (r_{Auto}).

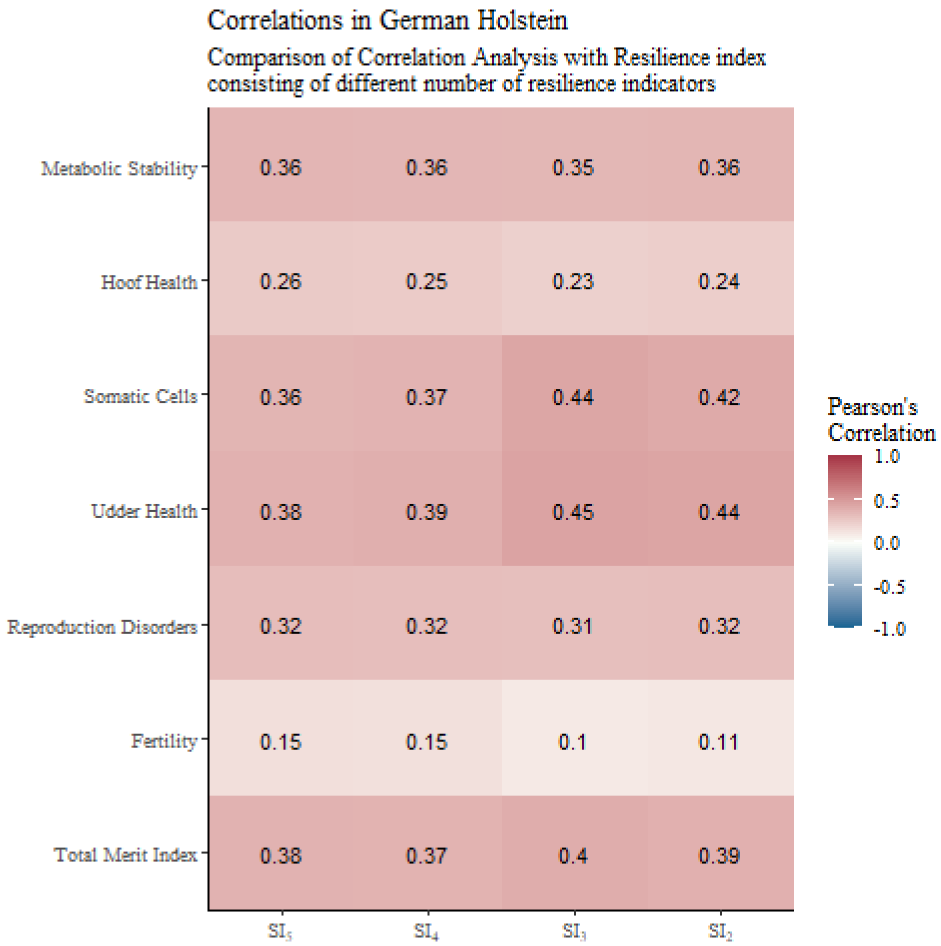


Figure 4. Comparison of resilience selection indices consisting of 5 (SI_5), 4 (SI_4), 3 (SI_3), or 2 (SI_2) resilience indicators based on the correlation to selection indices for functional and health traits. SI_5 consists of v, v_d, r_{Auto}, v_r, and v_{rd}; SI_4 consists of v, v_d, v_r, and v_{rd}; SI_3 consists of v, v_d, and v_r; SI_2 consists of v_d and v_r. v = variance of absolute daily milk yield; v_d = variance of deviations between observed and predicted absolute daily milk yield; r_{Auto} = autocorrelation of de- viations between observed and predicted absolute daily milk yield; v_r = variance of relative daily milk yield; v_{rd} = variance of deviations between observed and predicted relative daily milk yield.

CHAPTER FOUR

MAPPING GENES FOR RESILIENT DAIRY COWS BY MEANS OF ACROSS-BREED GENOME-WIDE ASSOCIATION ANALYSIS

F. Keßler[1*†], M. Zölch[1†], R. Wellmann[1], J. Bennewitz[1]

[1] Institute of Animal Science, University of Hohenheim, 70599 Stuttgart, Germany

†Franziska Keßler and Maximilian Zölch should be considered joint first author.

*Corresponding author: franziska.kessler@uni-hohenheim.de

Published in BMC Genomics (2025), Volume 26 (879), pp. 1–12

https://doi.org/10.1186/s12864-025-11940-z

ABSTRACT

Background Indicator traits based on variance and autocorrelation of longitudinal data are increasingly used to measure resilience in animal breeding. While these traits show promising heritability and can be routinely collected, their genetic architecture remains poorly understood. We conducted GWAS for three resilience indicators across German Holstein (*n* = 2,300), Fleckvieh (*n* = 2,330), and Brown Swiss (*n* = 1,073) dairy cattle (*Bos Taurus*) populations. The indicators included variance (v_d) and autocorrelation (r_{Auto}) of deviations of observed from predicted daily milk yield and variance of relative daily milk yield (v_r). Additionally, we analysed a selection index combining these traits. Prior to GWAS, we examined population structure through multi-dimensional scaling (MDS) and LD patterns, revealing distinct genetic clusters for each breed and similar LD decay patterns.

Results The GWAS results confirmed the polygenic nature of resilience, with multiple genomic regions showing significant associations. Notable signals were detected on *BTA5* (v_r), *BTA14* (v_d), *BTA2* and *BTA8* (r_{Auto}) for single indicator traits. For selection index resilience, strong suggestive SNPs are located on *BTA4*, *BTA16*, *BTA21*, and *BTA27*. Detected regions overlapped with previously reported QTLs for performance, reproduction, longevity and health, providing new insights into the biological pathways underlying dairy cattle resilience.

Conclusions Our findings demonstrate that resilience indicators have a complex genetic architecture with both breed-specific and shared components, supporting their potential use in selective breeding programs while highlighting the importance of careful trait definition.

Keywords Resilience, Variance, Autocorrelation, Linkage Disequilibrium, GWAS, MDS, Dairy cattle

BACKGROUND

In a challenging environment with an increased incidence of external disturbances such as heat waves intensified by climate change [1], there is a growing need for performance-stable and healthy livestock. One option is to breed for resilience, i.e., for the ability of an individual to react to short-term disturbances and maintain or quickly restore its own homeostasis and performance level [2, 3].

Since directly measuring responses to each disturbance is impractical in commercial settings, indirect approaches using routinely collected longitudinal data have been developed. The most promising is the use of indicator traits to determine performance variability and recovery speed. Performance variability can be expressed by the fluctuation of daily milk yield. Therefore, the variance of deviations between observed and predicted daily milk yield (v_d) is calculated. The variance is small for cows with smooth lactation curves, but also for cows with low milk yield [2, 4, 5]. To addresses the influence of the milk production level, a second parameter is the variance of relative daily milk yield (v_r)[6]. This parameter is small for cows with smooth lactation curves that show a low decrease in milk yield during the lactation. The heritability for both variance-based indicator traits are moderate, in the range of 0.13 to 0.24 [4–6]. Furthermore, the genetic correlations with performance traits are desirable when the standardized v_r is used or v_d is corrected for the original performance level [5, 6]. Several studies have shown that resilient individuals have better values for health traits [5, 7, 8] or the productive lifetime [4, 9] than non-resilient cows. Recovery speed is captured by the autocorrelation (r_{Auto}) calculated from the deviations between observed and predicted daily milk yield of a cow over the time of one lactation. A resilient cow with fast recovery has a value for r_{Auto} near to 0 [2]. The heritability is low with an average of 0.05 across several studies and breeds, and genetic correlations with other traits were mostly desirable but rarely significant [5, 8, 10]. A selection index can combine different resilience indicators in an optimal way. Since the economic value of resilience is difficult to measure, it was not used to determine the weighting factors of the single indicator traits and alternative approaches were considered. Previous studies offer two options: On the one hand, the genetic correlation between resilience indicators and health and functional traits could be considered [11], on the other hand, the weighting factors could be optimized by maximizing the selection response in health traits when breeding for resilience [8]. The latter is used in the following.

While previous studies estimated heritabilities and genetic correlations [4–6], and discussed the power and accuracy of single resilience indicator traits [2, 12], deeper analysis of the genetic architecture are lacking. To our knowledge, there has been one GWAS of resilience indicators in dairy cows [13], pigs [14] and laying hens [15]. Their results indicate a polygenic nature of resilience, with many gene loci having a small effect. Chen et al. [13] detected a strong peak on *BTA14* for performance variability.

This study builds on this state of research and uses in-depth genomic analysis to analyze the genetic architecture and relationships to other traits. Therefore, the aim of this study was to assess the genetic architecture of several resilience indicator traits by GWAS in the three large German dairy cattle (*Bos Taurus*) breeds German Holstein (HF), German Fleckvieh (FV) and German Brown Swiss (BS) using imputed HD SNP genotypes. Since we performed an across-breed and a within-breed GWAS, we also studied the across- and within-breed LD pattern and the population structure. This provided us information on the genetic relationship between the three breeds and supports the interpretation of the GWAS results.

METHODS

Data processing and evaluation as well as statistical analyses were performed in software R 4.2.1 [16]. Genotype preparation, phasing, imputation and population analysis were done by using PLINK 1.9 and PLINK 2.0 [17] and Beagle 5.4 [18, 19]. ASReml-R 4.1.0 [20] was used for univariate estimation of breeding values and GCTA 1.94.1 [21] for GWAS with de-regressed GEBVs as phenotypes.

Materials

The dataset consists of 5,703 dairy cows of the breeds German Holstein (HF, *n* = 2,300), German Fleckvieh (FV, *n* = 2,330) and German Brown Swiss (BS, *n* = 1,073), originating from 48 farms. The farms are members of the breeding organization Rinderunion Baden-Württemberg e.V. (Herbertingen, Germany) and work with automatic milking systems. The milking data, consisting of yield per milking and start time of milking, from the automatic milking systems were longitudinally recorded between October 2017 and April 2024 and were provided by the Landeskontrollverband Baden-Württemberg e.V. (Stuttgart, Germany).

Animals in our study were genotyped with 50 K SNP chips. For HF, the Eurogenomics-MD-Chip was used in several versions. The merging of the chips and the imputation of undetermined SNPs were done by Vereinigte Informationssysteme Tierhaltung w.V. (Verden, Germany). Genotyping of FV and BS was done by Landeskontrollverband Bayern (Munich, Germany) and Bayerische Landesanstalt für Landwirtschaft (Grub, Germany) using Illumina BovineSNP50v2 BeadChip or DAC-BS50 Illumina. For both breeds, we obtained a standardized data set over the different chips, whereby missing SNPs were called with the population mean. We excluded SNPs on sex chromosomes, on undefined position, with minor allele frequency (MAF) < 0.03 or missing call rate > 0.01. The MAF threshold was stricter than in comparable studies [13, 22] in order to cause fewer false-positive results in the GWAS and was based on a study with a similar data set to our BS sample [23]. SNPs that are not included in the high-density reference panels were excluded, as they would be automatically removed during imputation. All genotypes were updated to the reference genome assembly ARS-UCD1.2 by manually replacing the existing coordinates with the updated ones [24]. SNPs, which are not listed in the ARS-UCD1.2, were excluded. This left 31,416 SNPs for HF, 34,238 SNPs for FV and 31,527 SNPs for BS.

A detailed overview of the size of the raw genotype and phenotype data and remaining data sets after filtering per breed can be found in the Supplementary (see Additional File 1).

Methods

Calculation of resilience indicator traits

Milk yields per milking were added up to daily milk yields, whereby the first milking was divided proportionally between the current and the previous day. Daily milk yields were filtered as follows. Days where the number of animals milked on the farm deviated by three standard deviations from the mean number of animals normally milked on the farm as well as the day before and after were removed for all animals on this farm. Furthermore, the day before and after an individual gap of an animal, meaning one or more days without available data, was removed. Lactations were considered from day 10 to day 305, and those with less than 50% coverage respectively 148 data points were excluded. For each lactation of each cow, a lactation curve was predicted using spline interpolation with *pspline* in R [25] with degrees of freedom set to 5 and data points weighted by the strength of assumed disturbances. Details are described in Keßler et al. [6].

We considered three resilience indicator traits. The variance of the deviations between observed and predicted absolute daily milk yield (v_d) was calculated as:

$$v_d(\mathbf{y}_{il}) = \frac{1}{n-1} * \sum_{t=10}^{n} \left((\boldsymbol{y}_{ilt} - \hat{\boldsymbol{y}}_{ilt}) - \overline{(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})} \right)^2$$

with $\boldsymbol{y}$ a *n*-vector with daily milk yields of a cow i in a certain lactation l, $\hat{\boldsymbol{y}}$ the vector with interpolated daily milk yields and t the lactation day. The variance of relative daily milk yields (v_r) in considered lactation period was calculated as:

$$v_r(\mathbf{y}_{il}) = \frac{1}{n-1} * \sum_{t=10}^{n} \left((\alpha_{il}\, \mathbf{y}_{il}) - \overline{(\alpha_{il}\, \mathbf{y}_{il})} \right)^2$$

with $\boldsymbol{y}$ a n-vector with daily milk yields of a cow i in a certain lactation l and the scaling factor $\alpha_{il} = \frac{100}{\sum_{t=10}^{n} y_{ilt}}$ with t the lactation day. The two parameters were logarithmized to conform to the assumption of normal distribution according to previous analyses in Keßler et al. [6].

The autocorrelation of the deviations between observed and predicted absolute daily milk yield (r_{Auto}) was calculated as:

$$r_{Auto}(\mathbf{y}_{il}) = \frac{cov(\mathbf{y}_{il} - \hat{\mathbf{y}}_{il})}{var(\mathbf{y}_{il} - \hat{\mathbf{y}}_{il})}$$

and in detail:

$$r_{Auto}(\mathrm{y}_{il}) = \frac{\frac{1}{n-2} * \sum_{t=2}^{n} \left(\left((\boldsymbol{y}_{ilt} - \hat{\boldsymbol{y}}_{ilt}) - \overline{(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})} \right) * \left((\boldsymbol{y}_{il,t-1} - \hat{\boldsymbol{y}}_{ilt}) - \overline{(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})} \right) \right)}{\frac{1}{n-1} * \sum_{t=1}^{n} \left((\boldsymbol{y}_{ilt} - \hat{\boldsymbol{y}}_{ilt}) - \overline{(\boldsymbol{y}_{il} - \hat{\boldsymbol{y}}_{il})} \right)^2}$$

Genetic Analysis

The resilience indicators described above were genetically analyzed separately for each breed and two different lactation groups. The first one, labelled *P* for primiparous, included phenotypes from the first lactation. For the second one, named *M* for multiple lactations, we added information also from higher lactations of the cows in *P* as repeated measurements. Thus, a univariate analysis was performed for each of six groups: first lacta-tion HF, all lactation HF, first lactation FV, all lactation FV, first lactation BS, all lactation BS. The animal model for the data sets with information about cows in the first lactation was:

$$y = Xb + Zu + e$$

with y vector of observations, u vector of additive genetic effects, e vector of residuals, and incidence matrices X and Z. The animal model for all lactations of the considered cows was:

$$y = Xb + Zu + Wpe + e$$

where pe is the vector of permanent environmental effects and W is the incidence matrix. The additive genetic effects u, the permanent environmental effects pe and the residual effects e were normally distributed with $u \sim N(0, G\sigma_u^2)$, $pe \sim N\left(0, I_{pe}\sigma_{pe}^2\right)$ and $e \sim N(0, I_e\sigma_e^2)$, whereby I are identity matrices. The genomic relationship matrix G was built according to VanRaden et al. [26]. The vector of fixed effects b comprises in each model age at first calving in month, herd-year-season effect and completeness of lactation data. In the second model the effect of the lactation separated in first and higher lactation was added. Season in herd-year-season was divided into spring from March to May, summer from June to August, autumn from September to November, and winter from December to February and completeness of lactation data was graded in ≥ 90%, 80%—< 90%, 70%—< 80%, 60%—< 70%, 50%—< 60%. In all analyses, effect levels with fewer than six animals are excluded. This left 1,370 HF cows for *P* and 1,538 HF cows for *M*, for FV 1,135 cows in *P* and 1,551 in *M* and for BS *P* includes data from 310 and *M* from 488 cows. For further analysis, we de-regressed the cow's additive genetic effects, i.e. their GEBV, by dividing the effects by their reliabilities and standardized them to a mean of 0 and a standard deviation of 1 within each group. We also calculated the heritability as the proportion of additive genetic variance of the total variance.

Additionally, a selection index (SI) was computed that combines the resilience indicators into a single trait. The selection index is a linear combination of the GEBVs of individual resilience indicators, with weights chosen to optimally describe overall resilience. Weighting factors were determined in Keßler et al. [8], by maximizing the selection response in health traits when selecting on resilience indicators based on the performance trait daily milk yield. The weighting factors were adopted from this study, which were estimated in the same data set [8]. The selection index was calculated as

$$SI(\mathrm{y}_i) = 0.65 * \tilde{v}_d(\mathbf{y}_i) + 0.35 * \tilde{v}_r(\mathbf{y}_i),$$

where $\tilde{v}_d(\mathbf{y}_i)$ and $\tilde{v}_r(\mathbf{y}_i)$ were GEBVs of the logarithmized, negated $v_d(\mathbf{y}_i)$ and $v_r(\mathbf{y}_i)$, for cow i. The selection index was calculated in both lactation groups, P and M, and all three breeds.

Imputation

For further analyses we imputed the 50 K genotypes to high-density genotypes. The following reference panels were used. For HF, we used data from 1,278 Australian Holsteins with 585,517 SNPs that were genotyped with the BovineHD Genotyping BeadChip [27]. High-density data from 3,439 FV cows and bulls including 629,028 SNPs genotyped with Illumina BovineHD Bead chip [28] and 192 BS individuals with 613,140 SNPs genotyped with Illumina Bovine-HD [23] were available. Similar to the 50 K genotype data, SNPs whose MAF was < 0.03, whose missing call rate was > 0.01 or which were found on sex chromosomes were removed. The positions of considered SNPs were updated to the reference genome ARS-UCD1.2 [24]. 522,726 SNPs in HF, 580,873 SNPs in FV and 503,971 SNPs in BS remained.

Reference panel data were phased using beagle 5.4 within each dataset. 50 K and high-density data of each breed were concorded with *conform-gt* and then imputed with beagle 5.4. According to [29], the effective population size Ne was set to 100. Apart from that, the default settings were used. SNPs with a dosage R-Squared < 0.75 are removed to maintain a sufficiently high imputation quality [19]. The final imputed data set contains 2,300 HF cows with 503,263 SNPs, 2,330 FV cows with 569,056 SNPs and 1,073 BS cows with 493,637 SNPs. For the across-breed population analysis, the imputed genotypes were merged with PLINK 1.9 [30], leaving 401,491 SNPs shared across all breeds.

Population Analysis

Population analyses were done in PLINK 1.9 for MDS and PLINK 2.0 for LD analysis [17]. Genomic relationship between the breeds was studied with a MDS based on imputed genotypes, considering only SNPs that remained in all three breeds after all filtering steps described above. The LD was analysed across breeds and breed-specific, using the maximum number of available SNPs in the imputed genotype datasets of each breed, respectively the merged imputed dataset after all filtering steps. The LD was calculated as the r2 [31]:

$$r^2 = \frac{\left(p_{A_1B_1} - p_{A_1}p_{B_1}\right)^2}{p_{A_1}p_{A_2}p_{B_1}p_{B_2}}$$

with p the allele frequency, A_1 and A_2 alleles on gene locus A and B_1 and B_2 alleles on gene locus B. The LD between pairs of SNPs that were a maximum of 1,000 SNPs or 3,000 kilobases apart was calculated.

Genome-wide association study

For each of the six groups defined above, a GWAS was performed for the resilience indicator traits and the selection index. We optimized the GWAS model by minimizing the difference of the genomic inflation factor lambda λ_{GC} to 1 in each breed. λ_{GC} is calculated as the ratio between the median of the observed chi-squared test statistics and the expected median of 0.455 [32]. The value should be close to 1 or slightly above [22, 33]. We therefore decided for a mixed linear model based association analysis ($MLMA$) for HF, a $MLMA$ excluding the GRM of the chromosome where the SNP is located ($MLM - LOCO$) for BS and a $MLM - LOCO$ corrected for a fixed effect of the principal components calculated based on the whole genome ($\mathrm{MLM} - \mathrm{LOCO}_{PCGenome}$) to account for population stratification for FV [21] ($\lambda_{GC}$of the selected GWAS are provided in the results, all λ_{GC} are provided in Additional File 2).

GWAS were performed using the following model:

$$y = \mu + Xb + Zu + e,$$

with y vector of de-regressed, standardized additive genetic effects of each animal derived from univariate analysis for each resilience indicator trait and the selection index, the population mean μ, fixed effects b with the incidence matrix X, including the reference allele coded with 0, 1 or 2, the vector of additive genetic effects u with $u \sim N(0, G\sigma_u^2)$ and G the genomic relationship matrix created according to Yang et al. [34], and the residual term e with $e \sim N(0, I_e\sigma_e^2)$. In $MLM - LOCO$ and $\mathrm{MLM} - \mathrm{LOCO}_{PCGenome}$, G is calculated for each chromosome separately and leaves out the chromosome, where the SNP to be tested for association is located. The vector b includes the additive effect of the candidate SNP to be tested for association and for $\mathrm{MLM} - \mathrm{LOCO}_{PCGenome}$ in FV a covariate of 20 principal components, which were calculated based on the whole genome with software GCTA [35]. For the calculation of GWAS in GCTA, the reference allele was specified in accordance with ARS-UCD1.2.

For across-breed evaluation, we pooled the p-values in data set P and data set M per resilience indicator using the package *poolr* in R [36]. We used the Fisher method, which is based on the chi²-statistic:

$$X^2 = -2\sum_{i=1}^{k} \ln(p_i)$$

with K number of tests (three) and pi the *p*-values of the GWAS.

The results of the single GWAS and pooled GWAS are shown as Manhattan plots, whereby two significance thresholds were defined. Genome-wide significance was determined using Bonferroni correction with, with N number of SNPs, and a less stringent, suggestive level of significance was set to $p \leq \frac{0.05}{N}$. For SNPs showing significant association at the stringent significance level, the Cattle QTL Database release 53 [27] was used to search for QTL in the range from 25 kB up- and downstream.

RESULTS

Heritabilities

Heritabilities were in the range of 0.1 to 0.15 for v_d. BS showed the highest h^2 with 0.23 (SE = 0.15) in P and 0.15 (SE = 0.07) in M. HF and FV were similar with 0.13 (SE = 0.05) and 0.12 (SE = 0.06) in P and 0.1 (SE = 0.03) and 0.13 (SE = 0.03) in M. Repeatability was 0.26 (SE = 0.02) in HF, 0.25 (SE = 0.03) in FV and 0.19 (SE = 0.05) in BS. For v_r FV showed the lowest h^2 with 0.04 (SE = 0.04) in P and 0.08 (SE = 0.03) in M, and BS the highest h^2 with 0.18 (SE = 0.15) in P and 0.2 (SE = 0.08) in M. HF ranged between them with 0.13 (SE = 0.04) in P and 0.15 (SE = 0.03) in M. Repeatabilities were higher than for v_d, with 0.32 (SE = 0.02) in HF, 0.35 (SE = 0.03) in FV and 0.4 (SE = 0.05) in BS. Estimates of h^2 for r_{Auto} were rarely significant and low with values between 0.03 in FV and 0.12 in BS. Repeatability's were 0.17 (SE = 0.02) for HF, 0.2 (SE = 0.03) for FV and 0.27 (SE = 0.06) for BS. Reliabilities for GEBVs were smaller in P data sets than in M data sets with an average difference of 0.1. The highest values in M were estimated in HF (0.37) and BS (0.33) for v_r and the lowest in HF (0.15) and FV (0.14). Reliabilities of v_d in M ranged around 0.29. Genetic correlation between the resilience indicator traits were analysed in a previous study and can be seen in Keßler et al. [6].

Population Analyses

The MDS (Fig. 1) shows three distinct clusters, each corresponding to one breed. The distances between the clusters are similar.

The r^2 of the LD decreases with increasing marker distance (Fig. 2). This can be observed across all breeds as well as within breeds. The strongest decline in LD can be observed in FV, the lowest in BS. The LD within the breeds is similar, which means that the across-breed analysis showed comparable results.

