UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

A phenotypic and genetic analysis of claw lesions in Total Mixed Ration Holstein cattle herds in South Africa

by

Robyn Clair Joubert

submitted in fulfilment of the requirements for the degree
PHILOSOPHIAE DOCTOR (ANIMAL SCIENCE)

in the Faculty of Natural and Agricultural Sciences
University of Pretoria
Pretoria

November 2024

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

SUPERVISORY COMMITTEE

Prof. E. van Marle-Köster University of Pretoria
Department of Animal and Wildlife Sciences
Pretoria
Hatfield
0002
South Africa

Dr Bernice Moster SA Stud Book and Animal Improvement Association
Bloemfontein
9301
South Africa

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

DECLARATION

I, Robyn Clair Joubert, declare that this dissertation, which I hereby submit for the degree PhD Animal Science at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at this or any other tertiary institution.

SIGNATURE:

DATE: 29 November 2024

ACKNOWLEDGEMENTS

The journey to this point has been long … so long that I find it almost impossible to even start creating a list of all the people that have helped me over the years. So let me start by thanking my Heavenly Father, for without Him, none of this would have been possible and I know that He is the one that put all the angels on my path along the way, each at exactly the right time.

There are three angels in particular that stand out, that have been a part of the journey from the very beginning to the end – my mom, Sue, my husband, Stoffel, and my supervisor, Esté. You three have believed in me and supported me every step of the way, even when it looked like the journey may be never-ending. I don't know how to thank you for everything that you have done! Thank you for late night debates and early morning meetings, for a quiet house and a calm heart, and for pushing me to keep on keeping on. You have been my rocks, my anchors, and my greatest inspiration. I also want to mention our children, Amelia and Ruben, who, while not often contributing to the quiet house, certainly gave me many, many joyful moments along the way and reminded me to always appreciate the truly important things in life.

My family has provided endless encouragement throughout this journey, starting with my grandparents, John and Denise, who paved the way at the very beginning – I am forever grateful to you both for setting such a beautiful example of unconditional love. To all – and I mean all – of the Catos, Punnetts, Jouberts, Meyers, Baxters, and Scheepers', none of the mini-milestone celebrations, good luck messages, sympathetic hugs, and shared prayers have gone unnoticed. Your support has meant the world to me.

I owe a huge debt of gratitude to my boss, Terry, for creating the space and opportunity for me to fulfil this lifelong dream – very patiently, I might add – and my team at Chemuniqué for their support during one too many 'PhD weeks'. I would also like to thank my co-supervisor, Dr Bernice Mostert, for her guidance, particularly regarding the genetic analyses, and Prof. Donagh Berry for being a practical soundboard whenever I got lost in the data.

I am grateful to those who gave up their time to help with this project, lending a helping hand with everything from data input and interpretation of coding language, to participating in many a scientific discussion and deliberation: Danielle Alberts, Jani de Vos, Jason Reding, Lize Erasmus, Simon Lashmar, and Storm Sanderson, as well as to all the participating farmers and the hoof trimmer, specifically Gert van Zyl and Lizetter Meyer, for allowing access to their data.

To the statisticians at the University of Pretoria, particularly Dr Strydom and Mr Masenge, thank you for your patience and for making statistical analysis more enjoyable than I thought was possible.

There have been many other friends, family, and colleagues that have contributed to this work: Prof. Nanette, my original muse, Mr Bloem, the data wizard, Kyle Venter, my p-value person, and my PC friends, Jackie, Richardt, and Alex, who have played a huge role in supporting this dream over the years.

This PhD was partially funded by Milk SA and made use of genotypes created in the Dairy Genomic Programme, which was funded by the Technology Innovation Agency, and I am truly grateful to these institutions for their contributions.

EXECUTIVE SUMMARY

Claw lesions represent a substantial health and welfare issue in South African Holstein cattle, particularly in herds managed intensively under total mixed ration (TMR) systems. The motivation for this study began with the necessity to understand both the prevalence and the genetic factors that contribute to this issue, aiming to enhance animal welfare and optimise herd management practices, including preventative hoof trimming. The thesis is presented in six chapters, starting with a general introduction and motivation, followed by a comprehensive review of available literature on claw health in dairy cattle, identifying key phenotypic traits and genetic markers associated with claw lesions. Chapters three to five were prepared in article format, with Chapter 3 published in *Tropical Animal Health and Production*, Chapter 4 currently under review by *Archives Animal Breeding*, and Chapter 5 prepared for submission to the *South African Journal of Animal Science*. The final chapter summarises the results of the study in comparison to previously published research in this area, aiming to identify gaps that future research should address, as well as offer suggestions to the dairy industry regarding the improvement of claw lesions in South African dairy animals.

ABSTRACT

Lameness due to claw lesions is a major hurdle for sustainable dairy production worldwide. Hoof trimming is used as a preventative measure, and key to future improvement strategies, providing phenotypic records for genetic interventions. This study aimed to evaluate hoof-trimming data in South African Holstein herds in total mixed ration (TMR) systems to determine the prevalence of claw lesions, investigate phenotypic and genetic parameters thereof, and explore the use of genomic information to provide insight into the underlying genetic architecture of claw lesion traits. Routine hoof-trimming appointments to five dairy herds in the central region of South Africa over a 10-year period, together with genotypes generated during the South African Dairy Genomic Programme provided the data for this study. More than 50% of cows presented with a lesion on any one foot, with digital dermatitis (DD) as the most commonly recorded lesion, followed by the non-infectious lesions sole ulcers (SU), sole haemorrhage (SH), and white line (WL) lesions, most of which occurred in the rear feet. The relationships between housing systems, individual feet, and the different lesions was analysed using chi-square tests as well as correspondence analysis (CA); SU and SH were strongly associated with each other, as were DD and interdigital phlegmon (IP), and SH and WL. These associations between lesions could be used to inform a more simplified approach to lesion recording systems, and contribute to practical prevention strategies on-farm. Phenotypic correlations between individual lesions and groups (infectious, non-infectious, and total lesions) were investigated using Spearman correlation tests. Moderate to strong relationships were observed among non-infectious lesions SH, SU, and WL (0.425–0.576), with the occurrence of SU and WL being strongly positively associated with total non-infectious lesions (0.543–0.576). Similarly, the infectious lesion DD was positively correlated with total infectious lesions (0.984). The estimated heritability of lesion categories varied between 0.008 for total lesions to 0.05 for the total non-infectious lesions category. A genome-wide association study for non-infectious lesions was performed using EMMAX, leading to the identification of one genome-wide significant single nucleotide polymorphism (SNP) and 15 genome-wide suggestive SNP. Candidate genes associated with the significant SNP on chromosome 25 related to abnormal skin morphology, immunity, and inflammation. From the literature, and this study, it is clear that claw lesions are highly polygenic. Differences among definitions and descriptions add to the complexity of the analyses. This study represents the first attempt to investigate claw lesions in South Africa using a combination of phenotypic and genetic data. The results confirmed the lack of adequate phenotypic data for genetic and genomic analyses, due to a lack of consistent farmer recording as well as a lack of coherence among data recording systems. Underlying genetic variability was confirmed and holds potential for further research but this requires consistent and complete phenotypic claw data. The prevalence of lameness remains high and a simplified and standardised recording system will be a first step in improving participation in national recording schemes for applicable research to reduce the incidence of this painful and costly disorder.

THESIS OUTPUTS

Published in peer-reviewed journals

Joubert, R.C., Strydom, H.F., Van Marle-Köster, E., 2024. Routine hoof-trimming data provides insight into the occurrence of claw lesions in Holstein herds in the central region of South Africa. *Tropical Animal Health and Production* 55:395. https://doi.org/10.1007/s11250-023-03814-x

Submitted for publication in peer-reviewed journals

Joubert, R.C., Moster, B.E., Masenge, A., Van Marle-Köster, E., 2024. Phenotypic and genetic analyses of claw lesions in TMR Holstein herds in South Africa.

International congresses

Joubert, R.C., Strydom, H.F., Van Marle-Köster, E., 2023. 316 Routine Claw Trimming Data Provides Insight into the Occurrence of Claw Lesions Holstein Herds in the Central Region of South Africa. *Journal of Animal Science*, *ASAS Annual 2023 Meeting Abstracts* 101(3):250–251.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

ADHB	Agriculture and Horticulture Development Board
ARC	Agricultural Research Council
avg.	average
AX	axial fissure
BCS	body condition score
BLUP	best linear unbiased prediction
CA	correspondence analysis
CC	corkscrew claw
DALRRD	Department of Land Reform and Rural Development
DD	digital dermatitis
DDID	digital and interdigital dermatitis
DGP	Dairy Genomic Programme
DL	dirt lot
DMI	dry matter intake
EFSA	European Food Safety Authority
FAO	Food and Agriculture Organization of the United Nations
FS	free-stall
GWAS	genome-wide association study
HE	heel erosion
HG	hardship groove
ICAR	International Committee on Animal Recording
ID	interdigital dermatitis
IH	interdigital hyperplasia
IL	infectious lesions
ILC	International Lameness Committee
IP	interdigital phlegmon
LRT	likelihood ratio test
LT	lameness treatment
MAF	minor allele frequency
NL	non-infectious lesions
OECD	Organisation for Economic Co-operation and Development
QTL	quantitative trait loci
SH	sole haemorrhage
SNP	single nucleotide polymorphism
SU	sole ulcer
temp.	temperature
TL	total lesions
TMR	total mixed ration
TS	thin sole
TU	toe ulcer
UK	United Kingdom
US	United States
VF	vertical fissure
WL	white line
WLDS	white line disease and separation

CHAPTER 1

GENERAL INTRODUCTION AND MOTIVATION FOR STUDY

1 General introduction and motivation for study

1.1 Introduction

As the fourth-largest agricultural sector in South Africa, dairy production contributes significantly to food security and has an important role in creating employment and income (DALRRD, 2021). According to Statistics South Africa, results of Census 2022 showed that the population of South Africa was 62 million (Statistics SA, 2023), and the United Nations report, *World Population Prospects 2022*, projects that the population of sub-Saharan Africa will double by 2050. Nutritional demand, including the demand for milk and dairy products, is increasing as a result of population growth, increasing incomes, and dietary changes (OECD/FAO, 2022). The dairy industry is facing several challenges to meet the increased demand in a responsible and sustainable manner.

Numerous technologies have enabled the dairy cattle industry worldwide to be highly advanced with regard to breeding and genetics (Miglior *et al.*, 2017; Visser *et al.*, 2020). Artificial insemination revolutionised the animal breeding industry (Lidder & Sonnino, 2011; Fleming *et al.*, 2018), having a major impact on the dissemination of semen around the world and, due to semen being stored, provided a DNA repository for the establishment of reference populations for genomic evaluations (Lidder & Sonnino, 2011). Since the development of milk recording schemes, progeny testing, and selection tools such as best linear unbiased prediction (BLUP), the dairy industry worldwide has been characterised by significant progress, especially in production traits such as milk yield (Brotherstone & Goddard, 2005, Moore & Hasler, 2017).