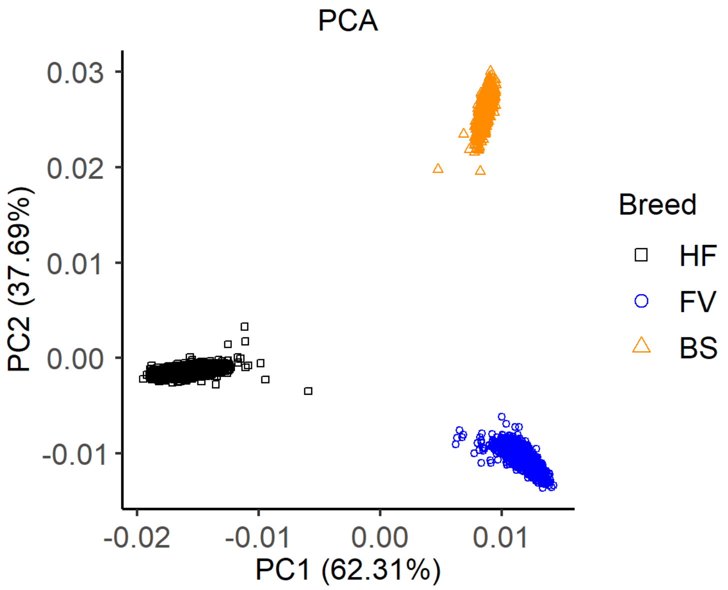


Fig. 1: Genomic relationship between the breeds HF, FV and BS represented in a MDS-plot

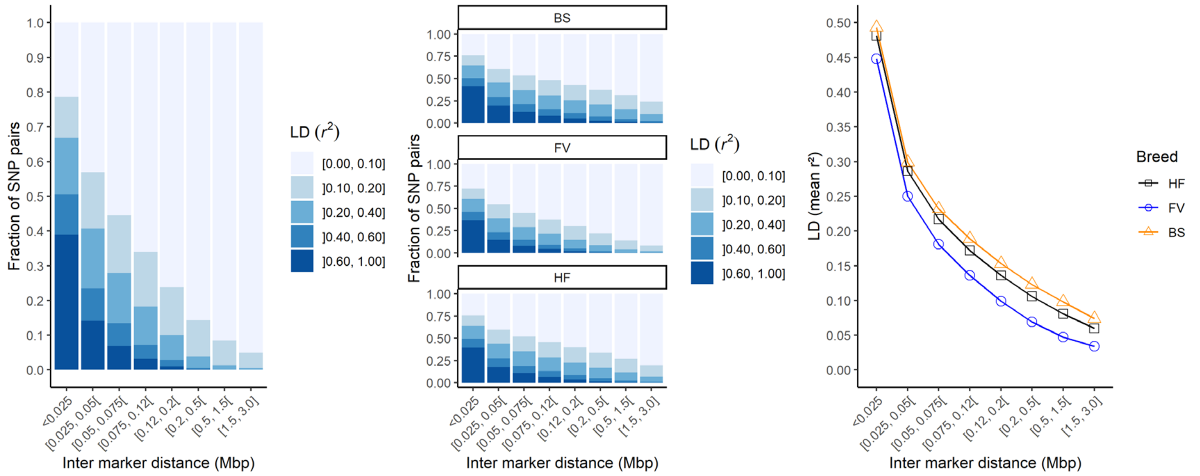


Fig. 2: The decay of mean r² as a function of physical distance for breeds HF, FV and BS analyzed jointly (left), separated by breed (middle) and compared between the breeds (right)

Genome-wide association study

Table 1 shows the values of λ_{GC} for MLMA in HF, $MLM - LOCO$ in BS and $\mathrm{MLM} - \mathrm{LOCO}_{PCGenome}$ in FV. Based on these values, we decided on the respective method for the GWAS. Our aim was to detect significant SNPs as accurately as possible without the inflation of false-positive results, therefore λ_{GC} should be close to 1 or slightly above. Since the other methods considered led to a strong inflation of false-positive results

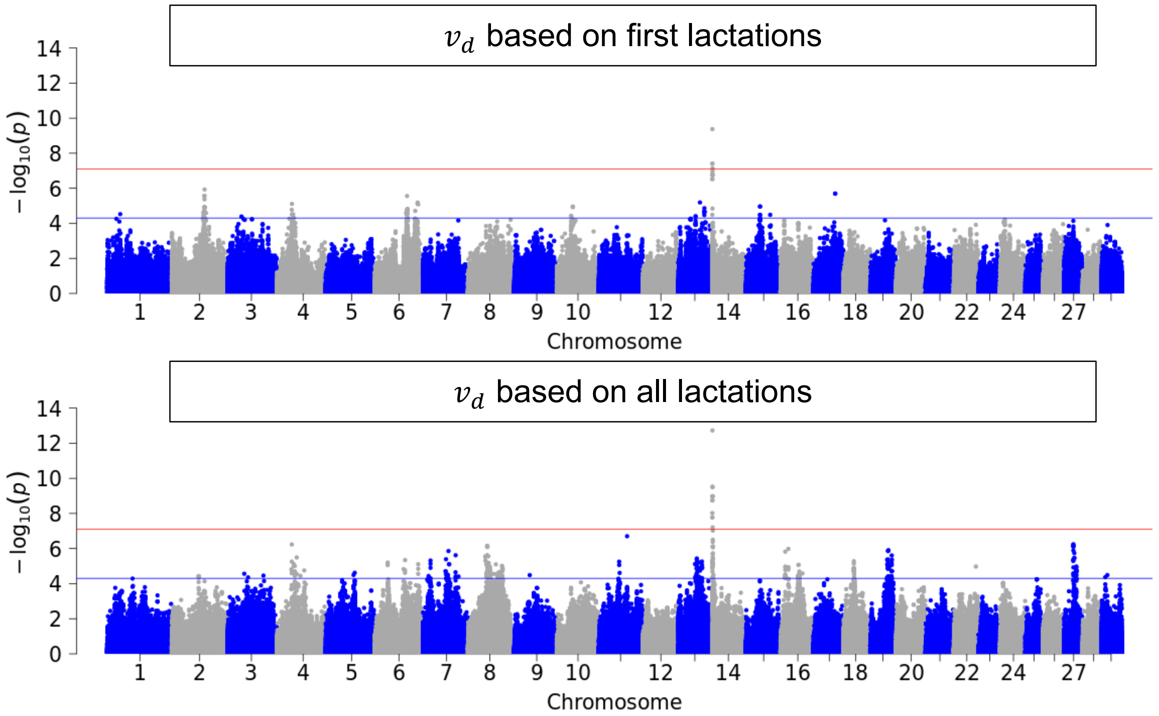
(λ_{GC} >1.5) in HF [see Additional File 2], we decided to use the conservative $MLMA$ approach.

Table 1 Genomic inflation factors λ_{GC} for GWAS in German Holstein, German Fleckvieh, German Brown Swiss and pooled data sets of first lactation (P) and first and higher lactations (M) for resilience indicator traits

German Holstein		**German Fleckvieh**		**German Brown Swiss**		**Across-Breed**	
P	*M*	*P*	*M*	*P*	*M*	*P*	*M*
0.811	0.805	1.197	1.374	1.140	1.242	1.081	1.253
0.811	0.810	1.155	1.373	1.153	1.191	1.084	1.251
0.842	0.823	1.117	1.353	1.103	1.164	1.048	1.233
0.822	0.807	1.185	1.374	1.142	1.198	1.099	1.235

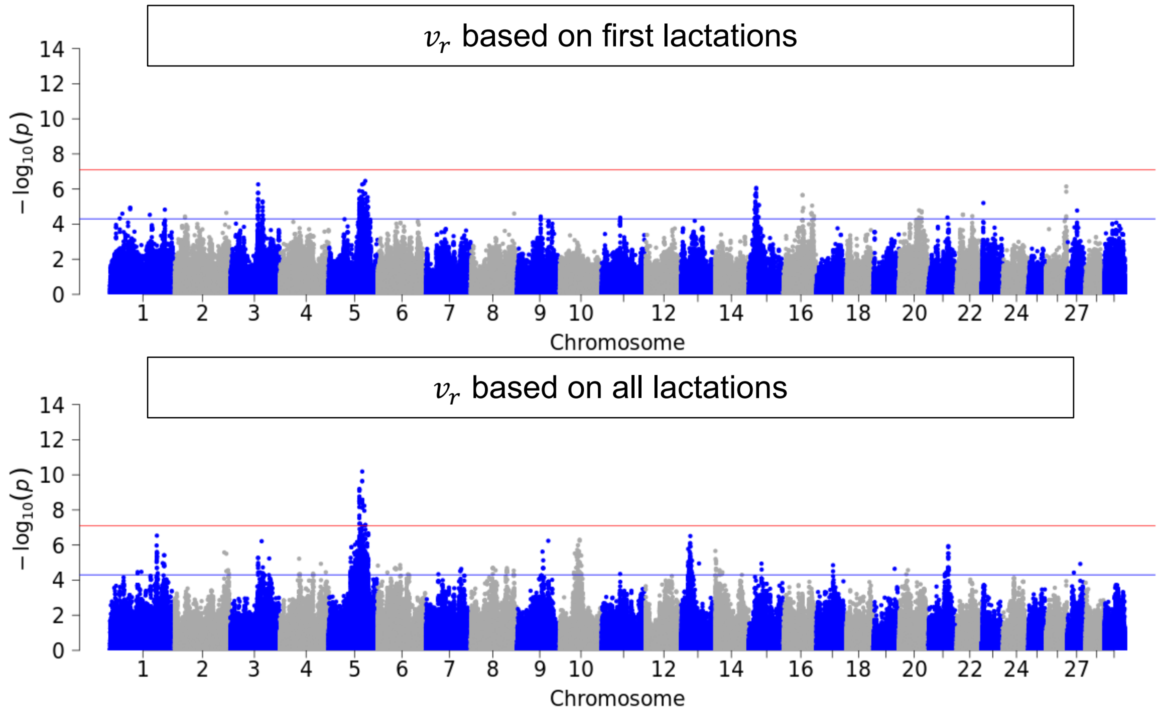
v_d **– variance of deviations between observed and predicted absolute daily milk yield**
v_r **– variance of relative daily milk yield**
r_{Auto} **– autocorrelation of deviations between observed and predicted absolute daily milk yield**
SI**– selection index resilience composed of single resilience indicators**

Figures 3, 4, 5 and 6 illustrate the results of GWAS for each resilience indicator trait after pooling p-values across breeds for first and for all available lactations. Genome-wide significant SNPs were found for v_d in the first lactation and for all single resilience indicator traits in the data set with all available lactations. SNPs that reached the suggestive significance threshold were found for all traits and groups, also for SI. These SNPs were distributed through-out the genome, with the variance-based indicators showing more significant SNPs. For the sake of completeness, the Manhattan plots can be viewed separately by breed in the Supplementary (see Additional File 4).


v_d based on first lactations

v_d based on all lactations

Fig. 3: Manhattan-Plot of pooled p-values from single GWAS in the three breeds


v_r based on first lactations

v_r based on all lactations

Fig. 4: Manhattan-Plot of pooled p-values from single GWAS in the three breeds German Holstein, German Fleckvieh and German Brown Swiss for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first lactation (top) and first and higher lactations (bottom)

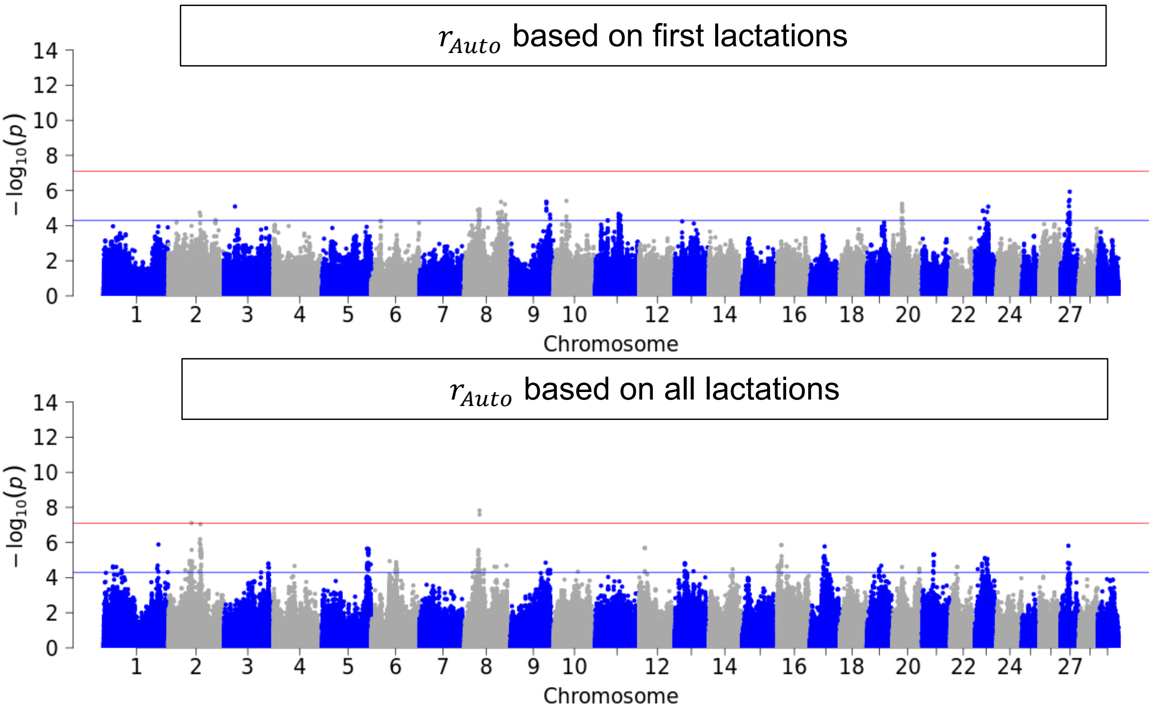


Fig. 5: Manhattan-Plot of pooled p-values from single GWAS in the three breeds German Holstein, German Fleckvieh and German Brown Swiss for resilience indicator trait r_{Auto}, which is the autocorrelation in first lactation (top) and first and higher lactations (bottom)

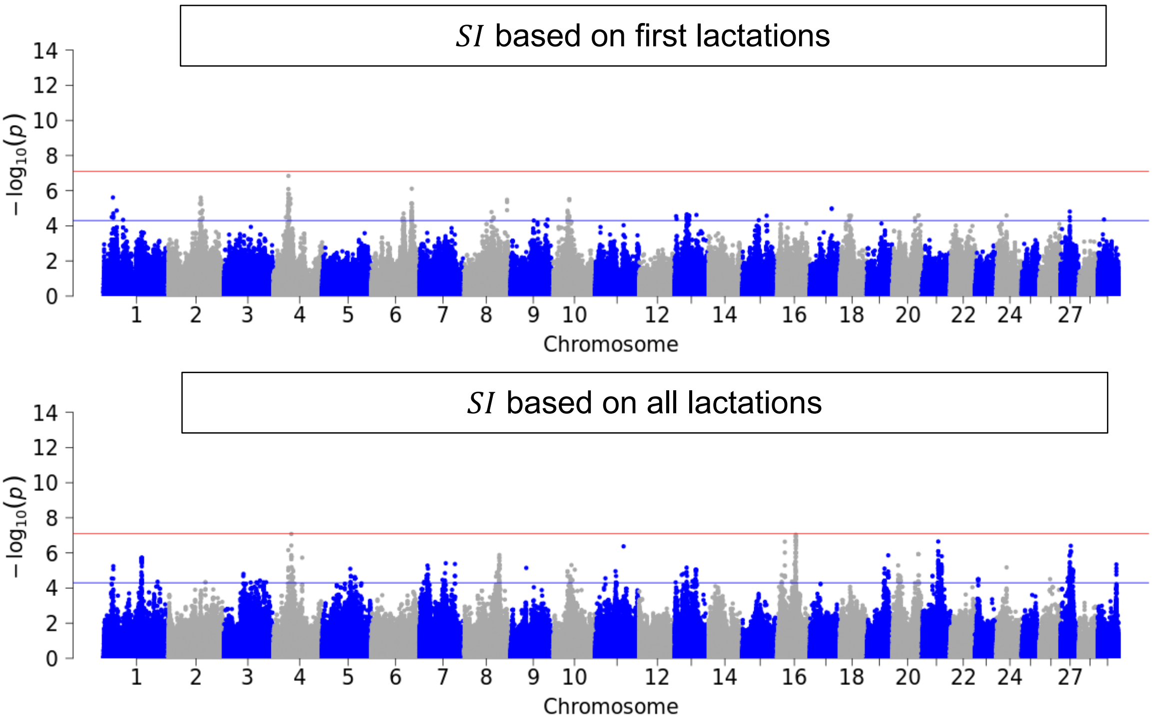


Fig. 6: Manhattan-Plot of pooled p-values from single GWAS in the three breeds German Holstein, German Fleckvieh and German Brown Swiss for the resilience selection index SI computed from resilience indicator traits calculated from daily milk yield in first lactation (top) and first and higher lactations (bottom)

Number of suggestive and genome-wide significant SNPs can be seen in Table 2, while the name of the genome-wide significant SNPs and their base pair positions can be viewed in the Supplementary [see Additional File 3]. According to previous studies [e.g. [37, 38], most correlated QTL potentially influence milk yield, reproductive performance, body condition or longevity. Furthermore, QTL associated with udder, metabolic and claw health as well as immunological parameters were found (see Additional File 3 for an overview).

Table 2: Number of significant SNPs for resilience indicator traits based on suggestive ($\boldsymbol{p} < \boldsymbol{5 * 10^{-5}}$) and genomewide ($\boldsymbol{p} \leq \frac{\mathbf{0.05}}{\boldsymbol{Number\ of\ SNPs}}$) significance threshold for first lactation of ($\boldsymbol{P}$) and for first and higher lactations of cows ($\boldsymbol{M}$)

Significance of the SNP	v_d		v_r		r_{Auto}		SI	
	P	***M***	***P***	***M***	***P***	***M***	***P***	***M***
Genome-wide	4	13	0	38	0	3	0	0
Suggestive	93	379	214	716	84	234	196	441

v_d **– variance of deviations between observed and predicted absolute daily milk yield**

v_r **– variance of relative daily milk yield**

r_{Auto} **– autocorrelation of deviations between observed and predicted absolute daily milk yield**

SI **– selection index resilience composed of single resilience indicators**

DISCUSSION

General discussion

In Germany, there are hardly any studies that compare and, above all, combine the genomic data from HF, FV and BS, likely also due to the division of breeding value estimation between different organisations. We matched the three data sets, which enabled us to increase our data basis and thus our power. In addition, we can draw conclusions about all three breeds, whereas analysing the BS alone would have been critical due to the small number of individuals. Multibreed analyses lead to a higher accuracy of estimates for breeds with small reference populations [39], like BS, and also allow estimates for crossbred animals, for example when estimating genomic breeding values [40]. For purebred, large reference populations a single breed analysis would be more advantageous [41], which is why we did a two-step analysis: run the mixed-linear model and the genome-wide association study for each breed in the first step, and combine the results in a second step. Heritabilities in our data set were in the range with previous studies with Holstein Friesian [4, 5, 10]. Higher heritabilities with higher standard errors in BS could be due to the limited number of individuals and farms, which is why fewer estimations of variance components per trait were significant. The inclusion of all lactations of the individuals compared to only the first lactation tended to explain a higher proportion of the total variance, captured by the permanent environment effect.

Population analysis

The breeds studied are genetically different, which was as expected and previously reported for the same breeds in Switzerland [42]. The number of SNPs considered was > 300,000 and the decrease in LD with increasing distance between SNPs was similar in all breeds. Thus, all three breeds could be analysed and discussed jointly in the GWAS [43]. For the subsequent search for QTL associated with the genome-wide significant SNPs for resilience indicators, a window had to be defined. This is limited by the useful LD between SNP and QTL, which was described by de Roos et al. [40] and Sargolzaei et al. [44] with r^2>0.3. In our study, we observed a mean r^2>0.4 in a distance of up to 25 kb. In addition, as this was an across-breed study, we were more stringent with the window size.

Genomewide-association study

The inflation factor λ_{GC} was close to 1 or slightly above for most of the data sets (Table 1) and only for FV first and higher lactations above 1.3. This suggests that the p-values of the GWAS might be slightly inflated for the latter, but not for the remaining data sets. A conservative approach with λ_{GC} <1 was chosen for HF, as the other methods tested resulted in highly inflated results. The pooled, across-breed analysis showed that resilience indicators are polygenic traits influenced by many gene loci. This was shown by the high number of suggestive significant SNPs distributed across the entire genome and the small number of genome-wide significant SNPs. Similar results were reported by previous studies about resilience indicators in laying hens [15], pigs [14] and dairy cows [13]. Chen et al. [13] reported a strong peak on *BTA14*, whereby the milk yield level had a significant causal effect on the performance variability over several lactations. QTL that are closely adjacent to our genome-wide significant SNPs simultaneously influence several traits of performance, fertility and health [45]. The inclusion of repeated measurements per individual led to a higher power of the GWAS. In contrast to the data set of the first lactation, genome-wide significant SNPs were found for r_{Auto} and v_r in the data set including all lactations. For v_d, there was an increase in the number of genome-wide significant SNPs when all lactations were considered rather than just the first.

However, they did not share their genetic backgrounds, i.e. different genome regions influence different resilience indicators. This was previously described in Chen et al. [13] for traits similar to our v_d and r_{Auto} and were expected from us, because previous analysis of genetic correlation between single resilience indicator traits showed only less to moderate correlation, which can be interpreted as different traits[6].

Common genetic background of resilience and other traits

Genomic regions that have a strong effect on our resilience indicators influence milk yield, milk ingredients, health and fertility traits. A significant genetic effect on the resilience indicator $\boldsymbol{v_r}$ occurs from *BTA5*, in the region of the genes *CACNG2*, *EIF3D*, *IFT27* and *PVALB*, which influence milk yield, and next to *5s_RNA*, which influences the amount of milk fat [37]. With *7SK*, $\boldsymbol{r_{Auto}}$ on *BTA8* also has a milk yield-regulating gene in the analysed window. A significant effect of $\boldsymbol{v_d}$ were detected on *BTA14* in a region in which pleiotropic genes have an effect on milk quantity and ingredients, especially milk fat acids [46]. Known genes are for example *DGAT1*, *ARHGAP39*, *bta-mir-2308*, *LRRC24*, *CPSF1*, *RECQL4*, *PLEC*, *PPP1R16A*, *MFSD3*, *GPT*, *KIFC2*, *CYHR1*, *TONSL* or *FOXH1* [37, 38, 45]. A strong antagonism between the SNP effects on the amount of milk fat and the amount of milk and milk protein yield is known for *PLEC* and *PPP1R16A* [38]. An unbalanced fat-to-protein ratio can be a sign of a negative energy balance and metabolic diseases [47, 48], which is why animals with a strong genetic antagonism may be less resilient. In addition, this shared genetic background of performance and resilience influences the stability of milk and milk fat yield under heat stress [49] and the overall profitability of a dairy cow [50], which was also described in Poppe et al. [51].

Jiang et al. [38] reported a QTL next to *MRPS35* on *BTA5*, which is in a high LD with genome-wide significant SNPs for v_r, influencing pregnancy and conception rate, and Cochran et al. [45] a QTL on *CPSF1*, influencing conception rate and v_d. Galliou et al. [52] detected on *BTA2* in a genomic region with an effect on r_{Auto}, QTL for heifer reproduction traits that may also affect reproduction in cows. Health indicator traits like the somatic cell score for mastitis [45] or the concentration of beta-hydroxybutyrat (BHB) in milk for ketosis [53] are affected by genomic regions on *BTA14*, also influencing v_d. This is confirmed by a study with the EBV of mastitis, showing a significant influence in the same genomic area [54].

The selection index SI was not influenced by genome-wide significant SNPs, but strong suggestive peaks emerged on *BTA4*, *BTA16*, *BTA21* and *BTA27*. QTL on these chromosomes influence milk yield and especially milk fat, longevity and reproduction ability. This underlines the polygenic characteristics of resilience.

Breeding for resilience

Breeding for resilience to increase recovery speed and reduce performance variability reduces sensitivity to external disturbances. The current approach of using indicator traits calculated on the basis of longitudinal data seems promising: moderate heritabilities and desirable correlations with other traits have been shown in previous studies [4–7, 10, 55]. The combination of different indicator traits is suitable for integration into practical breeding [11]. For example, the weighting factors can be determined by maximizing selection response in functional and health traits. In this way, performance and functionality are combined and mediated. Because of favorable genetic correlations, breeders could use this EBV in addition to the total merit index to more easily identify sires that combine yield, longevity and health [8]. There are two main points in favor of breeding for resilience: First, no extra data collection is necessary for breeding value estimation [2]. Second, in some breeds, little or no health traits are recorded; breeding for resilience could improve animal health [6, 8]. A homogeneous, healthy herd with stable performance is easier to manage and more profitable [2, 51]. In the future, the suitability of other statistical parameters as resilience indicator traits [12] and new longitudinal measured phenotypes (e.g. activity data, omics data) will be studied [7, 56].

CONCLUSION

Our study demonstrated clear genetic differentiation between German populations of HF, FV, and BS breeds, while showing similar patterns of LD decay across breeds. Significant heritabilities for resilience indicators were estimated across all three breeds. GWAS results revealed the polygenic nature of resilience, with significant SNPs distributed across multiple BTA. Genome-wide significant SNPs for v_d were found on *BTA14*, for v_r on BTA5 and for r_{Auto} on *BTA2* and *BTA8*, which indicate a different genetic background. A selection index combined of v_d and v_r was mainly influenced by SNPs on *BTA4*, *BTA16*, *BTA21* and *BTA27*. We found strong links with QTL affecting production, health and fertility, which confirms the complex genetic architecture of resilience. Notably, analyzing resilience across multiple lactations increased statistical power and revealed additional significant associations compared to first-lactation analysis.

REFERENCES

1. Hansen J, Sato M, Ruedy R. Perception of climate change. Proc Natl Acad Sci U S A. 2012;109:E2415–23. https://doi.org/10.1073/pnas.1205276109.
2. Berghof TVL, Poppe M, Mulder HA. Opportunities to improve resilience in animal breeding programs. Front Genet. 2018;9:692. https://doi.org/10.3389/fgene.2018.00692.
3. Colditz IG, Hine BC. Resilience in farm animals: biology, management, breeding and implications for animal welfare. Anim Prod Sci. 2016;56:1961–83. https://doi.org/10.1071/AN15297.
4. Chen S-Y, Boerman JP, Gloria LS, Pedrosa VB, Doucette J, Brito LF. Genomic-based genetic parameters for resilience across lactations in North American Holstein cattle based on variability in daily milk yield records. J Dairy Sci. 2023;106:4133–46. https://doi.org/10.3168/jds.2022-22754.
5. Poppe M, Veerkamp RF, van Pelt ML, Mulder HA. Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. J Dairy Sci. 2020;103:1667–84. https://doi.org/10.3168/jds.2019-17290.
6. Keßler F, Wellmann R, Chagunda MGG, Bennewitz J. Resilience indicator traits in three dairy cattle breeds in Baden-Württemberg. J Dairy Sci. 2024. https://doi.org/10.3168/jds.2023-24305.
7. van Dixhoorn I, de Mol RM, Schnabel SK, van der Werf J, van Mourik S, Bolhuis JE, et al. Behavioral patterns as indicators of resilience after parturition in dairy cows. J Dairy Sci. 2023. https://doi.org/10.3168/jds.2022-22891.
8. Keßler F, Wellmann R, Chagunda MGG, Bennewitz J. Toward a resilience selection index with indicator traits in German Holstein dairy cattle. J Dairy Sci. 2025;108:726–34. https://doi.org/10.3168/jds.2024-25323.
9. Wang A, Brito LF, Zhang H, Shi R, Zhu L, Liu D, et al. Exploring milk loss and variability during environmental perturbations across lactation stages as resilience indicators in Holstein cattle. Front Genet. 2022;13:1031557. https://doi.org/10.3389/fgene.2022.1031557.
10. Wang A, Su G, Brito LF, Zhang H, Shi R, Liu D, et al. Investigating the relationship between fluctuations in daily milk yield as resilience indicators and health traits in Holstein cattle. J Dairy Sci. 2024;107:1535–48. https://doi.org/1 0.3168/jds.2023-23495.

11. Meijer N, Bouwmeester-Vosman J, van Pelt M, de Jong G. Breeding for resilience in the Netherlands and Flanders: INTERBULL; 2024.
12. Ghaderi Zefreh M, Pong-Wong R, Doeschl-Wilson A. Validating statistical properties of resilience indicators derived from simulated longitudinal performance measures of farmed animals. Animal. 2024;18:101248. https://doi.org/10.1016/j.animal.2024.101248.
13. Chen SY, Gloria LS, Pedrosa VB, Doucette J, Boerman JP, Brito LF. Unravelling the genomic background of resilience based on variability in milk yield and milk production levels in North American Holstein cattle through GWAS and Mendelian randomization analyses. J Dairy Sci. 2023. https://doi.org/10.3168/ jds.2023-23650.
14. Mancin E, Maltecca C, Jiang J, Huang YJ, Tiezzi F. Capturing resilience from phenotypic deviations: a case study using feed consumption and whole genome data in pigs. BMC Genomics. 2024;25:1128. https://doi.org/10.1186/s 12864-024-11052-0.
15. Doekes HP, Bovenhuis H, Berghof TVL, Peeters K, Visscher J, Mulder HA. Research note: Genome-wide association study for natural antibodies and resilience in a purebred layer chicken line. Poult Sci. 2023;102(1):102312. https://doi.org/10.1016/j.psj.2022.102312.
16. R Core Team. R: A language and environment for statistical computing. 2022. https://www.R-project.org/. Accessed 9 Oct 2023.
17. Chang CC, Chow CC, Tellier LC, Vattikuti S, Purcell SM, Lee JJ. Second-generation PLINK: rising to the challenge of larger and richer datasets. Gigascience. 2015;4:7. https://doi.org/10.1186/s13742-015-0047-8.
18. Browning BL, Tian X, Zhou Y, Browning SR. Fast two-stage phasing of large-scale sequence data. Am J Hum Genet. 2021;108:1880–90. https://doi.org/10.1016/j.ajhg.2021.08.005.
19. Browning BL, Zhou Y, Browning SR. A one-penny imputed genome from next-generation reference panels. Am J Hum Genet. 2018;103:338–48. https://doi.org/10.1016/j.ajhg.2018.07.015.
20. Butler DG. Package ‘asreml’. 2018. https://asreml.kb.vsni.co.uk/wp-content/uploads/sites/3/2018/07/ASReml-Package.pdf.
21. Yang J, Zaitlen NA, Goddard ME, Visscher PM, Price AL. Advantages and pitfalls in the application of mixed-model association methods. Nat Genet. 2014;46:100–6. https://doi.org/10.1038/ng.2876.

22. Schneider H, Segelke D, Tetens J, Thaller G, Bennewitz J. A genomic assess-ment of the correlation between milk production traits and claw and udder health traits in Holstein dairy cattle. J Dairy Sci. 2023;106:1190–205. https://doi.org/10.3168/jds.2022-22312.
23. Dreher C, Wellmann R, Stratz P, Schmid M, Preuß S, Hamann H, Bennewitz J. Genomic analysis of perinatal sucking reflex in German Brown Swiss calves. J Dairy Sci. 2019;102:6296–305. https://doi.org/10.3168/jds.2019-16487.
24. Rosen BD, Bickhart DM, Schnabel RD, Koren S, Elsik CG, Tseng E, et al. De novo assembly of the cattle reference genome with single-molecule sequencing. Gigascience. 2020. https://doi.org/10.1093/gigascience/giaa021.
25. Ramsey J, Ripley B. pspline: Penalized Smoothing Splines. 2022. https://cran. r-project.org/web/packages/pspline/index.html. Accessed 29 Nov 2023.
26. VanRaden PM. Efficient methods to compute genomic predictions. J Dairy Sci. 2008;91:4414–23. https://doi.org/10.3168/jds.2007-0980.
27. van den Berg I, Ho PN, Nguyen TV, Haile-Mariam M, MacLeod IM, Beatson PR, et al. GWAS and genomic prediction of milk urea nitrogen in Australian and New Zealand dairy cattle. Genet Sel Evol. 2022;54:15. https://doi.org/10.1186/ s12711-022-00707-9.
28. Ertl J, Legarra A, Vitezica ZG, Varona L, Edel C, Emmerling R, Götz K-U. Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. Genet Sel Evol. 2014;46:40. https://doi.org/10.11 86/1297-9686-46-40.
29. Qanbari S, Pimentel ECG, Tetens J, Thaller G, Lichtner P, Sharifi AR, Simianer H. The pattern of linkage disequilibrium in German Holstein cattle. Anim Genet. 2010;41:346–56. https://doi.org/10.1111/j.1365-2052.2009.02011.x.
30. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MAR, Bender D, et al. PLINK: a tool set for whole-genome association and population-based link-age analyses. Am J Hum Genet. 2007;81:559–75. https://doi.org/10.1086/519 795.
31. Hill WG, Robertson A. Linkage disequilibrium in finite populations. Theor Appl Genet. 1968;38:226–31. https://doi.org/10.1007/BF01245622.
32. van den Berg S, Vandenplas J, van Eeuwijk FA, Lopes MS, Veerkamp RF. Significance testing and genomic inflation factor using high-density genotypes or whole-genome sequence data. J Anim Breed Genet. 2019;136:418–29. https://doi.org/10.1111/jbg.12419.

33. Yang J, Weedon MN, Purcell S, Lettre G, Estrada K, Willer CJ, et al. Genomic inflation factors under polygenic inheritance. Eur J Hum Genet. 2011;19:807–12. https://doi.org/10.1038/ejhg.2011.39.
34. Yang J, Benyamin B, McEvoy BP, Gordon S, Henders AK, Nyholt DR, et al. Common SNPs explain a large proportion of the heritability for human height. Nat Genet. 2010;42:565–9. https://doi.org/10.1038/ng.608.
35. Yin T, König S. Genome-wide associations and detection of potential candidate genes for direct genetic and maternal genetic effects influencing dairy cattle body weight at different ages. Genet Sel Evol. 2019;51:4. https://doi.org/10.1186/s12711-018-0444-4.
36. Cinar O, Viechtbauer W. The poolr package for combining independent and dependent p values. J Stat Soft. 2022;101:1–42. https://doi.org/10.18637/jss.v101.i01.
37. Pedrosa VB, Schenkel FS, Chen S-Y, Oliveira HR, Casey TM, Melka MG, Brito LF. Genomewide association analyses of lactation persistency and milk production traits in Holstein cattle based on imputed whole-genome sequence data. Genes. 2021;12:1830. https://doi.org/10.3390/genes12111830.
38. Jiang J, Ma L, Prakapenka D, VanRaden PM, Cole JB, Da Y. A large-scale genome-wide association study in U.S. Holstein cattle. Front Genet. 2019;10:412. https://doi.org/10.3389/fgene.2019.00412.
39. Frischknecht M, Pausch H, Bapst B, Signer-Hasler H, Flury C, Garrick D, et al. Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. BMC Genomics. 2017;18:999. https://doi.org/10.1186/s12 864-017-4390-2.
40. Karaman E, Su G, Croue I, Lund MS. Genomic prediction using a reference population of multiple pure breeds and admixed individuals. Genet Sel Evol. 2021;53:46. https://doi.org/10.1186/s12711-021-00637-y.
41. Misztal I, Steyn Y, Lourenco DAL. Genomic evaluation with multibreed and crossbred data. JDS Communications. 2022;3:156–9. https://doi.org/10.3168/jdsc.2021-0177.
42. Signer-Hasler H, Burren A, Neuditschko M, Frischknecht M, Garrick D, Stricker C, et al. Population structure and genomic inbreeding in nine Swiss dairy cattle populations. Genet Sel Evol. 2017;49:83. https://doi.org/10.1186/s1271 1-017-0358-6.
43. de Roos APW, Hayes BJ, Spelman RJ, Goddard ME. Linkage disequilibrium and

persistence of phase in Holstein-Friesian, Jersey and Angus cattle. Genetics. 2008;179:1503–12. https://doi.org/10.1534/genetics.107.084301.

44. Sargolzaei M, Schenkel FS, Jansen GB, Schaeffer LR. Extent of linkage disequilibrium in Holstein cattle in North America. J Dairy Sci. 2008;91:2106–17. https://doi.org/10.3168/jds.2007-0553.
45. Cochran SD, Cole JB, Null DJ, Hansen PJ. Discovery of single nucleotide polymorphisms in candidate genes associated with fertility and production traits in Holstein cattle. BMC Genet. 2013;14:49. https://doi.org/10.1186/1471-215 6-14-49.
46. Gebreyesus G, Buitenhuis AJ, Poulsen NA, Visker MHPW, Zhang Q, van Valenberg HJF, et al. Combining multi-population datasets for joint genome-wide association and meta-analyses: the case of bovine milk fat composition traits. J Dairy Sci. 2019;102:11124–41. https://doi.org/10.3168/jds.2019-16676.
47. Toni F, Vincenti L, Grigoletto L, Ricci A, Schukken YH. Early lactation ratio of fat and protein percentage in milk is associated with health, milk production, and survival. J Dairy Sci. 2011;94:1772–83. https://doi.org/10.3168/jds.2010-33 89.
48. Buttchereit N, Stamer E, Junge W, Thaller G. Short communication: genetic relationships among daily energy balance, feed intake, body condition score, and fat to protein ratio of milk in dairy cows. J Dairy Sci. 2011;94:1586–91. https://doi.org/10.3168/jds.2010-3396.
49. Macciotta NPP, Biffani S, Bernabucci U, Lacetera N, Vitali A, Ajmone-Marsan P, Nardone A. Derivation and genome-wide association study of a principal component-based measure of heat tolerance in dairy cattle. J Dairy Sci. 2017;100:4683–97. https://doi.org/10.3168/jds.2016-12249.
50. Nayeri S, Sargolzaei M, Abo-Ismail MK, Miller S, Schenkel F, Moore SS, Stothard P. Genome-wide association study for lactation persistency, female fertility, longevity, and lifetime profit index traits in Holstein dairy cattle. J Dairy Sci. 2017;100:1246–58. https://doi.org/10.3168/jds.2016-11770.
51. Poppe M, Veerkamp RF, Mulder HA, Hogeveen H. Observational study on associations between resilience indicators based on daily milk yield in first lactation and lifetime profitability. J Dairy Sci. 2022;105:8158–76. https://doi.org/10.3168/jds.2021-21532.
52. Galliou JM, Kiser JN, Oliver KF, Seabury CM, Moraes JGN, Burns GW, et al. Identification of loci and pathways associated with heifer conception rate in U.S. Holsteins. Genes. 2020. https://doi.org/10.3390/genes11070767.

53. Nayeri S, Schenkel F, Fleming A, Kroezen V, Sargolzaei M, Baes C, et al. Genome-wide association analysis for β-hydroxybutyrate concentration in milk in Holstein dairy cattle. BMC Genet. 2019;20:58. https://doi.org/10.1186/s 12863-019-0761-9.
54. Sahana G, Guldbrandtsen B, Thomsen B, Lund MS. Confirmation and finemapping of clinical mastitis and somatic cell score QTL in Nordic Holstein cattle. Anim Genet. 2013;44:620–6. https://doi.org/10.1111/age.12053.
55. Oloo R, Mrode R, Bennewitz J, Ekine-Dzivenu CC, Ojango JM, Gebreyohanes G, et al. Potential for quantifying general resilience of dairy cattle in sub-Saharan Africa using deviations in milk yield. Front Genet. 2023. https://doi.or g/10.3389/fgene.2023.1208158.
56. Poppe M, Mulder HA, van Pelt ML, Mullaart E, Hogeveen H, Veerkamp RF. Development of resilience indicator traits based on daily step count data for dairy cattle breeding. Genet Sel Evol. 2022;54:21. https://doi.org/10.1186/s12 711-022-00713-x.

SUPPLEMENTARY MATERIAL

Additional file 1 of *Mapping genes for resilient dairy cows by means of across-breed genome-wide association analysis*: **Provision of data set sizes before and after filtering**

Additional file 2 of *Mapping genes for resilient dairy cows by means of across-breed genome-wide association analysis*: **Provision of the genomic inflation factor λ_{GC} for each GWAS method**

Additional file 3 of *Mapping genes for resilient dairy cows by means of across-breed genome-wide association analysis*: **Provision of information of genome-wide significant SNPs and correlated QTL**

Additional file 4 of *Mapping genes for resilient dairy cows by means of across-breed genome-wide association analysis*: **Manhattan-Plots and QQ-Plots of each breed and lactation group**

Additional file 1: Provision of data set sizes before and after filtering

Table 3: Overview of the size of the phenotype and genotype data sets before and after processing

		BS	FV	HF
Dataset phenotypes	Initial number of individuals	3,608	8,943	8,474
	Initial number of lactations	5,038	15,472	13,517
	Number of individuals after filtering for at least 50 % of data points per lactation	1,465	4,614	4,204
	Number of lactations after filtering for at least 50 % of data points per lactation	2,505	9,494	8,111
Data set of genotypes	Initial number of genotypes 50K	1,073	2,330	2,300
	Initial number of usable SNPs 50K	38,482	40,864	45,613
	Number of individuals in the HD-genotyped reference sample	192	3,439	1,278
	Initial number of useable SNPs HD	613,140	629,028	585,517
	Number of imputed SNPs after excluding SNPs with MAF <0.03	493,637	569,056	503,263
Univariate analysis	Number of individuals in analysis of first lactation (P)	310	1,135	1,370
	Number of individuals in analysis of first and higher lactation (M)	477	1,551	1,538
	Number of lactations in analysis of first and higher lactation (M)	885	2,874	3,409
	Number SNPs considered in the relationship matrix	31,527	34,238	31,416
Genome-wide association analysis	Number of individuals in analysis of first lactation (P)	310	1,135	1,370
	Number of individuals in analysis of first and higher lactation (M)	477	1,551	1,538
	Number of lactations in analysis of first and higher lactation (M)	885	2,874	3,409
	Number SNPs considered in the genome-wide association analysis	493,637	569,056	503,263

Additional file 2: Provision of the genomic inflation factor λ_{GC} for each GWAS method

Table 4: Genomic inflation factor for different GWAS methods analyzing the variance of the deviation between observed and predicted daily milk yield v_d in primiparous (P) and multiparous (M) cows

Breed	**Lactation**	**MLMA**	**MLMA Loco**	**MLMA Loco PC_{Genome}**	**MLMA Loco $PC_{Chromosome}$**
German Holstein	P	0.811	2.257	1.621	0.503
German Holstein	M	0.805	2.798	1.908	0.548
German Fleckvieh	P	0.883	1.411	1.197	0.634
German Fleckvieh	M	0.840	1.703	1.374	0.676
German Brown Swiss	P	0.901	1.177	0.919	0.404
German Brown Swiss	M	0.881	1.287	1.004	0.376
Pooled data set	P	1.091			
Pooled data set	M	1.255			

MLMA – mixed linear model based association analysis

MLMA Loco – MLMA with excluding the genomic relationship matrix of the considered BTA

MLMA Loco PC_{Genome} – MLMA Loco corrected for 20 principal components calculated from the whole genome

MLMA Loco $PC_{Chromosome}$ – MLMA Loco corrected for 20 principal components calculated from the considered chromosome

Table 5: Genomic inflation factor for different GWAS methods analyzing the variance of the deviation between observed and predicted daily milk yield v_r in primiparous (P) and multiparous (M) cows

Breed	**Lactation**	**MLMA**	**MLMA Loco**	**MLMA Loco PC_{Genome}**	**MLMA Loco $PC_{Chromosome}$**
German Holstein	P	0.811	2.517	1.664	0.490
German Holstein	M	0.810	2.876	1.888	0.526
German Fleckvieh	P	0.864	1.345	1.155	0.628
German Fleckvieh	M	0.833	1.687	1.373	0.664
German Brown Swiss	P	0.902	1.194	0.889	0.391
German Brown Swiss	M	0.825	1.284	0.971	0.385
Pooled data set	P	1.090			
Pooled data set	M	1.278			

MLMA – mixed linear model based association analysis

MLMA Loco – MLMA with excluding the genomic relationship matrix of the considered BTA

MLMA Loco PC_{Genome} – MLMA Loco corrected for 20 principal components calculated from the whole genome

MLMA Loco $PC_{Chromosome}$ – MLMA Loco corrected for 20 principal components calculated from the considered chromosome

Table 6: Genomic inflation factor for different GWAS methods analyzing the variance of the deviation between observed and predicted daily milk yield r_{Auto} in primiparous (P) and multiparous (M) cows

Breed	**Lactation**	**MLMA**	**MLMA Loco**	**MLMA Loco PC_{Genome}**	**MLMA Loco $PC_{Chromosome}$**
German Holstein	P	0.842	2.409	1.710	0.538
German Holstein	M	0.823	2.649	1.847	0.559
German Fleckvieh	P	0.858	1.324	1.117	0.612
German Fleckvieh	M	0.828	1.702	1.353	0.659
German Brown Swiss	P	0.891	1.132	0.852	0.382
German Brown Swiss	M	0.853	1.270	0.997	0.413
Pooled data set	P	1.049			
Pooled data set	M	1.266			

MLMA – mixed linear model based association analysis

MLMA Loco – MLMA with excluding the genomic relationship matrix of the considered BTA

MLMA Loco PC_{Genome} – MLMA Loco corrected for 20 principal components calculated from the whole genome

MLMA Loco $PC_{Chromosome}$ – MLMA Loco corrected for 20 principal components calculated from the considered chromosome

Additional File 3: Provision of information of genome-wide significant SNPs and correlated QTL

Table 7: Name and Base-pair Position of genomewide significant SNPs ($p \leq \frac{0.05}{Number\ of\ SNPs}$) for the resilience indicators variance (v_d) and autocorrelation (r_{Auto}) of deviations between observed and predicted absolute daily milk yield, variance of relative daily milk yield (v_r) and a selection index resilience computed from the resilience indicator traits (SI) analyzed in across-breeds in first lactation (P) and first and higher lactations (M)

Trait Lactation	Marker Name	Chromosome	Base-pair Position
$\boldsymbol{v_d}$ P	BovineHD1400000204	14	487527
	BovineHD1400000206	14	494621
	BovineHD1400000216	14	550784
	BovineHD1400000281	14	854163
$\boldsymbol{v_d}$ M	ARS-BFGL-NGS-107379	14	862483
	BovineHD1400000188	14	403312
	BovineHD1400000199	14	452477
	BovineHD1400000200	14	454838
	BovineHD1400000204	14	487527
	BovineHD1400000206	14	494621
	BovineHD1400000216	14	550784
	BovineHD1400000275	14	827586
	BovineHD1400000281	14	854163
	BovineHD1400000283	14	865655
	BovineHD1400000286	14	876529
	BovineHD1400000287	14	883732
	BovineHD1400000324	14	1063078
$\boldsymbol{v_r}$ M	ARS-BFGL-NGS-72413	5	82061755
	ARS-BFGL-NGS-80785	5	75143850
	BovineHD0500021484	5	75039090
	BovineHD0500021485	5	75048931
	BovineHD0500021495	5	75088299
	BovineHD0500021496	5	75094522
	BovineHD0500021497	5	75098897
	BovineHD0500021498	5	75100664
	BovineHD0500021499	5	75109095
	BovineHD0500021500	5	75111711
	BovineHD0500021501	5	75115270
	BovineHD0500021502	5	75117210
	BovineHD0500021505	5	75129323

	BovineHD0500021508	5	75137447
	BovineHD0500022023	5	77146567
	BovineHD0500022699	5	79710128
	BovineHD0500023284	5	82057231
	BovineHD0500023286	5	82059684
	BovineHD0500023287	5	82060341
	BovineHD0500023289	5	82062576
	BovineHD0500023290	5	82064350
	BovineHD0500023291	5	82064946
	BovineHD0500023292	5	82065496
	BovineHD0500023293	5	82067669
	BovineHD0500023295	5	82077397
	BovineHD0500023297	5	82089704
	BovineHD0500023298	5	82094211
	BovineHD0500024876	5	87262266
	BovineHD0500024896	5	87377813
	BovineHD0500025559	5	89572280
	BovineHD0500025685	5	90038070
	BovineHD4100003858	5	75105523
	BovineHD4100003859	5	75124656
	BovineHD4100003886	5	82066707
	BovineHD4100003887	5	82070754
	BovineHD4100003888	5	82085293
	Hapmap40676-BTA-121691	5	75086818
	Hapmap50084-BTA-74042	5	75043240
r_{Auto} M	BTA-114769-no-rs	8	36910551
	BovineHD0200016228	2	56978160
	BovineHD0800011049	8	36865281

Table 8: Overview of traits influenced by with genome-wide significant SNPs ($p \leq \frac{0.05}{Number\ of\ SNPs}$) for the resilience indicators variance (v_d) and autocorrelation (r_{Auto}) of deviations between observed and predicted absolute daily milk yield, variance of relative daily milk yield (v_r) and a selection index resilience computed from the resilience indicator traits (SI) analyzed in across-breeds in first lactation (P) and first and higher lactations (M) correlated QTL

Trait influenced by associated QTL	$\boldsymbol{v_d}$ P	$\boldsymbol{v_d}$ M	$\boldsymbol{v_r}$ M	$\boldsymbol{r_{Auto}}$ M
Body weight			X	
Bone quality			X	
Bovine tuberculosis susceptibility		X		X
Calving Interval				X
Clinical mastitis	X	X		
Conception rate	X	X	X	
Connective tissue amount			X	
Curd firmness		X		
Curd solids yield		X		
Curd yield		X		
Dystocia			X	
First service conception				X
Heat tolerance	X	X		X
Ketosis	X	X		
Lean meat yield	X	X		
Lifetime profit index	X	X		
M. paratuberculosis susceptibility			X	
Marbling score	X	X		
Metabolic body weight		X		
Milk alpha-lactalbumin percentage	X	X		
Milk alpha-S1-casein percentage		X		
Milk beta-lactoglobulin percentage		X		
Milk butyric acid content	X	X		
Milk C14 index	X	X		
Milk C16 index	X	X		
Milk C18 index	X	X		
Milk calcium content	X	X		
Milk capric acid content	X	X		
Milk caprylic acid content	X	X		
Milk casein percentage	X	X		
Milk cholesterol content	X	X		
Milk citrate count		X		
Milk conjugated linoleic acid content	X	X		
Milk copper content	X	X		
Milk fat percentage	X	X	X	

Milk fat yield	X	X	X	
Milk fat-to-protein ratio	X	X		
Milk kappa-casein content	X	X		
Milk kappa-casein percentage	X	X		
Milk lactose yield	X	X		
Milk linoleic acid content	X	X		
Milk linolenic acid content	X	X		
Milk monounsaturated fatty acid content		X		
Milk myristic acid content	X	X		
Milk myristoleic acid content	X	X		
Milk oleic acid content	X	X		
Milk palmitic acid content	X	X		
Milk palmitoleic acid content	X	X		
Milk pentadecylic acid content	X	X		
Milk phosphorus content		X		
Milk polyunsaturated fatty acid content		X		
Milk potassium content	X	X		
Milk protein content	X	X		
Milk protein percentage	X	X		
Milk protein yield	X	X		
Milk riboflavin content	X	X		
Milk saturated fatty acid content	X	X		
Milk stearic acid content	X	X		
Milk tridecylic acid content		X		
Milk unsaturated fatty acid content		X		
Milk urea nitrogen content	X	X		
Milk yield	X	X	X	X
Milk zinc content	X	X		
Multiple birth			X	
Pregnancy rate	X	X	X	
Shear force			X	
Somatic cell count	X	X		
Somatic cell score	X	X		
Subcutaneous fat thickness		X		
Udder attachment	X	X		
Udder cleft	X	X		

Additional File 4: Manhattan-Plots and QQ-Plots of each breed and lactation group