In South Africa, approximately 600 000 lactating cows make up the national commercial dairy herd (Van Heerden, 2024), with the Holstein breed making up the majority (Banga *et al.*, 2014). Farmers in the dairy cattle industry primarily utilise two production methods, either the total mixed ration (TMR) system, or a management system based on pasture. TMR management, including free-stall and dirt-lot systems, is more popular in the inland regions of the country (including Limpopo, Gauteng, and the Free State), while coastal dairy farms in KwaZulu-Natal and the Eastern Cape are mostly pasture-based (Meissner *et al.*, 2013; Ducrocq *et al.*, 2022). The Western Cape generally represents a mixture of TMR and pasture-based systems. Despite the fact that the number of milk producers in South Africa decreased by 44% between January 2017 and January 2023 (from 1 583 to 891), total milk production increased by 2,9% (from 3 254 000 t to 3 350 000 t) over the same period (Milk SA, 2023). Internationally, and in South Africa, more cattle on fewer farms are characterised by increased productivity per animal due to improvements in nutrition and management, as well as genetic selection for milk yield, although this often also leads to an increase in the incidence of health-related welfare traits such as claw disorders and a negative effect on cow longevity (Barkema *et al.*, 2015; Muller & de Waal, 2016; Afonso *et al.*, 2020).

Animal health and longevity have always been a challenge for dairy farmers, as sick cows are less profitable compared to healthy cows due to lower milk yield, decreased fertility, increased labour and veterinary costs, and higher culling rates (Von Keyserlingk *et al.*, 2009; Cole & Van Raden, 2018). Over the past decade, ethical concerns surrounding farming methods have made animal production systems the focus of increased public scrutiny (Barkema *et al.*, 2015; Clark *et al.*, 2016; Cole & Van Raden, 2018). Consumers are becoming increasingly aware of where food comes from, and strong opinions regarding animal welfare and sustainable production means some consumers are willing and able to adjust their spending to suit their beliefs (Clark *et al.*, 2016; Stygar *et al.*, 2021). In addition, regulatory agencies demand the reduction of routine drug use for the welfare of food-producing animals and human consumption of animal products such as dairy (Barkema *et al.*, 2015; Egger-Danner *et al.*, 2015; Cole & Van Raden, 2018). Genetic improvement

of functional traits may reduce the use of antibiotics while increasing cow well-being (Egger-Danner *et al.*, 2015; Rexroad *et al.*, 2019). Divergent views of dairy producers and consumers, as well as between other stakeholders like researchers and policymakers, on whether animal welfare is an economically or socially important issue adds to the lack of progress in solving the problem. Improvements are more likely to be realised if animal welfare can be integrated within a broader concept of quality or sustainability and recognised to be interdependent, with mutual responsibility towards an improved, shared fate (Henchion *et al.*, 2022; Verbeke, 2023).

Production and health traits have successfully been included in genetic evaluations for dairy cattle, but improving welfare traits is more challenging due to constraints in effective routine recording and the low heritability of these traits (Miglior *et al.*, 2017; Visser *et al.*, 2020; Erasmus & Van Marle-Köster, 2021). In dairy herds globally, lameness, mastitis, and reproductive disorders are the highest-ranked health conditions in frequency and cost and are listed as the most important reasons for involuntary culling (Sadiq *et al.*, 2020, Barden, 2022). In addition to being a production-limiting condition, lameness in dairy cattle is widely regarded as one of the most important welfare issues that needs to be addressed as it undermines every one of the Five Freedoms of Animal Welfare (Ramanoon *et al.*, 2018, Barden, 2022).

The most frequent reason for lameness in dairy cattle is the occurrence of lesions on the animals' claw(s) (Van Nuffel *et al.*, 2015). Novel phenotypes relating to these traits need to be included in breeding objectives and a large number of accurate phenotypic recordings are required for genetic evaluations and accurate selection (Holmberg, 2007; Miglior *et al.*, 2017). In order to remain competitive and relevant, the South African dairy industry must meet the criteria for sustainable production regarding welfare of dairy animals. While genetic and genomic selection for the enhancement of health-related welfare traits presents considerable potential, it requires the acquisition of more phenotypic data (Barkema *et al.*, 2015; Visser *et al.*, 2020).

1.2 Motivation and aim of study

The *Journal of Dairy Science* published a special issue in 2017 to highlight 100 years of scientific and technical progress in dairy science (McNamara & Lucy, 2017). In several of these 100-year review articles, the most important challenges relate to functional traits that require solutions for improving cow health and welfare, including lameness and claw health traits (Miglior *et al.*, 2017; Von Keyserlingk & Weary, 2017). Similar to dairy production in the rest of the world, these are also the challenges for South African dairy farmers that require attention and solutions. In addition, even though the interest in health and welfare traits has increased, many herd management systems do not ensure that data capture for health and welfare-related traits is consistent and accurate, which leads to large variability in the accuracy of incidence reporting (Egger-Danner *et al.*, 2015; Donnely *et al.*, 2023). Despite growing awareness of how lameness affects animal welfare and productivity, and the fact that its primary causes have not changed in the last three decades, the prevalence of lameness in dairy herds has continued to escalate to unacceptable levels (Bell *et al.*, 2022; Mülling *et al.*, 2024).

Among functional traits, feet and leg problems, including claw lesions, are the most frequent reasons for involuntary culling (Egger-Danner *et al.*, 2015; Ring *et al.*, 2018). Lameness due to claw disorders causes dairy cows significant distress, discomfort, and pain, which has serious implications on animal welfare (Whay & Shearer, 2017; Sadiq *et al.*, 2019) and a profound effect on production and herd efficiency as a result of reduced milk yield, decreased reproductive performance, and increased involuntary culling (Afonso *et al.*, 2020; Bell *et al.*, 2022).

In South Africa, Du Plessis (2007) reviewed foot health in housed cattle, Mhlongo (2019) published the first article on the prevalence of claw lesions, and Van Marle-Köster *et al.* (2020) investigated the possibility of using hoof-trimming data to improve claw health. Other than these, claw health has not been investigated locally. In South Africa, a claw lesion database is largely unavailable in dairy operations, which is why one of the first objectives of the present study is to capture claw lesion records from several Holstein herds operating in a TMR system and establish a database to demonstrate how such data can be used to improve our understanding of how, why, and when claw lesions occur as an important measure to manage lameness and to estimate the genetic parameters of these traits.

One of the most significant challenges that currently confronts the dairy industry is the need to minimise both the prevalence and impact of claw lesions (Ring *et al.*, 2018; Sadiq *et al.*, 2020), but the diversity in their definitions, diagnosis, and recording makes this a complex problem to solve (Charfeddine & Pérez-Cabal, 2017; Afonso *et al.*, 2020). Data capturing methods can differ vastly both between and within countries and data is recorded by a number of different role players in the industry, including producers, consultants, veterinarians, and para-professionals such as hoof trimmers (Van Nuffel *et al.*, 2015). In addition, lameness levels recorded by the farmer may differ greatly from those recorded by trained professionals such as hoof trimmers (Heringstad *et al.*, 2018; Bell *et al.*, 2022). Standardising the system of claw lesion diagnosis and recording will provide the necessary data to identify lesions that occur most frequently in dairy cattle, enhancing our understanding of how these lesions impact herd performance. (DeFrain *et al.*, 2013).

Despite the challenges in measuring functional traits such as lameness, breeding for these traits is crucial for the overall welfare and productivity of dairy cattle (Miglior *et al.*, 2017). DNA markers, particularly single nucleotide polymorphisms (SNP), have a great variety of applications in genetics research and diagnostics (Van Marle-Köster & Nel, 2003; Wiggans *et al.*, 2017). While traditional selection in dairy cattle has been successful in improving milk production traits without the use of DNA markers, there has been limited progress in improving functional traits. Genomic information is valuable in studying the genetic mechanisms that underlie specific traits (Vukasinovic *et al.*, 2017). Recent developments over the past two decades and the availability of genomic technologies provide the opportunity to improve production efficiency to meet the increased demand for dairy, while simultaneously addressing the need for genetic improvement in welfare traits. The use of genomics in animal breeding has two main objectives – improving the accuracy of breeding value estimation and allowing for the inclusion of novel functional traits such as claw lesions (Cole & Van Raden, 2018; Fleming *et al.*, 2018). It is for these lowly heritable and difficult-to-measure traits that genomic data holds the most potential to provide insight into the genetic base and provide direction for genetic management and improvement (Egger-Danner *et al.*, 2015; Abdelsayed *et al.*, 2017).

1.3 Aim of the study

This study aimed to assess claw lesions in South African Holstein cattle through analyses of available hoof-trimming data from TMR herds in the central region of South Africa. The investigation included investigation of phenotypic trait associations and genetic parameters for infectious and non-infectious claw lesions. The objectives were as follows:

1. Assessment of routine claw-trimming data to provide insight into the occurrence and recording of claw lesions in these herds.
2. Phenotypic and genetic analyses of claw lesions using pedigree records and available hoof-trimming data.
3. Performing genome-wide association studies (GWAS) on claw lesions to identify genomic regions associated with incidence of different types of claw lesions.

References

Afonso, J.S., Bruce, M., Keating, P., Raboisson, D., Clough, H., Oikonomou, G., Rushton, J., 2020. Profiling detection and classification of lameness methods in British dairy cattle research: A systematic review and meta-analysis. *Front. Vet. Sci*. 7:542. https://doi.org/10.3389/fvets.2020.00542

Banga, C.B., Neser, F.W.C., Garrick. D.J., 2014. Breeding objectives for Holstein cattle in South Africa. *S. Afr. J. Anim. Sci.* 44(3):199–214. http://dx.doi.org/10.4314/sajas.v44i3.1

Barden, M., 2022. Genetic and metabolic aspects of claw horn lesion aetiopathogenesis in Holstein cows. PhD thesis, University of Liverpool.

Barkema, H.W., von Keyserlingk, M.A.G., Kastelic, J.P., Lam, T.J.G.M., Luby, C., Roy, J.-P., LeBlance, S.J., Keefe, G.P., Kelton, D.F., 2015. Invited review: Changes in the dairy industry affecting dairy cattle health and welfare. *J. Dairy Sci.* 98(11):7426–7445. https://doi.org/10.3168/jds.2015-9377

Bell, N., Bacon, D., Craven, E., Crowe, S., Newsome, R., Oikonomou, G., Pedersen, S., Reader, J., Wilson, J., 2022. Dairy cattle lameness: A roundtable discussion. *Livestock* 27(Sup3):S1–S11. https://doi.org/10.12968/live.2022.27.S1.115

Brotherstone, S. & Goddard, M., 2005. Artificial selection and maintenance of genetic variance in the global dairy cow population. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 360(1459):1479–1488. https://doi.org/10.1098/rstb.2005.1668

Charfeddine, N. & Pérez-Cabal, M.A., 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100(1):653–665. https://doi.org/10.3168/jds.2016-11434

Clark, B., Stewart, G.B., Panzone, L.A., Kyriazakis, I., Frewer, L.J., 2016. A systematic review of public attitudes, perceptions and behaviours towards production diseases associated with farm animal welfare. *J. Agric. Environ. Ethics* 29(3):455-478. https://doi.org/10.1007/s10806-016-9615-x

Cole, J.B. & van Raden, P.M., 2018. Symposium review: Possibilities in an age of genomics: The future of selection indices. *J. Dairy Sci.* 101(4):3686–3701. https://doi.org/10.3168/jds.2017-13335

DALLRD, 2021. A profile of the South African dairy market value chain. http://webapps1.daff.gov.za/AmisAdmin/upload/Dairy%20Market%20Value%20Chain%20Profile%202021.pdf. Accessed 23 October 2024.

DeFrain, J.M., Socha, M.T., Tomlinson, D.J., 2013. Analysis of foot health records from 17 confinement dairies. *J. Dairy Sci.* 96(11):7329–7339. https://doi.org/10.3168/jds.2012-6017

Donnely, M.R., Hazel, A.R., Hansen, L.B., Heins, B.J., 2023. Health Treatment Cost of Holsteins in Eight High-Performance Herds. *Anim.* 13:2061. https://doi.org/10.3390/ani13132061

Ducrocq, V., Cadet, A., Patry, C., van der Westhuizen, L., van Wyk, J.B., Neser, F.W.C., 2022. Two approaches to account for genotype-by-environment interactions for production traits and age at first calving in South African Holstein cattle. *Genet. Sel. Evol.* 54:43. https://doi.org/10.1186/s12711-022-00735-5

Du Plessis, I., 2007. Foot health in housed cattle: A review. *S. Afr. J. Anim. Sci.* 8:11–17.

Egger-Danner, C., Cole, J.B., Pryce, J.E., Gengler, N., Heringstad, B., Bradley, A., Stock, K.F., 2015. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Anim.* 9(2):191–207. https://doi.org/10.1017/S1751731114002614

Erasmus, L. & van Marle-Köster, E., 2021. Moving towards sustainable breeding objectives and cow welfare in dairy production: a South African perspective. *Trop. Anim. Health Prod.* 53: 470. https://doi.org/10.1007/s11250-021-02914-w

Fleming, A., Abdalla, E.A., Maltecca, C., Baes, C.F., 2018. Invited review: Reproductive and genomic technologies to optimize breeding strategies for genetic progress in dairy cattle. *Arch. Anim. Breed.* 61(1):43–57. https://doi.org/10.5194/aab-61-43-2018

Henchion, M.M., Regan, Á., Beecher, M., MackenWalsh, Á., 2022. Developing 'smart' dairy farming responsive to farmers and consumer-citizens: A review. *Anim.* 12 (360). https://doi.org/10.3390/ani12030360

Heringstad, B., Egger-Danner, C., Charfeddine, N., Pryce, J.E., Stock, K.F., Kofler, J., Sogstad, A.M., Holzhauer, M., Fiedler, A., Müller, K., Nielsen, P., Thomas, G., Gengler, N., de Jong, G., Ødegård, C., Malchiodi, F., Miglior, F., Alsaaod, M., Cole, J.B., 2018. Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *J. Dairy Sci.* 101(6):1–21. https://doi.org/10.3168/jds.2017-13531

Holmberg, M., 2007. Genetic dissection of functional traits in dairy cattle. Doctoral dissertation. ISSN 1652-6880, ISBN 978-91-576-7391-6.

Lidder, P. & Sonnino, A., 2011. Current status of biotechnologies for the management of crop genetic resources. In: Lidder P, Sonnino A (Eds.) *Biotechnologies for the management of genetic resources for food and agriculture*, FAO.

McNamara, J.P. & Lucy, M.C., 2017. *Journal of Dairy Science* Volume 100 Special Issue: Introduction. *J. Dairy Sci.* 100(12):9892–9893.

Meissner, H.H., Scholtz, M.M., Palmer, A.R., 2013. Sustainability of the South African Livestock Sector towards 2050. Part 1: Worth and impact of the sector. *S. Afr. J. Anim. Sci.* 43(3), 282–297. http://dx.doi.org/10.4314/sajas.v43i3.5

Mhlongo, N.L., 2019. Evaluation of claw health of dairy cattle housed in dirt lot vs free stall in TMR systems in the central region of South Africa. Dissertation (MSc (Agric)), University of Pretoria.

Miglior, F., Fleming, A., Malchiodi, F., Brito, L.F., Martin, P., Baes, C.F., 2017. A 100-Year Review: Identification and genetic selection of economically important traits in dairy cattle. *J. Dairy Sci.* 100:10251–10271. https://doi.org/10.3168/jds.2017-12968

Milk SA, 2023. *Lacto Data* 26, June 2023.

Moore, S.G. & Hasler, J.F., 2017. A 100-Year Review: Reproductive technologies in dairy science. *J. Dairy Sci.* 100:10314–10331. https://doi.org/10.3168/jds.2017-13138

Muller, C.J.C. & de Waal, H.L., 2016. The effect of herd structure on the performance of dairy herds. *ARC News Letter Article*, Western Cape.

Mülling, C.K.W., 2024. Looking at their feet: A long and ongoing journey towards understanding lameness. In: *Proceedings of the 22nd International Symposium and 14th International Conference on Lameness in Ruminants*, 16–20 September 2024, Venice.

OECD/FAO, 2022. *OECD-FAO Agricultural Outlook 2022-2031*, OECD Publishing, Paris. https://doi.org/10.1787/f1b0b29c-en

Oehm, A.W., Knubben-Schweizer, G., Rieger, A., Stoll, A., Hartnack, S., 2019. A systematic review and meta-analyses of risk factors associated with lameness in dairy cows. *BMC Vet. Res.* 15:346. https://doi.org/10.1186/s12917-019-2095-2

Ramanoon, S.Z., Sadiq, M.B., Shaik Mossadeq, W.M., Mansor, R., Syed-Hussain, S.S., 2018. The impact of lameness on dairy cattle welfare: Growing need for objective methods of detecting lame cows and assessment of associated pain. *Animal Welfare.* http://dx.doi.org/10.5772/intechopen.75917

Rexroad, C. , Vallet, J., Matukumall, L.K., Reecy, J., Bickhart, D., Blackburn, H., Boggess, M., Cheng, H., Clutter, A., Cockett, N., Ernst, C., Fulton, J.E., Liu, J., Lunney, J., Neibergs, H., Purcell, C., Smith, T.P.L., Sonstegard, T., Taylor, J., Telugu, B., van Eenennaam, A., van Tassell, C.P., Wells, K., 2019. Genome to Phenome: Improving Animal Health, Production, and Well-Being – A New USDA Blueprint for Animal Genome Research 2018–2027. *Front. Genet.* 10:327. https://doi.org/10.3389/fgene.2019.00327

Ring, S.C., Twomey, A.J., Byrne, N., Kelleher, M.M., Pabiou, T., Doherty, M.L., Berry, D.P., 2018. Genetic selection for hoof health traits and cow mobility scores can accelerate the rate of genetic gain in

producer-scored lameness in dairy cows. *J. Dairy Sci.* 101(11), 10034–10047. https://doi.org/10.3168/jds.2018-15009

Sadiq, M.B., Ramanoon, S.Z, Mossadeq, W.M.S., Mansor, R., Hussain, S.S.S, 2019. Review: Dairy farmers' perceptions of and actions in relation to lameness management. *Anim.* 9(5):270. https://doi.org/10.3390/ani9050270

Sadiq, M.B., Ramanoon, S.Z., Mansor, R., Hussain, S.S.S., Mossadeq, W.M.S., 2020. Claw trimming as a lameness management practice and the association with welfare and production in dairy cows. *Anim.* 10(9):1515. https://doi.org/10.3390/ani10091515

Statistics SA, 2023. Census 2022. https://census.statssa.gov.za/#/. Accessed 6 November, 2024.

Stygar, A.H., Gómez, Y., Berteselli, G.V., Dalla Costa, E., Canali, E., Niemi, J.K., Llonch, P, Pastell, M., 2021. A Systematic Review on Commercially Available and Validated Sensor Technologies for Welfare Assessment of Dairy Cattle. *Front. Vet. Sci.* 8:634338. https://doi.org/10.3389/fvets.2021.634338. United Nations, 2022. United Nations Department of Economic and Social Affairs, Population Division. *World Population Prospects 2022: Summary of Results*. UN DESA/POP/2022/TR/NO. 3.

Van Marle-Köster, E., Mhlongo, N.L, Tucker, J., 2020. Hoof trimming data for improving claw health in South African dairy cattle: Understanding claw health can improve cow comfort and welfare. In: *IDF Animal Health Report N° 14*. International Dairy Federation. https://shop.fil-idf.org/products/idf-animal-health-report-n-14. Accessed 25 March, 2023.

Van Marle-Koster, E. & Nel, L.H., 2003. Genetic markers and their application in livestock breeding in South Africa: A review. *S. Afr. J. Anim. Sci.* 33(1):1–10. https://hdl.handle.net/10520/EJC94317

Van Nuffel, A., Zwertvaegher, I., Pluym, L., van Weyenberg, S., Thorup, V.M., Pastell, M., Sonck, B., Saeys, W., 2015. Lameness Detection in Dairy Cows: Part 1. How to Distinguish between Non-Lame and Lame Cows Based on Differences in Locomotion or Behavior. *Animals* 5:838–860. https://doi.org/10.3390/ani5030387

Verbeke, W., 2009. Stakeholder, citizen and consumer interests in farm animal welfare. Anim. Welfare 18(4):325–333. https://doi.org/10.1017/S0962728600000725

Visser, C., van Marle-Köster, E., Myburgh, H., de Freitas, A., 2020. Phenomics for sustainable production in the South African dairy and beef cattle industry. *Animal Front.* 10(2):12–18. https://doi.org/10.1093/af/vfaa003

Von Keyserlingk, M.A.G., Rushen, J., de Passillé, A.M., Weary, D.M., 2009. Invited review: The welfare of dairy cattle—Key concepts and the role of science. *J. Dairy Sci.* 92(9):4101–4111. https://doi.org/10.3168/jds.2009-2326

Von Keyserlingk, M.A. & Weary, D.M., 2017. A 100-year review: Animal welfare in the Journal of Dairy Science—The first 100 years. *J. Dairy Sci.* 100(12):10432-10444. https://doi.org/10.3168/jds.2017-13298

Vukasinovic, N., Bacciu, N., Przybyla, C.A., Boddhireddy, O., DeNise, S.K., 2017. Development of genetic and genomic evaluation for wellness traits in US Holstein cows. *J. Dairy Sci*. 100:428–438. https://doi.org/10.3168/jds.2016-11520

Whay, H. & Shearer, J., 2017. The Impact of Lameness on Welfare of the Dairy Cow. *Vet. Clin. North Am. Food Anim. Pract*. 33:153–164. http://dx.doi.org/10.1016/j.cvfa.2017.02.008

Wiggans, G.R., Cole, J.B., Hubbard, S., Sonstegard, T.S., 2017. Genomic Selection in Dairy Cattle: The USDA Experience. *Annu. Rev. Anim. Biosci.* 5:309–327. https://doi.org/10.1146/annurev-animal-021815-111422

CHAPTER 2

LITERATURE REVIEW

2 Literature review

2.1 Introduction

Lameness is generally regarded as one of the most significant cow welfare issues that needs to be addressed in the dairy industry, and it is directly linked to claw health (Croué *et al.*, 2019; Garvey, 2022). Finding sustainable solutions to improve claw lesions is complicated due to the disparity of methods to identify, record, and manage these disorders (Oehm *et al.*, 2019; Afonso *et al.*, 2020). In addition to quantitative approaches, genomic information holds promise to understand the genetic mechanism and identifying genes related to claw disorders (Sölzer *et al.*, 2022).