Figure 7: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience indicator trait v_d, which is the variance of deviation between observed and predicted absolute daily milk yield in first and higher lactations

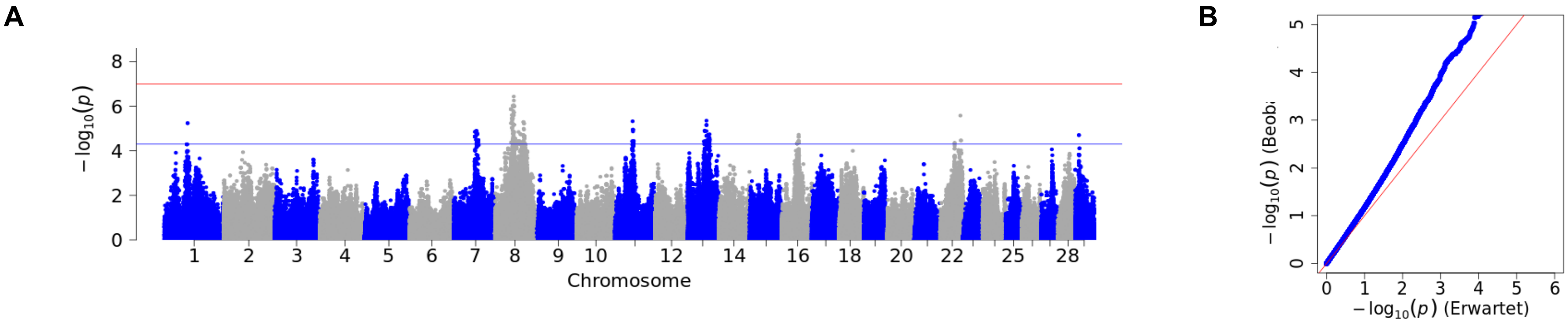


Figure 8: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first and higher lactations

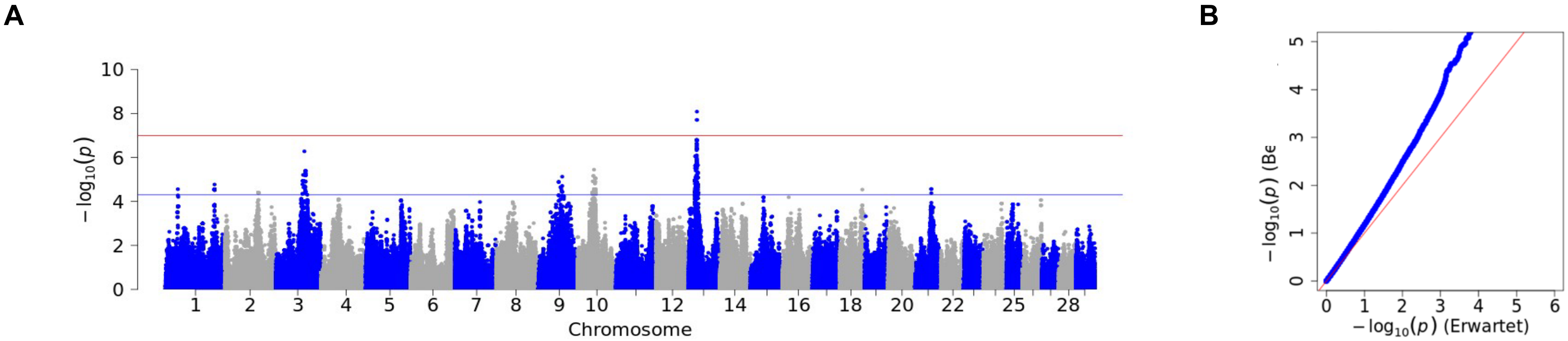


Figure 9: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience indicator trait $\boldsymbol{r_{Auto}}$, which is the autocorrelation of deviation between observed and predicted daily milk yield, in first and higher lactations

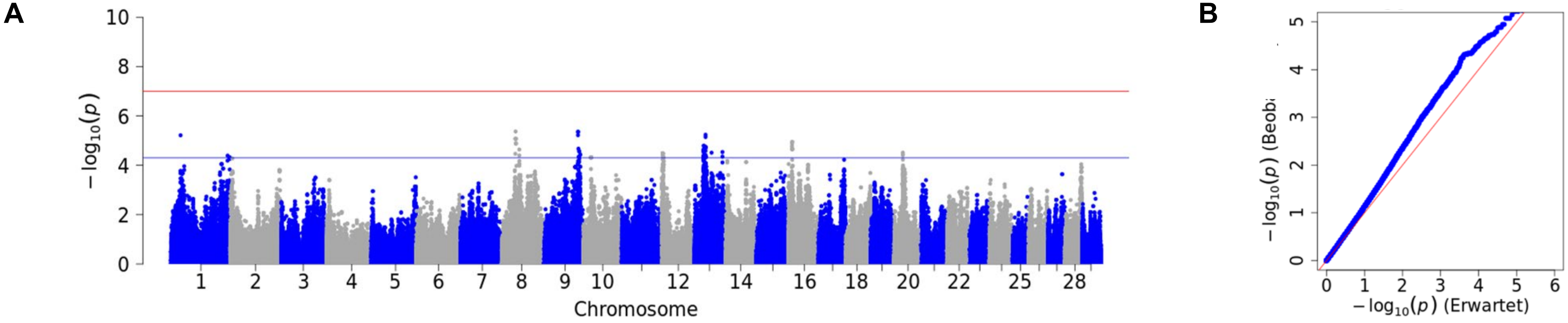


Figure 10: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience selection index $\boldsymbol{SI}$ computed from resilience indicator traits in first and higher lactations

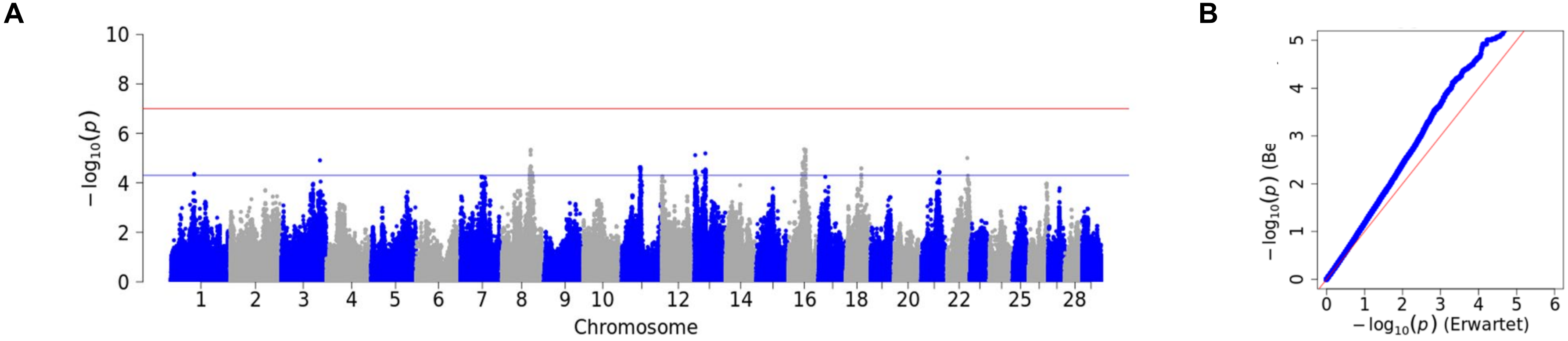


Figure 11: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience indicator trait v_d, which is the variance of deviation between observed and predicted absolute daily milk yield in first lactation

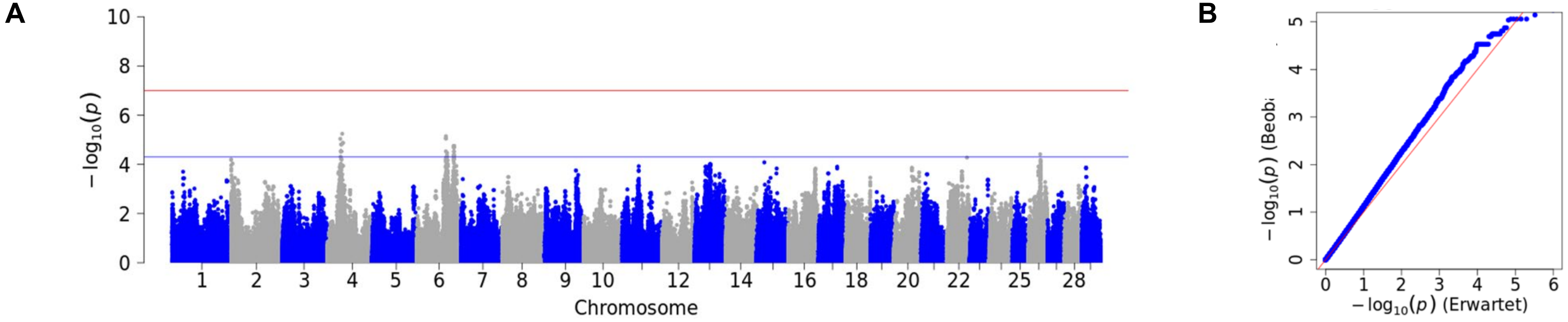


Figure 12: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first lactation

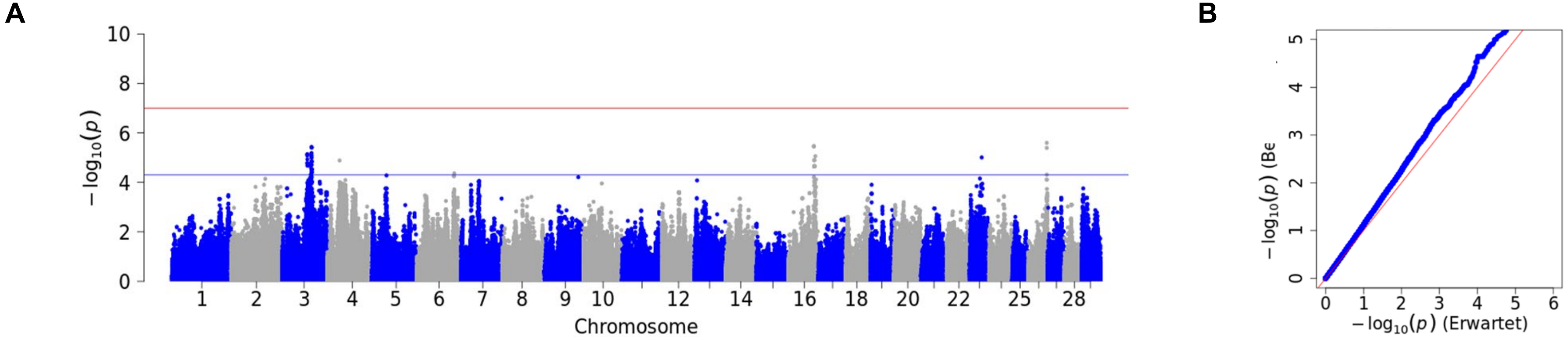


Figure 13: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience indicator trait $\boldsymbol{r_{Auto}}$, which is the autocorrelation of deviation between observed and predicted daily milk yield, in first lactation

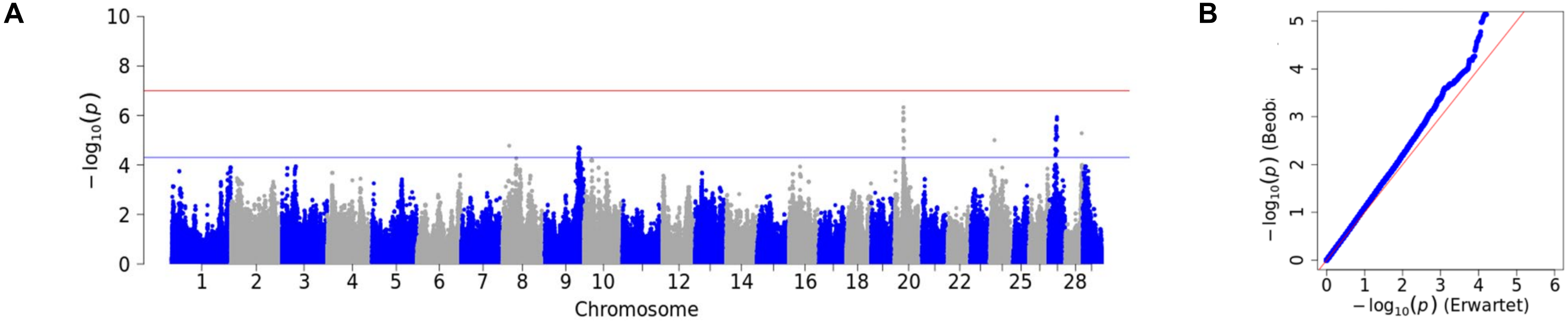


Figure 14: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Brown Swiss for the resilience selection index $\boldsymbol{SI}$ computed from resilience indicator traits in first lactation

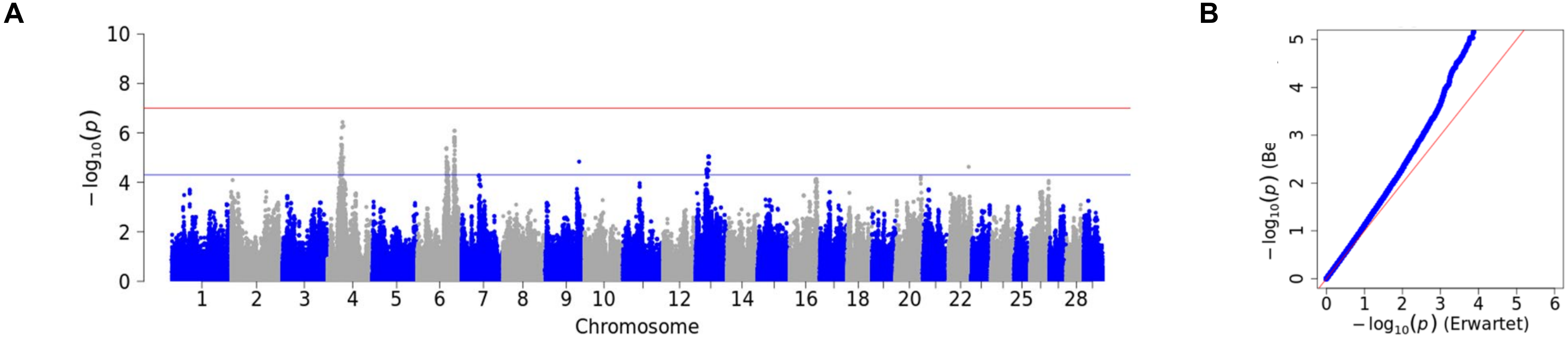


Figure 15: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience indicator trait v_d, which is the variance of deviation between observed and predicted absolute daily milk yield in first and higher lactations

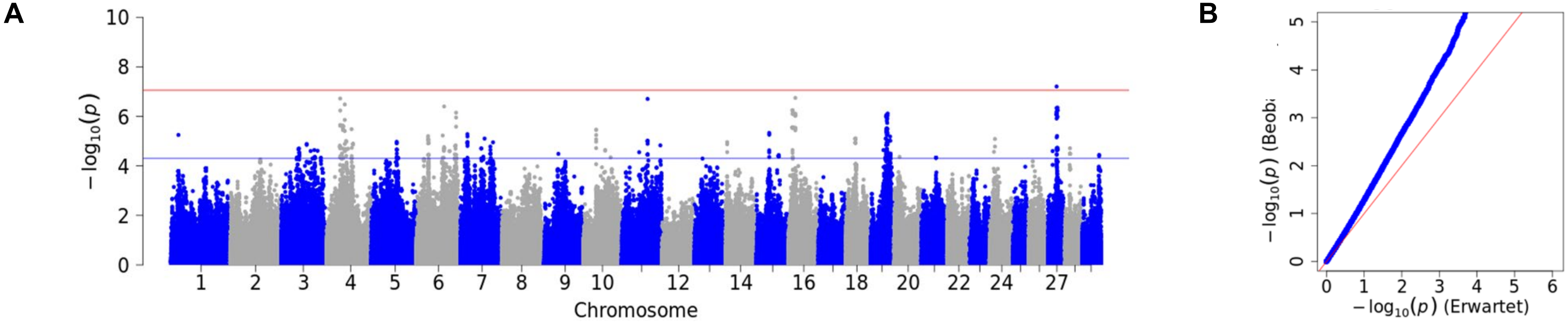


Figure 16: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first and higher lactations

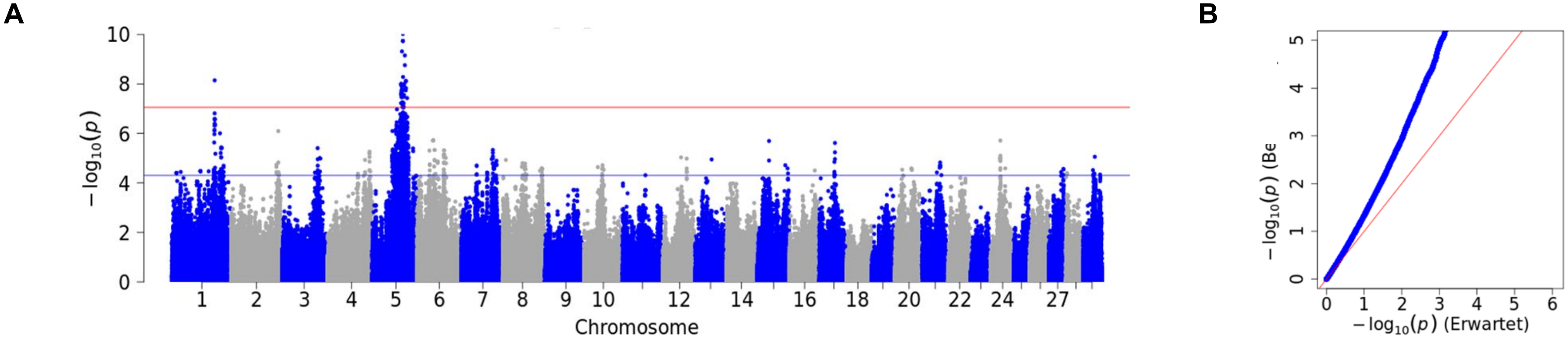


Figure 17: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience indicator trait r_{Auto}, which is the autocorrelation of deviation between observed and predicted daily milk yield, in first and higher lactations

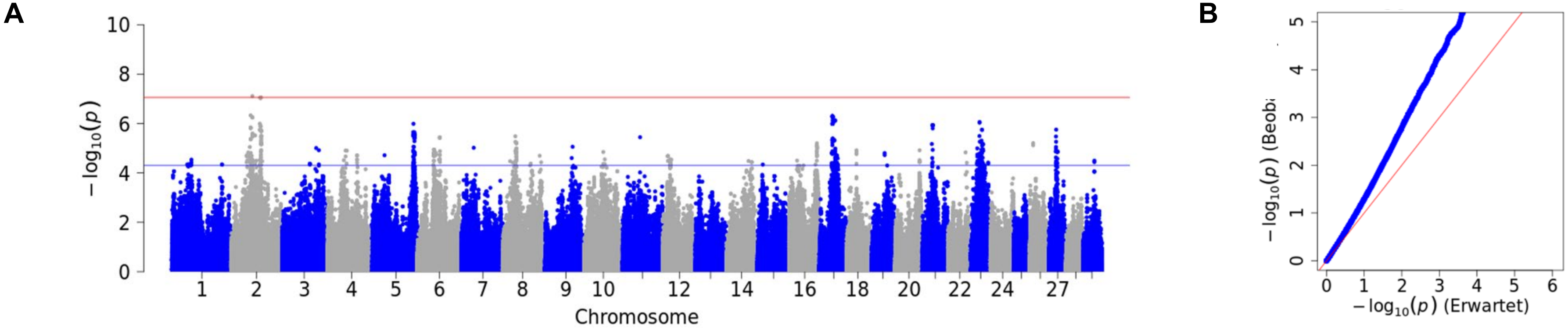


Figure 18: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience selection index SI computed from resilience indicator traits in first and higher lactations

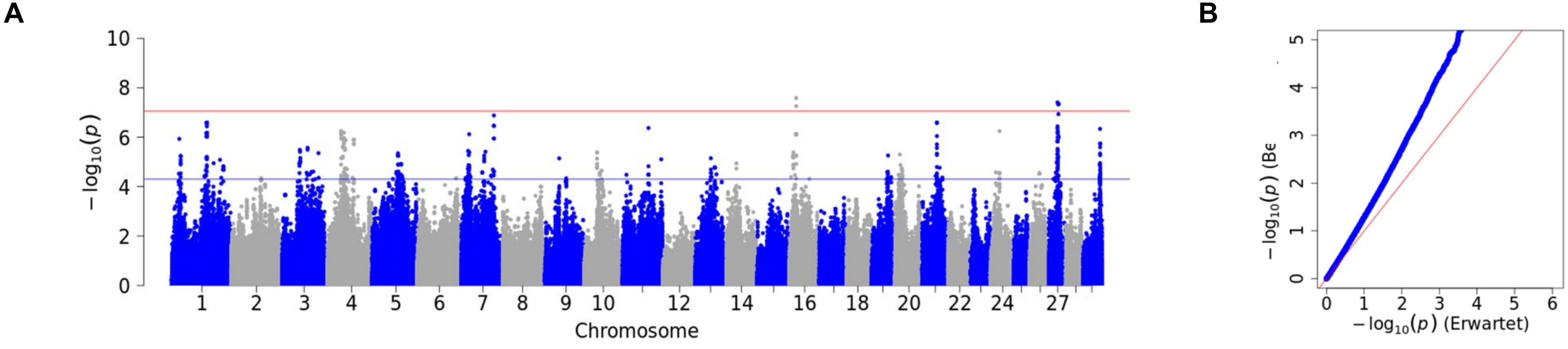


Figure 19: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience indicator trait v_d, which is the variance of deviation between observed and predicted absolute daily milk yield in first lactation

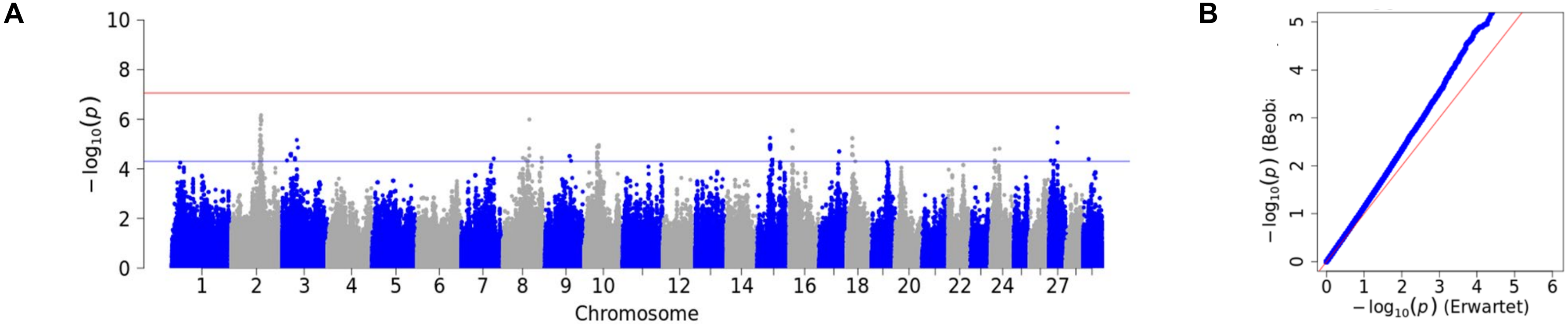


Figure 20: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first lactation

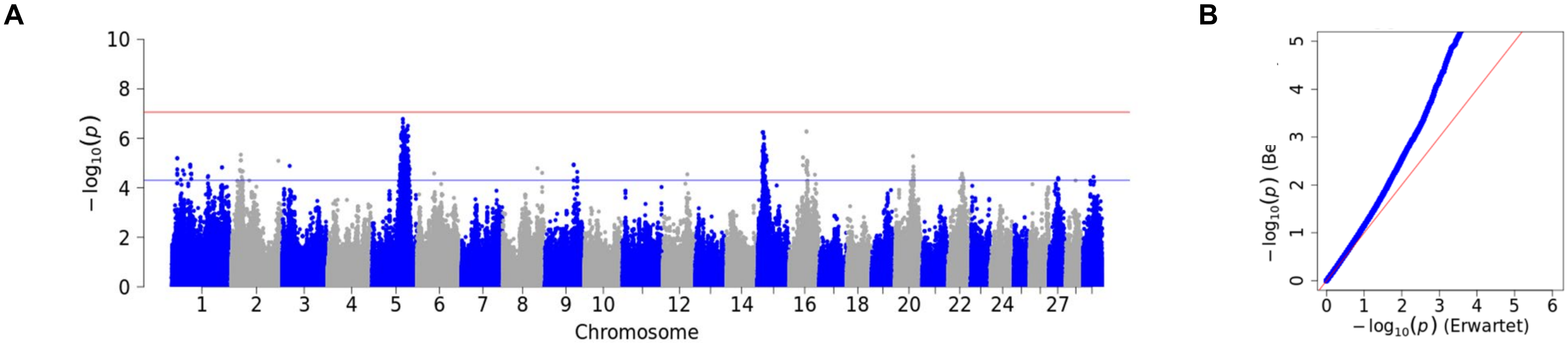


Figure 21: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience indicator trait $\boldsymbol{r_{Auto}}$, which is the autocorrelation of deviation between observed and predicted daily milk yield, in first lactation