This review will focus on the aetiology, risk factors, recording, and occurrence of claw lesions in Holstein cattle, as well as reviewing current knowledge regarding genetic investigations into claw health traits. The potential of genomics as a tool for finding solutions for future genetic improvement will also be discussed.

2.2 Claw lesions: Categorisation and risk factors

Although injuries to the nervous or musculoskeletal systems may play a role, lameness is primarily caused by lesions of the claw (Van Nuffel *et al.*, 2015; Charfeddine & Pérez-Cabal, 2017). In addition, there are a number of other factors that may have a negative effect on dairy cow locomotion, including flooring that is hard, wet, or slippery, cow age, and stage of gestation (Van Nuffel *et al.*, 2015). In this review, lameness is considered to include changes in locomotion as a result of painful claw lesions, which are classified into two categories according to their aetiology and pathogenesis. Infectious lesions include digital dermatitis (DD), interdigital dermatitis (ID), heel erosion (HE), and interdigital phlegmon or foot rot (IP). These generally affect the skin of the animal, and are influenced by environmental hygiene factors (Barden, 2022; Garvey, 2022). Non-infectious lesions are usually caused by mechanical and/or metabolic factors affecting the claw and include sole ulcer (SU), sole haemorrhage (SH), and white line disease (WL) (Buch *et al.*, 2011; Sadiq *et al.*, 2020).

As indicated in Figure 2.1, a complex combination of environmental and animal factors, together with the presence of certain microbial pathogens, contributes to the severity of claw disorders, which makes it particularly difficult to eradicate these in dairy herds (Randall *et al.*, 2015; Garvey, 2022). Infectious lesions tend to increase when cows' feet are exposed to wet or muddy environments, poor hygiene, and poor foot bath management. The risk factors that influence the development of non-infectious lesions include a lack of or improper claw trimming, poorly designed housing and/or flooring, nutritional factors, and the presence of post-calving metabolic disorders (EFSA, 2009; Garvey, 2022). In their meta-analysis, Oehm *et al.* (2019) reported five significant risk factors, including body condition score (BCS), overgrowth of the claw, stage of lactation, herd size, and parity, although more than 120 individual risk factors were identified. Many non-infectious claw lesions seem to be triggered by a low BCS, i.e. less than 2.5 (Oehm *et al.*, 2019, Barden, 2022). This often happens during early lactation, when cows mobilise adipose tissue (Randall *et al.*, 2015; Bell *et al.*, 2022). In addition, lame cows lie down more often and are less able to compete with herd mates at the feed bunk, leading to lowered feed intake, and a further decrease in BCS (Randall *et al.*, 2015). There likely exists a vicious cycle of association between lameness and BCS, with mutual causality being anecdotally reported (Oehm *et al.*, 2019; Bell *et al.*, 2022).

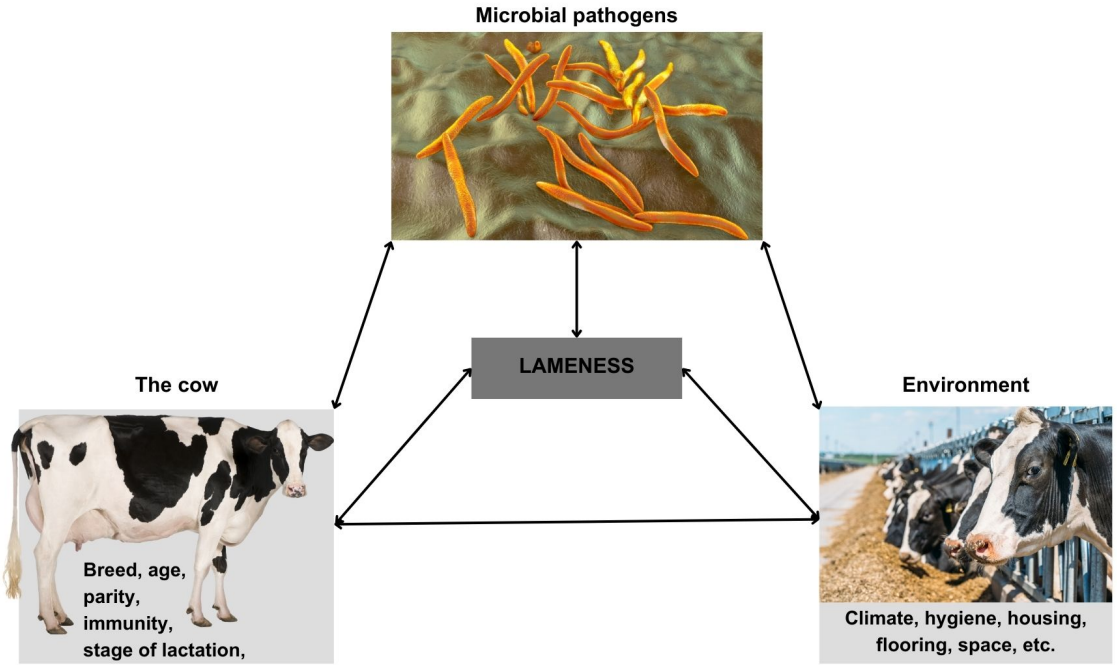


Figure 2.1 Factors contributing to claw lesions and lameness in dairy cattle, as adapted from Garvey (2022)

Overgrowth of the claw has a significant effect on the balance of weight-bearing within and between claws due to claw horn being produced faster than it is worn down, predisposing cows to SU and WL, especially in the hind limb claws. Claw overgrowth is promoted by exposure of cows to solid surfaces such as concrete (Shearer & Van Amstel, 2007, Barden, 2022).

Cows tend to have the highest risk of lameness during the first third of lactation, likely as a result of changes in their environment and nutrition during the transition period (Oberbauer *et al.*, 2013; Oehm *et al.*, 2019). Infectious lesions are generally predominant in early lactation, with the incidence of DD and IP being greatest during the first 60 days of lactation, while the incidence of non-infectious lesions tends to follow a typical lactation curve (DeFrain *et al.*, 2013). An investigation by Solano *et al.* (2016) further evaluated the claw lesion prevalence across different stages of lactation and parity. They found that the prevalence of DD was higher in first-lactation cows in mid- and late-lactation, whereas multiparous cows showed the greatest incidence at peak lactation. They also reported that cows had higher odds of SU and WL later in lactation, regardless of parity.

The association between claw lesions and parity has been well reported in the literature (Weber *et al.*, 2013; Solano *et al.*, 2016). The ratio of infectious to non-infectious lesions decreases as lactation number increases (DeFrain *et al.*, 2013). Older cattle tend to present with higher incidence of non-infectious lesions, potentially due to wear and tear on claws that accumulates as cows age (Van der Waaij *et al.*, 2005; Cook & Nordlund, 2009), while they experience a lower incidence of DD, possibly as a result of developing immunity to specific pathogen challenges over time (Somers *et al.*, 2005; Chapinal *et al.*, 2013).

There is a complex relationship between animal welfare and the size of the herd, affected by many factors, including management, rate of herd expansion, and the staff complement. Although a limited number of studies have thoroughly examined the impact of herd size on animal health and welfare, Barker *et al.* (2009) reported that larger herds had an increased risk for developing claw disorders, while Barkema *et al.* (2015) reported an inconsistent association between herd size and animal welfare. Equivocal results regarding the

association between lameness and herd size were also reported by Oehm *et al.* (2019), although they concluded that individual animals in larger herds were more prone to lameness.

In addition to the factors discussed above, there are a multitude of other risk factors that contribute to claw lesions, including seasonal effects, housing and flooring effects, and the presence of certain lesions as a precursor to the development of others (Shearer & Van Amstel, 2007; Solano *et al.*, 2016). Infectious lesions tend to be more common during the cooler months of the year, while non-infectious lesions are more common during warmer months (Shearer & Van Amstel, 2007; DeFrain *et al.*, 2013). The occurrence of claw lesions may be related to surface properties of the floor and the duration of contact, as well as the presence of moisture, especially in the form of urine and faeces (Du Plessis, 2007; Cook & Nordlund, 2009). Abrasive concrete floors cause excessive wear on the claw, which results in the development of thin soles and toe ulcers (TU) (Shearer & Van Amstel, 2007). Although Somers *et al.* (2005) found no structural differences in claw horn growth and wear between cows kept on different floors, Solano *et al.* (2016) reported that the odds of developing SU and WL were more than two times higher in cows in free-stall housing systems versus those on deep-bedded packs. Confinement conditions limit cows to a smaller area and increase their exposure to hard walkways, manure slurry, and moisture, which predisposes them to developing infectious claw lesions (Shearer & Van Amstel, 2007, Cook & Nordlund, 2009). The presence of certain non-infectious lesions may make cows more susceptible to developing other claw lesions. Cows that present with interdigital hyperplasia (IH) have greater odds of developing DD and cows with other claw horn lesions have greater odds of developing WL (Solano *et al.*, 2016). In turn, cows with SH have higher odds of presenting with SU (DeFrain *et al.*, 2013; Solano *et al.*, 2016). The intricate interplay of internal and external risk factors adds to the challenge of developing effective solutions for improving claw health in dairy cattle.

2.3 Recording and management of claw lesions

Claw lesions present a complex problem to solve due to the diversity of approaches employed in trait definition and recording (Charfeddine & Pérez-Cabal, 2017; Afonso *et al.*, 2020). Regular claw trimming by trained professionals provides the most dependable data to describe claw health, although data from veterinarians, automated sensors, and other scoring protocols may also add useful information (Herinsgtad *et al.*, 2018).

Dairy producers need to be cognisant of how many lame cows are in their herd and how severely they are considered to be lame in order to address this issue. Identifying the underlying cause of the issue is critical in order for optimal management intervention (Somers & O'Grady, 2015; Afonso *et al.*, 2020). Locomotion scoring can be useful to assess the incidence of lameness, and there are several well-documented locomotion scoring systems (Shearer *et al.*, 2004; Van Nuffel *et al.*, 2015). In 2008, the dairy industry in the United Kingdom adopted the Dairy Mobility Scoring System developed by the Agriculture and Horticulture Development Board (AHDB) as the standard tool for assessing lameness. However, Afonso *et al.* (2020) found that investigators made use of several other methods as well. In the literature, approximately 20 different approaches to locomotion scoring have been identified, each differing with respect to their definition of lameness, gait characteristics, postures, and scales (Van Nuffel *et al.*, 2015; Oehm *et al.*, 2019). Since Manson & Leaver first described locomotion scoring in cattle in 1988 using a nine-point scale, at least 10 research teams have amended their original scoring system by adding and/or amending the visual indicators to look for. Locomotion scoring is deemed to be a useful indicator trait for susceptibility to claw disorders (Laursen *et al.*, 2009; Weber *et al.*, 2013). Most commonly applied system is that proposed by Sprecher *et al.* (1997) using a visual assessment of back posture and gait to score an individual on a scale of 1 to 5 (Table 2.1). Table 2.1 also indicates the estimated relationship of locomotion score to reduction in percentage dry matter intake (DMI) and milk yield, as reported by Robinson & Juarez (2003).

Table 2.1 Locomotion scoring by assessment of back posture and gait abnormalities and the effect on DMI and milk yield, as adapted from Sprecher et al. (1997) and Robinson & Juarez (2003)

Locomotion score (LS)	Description	Assessment	Reduction in DMI (%)	Reduction in milk yield (%)
1	Normal	Level back while standing and walking, normal gait	0	0
2	Mildly lame	Level back while standing, arched back while walking	2	1
3	Moderately lame	Rounded back while standing and walking, short-strided gait	5	3
4	Lame	Bent back while standing and walking, favouring of one or more limbs, deliberate gait	17	7
5	Severely lame	Bent back while standing and walking, severe aversion to bear weight on one or more limbs	36	16

Despite the existence of a standardised claw diagram developed by Shearer *et al.* (2002) that designates specific zones within the cattle claw and digit for the capture of lameness data in dairy herds (Figure 2.2), the various claw lesion identification systems used by claw trimmers tend to define lesions and their occurrence differently (Table 2.2). Many researchers fail to report sufficient detail regarding their assessment of claw health, locomotion, or lameness, even though these may have a significant impact on the scoring (Van Nuffel *et al.*, 2015; Charfeddine & Pérez-Cabal, 2017). Several meta-analyses have been performed in an attempt to pool data in this field of study; however, it is clear that the range of definitions, study designs, and data analysis hampers the industry's ability to compare results and assess the effectiveness of lameness management interventions (Afonso *et al.*, 2020; Sadiq *et al.*, 2020).

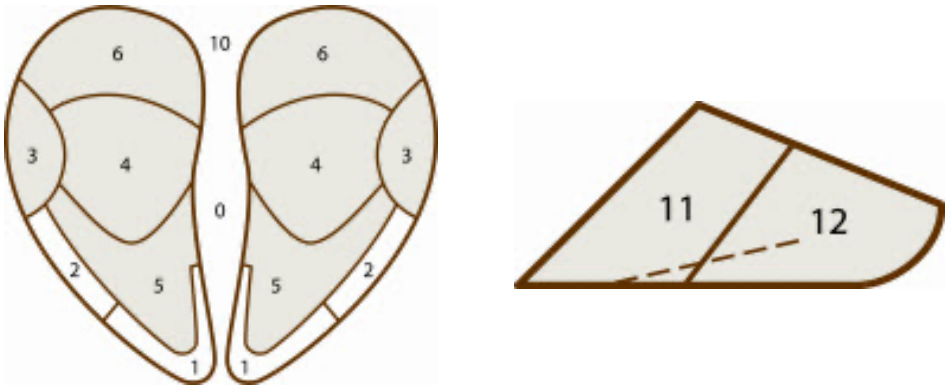


Figure 2.2 Standardised claw diagram designating specific claw zones for lesion recording: abaxial (outside) view (left), axial (inside) view (right). The dotted line represents the white line of the axial wall (Shearer et al., 2002)

Despite the economic impact of claw disorders being well reported (Cha *et al.*, 2010; Oberbauer *et al.*, 2013), the estimation of losses is done using different methodologies, and costs are split between direct and indirect costs, further complicating the process of evaluation (Assadi-Alamouti, 2022). Direct costs include treatment costs including the trimmer and veterinarian and the cost of discarded milk in the case of antibiotic withdrawal periods, and these are generally easy to quantify. Indirect costs include a reduction in milk yield, extension of the calving interval, and premature culling, and are often considered hidden costs because the farmer is not always aware of their magnitude (Ózsvári, 2017; Assadi-Alamouti, 2022).

The literature suggests that claw trimming is an important tool for the improvement of cow welfare through preventing and treating claw lesions (Heringstad *et al.*, 2018; Sadiq *et al.*, 2020). Several studies have investigated the association between production, welfare, and claw trimming; however, investigating the real effect of claw trimming is constrained by vague descriptions of the lesions and trimming methodology (Charfeddine & Pérez-Cabal, 2017; Oehm *et al.*, 2019).

In collaboration with the International Lameness Committee (ILC), Zinpro Corporation developed the *Claw Lesion Identification in Dairy Cattle* brochure in 2008, representing the first worldwide agreement on how to identify claw lesions, establish naming conventions, and implement record-keeping practices (Zinpro® Corporation, 2008). Two other common lesion identification systems have been identified. The *Bovine Hoof Lesion Identification and Severity Score Sheet* developed by Karl Burgi, Dörte Döpfer and Nigel B. Cook classifies claw lesions on a simple scale by grouping lesions together into six categories and then scoring them on severity (1 = mild, 2 = moderate, 3 = severe). The Functional Traits Working Group of the International Committee for Animal Recording (ICAR) developed the *ICAR Claw Health Atlas* in 2015, and updated it in 2020 (ICAR, 2020). In South Africa, three hoof trimmers provide this service to the dairy industry, each utilising one or a combination of these three systems (Table 2.2).

Claw lesions occur more frequently in the rear feet, primarily because these hooves are more exposed to moisture related to urine and faeces, along with experiencing increased strain on the rear limbs due to differences in anatomy when compared to the front limbs (Manske *et al.*, 2002; Chapinal *et al.*, 2013).

Lameness recorded on-farm by the producer often differs significantly from that recorded by trained professionals such as hoof trimmers (Sánchez-Molano *et al.*, 2019: Bell *et al.*, 2022). This is indicated by the wide variation in lameness prevalence reported in the literature – from 10% to over 80% (Somers & O'Grady, 2015; Croué *et al.*, 2019). Researchers agree that lameness is generally under-recorded by farmers by between 25% and 50%, and its importance in cow health and welfare, as well as farm profitability is also generally underestimated (Sadiq *et al.*, 2019; Ranjbar *et al.*, 2020).

The infectious lesions HE and IP as indicated in Table 2.2 are generally described similarly by these three systems (Figure 2.3), as are SU and WL, whereas the definitions of DD and TU differ significantly between the three systems. Sole fracture or heel ulcer occurs only in the ABC system, while CC and axial fissure are absent in that system but present in the other two.

Table 2.2 Comparison of different claw lesion identification recording systems for those claw lesions that are described in each of these three methodologies: ABC, ICAR, and ILC

Disorder (abbreviation)	Description (ABC chart)	Description (ICAR)	Description (ILC)
Heel erosion (E or HE), or heel horn erosion (HHE)	Starts as small pock marks of erosion and can develop to a large V-shaped fissure across the heel with multiple layers	V-shaped bulb erosion, sometimes extending to the corium	Irregular depressions or V-shaped erosion of the heel
Digital dermatitis (D or DD), or heel wart (HW)	Severity varies from small erosion between claws or in interdigital cleft to strawberry granulomas and/or ulceration	Infection of digital and/or interdigital skin, painful ulceration, hyperkeratosis	Hard, hairy, sores and growths that look like warts
Foot rot (F), or interdigital phlegmon (IP)	Starts as a slight separation of interdigital skin with little swelling and can develop to separation and severe swelling around coronary band	Painful, foul-smelling swelling of the foot with sudden lameness	Swelling of the foot with a noticeable foul odour
Axial fissure (X or AX), or axial horn fissure (HFA)		Vertical crack in the inner claw wall	Deep groove on the interior surface of the claw wall
Sole ulcer (S or U or SU)	Haemorrhage with exposure of the corium	Opening of the sole horn, possibly presenting a necrotic corium	Raw sore between the sole and heel on the inner side of the outside hind claw
Toe ulcer (T or TU)	Starts as a small fissure at the white line in the toe area and can develop into widespread necrosis of the corium in the toe	Ulcer on the toe	Rupture in the white line or sole at the toe
White line disease (W or WL)	Separation of the white line leading to an abscess and/or fissure extending to the coronary band	Separation of the white line	A rupture between the sole and the wall, sometimes with abscessation
Sole fracture (SF), or heel ulcer (HU)	Starts as a small fissure at the junction of the heel and sole and can lead to separation of a large area of the sole		
Corkscrew (C), or corkscrew claw (CC)		Torsion of inner or outer claw	Fast, uneven growth of the claw with rotation

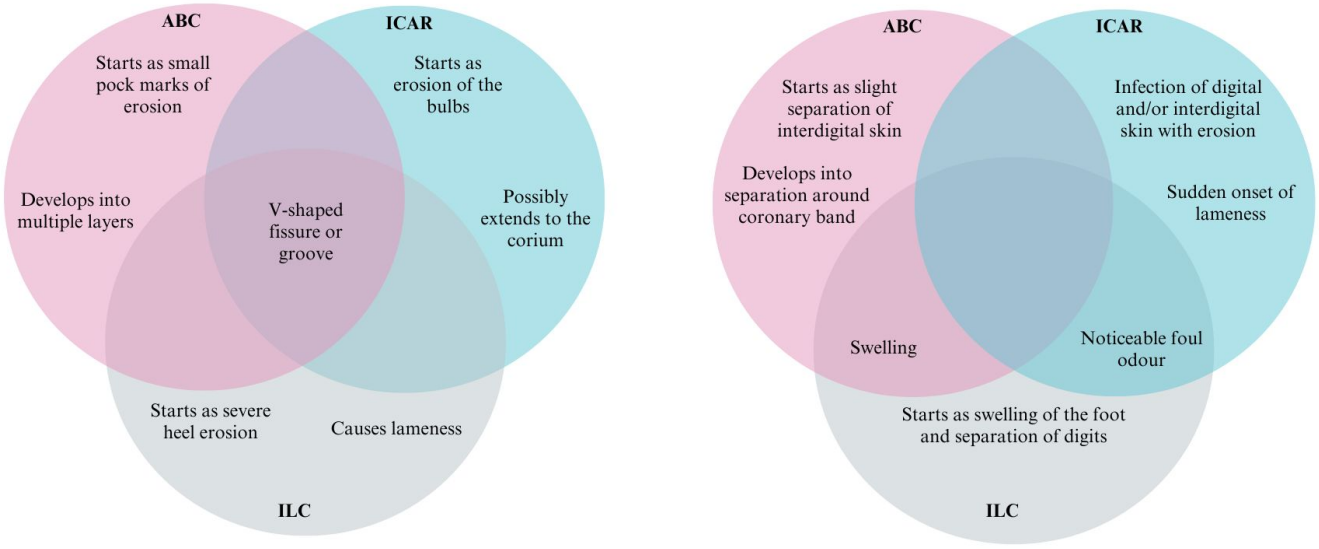


Figure 2.3 Venn diagrams illustrating the overlap in descriptions for heel erosion (left) and interdigital phlegmon (right) between three different claw lesion identification strategies

2.4 Phenotypic and genetic parameters

One of the major factors that has caused poor welfare in dairy cows must be the historic, long-term selection for production traits (EFSA, 2009). It is essential to integrate animal health and welfare traits into breeding programmes, with genetic selection being key to the sustained improvement of claw health in dairy cattle. (Heringstad *et al.*, 2018; Lai *et al.*, 2020).