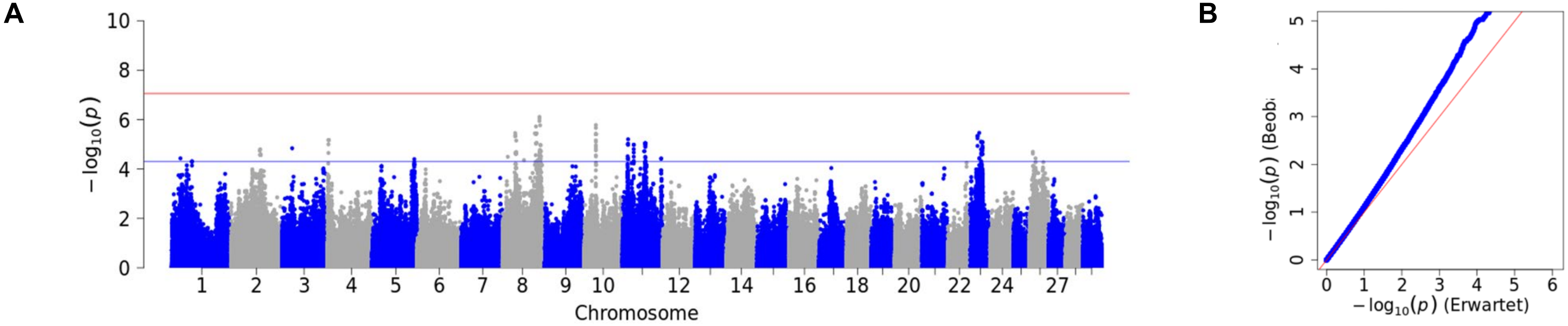


Figure 22: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Fleckvieh for the resilience selection index $\boldsymbol{SI}$ computed from resilience indicator traits in first lactation

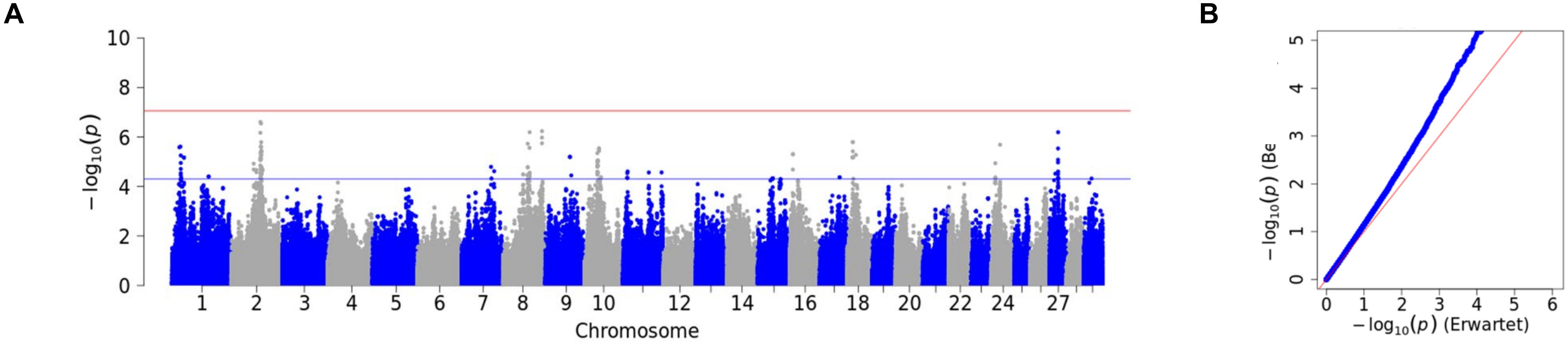


Figure 23: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience indicator trait v_d, which is the variance of deviation between observed and predicted absolute daily milk yield in first and higher lactations

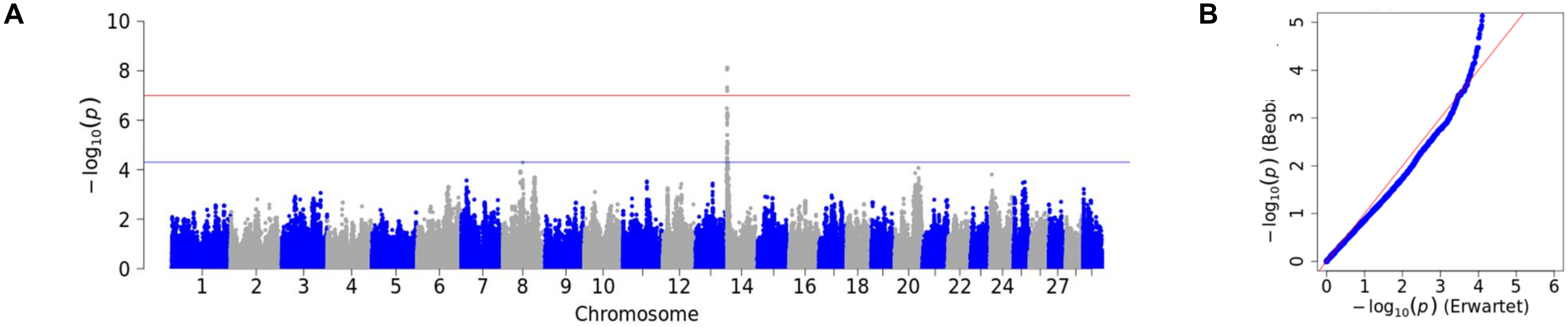


Figure 24: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first and higher lactations

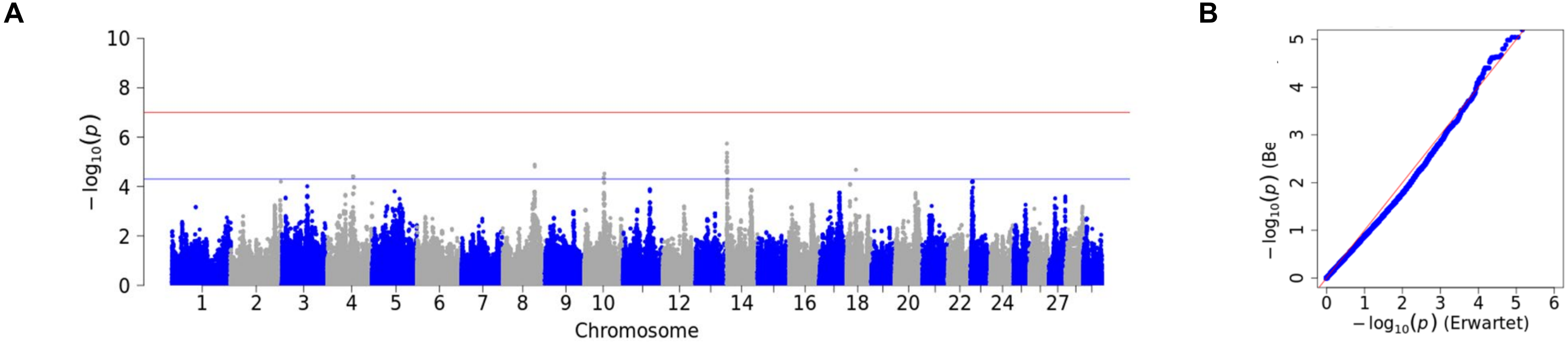


Figure 25: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience indicator trait r_{Auto}, which is the autocorrelation of deviation between observed and predicted daily milk yield, in first and higher lactations

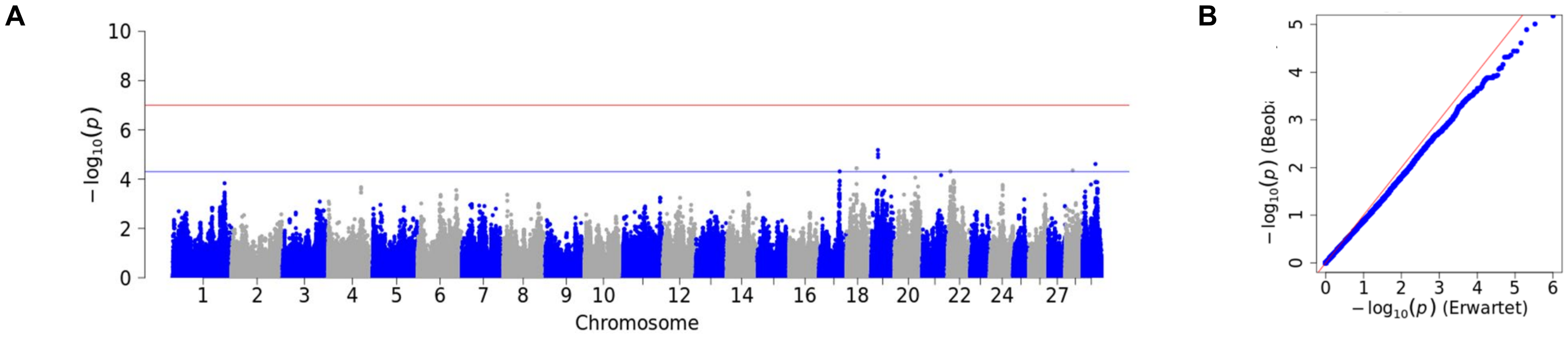


Figure 26: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience selection index SI computed from resilience indicator traits in first and higher lactations

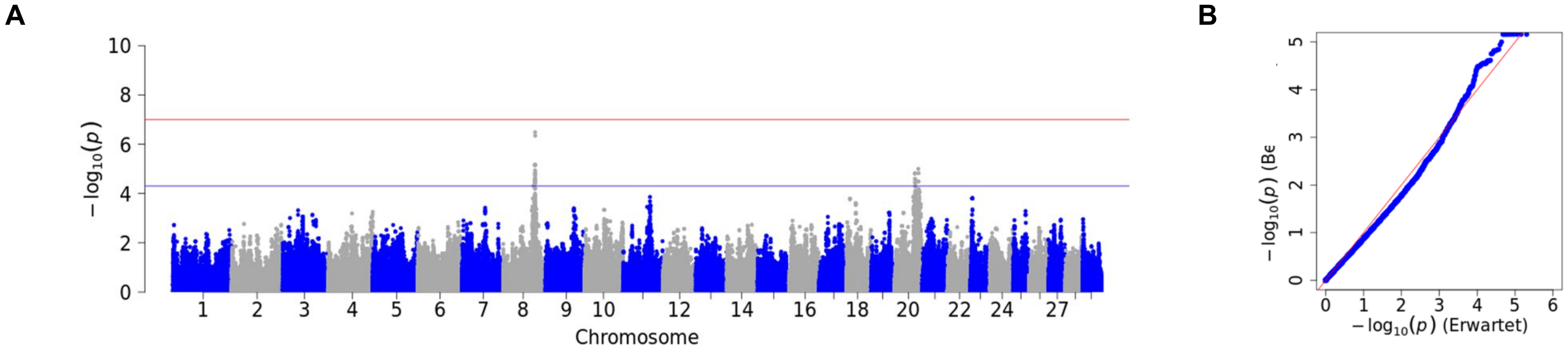


Figure 27: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience indicator trait v_d, which is the variance of deviation between observed and predicted absolute daily milk yield in first lactation

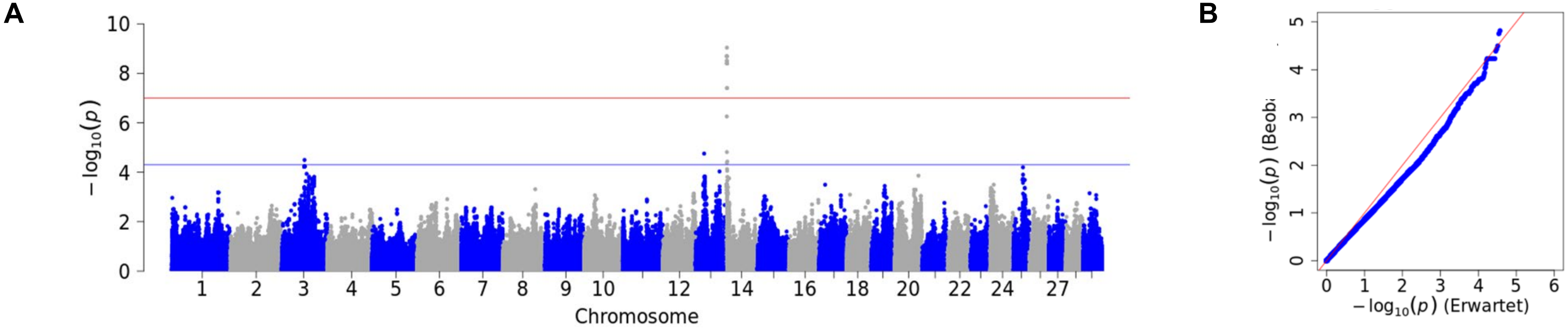


Figure 28: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience indicator trait v_r, which is the variance of relative daily milk yield in first lactation

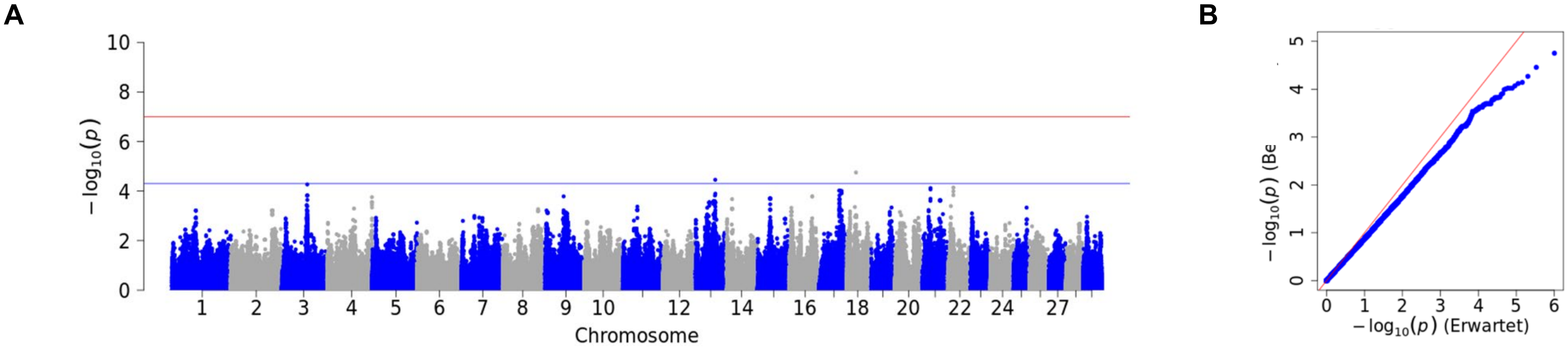


Figure 29: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience indicator trait r_{Auto}, which is the autocorrelation of deviation between observed and predicted daily milk yield, in first lactation

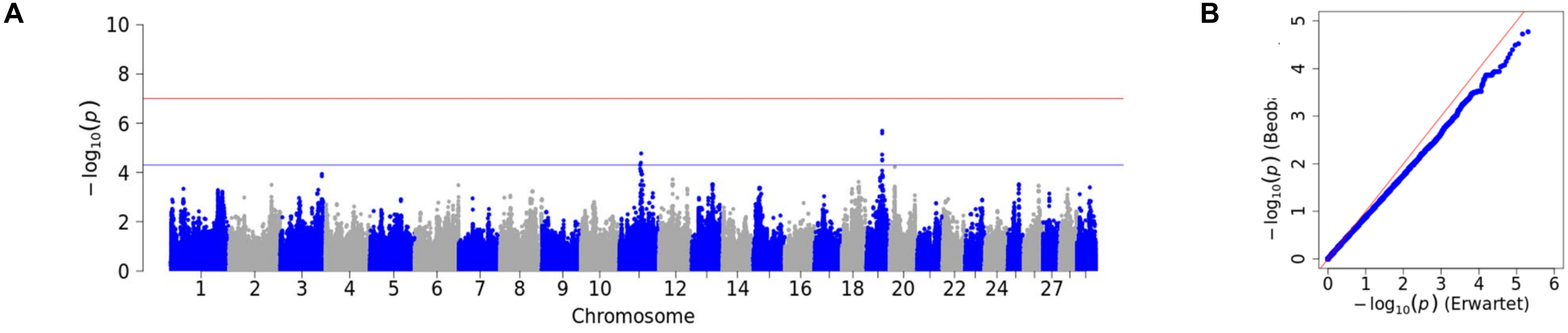
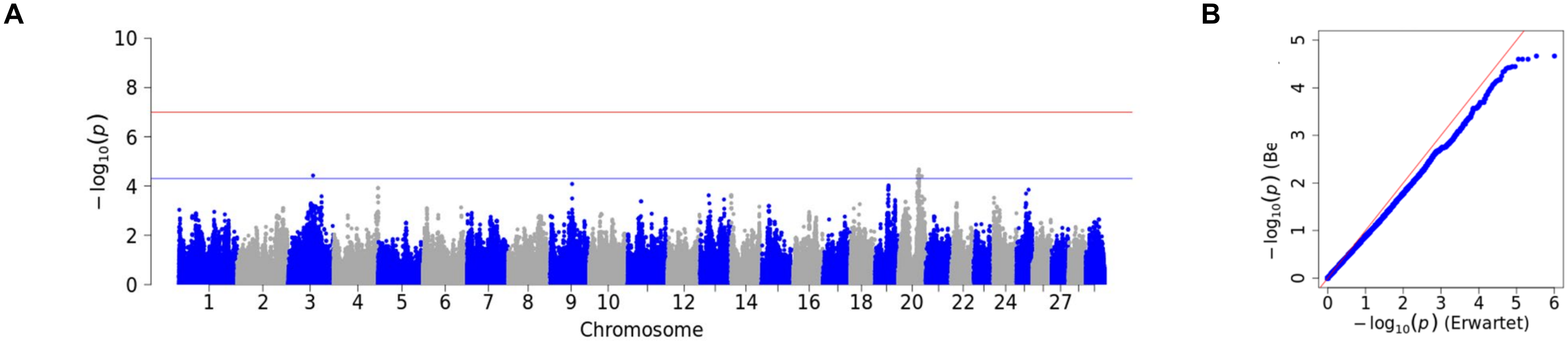


Figure 30: Manhattan-Plot (A) and Q-Q-Plot (B) of p-values from GWAS in German Holstein for the resilience selection index SI computed from resilience indicator traits in first lactation



GENERAL DISCUSSION

Breeding goals change over time. They are adapted to the demands of farmers and consumers, the requirements of the production environment, as well as political and social circumstances. In dairy cattle breeding, the focus shifted worldwide from performance a balanced combination of performance, health and fertility. Nowadays, novel traits, like feed or methane efficiency and resilience, are being studied and might be integrated into breeding goals in the future. At this, initiatives to make these traits measurable and evaluable on the large scale, such as the so-called sniffer technology to measure methane emissions, enable the inclusion of these traits into the breeding programs (Miglior et al. 2017; Lora et al. 2020). This thesis focuses on the topic of resilience and examines it in the German dairy cattle populations: German Holstein (HF), German Fleckvieh (FV) and German Brown Swiss (BS). In particular, various quantitative-genetic parameters of a novel trait need to be studied to understand the genetic background and correlations with other traits in the population concerned before it can be integrated into a breeding goal. These include heritabilities, repeatabilities, genetic correlations, economic values, phenotypic means and phenotypic variances in the current population (Simianer et al. 2021; Wolfová and Wolf 2013).

First, a novel trait or its underlying concept must be clearly defined and the trait collection described. These and the differentiation from other traits and concepts were described in **chapter one**.

Accordingly, the genetic parameters for various resilience indicator traits were estimated and interpreted in **chapter two**. It was found that resilience measured by the time series indicator traits is heritable and correlated with performance traits. The differences between the breeds were small. From a methodological point of view, logarithmization of the resilience indicator traits is recommended to satisfy the assumption of normal distribution. Economic values and correlations to functional and health traits are still missing for integration into the total merit index of a breeding program. This was the subject of **chapter three** for the HF. For each animal, an EBV per resilience indicator trait was estimated, whose correlations to the other traits for which an EBV was available were analyzed. The correlations for resilience indicator traits based on the time series parameter variance with health traits were significant and desired, while the correlation analysis between the autocorrelation and health traits were undesirable or non-significant. Since there are no economic values for resilience yet, the weighting factors for single resilience indicator traits in a selection index resilience were determined by maximizing the joint breeding response in the selection index health. The result was a selection index resilience with desirable correlations to single health traits. This means that individuals with a high EBV in the selection index resilience are yield-stable and healthy.

Since resilience is a new trait complex, little is known about its genetic architecture. **Chapter four** uses genome-wide association studies (GWAS) to unravel information on significantly affecting genomic regions. These were carried out for all breeds and concluded at the end by pooling the p-values of the GWAS statistics. The results showed that resilience is a polygenic trait with only few significant trait-associated SNPs.

In summary, mainly all requirements for the implementation of a trait resilience in the breeding value estimation of the HF could be fulfilled with this work. Variance components, heritabilities, and correlations with further traits were estimated and usable for breeding. An alternative method for determining the weighting factors of single resilience indicator traits in a selection index resilience was successfully tested to circumvent the problem of missing economic weights. This methodology, described and discussed in the **second chapter**, can be adapted to the FV and BS, so that a transfer into the breeding practice for these breeds is possible. To increase the understanding of resilience, the breeding value points of the resilience indicator traits are converted into measurable parameters such as milk loss per lactation or the average number of disturbances in the following **general discussion**. In addition, future developments of resilience are discussed.

Correlations between resilience indicator traits and health and functional traits

Chapter three presented the results of the correlation analyses between resilience indicator traits and health and functional traits in the HF population. Pearson correlations between EBV were analyzed, whereby a high EBV and a positive correlation coefficient are desired. The consideration of FV and BS would have gone beyond the scope of the publication, but will be added below. The same methodology as described in **chapter three** was adapted to between 850 and 1,227 individuals of the BS breed and to between 1,059 and 1,508 individuals of the FV breed. The number of observations differed between traits, because EBV with an accuracy < 15 % were excluded. While 13 single health traits are implemented in the breeding value estimation for HF and combined in a selection index health (Vereinigte Informationssysteme Tierhaltung w.V. 2024), only EBV for mastitis, milk fever, early fertility disorders and cysts are recorded for FV and BS, according to the official genetic evaluation for these breeds, carried out by ZuchtData (Vienna, Austria). As with HF, high EBV should be considered desirable and interpreted as healthy animals (Fürst 2023). Since the end of 2024, there have also been EBV for claw health (Fürst et al. 2023), but these were not available to our analyses. Therefore, a similar selection index to the health selection index in HF is named fitness ($\mathrm{SI}_{\mathrm{fitness}}$) and made up of the traits longevity, yield persistency, fertility, calving ease, vitality, udder health and milkability (Fürst 2023).

The results for BS and FV are shown in Figure 3 with generally weaker correlations than in HF (results shown in Figure 1 in chapter three). The analysis in BS showed similar results to HF with significant positive and desired correlations between variance-based resilience indicator traits and the EBV for health and functional traits. In contrast, the correlations with $\mathrm{r}_{\mathrm{Auto}}$ were undesired negative and less significant. Negative correlations between variance-based resilience indicator traits and fertility and metabolic diseases were found for FV, indicating that resilient individuals are more affected by cysts, early fertility disorders and milk fever. One reason for this could be different data collection periods. For example, milk fever is only detected in the first 10 days after calving in FV and BS; this period is not considered at all when calculating the resilience indicator traits. In HF, the data collection period is up to the 50th lactation day. Cysts are only recorded between the 30th and 150th lactation day, which cover only half of the considered period of time for the calculation of the resilience indicator traits. For a more precise analysis of the correlations, it is advisable to calculate the resilience indicator traits for individual lactation periods. In FV, $\mathrm{r}_{\mathrm{Auto}}$ is significantly negative correlated with any traits, which implies that more resilient animals with a shorter recovery time, have poorer EBV for health. This is in line with our findings in the HF population (**chapter three**), but contrary to comparable studies (Poppe et al. 2020; Chen et al. 2023a). EBV for health indicate the frequency of a disease, it is not mandatory that there is a connection between them and $\mathrm{r}_{\mathrm{Auto}}$. With a long recovery period per disease, fewer individual diseases can be detected, which may have led to the negative correlation.