The most prevalent lesions worldwide are DD, SU, and WL (Christen *et al.*, 2015; Shearer & Van Amstel, 2017). A number of researchers have attempted to investigate phenotypic associations between individual claw lesions and reported inconsistent results. Correlations between SH, SU, and WL vary from positive to negative (Van der Waaij *et al.*, 2005; Häggman & Juga, 2013), while some researchers have reported strong positive correlations between individual lesions as well (Capion *et al.*, 2009). Differences in results are mainly the result of differences in lesion categorisation and scoring methodology, and this adds a level of complication to the investigation.

Although the environment and management of animals notably influence the occurrence of claw lesions, variation can be observed between cows. The presence of adequate genetic variability in traits based on trimming data supports the feasibility of genetic evaluations to improve claw health (Chapinal *et al.*, 2013; Miglior *et al.*, 2017). Some international breeding programmes include lameness or predictor traits thereof such as claw lesions and conformation scores (Miglior *et al.*, 2005; Abdelsayed *et al.*, 2017; Ring *et al.*, 2018). However, genetic improvement in lameness is generally hampered by low heritability, with reports ranging from 0.0005 to 0.16 (Table 2.3), although the large variation in and poor quality of lameness recording probably means these have been underestimated (Afonso *et al.*, 2020; Bell *et al.*, 2022).

Claw disorders are generally scored as binary traits and analysed either by linear animal models, which ignore repeated incidence, or threshold models that take multiple occurrences into account (Chapinal *et al.*, 2015; Malchiodi *et al.*, 2017). More advanced models offer the advantage of increased use of the available

information, but linear modelling is often chosen because it is quick and easy, while largely providing similar results (Pérez-Cabal & Charfeddine, 2015; Heringstad *et al.*, 2018). **Table 2.3 summarises** the heritability estimates based on hoof-trimming data that have been reported for the most common claw disorders. These tend to vary depending on which model is used, with estimates from logistic and threshold models tending to be slightly higher than those from linear animal models (Heringstad *et al.*, 2018).

Table 2.3 Heritability estimates of claw disorders in Holstein cattle

Model	DD	ID	HE	IP	IH	SH	SU	WL
Linear								
Swalve *et al.*, 2008	0.08	0.09	-	-	-	-	0.07	0.05
Van der Spek *et al.*, 2013	0.04		-	-	0.14	0.02	0.03	0.04
Pérez-Cabal & Charfeddine, 2015	0.02		-	0.01	0.01	-	0.04	0.02
Malchiodi *et al.*, 2017	0.07	0.01	-	-	0.04	0.02	0.04	0.02
Oliveira Junior *et al.*, 2021	0.11		0.02	-	-	0.03	0.04	0.02
Threshold								
Van der Waaij *et al.*, 2005	0.10	0.05	-	-	0.10	0.08	0.01	0.02
Swalve *et al.*, 2008	0.13	0.20	-	-	-	-	0.17	0.10
Pérez-Cabal & Charfeddine, 2015	0.14		-	0.06	0.39	-	0.15	0.09
Malchiodi *et al.*, 2017	0.16	0.13	-	-	0.19	0.09	0.14	0.06
Logistic								
Koenig *et al.*, 2005	0.073		-	-	0.11	-	0.086	-
Häggman & Juga, 2013	0.13	0.03	0.02	-	-	0.02	0.08	0.04

DD: digital dermatitis; ID: interdigital dermatitis; HE: heel erosion; IP: interdigital phlegmon; IH: interdigital hyperplasia; SH: sole haemorrhage; SU: sole ulcer; WL: white line disease or white line separation

According to the studies referenced in Table 2.3, in terms of the infectious lesions, DD (0.07–0.16) and IH (0.01–0.39) tend to have the highest heritability and IP (0.01–0.06) tends to have the lowest, while SU generally has the highest estimated heritability under the non-infectious lesions (0.03–0.17), with the estimated heritability of SH tending to be the lowest at between 0.02 and 0.09.

While some researchers estimated the heritability of DD and ID separately, others combined these into a single trait. Although these studies used varying methodologies to define and record claw traits, as well as varying numbers of cows in their analyses, the heritability estimates for individual traits are generally consistent. Some claw lesions occur at a lower frequency than others but may be grouped together under their common aetiology, risk factors, or biological causes in order to increase the sample size for evaluation and heritability estimation (Heringstad *et al.*, 2018). It was suggested by Buch *et al.* (2011) to group claw disorders into categories related to hygiene (DD and HE) and feed (SH and SU), while Ødegård *et al.* (2013) created categories for traits related to laminitis (SH, SU, and WL) and infectious traits (DD, HE, and IP). On the other hand, Chapinal *et al.* (2013) classified lesions into three categories – infectious or partly infectious lesions (DD, HE, and IP), horn lesions that are influenced by metabolic or mechanical aspects (SH, SU, and WL), and other lesions (IH, fissures, thin soles, and CC).

Genetic correlations between individual claw disorders tend to be low, ranging from -0.18 between DD and SU to +0.18 between SU and IH (der Waaij *et al.,* 2005). Categorising claw diseases into two groups (DD and HE versus SH and SU), Buch *et al.* (2011) found high correlations between traits within the groups (+0.87 and +0.73, respectively), but low correlations between traits in different groups (≤ +0.23). The low correlation (+0.08) they found between the two groups of lesions was confirmed by Chapinal *et al.* (2013).

Digital dermatitis has positive correlations with all the other claw diseases, with the largest being with IH at +0.57 (Malchiodi *et al.*, 2017).

In spite of their low heritability, researchers agree that there is sufficient genetic variability for genetic selection to be a viable option for improving claw traits in dairy cattle (Van der Spek *et al.*, 2013; Pérez-Cabal & Charfeddine, 2015). A number of European and Scandinavian countries, including the Netherlands, Denmark, Finland, Sweden, and Norway have implemented routine genetic evaluation of claw health and results indicate that it is possible to produce reliable breeding values using data currently available (Heringstad *et al.*, 2018). However, achieving high selection accuracy will require improved data recording of lameness and claw health traits to offset the low heritability (Ring *et al.*, 2018). Using technology and automation to collect these data may offer the solution. A number of technologies exist that may aid in the automatic recording of claw lesions, e.g. pedometers, digital scanners, and even machine learning, although these are still being refined and validated (Rexroad *et al.*, 2019; Afonso *et al.*, 2020; Barden, 2022).

In South Africa, claw data is not routinely collected by producers, although some dairy farmers employ hoof trimmers to perform preventative trimming or lameness interventions as needed. In addition, participation of dairy cows in milk recording falls short when compared to global standards. In 2018, only approximately 13% of the national herd participated in official milk recording with either the Agricultural Research Council (ARC) or SA Stud Book (https://my.icar.org/stats/list). This has resulted in limited pedigrees and smaller complete datasets being available for genetic analysis.

2.5 Genomic analyses

From the literature, it is clear that claw lesions are complex with regard to their aetiology, identification, recording and management (Charfeddine & Pérez-Cabal, 2017; Afonso *et al.*, 2020). Due to the lack of accurate and consistent recordings of claw lesions, heritability estimates remain low and the inclusion of these traits for genetic evaluations limited.

Since the development of cattle linkage maps in the 1990s, researchers around the world have studied quantitative trait loci (QTL) affecting a variety of traits in dairy cattle in order to make improved selection decisions (Ahswell *et al.*, 2004). The completion of the bovine genome sequencing in 2009 (Tellam *et al.*, 2009) represents one of the most significant breakthroughs in cattle genetic improvement in recent decades (Gutierrez-Reinoso *et al.*, 2021; Barbosa *et al.*, 2023; Hossein-Zadeh, 2024). Thereafter, several assays were developed that were able to quickly and cost-effectively genotype a large number of single nucleotide polymorphisms (SNP) (Wiggans *et al.*, 2017). A number of countries now routinely include genomic information in their genetic evaluation systems, including the United States, New Zealand, Australia, and Canada (Wiggans *et al.*, 2017). Today, SNP are the most widely used tool in livestock genomics because they allow for relatively fast, reliable, and inexpensive determination of multiple genetic differences (Sender *et al.*, 2013, Gurgul *et al.*, 2014).

Including genomic information in genetic evaluations has had a positive impact on dairy cattle improvement programmes (Erasmus & Van Marle-Köster, 2021; Wiggans & Carrillo, 2022). A very large number of genotypes (over 6.5 million in 2022) have been produced worldwide (Wiggans & Carrillo, 2022), and these are used in a multitude of genomic analyses, including studies related to population diversity and selection signatures, as well as genome-wide association studies (Barbosa *et al.*, 2023; Ma & Lin, 2024). Genome-wide association studies (GWAS) facilitate comprehensive genome screening by employing numerous SNP spread throughout the genome, allowing researchers to detect genetic variants related to specific traits (Meredith *et al.*, 2012) in order to evaluate associations between common genetic variants with phenotypic

differences in a trait (Sahana *et al.*, 2014). Currently, a medium-density SNP chip with approximately 50 000 markers is widely used for GWAS in dairy cattle. The SNP may be co-inherited with ungenotyped causal variants due to their proximity and so can act as proxies for these (Meredith *et al.*, 2012).

In the early years, most studies focused on production traits, but this has shifted towards more research into traits related to health and welfare (Gutierrez-Reinoso *et al.*, 2021). Today, GWAS have been successfully used in dairy cattle as an initial screening tool to detect and quantitative trait loci (QTL) regions for health traits in countries other than South Africa (Meredith *et al.*, 2012; Sahana *et al.*, 2014). The first GWAS on claw disorders was published by Van der Spek *et al.* (2015). Although they found a number of SNP associated with claw disorders, they did not identify genes with a major effect due to the low power of the study. Thereafter, several researchers have performed genomic studies on claw health in dairy cattle and reported several candidate genes related to specific lesions (Table 2.4).

A number of candidate genes were found to be associated with infectious lesions as a group, including *CDAC7* and *ZAK* on BTA 2, *CD1E* on BTA 3, and *PEL12* and *AHSA1* on BTA 10 (Malchiodi *et al.*, 2018). When studying DD and IH, two candidate genes were found on BTA 3 related to immunity and inflammation: *FPGT* and *TNN13K* (Sánchez-Molano *et al.*, 2019). In addition, there seems to be a promising candidate gene (*EPYC*) related to these two lesions on BTA 5 that is related to a form of Ehlers-Danlos syndrome, which causes soft and hyper-extensible skin, delayed wound healing, and skin fragility (Croué *et al.*, 2019). Both DD and IH were investigated as individual traits by Lai *et al.* (2020) and Sölzer *et al.* (2022), who found candidate genes related to immune response, cell formation, wound healing, and stress response on several chromosomes, although none in common.

In their investigation of non-infectious lesions as a group, Malchiodi *et al.* (2018) found a number of candidate genes related to cell, collagen, and cartilage formation, as well as genes related to immunity and inflammation, mostly located on BTA 5, whereas Lai *et al.* (2021) found candidate genes related to bone mineralisation (*RASSF2* and *WDR37*) and skeletal development (*DIP2C*) on BTA 13. Investigations into specific non-infectious lesions revealed several candidate genes for SU on BTA 8 related to cell apoptosis (*DCAF12*), delayed wound healing, hyperkeratosis, skin lesions, and thin skin (*B4GALT1* and *GALT*), and bone mineralisation (*APTX* and *GULO*) (Lai *et al.*, 2021). Candidate genes associated with immune response (*PLPP3*, *C8A*, and *C8B*) were identified on BTA 3 for WL and SH (Li *et al.*, 2023). Table 2.4 provides a summary of potential candidate genes identified in recent studies, although here, again, results have been discordant due to differences in lesion categorisation and research methodology (Croué *et al.*, 2019; Lai *et al.*, 2020).

The limitations experienced in analysing claw lesions, i.e. different identification and recording systems, different classification methodologies, and different methods of statistical analysis, carry through to genomic analysis. There does not seem to be consensus regarding the best method for genomic analysis, as the studies referenced here represent a wide variety of population sizes, array densities, and QTL mapping methodologies (Malchiodi *et al.*, 2018, Sánchez-Molano *et al.*, 2019; Croué *et al.*, 2019; Lai *et al.*, 2020; Lai *et al.*, 2021; Sölzer *et al.*, 2022; Li *et al.*, 2023). This may explain the fact that, despite the discovery of several significant QTL, the literature shows little consistence in the candidate genes identified thus far (Lai *et al.*, 2020).

Table 2.4 Selected references for the identification of candidate genes for claw lesions in dairy cattle

Claw lesion/category	BTA	Candidate gene	Candidate gene relevance
Infectious lesions[1]	2	CDAC7	Cell proliferation and apoptosis
	2	ZAK	Embryonic digit formation
	3	CD1E	Immune response
	10	PEL12	Immunity
	10	AHSA1	Response to stress
Digital dermatitis[2]	2	CXCR4, MGAT5	Immune responsiveness
	7	CACNA1A	Immunologic reaction
	10	NEO1	Cell growth and differentiation
	10	DAPK2	Immune response
	10	USP3	Protein ubiquitination
	19	KRT33A, KRT33B	Keratin formation
	20	AHRR SLC9A3	Immune response
	20	TERT	Wound healing and hyperplasia
Digital dermatitis and interdigital hyperplasia[3]	3	FPGT	Cell recognition, inflammation, immunity
	3	TNN13K	Inflammatory response
	5	EPYC	Ehlers-Danlos syndrome
	23	EDN1	Inflammatory response
Interdigital hyperplasia[4]	8	UBQLN1	Protein degradation
	11	WDPCP	Collective cell movement and cilia formation
	22	ITPR1	Stress response
Non-infectious lesions[5]	5	TULP3	Cartilage development, embryonic digital formation
	5	RERG	Collagen fibril organisation
	5	CHST11	Epidermis formation
	5	STYK1	Immune response
	5	PPARA	Inflammatory response
	6	BDH2	Collagen metabolic processes
	13	RASSF2, WDR37	Bone mineralisation
	13	DIP2C	Mutations associated with skeletal dysplasia
	16	HMGB1	Epithelial cell differentiation
	21	BDKRB1	Immune response
	25	PLOD3	Epidermis formation
	25	SH2B2	Immune response
	28	GALNT2	Cell growth
Sole ulcer[6]	6	GC gene	Immune response
	8	APTX, GULO	Bone mineralisation
	8	B4GALT1, GALT	Delayed healing, hyperkeratosis, skin lesions, thin skin
	8	DCAF12	Regulation of apoptosis
	13	C20orf202	Na/K/2Cl co-transporter mechanisms
	17	TMEM132B	Cell adhesion
White line disease[7]	3	PLPP3	Immune response
Sole haemorrhage[8]	2	GPR17	Inflammatory response
White line disease and sole haemorrhage [7]	3	C8A and C8B	Immune response

References: [1]Machiodi *et al.*, 2018. [2]Lai *et al.*, 2020; Sölzer *et al.*, 2022. [3]Croué *et al.*, 2019; Sánchez-Molano *et al.*, 2019. [4]Sölzer *et al.*, 2022. [5]Machiodi *et al.*, 2018; Lai *et al.*, 2021. [6]Lai *et al.*, 2021; Sölzer *et al.*, 2022. [7]Li *et al.*, 2023. [8]Sánchez-Molano *et al.*, 2019.

For most functional and welfare-related traits, including claw health, the availability of sufficient objective records remains limited, so available heritability estimates are low and, therefore, genetic progress is slow (Holmberg, 2007; Egger-Danner *et al.*, 2015). Genomic data, therefore, provides valuable additional

information to be used at the genome level for studying the underlying genetic mechanisms affecting a specific trait, and for possible inclusion in genomic evaluations (Vukasinovic *et al.*, 2017). Improving the reliability of breeding values is often purported to be the most significant benefit of genomic selection, but Cole & Van Raden (2018) also list other advantages, including the identification of genes that influence economically important traits, especially those with low heritability.

2.6 Conclusion

The occurrence of claw lesions is significantly influenced by management and environmental factors and the remaining genetic component is highly complex and heterogenous. Recording of phenotypes varies due to inconsistencies in scoring systems, grouping of traits, and evaluation methodologies, a phenomenon that seems to carry through to genetic evaluation of these traits as well. In addition to the fact that these traits generally have low heritability, this variation in methodologies further contributes to challenges in the estimation of heritability with the aim of making genetic progress in claw health. Genomic information seems to hold potential to address this issue. To date, most of the candidate genes reported in the literature are related to inflammatory processes and immune response, together with various cell proliferation processes, which is expected due to the complex biological pathways involved in these processes. Although farm management may be the most effective short-term method for improving lameness in dairy herds, the literature indicates that combining genomic technologies with management remains the most effective and sustainable long-term solution.

References

Afonso, J.S., Bruce, M., Keating, P., Raboisson, D., Clough, H., Oikonomou, G., Rushton, J., 2020. Profiling detection and classification of lameness methods in British dairy cattle research: A systematic review and meta-analysis. *Front. Vet. Sci*. 7:542. https://doi.org/10.3389/fvets.2020.00542

Ashwell, M.S., Heven, D.W., Sonstegard, T.S., Van Tassel, C.P., Da, Y., Van Raden, P.M., Ron, M., Weller, J.I., Lewin, H.A., 2004. Detection of quantitative trait loci affecting milk production, health, and reproductive traits in Holstein cattle. *J. Dairy Sci.* 87(2):468–475. https://doi.org/10.3168/jds.S0022-0302(04)73186-0

Assadi-Alamouti, A., 2022. Economic Losses Associated with Lameness in Dairy Herds. In: *The 2nd Regional Conference on Cow Comfort & Lameness.* 18–20 July 2022, University of Tehran, Iran.

Barbosa, B.L., Silva, A.P.S., Castro, D.P., Castro, G.C., Silva, T.S., Vieira, R.B., Silva, L., Torres, T.S., Pereira, E.H.U., Silva, L.R.G., Borges, L.S., Oliveira, M.B., Sarmento, J.L.R., 2023. Overview of the use of genomic data in animal breeding. *Ciência Rural* 53(10):e20220350. http://doi.org/10.1590/0103-8478cr20220350

Barden, M., 2022. Genetic and metabolic aspects of claw horn lesion aetiopathogenesis in Holstein cows. PhD thesis, University of Liverpool.

Barker, Z.E., Amory, J.R., Wright, J.L., Mason, S.A., Blowey, R.W., Green, L.E., 2009. Risk factors for increased rates of sole ulcers, white line disease, and digital dermatitis in dairy cattle from twenty-seven farms in England and Wales. *J. Dairy Sci*. 92:1971–1978. https://doi.org/10.3168/jds.2008-1590

Barkema, H.W., von Keyserlingk, M.A.G., Kastelic, J.P., Lam, T.J.G.M., Luby, C., Roy, J.-P., LeBlance, S.J., Keefe, G.P., Kelton, D.F., 2015. Invited review: Changes in the dairy industry affecting dairy cattle health and welfare. *J. Dairy Sci.* 98(11):7426–7445. https://doi.org/10.3168/jds.2015-9377

Bell, N., Bacon, D., Craven, E., Crowe, S., Newsome, R., Oikonomou, G., Pedersen, S., Reader, J., Wilson, J., 2022. Dairy cattle lameness: A roundtable discussion. *Livestock* 27(Sup3):S1–S11. https://doi.org/10.12968/live.2022.27.S1.115

Buch, L.H., Sørensen, A.C., Lassen, J., Berg, P., Eriksson, J.-Å., Jakobsen, J.H., Sørensen, M.K., 2011. Hygiene-related and feed-related hoof diseases show different patterns of genetic correlations to clinical mastitis and female fertility. *J. Dairy Sci.* 94(3):1540–1551. https://doi.org/10.3168/jds.2010-3137

Capion, N., Thamsborg, S.M., Enevoldsen, C., 2009. Prevalence and severity of foot lesions in Danish Holstein heifers through first lactation. *Vet. J.* 182:50–58. https://doi.org/10.1016/j.tvjl.2008.05.026

Cha, E., Hertl, J.A., Bar, D., Gröhn, Y.T., 2010. The cost of different types of lameness in dairy cows calculated by dynamic programming. *Prev. Vet. Med.* 97(1):1–8. https://doi.org/10.1016/j.prevetmed.2010.07.011

Chapinal, N., Koeck, A., Sewalem, A., Kelton, D.F., Mason, S., Cramer, G., Miglior, F., 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. *J. Dairy Sci.* 96:2596–2604. https://doi.org/10.3168/jds.2012-6071

Charfeddine, N. & Pérez-Cabal, M.A., 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100:653–665. https://doi.org/10.3168/jds.2016-11434

Christen, M., Bergsten, C., Burgstaller, J., Capion, N., Charfeddine, N., Clarke, J., Daniel, V., Döpfer, D., Fiedler, A., Fjeldaas, T., Heringstad, B., Cramer, G., Kofler, J., Mueller, K.R., Nielsen, P., Oakes, E., Ødegård, C., O'Driscoll, K.J., Pryce, J.E., Steiner, A., Stock, K.F., Thomas, G., Ulvshammar, K., Holzhauer, M., Cole, J.B., Egger-Danner, C., Kowalski, Z., Petreny, N., Burke, M., Buček, P., Journaux, L., Coffey, M., Hunlun, C., Radzio, D., 2015. Recording of claw and foot disorders in

dairy cattle: Current role and prospects of the international harmonization initiative of ICAR. *ICAR Tech. Series* 19:157–165, 2015.