The FV and BS breeds are dual-purpose breeds and the total EBV includes meat performance (18% in FV, 5% in BS) (Fürst 2023). Resilience indicator traits based on daily milk yield may not capture all responses to disturbances. The reaction can be various; thus a change in body weight is also possible. A study with HF showed that the response to disturbances can be measurable in milk yield, body weight or both traits together (Ben Abdelkrim et al. 2021). The focus on meat in the total EBV of FV may have resulted in differences in the direction and strength of the analyzed correlations compared to HF. In

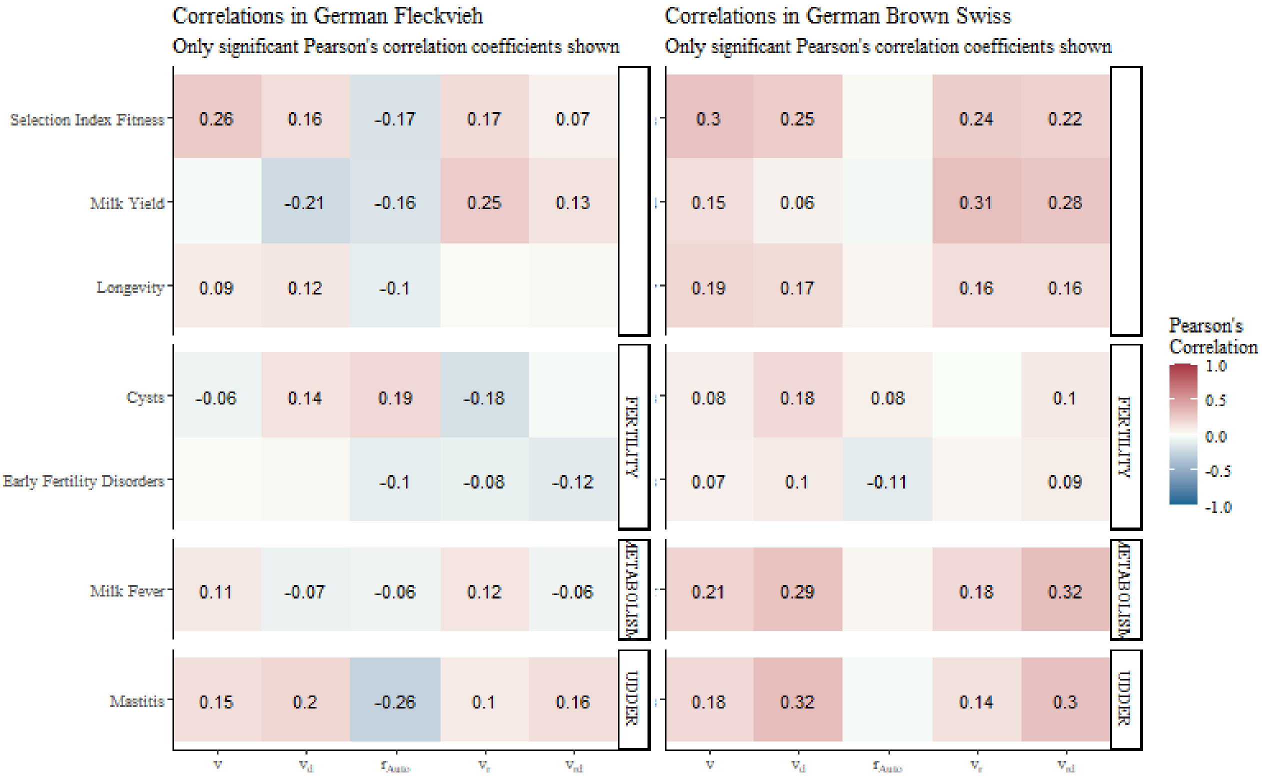


Figure 3: Correlations between estimated breeding values for resilience indicator traits and health and functional traits in German Fleckvieh and German Brown Swiss with resilience indicator traits variance of absolute (v) and relative $(\mathrm{v}_{\mathrm{r}})$ daily milk yield, variance of deviations between observed and predicted absolute $(\mathrm{v}_{\mathrm{d}})$ and relative $(\mathrm{v}_{\mathrm{rd}})$ daily milk yield and autocorrelation of deviations between observed and predicted absolute daily milk yield

FV, it is therefore advisable to calculate resilience indicator traits on the basis of body weight data.

A selection index resilience for German Fleckvieh and German Brown Swiss

A resilience selection index for HF was developed in **chapter three**. A selection index combines several traits to achieve joint breeding progress in the considered traits during selection. The weighting factors are thereby generally based on their economic value, with the aim of maximizing marginal utility (William and Simianer 2017). As discussed in **chapter three**, it is currently not possible to define economic weights for resilience indicator traits. The weighting factors were therefore determined to maximize the breeding response in the health selection index. This method can also be applied to FV and BS. As there is no selection index based solely on health traits, $\mathrm{SI_{fitness}}$ is used for these two breeds. It is composed of longevity, persistency, fertility, calving ease, vitality, udder health and milkability (Fürst 2023). Results show that breeding for resilience leads to a positive trend in $\mathrm{SI_{fitness}}$. This is stronger in BS (shown in Table 3) than in FV (shown in Table 2).

The differences in the optimized $\mathrm{SI_{resilience}}$ are primarily based on the differences between $\mathrm{SI_{health}}$ and $\mathrm{SI_{fitness}}$. In HF, $\mathrm{v_r}$ recommended itself as a component of the index, possibly because of the strong correlations with the single EBV of metabolic health traits, which were not collected in FV and BS. On the contrary, in $\mathrm{SI_{fitness}}$ of BS and FV the EBV for fertility and persistency have a higher value. For fertility, the correlations were stronger, in the desired direction or more significant for v or $\mathrm{v_d}$ than $\mathrm{v_r}$. The persistency, not included in the optimization of HF, is best represented by v: A high variance in absolute daily milk yield can be caused by a steep drop in performance towards the end of lactation.

The selection response in $\mathrm{SI_{health}}$ was highest in HF, as fewer and similar traits were combined in $\mathrm{SI_{health}}$ than in $\mathrm{SI_{fitness}}$. In the comparison between BS and FV, the selection response was greater in BS, possibly because milkability is excluded in $\mathrm{SI_{fitness}}$. As the correlations of traits in $\mathrm{SI_{fitness}}$ with $\mathrm{v_{rd}}$ and in FV with $\mathrm{v_r}$ are too weak or undesirable, these resilience indicator traits are not taken into account by the algorithm in the optimization of $\mathrm{SI_{resilience}}$ according to $\mathrm{SI_{fitness}}$. Overall, the strongest correlation with $\mathrm{SI_{fitness}}$ is with v in both breeds, with the main factor behind the increased weighting of v is likely to be the persistence of performance.

Table 2: Different selection indices resilience with the weighting factor of each considered resilience indicator trait, heritability (h^2) of the resilience selection index $\mathrm{SI}_{\mathrm{resilience}}$, correlation coefficient (r) for correlation between resilience selection index $\mathrm{SI}_{\mathrm{resilience}}$ and selection index $\mathrm{SI}_{\mathrm{fitness}}$, and breeding response $(\mathrm{R}_{\mathrm{SI}_{\mathrm{fitness}}})$ in $\mathrm{SI}_{\mathrm{fitness}}$ for German Fleckvieh

Resilience selection index consisting of					$\mathrm{h}^2\mathrm{SI}_{\mathrm{resilience}}$	r	$\mathrm{R}_{\mathrm{SI}_{\mathrm{fitness}}}$
v	v_{d}	$\mathrm{r}_{\mathrm{Auto}}$	v_{r}	v_{rd}			
0.676	0.324				0.153	0.276	0.108
0.677	0.323	0.000			0.152	0.276	0.108
0.683	0.317	0.000	0.000		0.151	0.276	0.107
0.706	0.294	0.000	0.000	0.000	0.147	0.276	0.106

[1] Description of resilience indicator traits can be found in Table 1

Table 3: Different selection indices resilience with the weighting factor of each considered resilience indicator trait, heritability (h^2) of the resilience selection index $\mathrm{SI}_{\mathrm{resilience}}$, correlation coefficient (r) for correlation between resilience selection index $\mathrm{SI}_{\mathrm{resilience}}$ and selection index $\mathrm{SI}_{\mathrm{fitness}}$, and breeding response $(\mathrm{R}_{\mathrm{SI}_{\mathrm{fitness}}})$ in $\mathrm{SI}_{\mathrm{fitness}}$ for German Brown Swiss

Resilience selection index consisting of					$\mathrm{h}^2\mathrm{SI}_{\mathrm{resilience}}$	r	$\mathrm{R}_{\mathrm{SI}_{\mathrm{fitness}}}$
v	v_{d}	$\mathrm{r}_{\mathrm{Auto}}$	v_{r}	v_{rd}			
0.274	0.388		0.338		0.249	0.305	0.152
0.265	0.391	0.000	0.344		0.249	0.305	0.152
0.585	0.298	0.000	0.117	0.000	0.225	0.310	0.147
0.724	0.276				0.221	0.312	0.147

[1] Description of resilience indicator traits can be found in Table 1

Heritabilities of $\mathrm{SI}_{\mathrm{resilience}}$ were moderate, which enables selective breeding. The combination of resilience indicator traits increases heritability compared to the results of single resilience indicator traits (see results in **chapters two** and **three**). All three optimizations have in common that the optimal index does not contain all available resilience indicator traits. A selection index consisting of two resilience indicator traits is recommended in HF and FV, and an index of three in BS. This also reduces the computing capacity required and increases comprehensibility, which is important, because in the end farmers apply what they understand (Ule et al. 2023). In any case, $\mathrm{v_d}$ led to an improvement in health and functional traits across all breeds, showed significant heritability and desired genetic correlations. This is confirmed by other studies across species and breeds (Mengistu et al. 2022; Poppe et al. 2020; Doekes et al. 2023). In contrast, $\mathrm{r_{Auto}}$ is excluded by optimization or considered with low weighting factors. It is likely to have biological significance, but a statistically meaningful integration is difficult. As discussed in **chapter four**, modeling the deviations, which can have a major influence on $\mathrm{r_{Auto}}$, is challenging. Furthermore, $\mathrm{r_{Auto}}$ is more sensitive to the frequency of data collection than variance-based parameters (Ghaderi Zefreh et al. 2024). On the other hand, the optimization on existing traits may not be sufficient, as $\mathrm{r_{Auto}}$ is a novel trait indicating the recovery time from unknown disturbances, which is not captured by existing traits. It may be advisable to use a trait other than daily milk yield, as, for example, daily step counts, which showed more significant results in $\mathrm{r_{Auto}}$ (Poppe et al. 2022b).

Practical significance of resilience indicator traits

Resilience indicator traits are abstract. Unlike milk yield, for example, they cannot be directly measured and are more difficult to understand. In the following, differences between levels of EBV are therefore expressed in milk gain or loss per lactation, number of disturbances and disturbance days as well as effects at the test day data. In each breed (HF with $\mathrm{n} = 2300$, FV with $\mathrm{n} = 2330$, and BS with $\mathrm{n} = 1073$) EBV were estimated using a 5-fold cross-validation. The calculation of the resilience indicator traits and the univariate estimation model correspond to the methodology in **chapter four**. In each repetition, 4/5 of the individuals were selected as reference population and the remaining 1/5 of the individuals formed the validation population for which the EBV were predicted, based on the estimates of the reference population using genotypic information.

To translate the EBV for resilience indicator traits into practice, the definition of a disturbance was first determined. Based on CRV (2024), a disturbance starts as soon as the observed milk yield drops below 97 % of the expected milk yield and ends as soon as 95 % of the original yield is reached again. To exclude noise, a disturbance is only counted if the observed yield deviates from the expected yield by more than 15 % on at least one day. From the raw data, the sum of the deviations between observed and expected performance (whether positive or negative) between the 10th and 305th day of lactation (MLT), the sum of deviations during disturbance (MLD), the number of days with disturbances (DD) and the number of disturbances (DE) per animal and lactation were calculated. The deviations in milk yield MLT and MLD are converted and represent the milk loss (reading: individual A with an EBV of 90 and value in MLT of 300 kg produced less milk than individual B with an EBV of 110 and value in MLT of 100 kg). Contents of milk fat in % (MFC), milk protein in % (MPC), milk urea in mg/dl (MUC), and milk lactose in % (MLC) and somatic cell counts (SCC) were available (overview of the traits can be found in Table 1). For the latter, the mean value of all test days per lactation was calculated. The regression of each individual test day, taking into account repeated measurements, was tested but showed similar results (results not shown). Traits were regressed on the EBV from the validation runs, as follows:

$$\mathbf{y} \sim \beta_0 + \beta_1 * \mathbf{RI} + \mathbf{pe} + \mathbf{e},$$

with $\mathbf{y}$ the phenotypic observations, β_0 the intercept and $\beta_1$the effect of the resilience indicator trait EBV $\mathbf{RI}$ on $\mathbf{y}$. An individual can be included in the regression with several lactations, in which case $\mathbf{pe}$ is added as a vector of repeated measurements and $\mathbf{e}$ is the residual. For each breed, the optimized $\mathrm{SI}_{\mathrm{resilience}}$ from the previous chapter was used and its integrated single resilience indicator traits. Additionally, the results for $\mathrm{r}_{\mathrm{Auto}}$ were shown for each breed.

Table 1. Overview and description of traits considered in the general discussion

Trait	Description
v	Log variance of the observed absolute daily milk yield
$\mathrm{v_d}$	Log variance of deviation between observed absolute and predicted daily milk yield
$\mathrm{r_{Auto}}$	Lag-1-Autocorrelation of deviation between observed absolute and predicted daily milk yield
$\mathrm{v_r}$	Log variance of relative daily milk yield
$\mathrm{v_{rd}}$	Log variance of deviation between observed relative and predicted daily milk yield
MFC	Milk fat content
MLC	Milk lactose content
MLD	Summarised milk loss over a lactation from the 10th to the 305th day of lactation of an animal during defined disturbances
MLT	Summarised milk loss over a lactation from the 10th to the 305th day of lactation of an individual
MPC	Milk protein content
MUC	Milk urea content
SSC	Somatic cell count in milk
DD	Sum of days with a defined disturbance between the 10th and 305th day of lactation of an individual per lactation
DE	Sum of the defined disturbances per lactation and animal

Table 1: Phenotypic variations in traits from milk performance test and disruptive influences by a breeding value in the selection index resilience of 90, 100 (population mean) and 110 in German Holstein (non-significant results [p-value > 0.05] are marked in gray)

RI[1]	EBV	$\varnothing_{\mathrm{MPC}}$	Δ_{MPC}	$\varnothing_{\mathrm{MFC}}$	Δ_{MFC}	$\varnothing_{\mathrm{MUC}}$	Δ_{MUC}	$\varnothing_{\mathrm{MLC}}$	Δ_{MLC}	$\varnothing_{\mathrm{SCC}}$	Δ_{SCC}
$\mathrm{v_d}$	90	3.40	-0.08	3.78	-0.14	18.45	-0.22	4.87	-0.03	463.11	80.00
	100	3.48	0.00	3.88	0.00	21.37	0.00	4.83	0.00	370.25	0.00
	110	3.55	0.08	3.91	0.14	20.45	0.22	4.87	0.03	222.38	-80.00
$\mathrm{r_{Auto}}$	90	3.52	-0.01	3.84	-0.07	20.22	-0.68	4.85	0.01	346.01	22.94
	100	3.47	0.00	3.90	0.00	21.06	0.00	4.82	0.00	270.73	0.00
	110	3.52	0.01	4.56	0.07	25.05	0.68	4.82	-0.01	40.11	-22.94
$\mathrm{v_r}$	90	3.53	0.01	3.98	0.03	23.10	0.73	4.78	-0.04	284.09	38.32
	100	3.51	0.00	3.86	0.00	21.11	0.00	4.83	0.00	308.87	0.00
	110	3.52	-0.01	4.01	-0.03	20.90	-0.73	4.86	0.04	247.69	-38.32
$\mathrm{SI_{resilience}}^2$	90	3.23	-0.06	3.69	-0.10	21.48	0.22	4.62	-0.04	428.84	95.40
	100	3.47	0.00	3.86	0.00	21.23	0.00	4.82	0.00	361.65	0.00
	110	3.58	0.06	3.98	0.10	20.54	-0.22	4.85	0.04	273.84	-95.40

		$\varnothing_{\mathrm{MLT}}$	Δ_{MLT}	$\varnothing_{\mathrm{MLD}}$	Δ_{MLD}	$\varnothing_{\mathrm{DD}}$	Δ_{DD}	$\varnothing_{\mathrm{DE}}$	Δ_{DE}
$\mathrm{v_d}$	90	307.41	27.97	203.19	27.38	35.08	2.89	5.38	0.58
	100	257.94	0.00	201.32	0.00	37.83	0.00	5.70	0.00
	110	228.69	-27.97	164.83	-27.38	33.43	-2.89	5.18	-0.58
$\mathrm{r_{Auto}}$	90	260.59	2.24	202.69	-1.82	38.43	-0.72	5.70	-0.30
	100	251.99	0.00	197.34	0.00	37.65	0.00	5.88	0.00
	110	247.74	-2.24	295.32	1.82	56.67	0.72	5.33	0.30
$\mathrm{v_r}$	90	242.27	8.18	185.79	12.81	37.04	2.77	5.57	0.49
	100	256.63	0.00	196.92	0.00	37.56	0.00	5.63	0.00
	110	226.55	-8.18	170.37	-12.81	32.74	-2.77	4.91	-0.49
$\mathrm{SI_{resilience}}^2$	90	448.94	30.55	391.39	32.75	65.00	4.30	10.00	0.82
	100	250.69	0.00	190.19	0.00	36.47	0.00	5.72	0.00
	110	225.56	-30.55	163.79	-32.75	32.94	-4.30	4.97	-0.82

[1] RI – resilience indicator trait; overview of trait abbreviations can be found in Table 1

[2] $\mathrm{SI_{resilience}}$ – selection index resilience calculated as $0.654 * v_d + 0.346 * v_r$

Ø – mean of the trait in all individuals with the same EBV for the resilience indicator trait (intercept of regression analysis)

Δ – deviation of the group of all individuals with the same EBV for the resilience indicator trait to the population mean (slope of regression analysis)

Table 4: Phenotypic variations in traits from milk performance test and disruptive influences by a breeding value in the selection index resilience of 90, 100 (population mean) and 110 in German Fleckvieh (non-significant results [p-value > 0.05] are marked in gray)

RI¹	EBV	$Ø_{MPC}$	$Δ_{MPC}$	$Ø_{MFC}$	$Δ_{MFC}$	$Ø_{MUC}$	$Δ_{MUC}$	$Ø_{MLC}$	$Δ_{MLC}$	$Ø_{SCC}$	$Δ_{SCC}$
v	90	3.56	-0.01	3.99	0.04	20.45	-0.09	4.87	-0.03	194.70	2.73
	100	3.60	0.00	4.08	0.00	21.38	0.00	4.85	0.00	228.14	0.00
	110	3.58	0.01	4.01	-0.04	22.38	0.09	4.87	0.03	206.10	-2.73
v_d	90	3.54	-0.04	4.14	-0.03	21.86	0.05	4.83	-0.01	495.67	13.05
	100	3.58	0.00	4.07	0.00	21.80	0.00	4.84	0.00	202.61	0.00
	110	3.63	0.04	4.16	0.03	21.34	-0.05	4.84	0.01	205.94	-13.05
r_{Auto}	90	3.69	0.06	4.24	-0.04	20.43	-0.78	4.93	0.04	141.15	-21.59
	100	3.60	0.00	4.10	0.00	21.62	0.00	4.83	0.00	226.54	0.00
	110	3.41	-0.06	3.74	0.04	21.15	0.78	4.88	-0.04	81.39	21.59
$SI_{resilience}{}^2$	90	3.54	-0.03	4.35	0.02	21.79	-0.04	4.80	-0.03	209.01	9.08
	100	3.60	0.00	4.12	0.00	21.83	0.00	4.84	0.00	248.10	0.00
	110	3.64	0.03	4.00	-0.02	22.24	0.04	4.86	0.03	293.34	-9.08
		$Ø_{MLT}$	$Δ_{MLT}$	$Ø_{MLD}$	$Δ_{MLD}$	$Ø_{DD}$	$Δ_{DD}$	$Ø_{DE}$	$Δ_{DE}$		
v	90	203.49	4.91	143.47	5.24	32.44	1.31	5.54	0.38		
	100	182.62	0.00	123.88	0.00	31.65	0.00	5.35	0.00		
	110	176.29	-4.91	124.20	-5.24	28.87	-1.31	5.16	-0.38		
v_d	90	199.81	14.34	126.18	14.87	30.67	1.36	5.71	0.34		
	100	192.48	0.00	129.10	0.00	32.43	0.00	5.63	0.00		
	110	179.75	-14.34	122.91	-14.87	32.15	-1.36	5.29	-0.34		
r_{Auto}	90	115.61	-18.41	71.44	-16.58	14.20	-3.94	2.90	-0.86		
	100	182.05	0.00	125.20	0.00	32.70	0.00	5.25	0.00		
	110	172.19	18.41	89.50	16.58	28.00	3.94	5.00	0.86		
$SI_{resilience}{}^2$	90	215.57	10.87	136.15	11.59	30.50	1.83	5.07	0.50		

	100	191.15	0.00	138.93	0.00	33.95	0.00	5.51	0.00
	110	200.26	-10.87	154.32	-11.59	37.73	-1.83	6.64	-0.50

[1] RI – resilience indicator trait; overview of trait abbreviations can be found in Table 1

[2] $\mathrm{SI}_{\mathrm{resilience}}$ – selection index resilience calculated as $0.676 * v + 0.324 * v_d$

Ø – mean of the trait in all individuals with the same EBV for the resilience indicator trait (intercept of regression analysis)

Δ – deviation of the group of all individuals with the same EBV for the resilience indicator trait to the population mean (slope of regression analysis)

Table 5: Phenotypic variations in traits from milk performance test and disruptive influences by a breeding value in the selection index resilience of 90, 100 (population mean) and 110 in German Brown Swiss (non-significant results [p-value > 0.05] are marked in gray)

RI[1]	EBV	$Ø_{\mathrm{MPC}}$	Δ_{MPC}	$Ø_{\mathrm{MFC}}$	Δ_{MFC}	$Ø_{\mathrm{MUC}}$	Δ_{MUC}	$Ø_{\mathrm{MLC}}$	Δ_{MLC}	$Ø_{\mathrm{SCC}}$	Δ_{SCC}
	90	3.66	0.03	4.40	0.09	26.50	0.93	4.84	-0.02	236.14	7.64
v	100	3.64	0.00	4.28	0.00	23.73	0.00	4.84	0.00	227.80	0.00
	110	3.55	-0.03	4.13	-0.09	23.38	-0.93	4.88	0.02	226.37	-7.64
	90	3.65	-0.03	4.20	-0.09	24.49	0.07	4.81	-0.01	216.21	21.45
$\mathrm{v_d}$	100	3.63	0.00	4.21	0.00	23.59	0.00	4.84	0.00	184.52	0.00
	110	3.65	0.03	4.36	0.09	24.21	-0.07	4.83	0.01	191.41	-21.45
	90	3.70	0.02	4.39	-0.02	23.46	-0.03	4.87	0.00	175.98	20.89
$\mathrm{r_{Auto}}$	100	3.62	0.00	4.20	0.00	23.72	0.00	4.90	0.00	178.95	0.00
	110	3.88	-0.02	4.61	0.02	22.95	0.03	4.77	0.00	156.06	-20.89
	90	3.64	0.04	4.10	0.09	23.82	0.75	4.89	-0.02	163.76	8.55
$\mathrm{v_r}$	100	3.62	0.00	4.30	0.00	23.57	0.00	4.86	0.00	205.14	0.00
	110	3.58	-0.04	4.08	-0.09	22.05	-0.75	4.84	0.02	189.60	-8.55
	90	4.06	0.02	4.92	0.05	28.09	0.91	4.74	-0.03	308.38	19.40
$\mathrm{SI_{resilience}}$[2]	100	3.65	0.00	4.21	0.00	23.06	0.00	4.85	0.00	204.01	0.00
	110	3.66	-0.02	4.53	-0.05	24.97	-0.91	4.88	0.03	93.24	-19.40
		$Ø_{\mathrm{MLT}}$	Δ_{MLT}	$Ø_{\mathrm{MLD}}$	Δ_{MLD}	$Ø_{\mathrm{DD}}$	Δ_{DD}	$Ø_{\mathrm{DE}}$	Δ_{DE}		
v	90	142.46	5.68	70.17	4.35	20.89	1.35	3.78	0.00		
	100	172.57	0.00	109.31	0.00	25.51	0.00	4.07	0.00		

	110	150.96	-5.68	78.27	-4.35	20.00	-1.35	3.00	0.00
v_d	90	229.98	19.70	154.40	15.66	30.22	2.31	5.22	0.22
	100	186.63	0.00	113.24	0.00	24.81	0.00	4.05	0.00
	110	193.43	-19.70	136.99	-15.66	29.55	-2.31	4.73	-0.22
r_{Auto}	90	182.39	9.97	114.91	12.92	27.20	3.36	3.80	0.20
	100	150.16	0.00	76.49	0.00	19.09	0.00	3.37	0.00
	110	169.70	-9.97	89.91	-12.92	15.83	-3.36	2.33	-0.20
v_r	90	120.99	3.45	68.67	6.40	21.23	1.77	3.23	0.21
	100	176.26	0.00	109.74	0.00	25.99	0.00	4.31	0.00
	110	254.06	-3.45	183.40	-6.40	39.08	-1.77	6.81	-0.21
$SI_{resilience}$[2]	90	204.22	12.31	124.86	11.61	30.33	2.51	5.83	0.20
	100	192.26	0.00	125.67	0.00	29.49	0.00	4.51	0.00
	110	135.51	-12.31	33.63	-11.61	9.50	-2.51	2.00	-0.20

[1] RI – resilience indicator trait; overview of trait abbreviations can be found in Table 1

[2] $SI_{resilience}$ – selection index resilience calculated as $0.274 * v + 0.388 * v_d + 0.338 * v_r$

Ø – mean of the trait in all individuals with the same EBV for the resilience indicator trait (intercept of regression analysis)

Δ – deviation of the group of all individuals with the same EBV for the resilience indicator trait to the population mean (slope of regression analysis)

Table 3, Table 4 and Table 5 show the results, with the mean of all individuals per EBV group as the intercept of the regression and the slope multiplicated with the difference in EBV points as the deviation. Non-significant results were colored gray. In all breeds, the individuals showed changes in the analyzed traits depending on their resilience. Resilient animals lost less milk per lactation compared to their less resilient fellows. Although an increase in milk yield of up to 30 kg in HF, 20 kg in BS and 15 kg in FV per lactation selecting on $\mathrm{v_d}$ seems a small improvement, the test day results shows that also the milk ingredients of resilient cows are higher. In HF, a difference of ten breeding value points for $\mathrm{v_d}$ could result in a gain of 0.08% in MPC and of 0.14% in MFC. Similar trend was found for FV in MPC with an increase of 0.04% and for BS in MFC of 0.09%. The milk price in Germany is indexed to a milk fat content of 4% and a milk protein content of 3.4%, whereby deviations are rewarded with premiums or discounts. Resilient cows therefore tend to produce more milk with higher ingredients and thus could generate a higher economic income. This is in line with Poppe et al. (2022a), who calculated a higher lifetime gross margin for resilient cows in a comprehensive approach, and with Berghof et al. (2018), who showed an economic benefit in their study, however being based on assumptions instead of real data.

The test day traits also provide information on animal health and ruminant-adequate nutrition. Although cattle breeds differ in their milk composition, previous studies have shown that the same principles and threshold values can be assumed for HF, FV and BS (Glatz-Hoppe et al. 2019b). The desired MPC is approximately between 3.0 and 3.8 % and MFC between 3.0 and 4.8 % (Spiekers et al. 2009; Glatz-Hoppe et al. 2019a), whereby individuals in our study were in this range. The higher MPC, the better the energy supply for protein synthesis by the rumen microbes and the higher MFC, the more energy is available to the individual from structured crude fiber (Volling and Krömker 2007). Resilient animals seem to utilize more energy from the feed and convert it into milk ingredients than their less resilient stablemates. Attention should be paid to MPC and MFC to avoid falling (too far) into a negative net energy balance, especially at the beginning of lactation. Thereby, both parameters should not be too far apart, which in turn indicates metabolic disorders such as acidosis or ketosis (Heuer et al. 2000; Glatz-Hoppe et al. 2019a; Duffield et al. 1997). Besides the fat-protein-quotient, MUC provides information about the protein supply. The above-average amount of urea in the milk is caused by an oversupply of protein in the ration. This can lead to fertility problems and indicates that feeding costs can be reduced. A below-average urea content indicates that the cow is undersupplied and cannot exploit its performance potential (Biswajit et al. 2010). The normal range of MUC is 15 to 30 mg/dl (Spiekers et al. 2009). All three breeds are within this range, with BS showing slightly higher values than the other two. This corresponds to previous studies (Glatz-Hoppe et al. 2019b). The regression shows no clear direction within a breed. However, individuals with a short recovery phase (resilient according to $\mathrm{r}_{\mathrm{Auto}}$) have higher urea levels, while animals with few fluctuations in performance (resilient according to variance-based parameters) have lower urea levels. This corresponds to the results of the correlation analysis, in which $\mathrm{r}_{\mathrm{Auto}}$ correlated negatively with the health traits in HF (**chapter three**), i.e. healthy individuals have a longer recovery time.

MLC is more stable with values of 4.6 to 4.8 %, whereby the level decreases in all breeds over the lactations (Glatz-Hoppe et al. 2019b). A drop in MLC can be observed in udder diseases (Spiekers et al. 2009) and with increasing somatic cell counts (Alessio et al. 2016). This can be confirmed in HF, where resilient animals have significant increasing MLC and decreasing SCC and is underlined by the same trend in FV and BS. SCC serves as an indicator for udder diseases due to its positive correlations with mastitis (Coffey et al. 1986). It increases over lactations and tends to be higher for HF than for FV and BS (Glatz-Hoppe et al. 2019b). The lack of significance of the regression of SCC on resilience may be due to the small number of individuals per EBV level, as outliers could have a biasing effect. However, previous studies have already shown correlations between resilience indicator traits and mastitis prevalence (Kok et al. 2021).

In accordance with the definition described above, we have finally added how many different disturbance events and disturbance days the individuals suffer from. Across all breeds, individuals with high desired breeding values in variance-based resilience indicator traits and optimized selection indices resilience were less sensitive to environmental influences. Differences in the number of DE between levels of EBV were similar to results from Holstein Friesian in the Netherlands (Meijer et al. 2024). Also, number of days under disturbance DD in BS is in line with this study. In contrast, in FV resilient animals (high EBV in $\mathrm{r}_{\mathrm{Auto}}$) suffer from higher values in DE and DD with the same but non-significant trend in HF. Since the translation of the variance-based parameters appears plausible, this contradictory result is probably due to the calculation of the $\mathrm{r}_{\mathrm{Auto}}$. As previously discussed, $\mathrm{r}_{\mathrm{Auto}}$ is more sensitive to missing data, data modeling and the onset of disturbances (Ghaderi Zefreh et al. 2024; Le et al. 2024) with late onset disturbances tending to be harder to detect (Le et al. 2024; Ghaderi Zefreh et al. 2024).

Overall, the translation shows that breeding for resilience leads to a reduction in milk losses due to disturbances. In addition, milk ingredients can be positively influenced and, when interpreted as indicator traits, point to improved animal health. This is also confirmed by the assumed disturbance events and days per lactation using the variance-based resilience indicator traits from which the individual suffers. The methodology of the translation was a simple regression. This may not correspond to natural behavior, but polynomial regression did not reflect it better (results not shown). We assume that increasing the number of animals in each breed and improving the accuracy of the breeding value estimation by increasing the database would improve the validity of our results.

Comparison of the three breeds

In this study, data from herdbook cows of HF, FV and BS breeds raised in Baden-Württemberg were analyzed. They are the most important cattle breeds in southern Germany and are kept for milk production. FV and BS are dual-purpose breeds and the calves can also be marketed profitably for fattening. HF has the highest milk yield with 9,208 kg per year, followed by FV with 7,651 kg and BS with 7,572 kg (statistics from 2022). In contrast, BS produced the highest values for milk ingredients. In terms of lifetime productivity, the breeds differ in their longevity. The lifetime productivity of HF and BS is similar at around 31.5 thousand kg of milk, with BS living around 10 months longer at 47.5 months. At 26 thousand kg, FV achieves a slightly lower lifetime productivity, but at 39.5 months is utilized slightly longer than HF. Longevity and lifetime productivity tend to increase for all breeds (Bundesverband Rind und Schwein e.V. 2023). This could be due to the increased focus of dairy cattle breeding on improving functional and health traits in recent years. The analyses of genetic trends show a strong improvement of the genetic predisposition for better health in HF (Reents et al. 2024) and a stable upward trend in FV and BS (Fürst 2023).

Local and dual-purpose breeds are often considered healthier and more robust, and lower performance is accepted. The analysis of the test day data of Baden-Württemberg dairy cows in 2023 cannot confirm this: The causes of culling are similar in HF, FV and BS. Most culls are caused by infertility, followed by udder, hoof and metabolic diseases. A large proportion of diseases are not defined, which makes an exact evaluation difficult (Landesverband Baden-Württemberg für Leistungs- und Qualitätsprüfungen in der

Tierzucht e.V. 2023). Previous studies, however, have revealed differences between breeds. High-yielding dairy cow breeds appear to be more susceptible to udder and claw diseases and fertility problems (Bieber et al. 2019), external influences like heat (Mylostyvyi et al. 2021) and suffer from higher cortisol level, which indicates stress (Braun et al. 2022). On the other hand, the breeds seem to have different strategies for coping with difficult situations (Catellani et al. 2023). They may also differ in terms of resilience. We therefore compared the resilience indicator traits in the three breeds in **chapter two** and were only able to identify slight trend differences, some of which were contradictory. The results of Bonekamp et al. (2022) and Adriaens et al. (2023) confirm this, so we cannot prove any differences between breeds in general resilience. Depending on the environment and the type of disturbance, however, there may be differences in the specific resilience (Friggens et al. 2024). Further studies should therefore consider different breeds.

Outlook and further research approaches

Development of resilience indicator traits

Our analysis and previous studies show the validity of resilience indicator traits calculated based on the daily milk yield of dairy cows. They are heritable (Berghof et al. 2018; Poppe et al. 2020; Chen et al. 2023a), genetically correlated with other traits (Wang et al. 2022; Poppe et al. 2020), capture the response to unknown disturbances (Poppe et al. 2021; Ghaderi Zefreh et al. 2024) and selection for them can lead to selection response in functional and health traits. Nevertheless, this is just the first step and there are many starting points for continuing and intensifying resilience research in the livestock sector.

Statistical methods for quantifying resilience are currently being tested and continuously improved. The variance and autocorrelation of longitudinally measured performance traits initially proved to be the most promising, but further resilience indicator traits are constantly being defined and validated. The variance has turned out to be a stable indicator across species, breeds and traits, while autocorrelation should be treated with caution. Our study met the requirements for data density of intervals of less than three days and the length of the data collection period of at least 50 observations to obtain robust results (Ghaderi Zefreh et al. 2024). Nevertheless, the low significance in the analysis and higher error rates indicate a great need for further research for $\mathrm{r}_{\mathrm{Auto}}$. Possibly, the area under the curve of expected to the observed performance could be used to indicate recovery time, because it shows more stable results in validation tests (Ghaderi Zefreh et al. 2024; Mancin et al. 2024b; Le et al. 2024). Individual packages are already available for the statistical software R to examine livestock data sets for the ability of being resilient, e.g. from Barreto-Mendes et al. (2022) or Rohmer et al. (2023).

A major challenge in the methodology is the modelling of the expected trait values. Therefore, various concept- and data-based methods were tested (Friggens et al. 2024; Codrea et al. 2011; Poppe et al. 2020; Chen et al. 2023a) and the possibility of measuring resilience for animal groups (e.g., kept together in one pen or batch) or herds is evaluated (Le et al. 2024; Rikkers et al. 2023). There is a lot of dynamism in the development of statistical methods for measuring resilience, which raises the question of what kind of resilience we are looking for. We either speak of holistic resilience or specify it for individual types of disturbance or affected traits (Friggens et al. 2024; Knap and Doeschl-Wilson 2020). We should be aware that no individual can be immune to all disturbances worldwide anytime (Strandberg et al. 2013). It is therefore worth studying the biological background and correlations in more detail to gain a deeper understanding of resilience. Furthermore, a combination of several resilience indicator traits and traits is recommended, because individuals respond differently and with one or more traits to disturbances with more or less overlaps (Ben Abdelkrim et al. 2021; Le et al. 2024).

Firstly, resilience indicator traits could be applied to non-performance-related traits. The applied resilience indicator traits in this study, based on daily milk yield, reflect performance resilience despite being desirably correlated with functional and health traits (Bedere et al. 2022). Simple approaches include analyzing step counts (Poppe et al. 2022b), feed intake (Homma et al. 2021) or activity times (van der Zande et al. 2020), whose data could be available on a large scale in the future thanks to advancing digitalization (Schokker et al. 2022). Activity data such as eating, resting or standing times, and rumination activity, as well as their variances and periodicities serve as proxies for diseases in the transit phase of dairy cows (van Dixhoorn et al. 2023). Combined with physiological parameters such as body temperature, heart and breathing rate or the condition of the udder, the probability and severity of the occurrence of diseases after parturition can be predicted in advance. The change in blood parameters around the time of parturition was additionally analyzed and showed that animals with blood counts indicating inflammatory reactions had a higher prevalence for diseases at the beginning of lactation (van Dixhoorn et al. 2018).

Overall, consideration of metabolites in the research question contributes to a more comprehensive understanding of resilience: With regard to disease resilience, resilient pigs showed higher lymphocyte, hemoglobin and hematocrit but lower neutrophil levels after a disturbance. These blood parameters are part of the immune response to pathogens and a high value can be interpreted as a stronger response and desired (Bai et al. 2020). This is confirmed by Laghouaouta et al. (2021), which examined haptoglobin in the blood of pigs after vaccination. The concentration of this protein increases in response to infections, inflammation, trauma or stress. The study showed that resilient animals exhibited a lower increase in haptoglobin and at the same time a positive, desired deviation in body weight. In another example, cows experienced a change in the proportion of certain blood parameters in the total volume when exposed to increasing heat (Velayudhan et al. 2022). The consideration of the three studies shows the importance of fundamental knowledge of metabolites and their functions, as this knowledge of biological causality is required to interpret changes in their concentrations correctly as resilient or non-resilient. At the same time, not every assumed connection can be proven; for example, a study on the correlation between natural antibodies and resilience indicator traits based on body weight and laying performance in laying hens showed no significant results (Doekes et al. 2023; Berghof et al. 2024).

In less invasive studies, milk metabolites in goat's milk from test day samples were analyzed as a basis for resilience indicator traits (Abdelkrim et al. 2023; Ithurbide et al. 2023). The milk metabolite profiles of early and late lactation allow an assessment of resilience to nutritional disturbances (Abdelkrim et al. 2023). Subsequently, individuals grouped a priori with low longevity showed significantly higher variance in different metabolites, which was interpreted as non-resilient. The significantly different metabolites indicate higher oxidative stress, higher inflammation and greater mobilization of body fat reserves (Ithurbide et al. 2023). Billa et al. (2020) measured differences in the concentration of the same milk metabolites under feed restriction in two different dairy cattle breeds. These in turn were significantly correlated with the energy balance of the dairy cows, which emphasizes the importance of paying attention to milk metabolites in determining resilience.

In recent years, breeding has focused on the microbiome, its heritability, composition and abundance. It influences and mediates the performance, health and efficiency of livestock (Forcina et al. 2022). Initial studies in rabbits (Casto-Rebollo et al. 2023) and pigs (Mancin et al. 2024a) show that the composition and abundance of the microbiota of resilient and non-resilient animals differ and could therefore serve as an indicator of resilience.

Despite the many studies, there are still new approaches to studying resilience along the omics cascade (Zhu et al. 2022). Phenomics, the observation of visible or measurable trait expression, is widely considered in previous resilience studies. Research on metabolomics, proteomics and microbiomics has been initiated but could be further expanded in the future. To our knowledge, there is currently still a research gap in the analysis of transcriptomics. There are numerous previous studies on heat tolerance that have shown up- und down-regulation if genes under different thermal conditions (Velayudhan et al. 2022; Collier et al. 2006; Kim et al. 2020). It is therefore likely that differences in gene expression also have an impact on resilience.

Further genomic analysis

Resilience has been analyzed in **chapter four** and by other studies using GWAS to decipher the genetic architecture. The results concur that resilience indicator traits are polygenic traits, hence being influenced by many gene loci with little effect (Doekes et al. 2023; Chen et al. 2023b). These results were to be assumed as the resilience indicator traits studied are based on milk yield and are therefore a classic quantitative trait (William and Simianer 2017). GWAS of milk yield show many SNPs with a significant influence on the trait expression and related genes distributed over the entire genome (Jiang et al. 2019; Schneider et al. 2023). A more detailed analysis and deeper insights would be possible by using whole genome data in the GWAS. This enables fine mapping of genes and a more precise assignment of biological backgrounds, which reveals gene loci that truly influence resilience (Mancin et al. 2024b). Due to the complexity of resilience, the classic GWAS may not be sufficient as a tool for a closer look at common genetic backgrounds with other traits. In this case, it is advisable to carry out local correlation analyses. Generally, genetic correlations are estimated across the entire genome as the means of all effects. However, single loci in the genome can jointly influence two traits positively, negatively or contrarily. Various tools have been developed to record this (Werme et al. 2022; Guo et al. 2021).

Another approach is the analysis of specific genome subsets and their influence on resilience indicator traits. Xiang et al. (2019) analyzed 30 genomic variants for 34 traits of Australian dairy cows and showed that the heritability per subset differs. This was confirmed by Schneider et al. (2024) when applied to milk yield and several health traits in the German population. The methodology also showed differences in the strength and direction of genetic correlations depending on the subset analyzed (Schneider et al. 2024).

A requirement for in-depth genomic analyses is a clear definition of the resilience indicator trait or resilience process to be studied. Once this has been done, causality studies can be conducted. Various methods are available, whereby the best known are Mendelian

Randomization (Sanderson et al. 2022) and structural equation systems (Gianola and Sorensen 2004). The former has already been carried out for resilience indicator traits based on daily milk yields and showed a significant causal effect of milk yield on the variance of the deviation of the expected from the observed daily milk yield (Chen et al. 2023b). This scaling effect is expected and was therefore taken into account in Poppe by correcting for milk yield (Poppe et al. 2020) and in our study by using the variance of relative milk yields (**chapter two to four**). Nevertheless, the study shows that causal relationships with resilience indicator traits exist (Chen et al. 2023b).

Concluding remarks

Resilience offers the opportunity to breed performance-stable, healthy and, to a certain extent, environmentally insensitive livestock. Despite the many open research approaches discussed above, resilience can be implemented directly in practical breeding in all important livestock species. Sufficient studies have shown that the variance of longitudinally recorded performance traits represents a new selection tool for breeders and provides additional information to existing EBV. To address remaining uncertainties, we recommend the publication of a selection index in addition to the existing total breeding value. Furthermore, the autocorrelation and area under the curve should be intensively studied as resilience indicator traits of recovery time. Such or a similar trait has not yet been implemented in breeding value estimation and captures a large proportion of the response to disturbances that are unknown today.

For further research on resilience in livestock, especially along the omics cascade, different disciplines of livestock research should co-operate. In addition to the final breeding aspect, extensive knowledge of physiological and biological processes in the organism is required to reveal resilience in a comprehensive manner.

Finally, it is important to involve farmers and breeders in practice on this journey to make them aware of the importance of resilient animals, especially in times of a constantly changing and increasingly demanding environment. The work in breeding research can only be successful if the selection tools we offer are also utilized in the barn.

References

Abdelkrim, A. Ben; Ithurbide, M.; Larsen, T.; Schmidely, P.; Friggens, N. C. (2023): Milk metabolites can characterise individual differences in animal resilience to a nutritional challenge in lactating dairy goats. In *animal* 17 (4), p. 100727. DOI: 10.1016/j.animal.2023.100727.

Adriaens, Ines; Bonekamp, Gerbrich; Napel, Jan ten; Kamphuis, Claudia; Haas, Yvette de (2023): Differences across herds with different dairy breeds in daily milk yield based proxies for resilience. In *Front. Genet.* 14, p. 1120073. DOI: 10.3389/fgene.2023.1120073.

Alessio, Dileta Regina Moro; Thaler Neto, André; Velho, João Pedro; Perreira, Ildemar Brayer; Miquelluti, David José; Knob, Deise Aline; Da Silva, Claudineli Gasparini (2016): Multivariate analysis of lactose content in milk of Holstein and Jersey cows1. In *SCA* 37 (4Supl1), p. 2641. DOI: 10.5433/1679-0359.2016v37n4Supl1p2641.

Bai, Xuechun; Putz, Austin M.; Wang, Zhiquan; Fortin, Frédéric; Harding, John C. S.; Dyck, Michael K. et al. (2020): Exploring Phenotypes for Disease Resilience in Pigs Using Complete Blood Count Data From a Natural Disease Challenge Model. In *Front. Genet.* 11, p. 216. DOI: 10.3389/fgene.2020.00216.

Barreto-Mendes, L.; La Torre, A. de; Ortigues-Marty, I.; Cassar-Malek, I.; Pires, J.; Blanc, F. (2022): How to approach the resilience of livestock exposed to environmental challenges? Quantification of individual response and recovery by means of differential calculus. In *Animal - Open Space* 1 (1), p. 100008. DOI: 10.1016/j.anopes.2022.100008.

Bedere, Nicolas; Berghof, Tom V. L.; Peeters, Katrijn; Pinard-van der Laan, Marie-Hélène; Visscher, Jeroen; David, Ingrid; Mulder, Han A. (2022): Using egg production longitudinal recording to study the genetic background of resilience in purebred and crossbred laying hens. In *Genet Sel Evol* 54 (1), p. 26. DOI: 10.1186/s12711-022-00716-8.

Ben Abdelkrim, A.; Tribout, T.; Martin, O.; Boichard, D.; Ducrocq, V.; Friggens, Nicolas C. (2021): Exploring simultaneous perturbation profiles in milk yield and body weight reveals a diversity of animal responses and new opportunities to identify resilience proxies. In *J. Dairy Sci.* 104 (1), pp. 459–470. DOI: 10.3168/jds.2020-18537.

Berghof, Tom V. L.; Bedere, Nicolas; Peeters, Katrijn; Poppe, Marieke; Visscher, Jeroen;

Mulder, Han A. (2024): The genetics of resilience and its relationships with egg production traits and antibody traits in chickens. In *Genet Sel Evol* 56 (1), p. 20. DOI: 10.1186/s12711-024-00888-5.

Berghof, Tom V. L.; Poppe, Marieke; Mulder, Han A. (2018): Opportunities to Improve Resilience in Animal Breeding Programs. In *Front. Genet.* 9, p. 692. DOI: 10.3389/fgene.2018.00692.

Bieber, Anna; Wallenbeck, Anna; Leiber, Florian; Fuerst-Waltl, Birgit; Winckler, Christoph; Gullstrand, Patricia et al. (2019): Production level, fertility, health traits, and longevity in local and commercial dairy breeds under organic production conditions in Austria, Switzerland, Poland, and Sweden. In *J. Dairy Sci.* 102 (6), pp. 5330–5341. DOI: 10.3168/jds.2018-16147.

Billa, P. A.; Faulconnier, Y.; Larsen, T.; Leroux, C.; Pires, J. A. A. (2020): Milk metabolites as noninvasive indicators of nutritional status of mid-lactation Holstein and Montbéliarde cows. In *Journal of Dairy Science* 103 (4), pp. 3133–3146. DOI: 10.3168/jds.2019-17466.

Biswajit, Roy; Brahma, B.; Ghosh, S.; Mandal, G.; Pankaj, P. (2010): Evaluation of Milk Urea Concentration as Useful Indicator for Dairy Herd Management: A Review. In *Asian J. of Animal and Veterinary Advances* 6 (1), pp. 1–19. DOI: 10.3923/ajava.2011.1.19.

Bonekamp, Gerbrich; Poppe, M.; ten Napel, J.; Kamphuis, C.; de Haas, Yvette; Adriaens, I. (2022): Comparison of milk yield based resilience indicators across dairy cattle breeds. Proceedings of 12th World Congress on Genetics Applied to Livestock Production. Wageningen Academic Publishers. Wageningen, Netherlands, 2022. Available online at https://www.wageningenacademic.com/pb-assets/wagen/WCGALP2022/27_002.pdf.

Braun, U.; Züblin, S.; Imhof, S.; Baumgartner, M. R.; Binz, T. M. (2022): Haarcortisolkonzentrationen bei Kühen verschiedener Rinderrassen, in natürlich gewachsenem und in nachgewachsenem Haar sowie in Haar verschiedener Körperstellen. In *Schweizer Archiv fur Tierheilkunde* 164 (10), pp. 695–703. DOI: 10.17236/sat00369.

Bundesverband Rind und Schwein e.V. (2023): Rinder- und Schweineproduktion in Deutschland 2022.

Casto-Rebollo, Cristina; Argente, María José; García, María Luz; Pena, Ramona Natacha; Blasco, Agustín; Ibáñez-Escriche, Noelia (2023): Selection for environmental variance shifted the gut microbiome composition driving animal resilience. In *Microbiome* 11 (1), p. 147. DOI: 10.1186/s40168-023-01580-4.

Catellani, A.; Mezzetti, M.; Minuti, A.; Cattaneo, L.; Trevisi, E. (2023): Metabolic and inflammatory responses reveal different adaptation to the transition period challenges in Holstein, Brown Swiss, and Simmental dairy cows. In *Italian Journal of Animal Science* 22 (1), pp. 388–397. DOI: 10.1080/1828051X.2023.2196995.

Chen, Shi-Yi; Boerman, Jacquelyn P.; Gloria, Leonardo S.; Pedrosa, Victor B.; Doucette, Jarrod; Brito, Luiz F. (2023a): Genomic-based genetic parameters for resilience across lactations in North American Holstein cattle based on variability in daily milk yield records. In *J. Dairy Sci.* 106 (6), pp. 4133–4146. DOI: 10.3168/jds.2022-22754.

Chen, Shi-Yi; Gloria, Leonardo S.; Pedrosa, Victor B.; Doucette, Jarrod; Boerman, Jacquelyn P.; Brito, Luiz F. (2023b): Unravelling the genomic background of resilience based on variability in milk yield and milk production levels in North American Holstein cattle through GWAS and Mendelian randomization analyses. In *Journal of Dairy Science* 0 (0). DOI: 10.3168/jds.2023-23650.

Codrea, M. C.; Højsgaard, S.; Friggens, Nicolas C. (2011): Differential smoothing of time-series measurements to identify disturbances in performance and quantify animal response characteristics: An example using milk yield profiles in dairy cows. In *J Anim Sci* 89 (10), pp. 3089–3098. DOI: 10.2527/jas.2010-3753.

Coffey, E. M.; Vinson, W. E.; Pearson, R. E. (1986): Potential of somatic cell concentration in milk as a sire selection criterion to reduce mastitis in dairy cattle. In *Journal of Dairy Science* 69 (8), pp. 2163–2172. DOI: 10.3168/jds.S0022-0302(86)80649-X.

Collier, R. J.; Stiening, C. M.; Pollard, B. C.; VanBaale, M. J.; Baumgard, L. H.; Gentry, P. C.; Coussens, P. M. (2006): Use of gene expression microarrays for evaluating environmental stress tolerance at the cellular level in cattle. In *Journal of animal science* 84 Suppl (suppl_13), E1-13. DOI: 10.2527/2006.8413_supplE1x.

CRV (2024): Breeding value Resilience. Statistical Indicators. Available online at https://www.cooperatie-crv.nl/wp-content/uploads/2024/03/E-47-Veerkracht-April-2024-Engels.pdf, updated on 3/22/2024, checked on 2/5/2025.

Doekes, Harmen P.; Bovenhuis, Henk; Berghof, Tom V. L.; Peeters, Katrijn; Visscher, Jeroen; Mulder, Han A. (2023): Research Note: Genome-wide association study for natural antibodies and resilience in a purebred layer chicken line. In *Poultry Science* 102 (1), p. 102312. DOI: 10.1016/j.psj.2022.102312.

Duffield, T. F.; Kelton, D. F.; Leslie, K. E.; Lissemore, K. D.; Lumsden, J. H. (1997): Use of test day milk fat and milk protein to detect subclinical ketosis in dairy cattle in Ontario. In *The Canadian Veterinary Journal* 38 (11), pp. 713–718.

Forcina, Giovanni; Pérez-Pardal, Lucía; Carvalheira, Júlio; Beja-Pereira, Albano (2022): Gut Microbiome Studies in Livestock: Achievements, Challenges, and Perspectives. In *Animals* 12 (23), p. 3375. DOI: 10.3390/ani12233375.

Friggens, N. C.; Ithurbide, M.; Lenoir, G. (2024): Getting to grips with resilience: Toward large-scale phenotyping of this complex trait. In *JDS Communications* 5 (6), pp. 761–766. DOI: 10.3168/jdsc.2023-0434.

Fürst, Christian (2023): Zuchtwertschätzung beim Rind. Grundlagen, Methoden und Interpretationen. ZuchtData EDV-Dienstleistungen GmbH. Available online at https://www.zuchtwert.at/downloads/ZWS/ZWS.pdf, updated on December 2023, checked on 1/30/2025.

Fürst, Christian; Schwarzenbacher, Hermann; Himmelbauer, Judith; Egger-Danner, Christa (2023): Neu: Zuchtwerte für Klauengesundheit für Fleckvieh und Brown Swiss. In *Rinderzucht Austria*, 12/6/2023. Available online at https://www.rinderzucht.at/nachricht/20231206-neu-zuchtwerte-fuer-klauengesundheit-fuer-fleckvieh-und-brown-swiss.html, checked on 1/30/2025.

Ghaderi Zefreh, M.; Pong-Wong, R.; Doeschl-Wilson, A. (2024): Validating statistical properties of resilience indicators derived from simulated longitudinal performance measures of farmed animals. In *animal* 18 (8), p. 101248. DOI: 10.1016/j.animal.2024.101248.

Gianola, Daniel; Sorensen, Daniel (2004): Quantitative genetic models for describing simultaneous and recursive relationships between phenotypes. In *Genetics* 167 (3), pp. 1407–1424. DOI: 10.1534/genetics.103.025734.

Glatz-Hoppe, J.; Mohr, E.; Losand, B. (2019a): Nutzung von Milchinhaltsstoffen zur Beurteilung der Versorgungssituation von Milchkühen. 2. Mitteilung:

Bewertungsschema zur Beurteilung der Inhaltsstoffe auf Betriebsebene. In *Züchtungskunde* 91 (6), pp. 449–473.

Glatz-Hoppe, Julia; Onken, F; Eggert, Anja; Mohr, E; Losand, B (2019b): Nutzung von Milchinhaltsstoffen zur Beurteilung der Versorgungssituation von Milchkühen 1. Mitteilung: Milchleistung und Inhaltsstoffe deutscher Milchrindrassen im Vergleich. In *Züchtungskunde* 91 (6), pp. 423–448. Available online at https://d-nb.info/1293661236/34#page=17.

Guo, Hanmin; Li, James J.; Lu, Qiongshi; Hou, Lin (2021): Detecting local genetic correlations with scan statistics. In *Nat Commun* 12 (1), p. 2033. DOI: 10.1038/s41467-021-22334-6.

Heuer, C.; van Straalen, W. M.; Schukken, Y. H.; Dirkzwager, A.; Noordhuizen, J.P.T.M. (2000): Prediction of energy balance in a high yielding dairy herd in early lactation: model development and precision. In *Livestock Production Science* 65 (1-2), pp. 91–105. DOI: 10.1016/S0301-6226(99)00177-3.

Homma, C.; Hirose, K.; Ito, T.; Kamikawa, M.; Toma, S.; Nikaido, S. et al. (2021): Estimation of genetic parameter for feed efficiency and resilience traits in three pig breeds. In *animal* 15 (11), p. 100384. DOI: 10.1016/j.animal.2021.100384.

Ithurbide, M.; Wang, H.; Fassier, T.; Li, Z.; Pires, J.; Larsen, T. et al. (2023): Multivariate analysis of milk metabolite measures shows potential for deriving new resilience phenotypes. In *Journal of Dairy Science* 106 (11), pp. 8072–8086. DOI: 10.3168/jds.2023-23332.

Jiang, Jicai; Ma, Li; Prakapenka, Dzianis; VanRaden, Paul M.; Cole, John B.; Da, Yang (2019): A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. In *Front. Genet.* 10, p. 412. DOI: 10.3389/fgene.2019.00412.

Kim, W. S.; Ghassemi Nejad, J.; Peng, D. Q.; Jung, U. S.; Kim, M. J.; Jo, Y. H. et al. (2020): Identification of heat shock protein gene expression in hair follicles as a novel indicator of heat stress in beef calves. In *animal* 14 (7), pp. 1502–1509. DOI: 10.1017/S1751731120000075.

Knap, Pieter W.; Doeschl-Wilson, Andrea (2020): Why breed disease-resilient livestock, and how? In *Genet Sel Evol* 52 (1), p. 60. DOI: 10.1186/s12711-020-00580-4.

Kok, A.; Tsousis, G.; Niozas, G.; Kemp, B.; Kaske, M.; van Knegsel, A. T. M. (2021): Short communication: Variance and autocorrelation of deviations in daily milk yield are related with clinical mastitis in dairy cows. In *animal* 15 (10), p. 100363. DOI: 10.1016/j.animal.2021.100363.

Laghouaouta, Houda; Pena, Ramona N.; Ros-Freixedes, Roger; Reixach, Josep; Díaz, Marta; Estany, Joan et al. (2021): A Methodology to Quantify Resilience in Growing Pigs. In *Animals* 11 (10), p. 2970. DOI: 10.3390/ani11102970.

Landesverband Baden-Württemberg für Leistungs- und Qualitätsprüfungen in der Tierzucht e.V. (2023): Jahresbericht 2023. Ergebnisse des Prüfungsjahres 2023. Stuttgart, Germany: LKV Beratungs- und Service GmbH. Available online at https://lkvbw.de/services/files/jahresberichte/A%20Jahresbericht%202023_web.pdf, checked on 2/26/2025.

Le, Vincent; Rohmer, Tom; David, Ingrid (2024): Identification and characterization of unknown disturbances in a structured population using high-throughput phenotyping data and measurement of robustness: application to growing pigs. In *Journal of animal science* 102, skae059. DOI: 10.1093/jas/skae059.

Lora, I.; Gottardo, F.; Contiero, B.; Zidi, A.; Magrin, L.; Cassandro, M.; Cozzi, G. (2020): A survey on sensor systems used in Italian dairy farms and comparison between performances of similar herds equipped or not equipped with sensors. In *Journal of Dairy Science* 103 (11), pp. 10264–10272. DOI: 10.3168/jds.2019-17973.

Mancin, Enrico; Maltecca, Christian; Huang, Yi Jian; Mantovani, Roberto; Tiezzi, Francesco (2024a): A first characterization of the microbiota-resilience link in swine. In *Microbiome* 12 (1), p. 53. DOI: 10.1186/s40168-024-01771-7.

Mancin, Enrico; Maltecca, Christian; Jiang, Jicaj; Huang, Yi Jian; Tiezzi, Francesco (2024b): Capturing resilience from phenotypic deviations: a case study using feed consumption and whole genome data in pigs. In *BMC Genomics* 25 (1), p. 1128. DOI: 10.1186/s12864-024-11052-0.

Meijer, Niek; Bouwmeester-Vosman, Jorien; van Pelt, Mathijs; de Jong, Gerben (2024): Breeding for resilience in the Netherlands and Flanders: INTERBULL. Available online at https://journal.interbull.org/index.php/ib/article/download/1926/1935.

Mengistu, Samuel Bekele; Mulder, Han A.; Bastiaansen, John W.M.; Benzie, John A.H.; Khaw, Hooi Ling; Trinh, Trong Quoc; Komen, Hans (2022): Fluctuations in growth are heritable and a potential indicator of resilience in Nile tilapia (Oreochromis niloticus). In *Aquaculture* 560, p. 738481. DOI: 10.1016/j.aquaculture.2022.738481.

Miglior, Filippo; Fleming, Allison; Malchiodi, Francesca; Brito, Luiz F.; Martin, Pauline; Baes, Christine F. (2017): A 100-Year Review: Identification and genetic selection of economically important traits in dairy cattle. In *Journal of Dairy Science* 100 (12), pp. 10251–10271. DOI: 10.3168/jds.2017-12968.

Mylostyvyi, Roman; Lesnovskay, Olena; Karlova, Lina; Khmeleva, Olena; Kalinichenko, Olena; Orishchuk, Oksana et al. (2021): Brown Swiss cows are more heat resistant than Holstein cows under hot summer conditions of the continental climate of Ukraine. In *JABB* 9 (4), pp. 1–8. DOI: 10.31893/jabb.21034.

Poppe, M.; Mulder, H. A.; Veerkamp, Roel F. (2021): Validation of resilience indicators by estimating genetic correlations among daughter groups and with yield responses to a heat wave and disturbances at herd level. In *J. Dairy Sci.* 104 (7), pp. 8094–8106. DOI: 10.3168/jds.2020-19817.

Poppe, M.; Veerkamp, Roel F.; Mulder, H. A.; Hogeveen, H. (2022a): Observational study on associations between resilience indicators based on daily milk yield in first lactation and lifetime profitability. In *J. Dairy Sci.* 105 (10), pp. 8158–8176. DOI: 10.3168/jds.2021-21532.

Poppe, M.; Veerkamp, Roel F.; van Pelt, M. L.; Mulder, H. A. (2020): Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. In *J. Dairy Sci.* 103 (2), pp. 1667–1684. DOI: 10.3168/jds.2019-17290.

Poppe, Marieke; Mulder, Han A.; van Pelt, Mathijs L.; Mullaart, Erik; Hogeveen, Henk; Veerkamp, Roel F. (2022b): Development of resilience indicator traits based on daily step count data for dairy cattle breeding. In *Genet Sel Evol* 54 (1), p. 21. DOI: 10.1186/s12711-022-00713-x.

Reents, Reinhard; Hüneke, Laura; Schmidtmann, Christin; Rensing, Stefan; vit (Vereinigte Informationssysteme Tierhaltung w.V.) (2024): Zucht verbessert Gesundheit und Funktionalität beim Milchrind. In *Züchtungskunde* 94 (1), pp. 27–33. DOI: ISSN.

Rikkers, Roxann S. C.; Ducro, Bart J.; van Binsbergen, Rianne; Kamphuis, Claudia (2023): Predicting dairy herd resilience on farms with conventional milking systems. In

Journal of Dairy Research, pp. 1–7. DOI: 10.1017/S0022029923000432.

Rohmer, Tom; Le, Vincent; David, Ingrid (2023): CRAN: Contributed Packages.

Sanderson, Eleanor; Glymour, M. Maria; Holmes, Michael V.; Kang, Hyunseung; Morrison, Jean; Munafò, Marcus R. et al. (2022): Mendelian randomization. In *Nat Rev Methods Primers* 2 (1), pp. 1–21. DOI: 10.1038/s43586-021-00092-5.

Schneider, Helen; Krizanac, Ana-Marija; Falker-Gieske, Clemens; Heise, Johannes; Tetens, Jens; Thaller, Georg; Bennewitz, Jörn (2024): Genomic dissection of the correlation between milk yield and various health traits using functional and evolutionary information about imputed sequence variants of 34,497 German Holstein cows. In *BMC Genomics* 25 (1), p. 265. DOI: 10.1186/s12864-024-10115-6.

Schneider, Helen; Segelke, Dierck; Tetens, Jens; Thaller, Georg; Bennewitz, Jörn (2023): A genomic assessment of the correlation between milk production traits and claw and udder health traits in Holstein dairy cattle. In *Journal of Dairy Science* 106 (2), pp. 1190–1205. DOI: 10.3168/jds.2022-22312.

Schokker, D.; Poppe, M.; Napel, J. ten; Athanasiadis, I. N.; Kamphuis, C.; Veerkamp, Roel F. (2022): Rapid turnover of sensor data to genetic evaluation for dairy cows in the cloud. In *Journal of Dairy Science* 105 (12), pp. 9792–9798. DOI: 10.3168/jds.2022-22113.

Simianer, Henner; Büttgen, Lisa; Ganesan, Amudha; Ha, Ngoc Thuy; Pook, Torsten (2021): A unifying concept of animal breeding programmes. In *Journal of Animal Breeding and Genetics* 138 (2), pp. 137–150. DOI: 10.1111/jbg.12534.

Spiekers, Hubert; Nußbaum, Hansjörg; Potthast, Volker (2009): Erfolgreiche Milchviehfütterung. Frankfurst am Main: DLG.

Strandberg, E.; Felleki, Majbritt; Fikse, W. F.; Franzén, J.; Mulder, H. A.; Rönnegård, L. et al. (2013): Statistical tools to select for robustness and milk quality. In *Advances in Animal Biosciences* 4 (3), pp. 606–611. DOI: 10.1017/S2040470013000162.

Ule, A.; Erjavec, K.; Klopčič, M. (2023): Influence of dairy farmers' knowledge on their attitudes towards breeding tools and genomic selection. In *animal* 17 (6), p. 100852. DOI: 10.1016/j.animal.2023.100852.

van der Zande, Lisette E.; Dunkelberger, Jenelle R.; Rodenburg, T. Bas; Bolhuis, J.

Elizabeth; Mathur, Pramod K.; Cairns, W. James et al. (2020): Quantifying Individual Response to PRRSV Using Dynamic Indicators of Resilience Based on Activity. In *Front. Vet. Sci.* 7, p. 325. DOI: 10.3389/fvets.2020.00325.

van Dixhoorn, I. D. E.; Mol, R. M. de; van der Werf, J. T. N.; van Mourik, S.; van Reenen, C. G. (2018): Indicators of resilience during the transition period in dairy cows: A case study. In *Journal of Dairy Science* 101 (11), pp. 10271–10282. DOI: 10.3168/jds.2018-14779.

van Dixhoorn, I.D.E.; Mol, R. M. de; Schnabel, S. K.; van der Werf, J.T.N.; van Mourik, S.; Bolhuis, J. E. et al. (2023): Behavioral patterns as indicators of resilience after parturition in dairy cows. In *Journal of Dairy Science*. DOI: 10.3168/jds.2022-22891.

Velayudhan, Silpa Mullakkalparambil; Brügemann, Kerstin; Alam, Shahin; Yin, Tong; Devaraj, Chinnasamy; Sejian, Veerasamy et al. (2022): Molecular, Physiological and Hematological Responses of Crossbred Dairy Cattle in a Tropical Savanna Climate. In *Biology* 12 (1). DOI: 10.3390/biology12010026.

Vereinigte Informationssysteme Tierhaltung w.V. (2024): Beschreibung der Zuchtwertschätzung für alle Schätzmerkmale bei den Milchrinderrassen für die vit mit der Zuchtwertschätzung beauftragt ist. Available online at https://www.vit.de/fileadmin/DE/Zuchtwertschaetzung/Zws_Bes_deu.pdf, updated on December 2024, checked on 1/30/2025.

Volling, O.; Krömker, V. (2007): Monitoring als Bestandteil des Tiergesundheitsmanagements. Available online at https://orgprints.org/9507/.

Wang, Ao; Brito, Luiz F.; Zhang, Hailiang; Shi, Rui; Zhu, Lei; Liu, Dengke et al. (2022): Exploring milk loss and variability during environmental perturbations across lactation stages as resilience indicators in Holstein cattle. In *Front. Genet.* 13, p. 1031557. DOI: 10.3389/fgene.2022.1031557.

Werme, Josefin; van der Sluis, Sophie; Posthuma, Danielle; Leeuw, Christiaan A. de (2022): An integrated framework for local genetic correlation analysis. In *Nat Genet* 54 (3), pp. 274–282. DOI: 10.1038/s41588-022-01017-y.

William, Alfons; Simianer, Henner (2017): Tierzucht. Selektion. Selektionsmethoden. Indexselektion. 2nd ed. Stuttgart, Germany: Eugen Ulmer.

Wolfová, M.; Wolf, J. (2013): Strategies for defining traits when calculating economic values for livestock breeding: a review. In *animal* 7 (9), pp. 1401–1413. DOI: 10.1017/S1751731113001018.

Xiang, Ruidong; van Berg, Irene den; MacLeod, Iona M.; Hayes, Benjamin J.; Prowse-Wilkins, Claire P.; Wang, Min et al. (2019): Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. In *Proc. Natl. Acad. Sci. U.S.A.* 116 (39), pp. 19398–19408. DOI: 10.1073/pnas.1904159116.

Zhu, Yingkun; Bu, Dengpan; Ma, Lu (2022): Integration of Multiplied Omics, a Step Forward in Systematic Dairy Research. In *Metabolites* 12 (3), p. 225. DOI: 10.3390/metabo12030225.

ACKNOWLEDGEMENT

Resilienz ist die Widerstandsfähigkeit eines Organismus, dank der er den wechselnden Bedingungen seiner Umwelt trotzt und sich von ihren Einflüssen erholt. Handelt es sich bei dem Organismus um einen Doktoranden und bei der Umwelt um eine Promotion, so findet er bestenfalls Unterstützung in seinem Umfeld. Ich möchte mich bei allen bedanken, die mich auf meinem Weg samt Höhen und Tiefen der vergangenen Jahre begleitet haben.

Zuallererst sei hier Prof. Dr. Jörn Bennewitz für die Überlassung des Themas und die stets hervorragende Betreuung als Doktorvater gedankt. Lieber Jörn, ich danke Dir für die überzeugenden Argumente die Promotion zu beginnen und die Unterstützung bis zu ihrem Abschluss, für ein stetiges Fördern und Fordern, für die Möglichkeit zu wachsen und neue Erfahrungen zu sammeln, für eine offene Tür und zwei Ohren in allen Forschungs- und Lebenslagen, und nicht zuletzt für ein freundschaftliches Miteinander und eine Arbeitsatmosphäre zum Wohlfühlen.

Ich danke Prof. Dr. Georg Thaller und Prof. Dr. Hans-Peter Piepho für die Bereitschaft die Aufgaben des Zweit- und Drittprüfers zu übernehmen. Außerdem möchte ich mich bei Prof. Dr. Mizeck Chagunda für die Betreuung bedanken. Dear Mizeck, thank you for your enthusiastic, optimistic manner, your passion for research and always encouraging words. You are an inspiration and I am delighted to have worked with you.

Einen wichtigen Unterstützer, ohne den es mit Sicherheit keine Doktorarbeit geben würde, fand ich in Dr. Dr. Robin Wellmann. Lieber Robin, ich bin überzeugt davon, dass Deine statistische Expertise einen höchst signifikanten, positiven Einfluss auf das vorliegende Ergebnis nahm. Und dank vieler gemeinsamer Stunden im R-Kurs verstehe ich auch die von Dir beigesteuerten Code-Zeilen – zumindest in absoluter Mehrheit gesehen. Vielen Dank!

Eine erfolgreiche Doktorarbeit entsteht nicht von allein, es bedarf Daten, Expertise, Finanzierung, Ideenreichtum, Leidenschaft, Manpower und vielem mehr. Daher bedanke ich mich bei allen Beteiligten des EIP-Projekts KlimaFit: Angefangen bei den Landwirten und ihren resilienten Milchkühen, bei den fleißigen Mitwirkenden in der Datenerhebung, bei all den Verbänden und Organisationen und ihren Mitarbeitenden. Es hat mir viel Spaß bereitet, Teil dieses Projekts zu sein. Stellvertretend ein großes Dankeschön an Elena Frenken, Dr. Pera Herold und Dr. Philipp Muth für die stets konstruktive, zuverlässige Zusammenarbeit.

Das resilienteste Individuum der eigenen Arbeit kann man nicht ohne Hilfe sein: Ein großes Dankeschön geht an alle Doktoranden und Mitarbeitenden des Fachgebiets Tiergenetik und Züchtung! Egal ob schwerwiegende Forschungsprobleme, persönliche Sinnkrisen, die Suche nach neuem Kaffee oder die Frage nach der besten Bar der Stadt – gemeinsam fand sich stets eine Lösung. Ich werde die konspirativen Kaffeepausen, die Gedankenspaziergänge während der Hunderunden, die hoch wissenschaftlichen Planungen von gemeinsamen Unternehmungen oder Doktorhüten und die unvergesslichen Exkursionen und Konferenzreisen vermissen. Ohne Euch wäre mein Büroalltag deutlich weniger bunt gewesen. Ein besonderes Dankeschön richtet sich an meine Bürogemeinschaften. Danke liebe Helen(e) für all das, was Du mir beigebracht hast, für Deine Betreuung und Unterstützung, für gemeinsame Road-Trips und Filmabende, für Dein Wissen und Deine Freundschaft. Vielen Dank lieber Maxi für unsere tolle Zusammenarbeit, für Dein Feingefühl, wenn es eben doch mal nicht so lief, und erholsame Freizeitevents ganz ohne Raum für die Wissenschaft.

Doch nicht nur im Büro wirken die Einflüsse der Umwelt, auch daheim. Daher geht ein großer Dank an Georg und Janine für ein Zuhause fernab meiner Heimat, in dem wir Tiefschläge gemeinsam überwunden und Erfolge gefeiert haben. Danke Euch für alles.

Diese Danksagung könnte ewig lang sein und ich hätte noch nicht alle bedacht, die es verdient hätten. Daher danke ich an dieser Stelle allen Wegbegleitern und Wegbereitern, allen Bekannten und Sportkameraden, allen Kommilitonen und Freunden für die stetige Unterstützung, aufbauende Worte, ausgleichende Freizeit- und Urlaubserlebnisse, unvergessliche Erfahrungen und Euren Glauben in meine Arbeit und mich. Ihr wart Seelsorger und Mentoren, Sprungtuch und Inspiration für mich. Ohne Euch wäre dieser Weg nicht gangbar gewesen, vielen Dank.

Der Abschluss dieser Danksagung, dieser Doktorarbeit und dieser gesamten Promotion soll den mir wichtigsten Menschen gehören: Ich danke von tiefsten Herzen meiner Familie, meinen Großeltern, meinen wundervollen, unterstützenden Eltern und meiner liebsten, kleinen Schwester. Danke, dass Ihr immer an mich glaubt, mich auf all meinen Wegen begleitet, mir alles ermöglicht und immer für mich da seid!

CURRICULUM VITAE

Personal Details

Name	Franziska Keßler
Date of Birth	21st February 1998
Place of Birth	Forst (Lausitz) – Germany

Education

since 07/2022	PhD student in Animal Breeding and Genetics University of Hohenheim, Stuttgart – Germany
2020 – 2022	Master of Science Agribusiness University of Hohenheim, Stuttgart – Germany
2016 – 2020	Bachelor of Science Agrarwirtschaft dual Hochschule Neubrandenburg, Neubrandenburg – Germany
2016 – 2018	Apprenticeship as a farmer Forst (Lausitz), Pritzwalk, Prenzlau – Germany
2016 – 2018	Abitur Friedrich-Ludwig-Jahn Gymnasium Forst Forst (Lausitz) – Germany

Practical Experience

01/2022 – 06/2022 & 12/2022 – 02/2023	Student assistant at the University of Hohenheim, Dpt. of Agricultural Markets
03/2021 – 04/2021	Internship in product management at Förster-Technik GmbH
03/2020 – 07/2020	Student assistant at the Agrargenossenschaft Forst eG
09/2019 – 01/2020	Student assistant at the Hochschule Neubrandenburg
07/2019 – 09/2019	Internship in calf expert team at the ForFarmers Beelitz GmbH

Stuttgart, 12.03.2025

Franziska Keßler

EIDESSTATTLICHE VERSICHERUNG

Eidesstattliche Versicherung über die eigenständig erbrachte Leistung

gemäß § 18 Absatz 3 Satz 5 der Promotionsordnung der Universität Hohenheim für die Fakultäten Agrar-, Natur- sowie Wirtschafts- und Sozialwissenschaften

1. Bei der eingereichten Dissertation zum Thema

   Breeding for resilient cows

   handelt es sich um meine eigenständig erbrachte Leistung.
2. Ich habe nur die angegebenen Quellen und Hilfsmittel benutzt und mich keiner unzulässigen Hilfe Dritter bedient. Insbesondere habe ich wörtlich oder sinngemäß aus anderen Werken übernommene Inhalte als solche kenntlich gemacht.
3. Ich habe nicht die Hilfe einer kommerziellen Promotionsvermittlung oder -beratung in Anspruch genommen.
4. Die Bedeutung der eidesstattlichen Versicherung und der strafrechtlichen Folgen einer unrichtigen oder unvollständigen eidesstattlichen Versicherung sind mir bekannt.

Die Richtigkeit der vorstehenden Erklärung bestätige ich. Ich versichere an Eides Statt, dass ich nach bestem Wissen die reine Wahrheit erklärt und nichts verschwiegen habe.

Stuttgart, 12.03.2025

Ort, Datum	Unterschrift

PUBLIKATION | 2025