Cole, J.B. & Van Raden, P.M., 2018. Symposium review: Possibilities in an age of genomics: The future of selection indices. *J. Dairy Sci.* 101(4):3686–3701. https://doi.org/10.3168/jds.2017-13335

Cook, N.B. & Nordlund, K.V., 2009. The influence of the environment on dairy cow behavior, claw health and herd lameness dynamics. *Vet. J.* 179(3):360–369. https://doi.org/10.1016/j.tvjl.2007.09.016

Croué, I., Michenet, A., Leclerc, H., Ducrocq, V., 2019. Genomic analysis of claw lesions in Holstein cows: Opportunities for genomic selection, quantitative trait locus detection, and gene identification. *J. Dairy Sci.* 102(7):6306–6318. https://doi.org/10.3168/jds.2018-15979

DeFrain, J.M., Socha, M.T., Tomlinson, D.J., 2013. Analysis of foot health records from 17 confinement dairies. *J. Dairy Sci.* 96(11):7329–7339. https://doi.org/10.3168/jds.2012-6017

Du Plessis, I., 2007. Foot health in housed cattle: A review. *S. Afr. J. Anim. Sci.* 8:11–17.

EFSA, 2009. Scientific opinion of the panel on animal health and animal welfare on a request from the commission on the risk assessment of the impact of housing, nutrition and feeding, management and genetic selection on leg and locomotion problems in dairy cows. *EFSA J.* 1142:1–57. https://doi.org/10.2903/j.efsa.2009.1142

Egger-Danner, C., Cole, J.B., Pryce, J.E., Gengler, N., Heringstad, B., Bradley, A., Stock, K.F., 2015. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Anim.* 9(2):191–207. https://doi.org/10.1017/S1751731114002614

Erasmus, L. & Van Marle-Köster, E., 2021. Moving towards sustainable breeding objectives and cow welfare in dairy production: a South African perspective. *Trop. Anim. Health Prod.* 53: 470. https://doi.org/10.1007/s11250-021-02914-w

Garvey, M., 2022. Review: Lameness in dairy cow herds: Disease aetiology, prevention and management. *Dairy* 2022(3):199–210. https://doi.org/10.3390/dairy3010016

Gutierrez-Reinoso, M.A., Aponte, P.M., Garcia-Herrer, M., 2021. Genomic Analysis, Progress and Future Perspectives in Dairy Cattle Selection: A Review. *Anim.* 11:599. https://doi.org/10.3390/ani11030599

Gurgul, A., Semik, E., Pawlina, K., Szmatoła, T., Jasielczuk, I., Bugno-Poniewierska, M., 2014. The application of genome-wide SNP genotyping methods in studies on livestock genomes. *J. Appl. Genet.* 55:197–208. https://doi.org/10.1007/s13353-014-0202-4

Häggman, J. & Juga, J., 2013. Genetic parameters for hoof disorders and feet and leg conformation traits in Finnish Holstein cows. *J. Dairy Sci.* 96(5):3319–3325. https://doi.org/10.3168/jds.2012-6334

Heringstad, B., Egger-Danner, C., Charfeddine, N., Pryce, J.E., Stock, K.F., Kofler, J., Sogstad, A.M., Holzhauer, M., Fiedler, A., Müller, K., Nielsen, P., Thomas, G., Gengler, N., de Jong, G., Ødegård, C., Malchiodi, F., Miglior, F., Alsaaod, M., Cole, J.B., 2018. Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *J. Dairy Sci.* 101(6):1–21. https://doi.org/10.3168/jds.2017-13531

Holmberg, M., 2007. Genetic dissection of functional traits in dairy cattle. Doctoral dissertation. ISSN 1652-6880, ISBN 978-91-576-7391-6.

Hossein-Zadeh, N.G., 2024. An overview of recent technological developments in bovine genomics. *Vet. Anim. Sci.* 25:100382. https://doi.org/10.1016/j.vas.2024.100382

International Committee for Animal Recording (ICAR), 2020. *ICAR claw health atlas*. https://www.icar.org/index.php/publications-technical-materials/technical-series-and-proceedings/atlas-claw-health-and-translations/. Accessed 1 November 2024.

International Committee for Animal Recording (ICAR) statistics, https://my.icar.org/stats/list, last access: 20 September 2024.

Koenig, S., Sharifi, A.R., Wentrot, H., Landmann, D., Eise, M., Simianer, H., 2005. Genetic parameters of claw and foot disorders estimated with logistic models. *J. Dairy Sci.* 88(9):3316–3325. https://doi.org/10.3168/jds.S0022-0302(05)73015-0

Lai, E., Danner, A.L., Famula, T.R., Oberbauer, A.M., 2020. Genome-Wide Association Studies Reveal Susceptibility Loci for Digital Dermatitis in Holstein Cattle. *Anim.* 10:11. https://doi.org/10.3390/ani10112009

Lai, E., Danner, A.L., Famula, T.R., Oberbauer, A.M., 2021. Genome-wide association studies reveal susceptibility loci for noninfectious claw lesions in Holstein dairy cattle. *Front. Genet.* 12:657375. https://doi.org/10.3389/fgene.2021.657375

Laursen, M.V., Boelling, D., Mark, T., 2009. Genetic parameters for claw and leg health, foot and leg conformation, and locomotion in Danish Holsteins. *J. Dairy Sci.* 92(4):1770–1777. https://doi.org/10.3168/jds.2008-1388

Li, B., Barden, M., Kapsona, V., Sánchez-Molano, E., Anagnostopoulos, A., Griffiths, B.E., Bedford, C., Dai, X., Coffey, M., Psifidi, A., Oikonomou, G., Banos, G., 2023. Single-step genome-wide association analyses of claw horn lesions in Holstein cattle using linear and threshold models. *Genet. Sel. Evol*. 55:16. https://doi.org/10.1186/s12711-023-00784-4

Ma, Q. & Lin, X., 2024. From GWAS to Breeding Practice: Genetic Research on Improving Milk Production in Cattle. *Anim. Mol. Breed*. 14(1):27–35.

Manson, F.A. & Leaver, J.D., 1988. The influence of concentrate amount on locomotion and clinical lameness in dairy cattle. *Anim. Sci.* 47(2):185–190. https://doi.org/10.1017/S0003356100003251

Manson, F.J. & Leaver, J.D., 1988. The influence of dietary protein intake and of hoof trimming on lameness in dairy cattle. *Anim. Sci.* 47(2):191–199. https://doi.org/10.1017/S0003356100003263

Malchiodi, F., Koeck, A., Mason, S., Christen, A.M., Kelton, D.F., Schenkel, F.S., Miglior, F., 2017. Genetic parameters for hoof health traits estimated with linear and threshold models using alternative cohorts. *J. Dairy Sci.* 100(4):2828–2836. https://doi.org/10.3168/jds.2016-11558

Malchiodi, F., Brito, L.F., Schenkel, F.S., Christen, A.M., Kelton, D.F., Miglior, F., 2018. Genome-wide association study and functional analysis of infectious and horn type hoof lesions in Canadian Holstein cattle. In: *World Congress on Genetics Applied to Livestock Production.* 11–16 February, Auckland, New Zealand

Manske, T., 2002. Hoof lesions and lameness in Swedish dairy cattle. Prevalence, risk factors, effects of claw trimming, and consequences for productivity. PhD thesis, Swedish University of Agricultural Sciences.

Meredith, B.K., Kearney, F.J., Finlay, E.K., Bradley, D.G., Fahey, A.G., Berry, D.P., Lynn, D.J., 2012. Genome-wide associations for milk production and somatic cell score in Holstein-Friesian cattle in Ireland. *BMC Genet.* 13(21). https://doi.org/10.1186/1471-2156-13-21

Miglior, F., Muir, B.L., Van Doormaal, B.J., 2005. Selection indices in Holstein cattle of various countries. *J. Dairy Sci.* 88(3):1255–1263. https://doi.org/10.3168/jds.S0022-0302(05)72792-2

Miglior, F., Fleming, A., Malchiodi, F., Brito, L.F., Martin, P., Baes, C.F., 2017. A 100-Year Review: Identification and genetic selection of economically important traits in dairy cattle. *J. Dairy Sci.* 100:10251–10271. https://doi.org/10.3168/jds.2017-12968

Milk SA, 2023. *Lacto Data* 26, June 2023.

Oberbauer, A.M., Berry, S.L., Belanger, J.M., McGoldrick, R.M., Pinos-Rodriquez, J.M., Famula, T.R., 2013. Determining the heritable component of dairy cattle foot lesions. *J. Dairy Sci.* 96(1):605–613. https://doi.org/10.3168/jds.2012-5485

Ødegård, C., Svendsen, M., Heringstad, B., 2013. Genetic analyses of claw health in Norwegian Red cows. *J. Dairy Sci.* 96(11):7274–7283. https://doi.org/10.3168/jds.2012-6509

Oehm, A.W., Knubben-Schweizer, G., Rieger, A., Stoll, A., Hartnack, S., 2019. A systematic review and meta-analyses of risk factors associated with lameness in dairy cows. *BMC Vet. Res.* 15:346. https://doi.org/10.1186/s12917-019-2095-2

Oliveira Junior, G.A., Schenkel, F.S., Alcantara, L., Houlahan, K., Lynch, C., Baes, C.F., 2021. Estimated genetic parameters for all genetically evaluated traits in Canadian Holsteins. *J. Dairy Sci.* 104(8):9002–9015. doi:10.3168/jds.2021-20227. https://doi.org/10.3168/jds.2021-20227

Ózsvári, L., 2017. Economic Cost of Lameness in Dairy Cattle Herds. *J. Dairy Vet. Anim. Res*. 6(2):00176

Pérez-Cabal, M.A. & Charfeddine, N., 2015. Models for genetic evaluations of claw health traits in Spanish dairy cattle. *J. Dairy Sci.* 98(11):8186-8194. https://doi.org/10.3168/jds.2015-9562

Randall, L.V., Green, M.J., Chagunda, M.G.G., Mason, C., Archer, S.C., Green, L.E., Huxley, J.N., 2015. Low body condition predisposes cattle to lameness: An 8-year study of one dairy herd. *J. Dairy Sci.* 98(6):3766–3777. https://doi.org/10.3168/jds.2014-8863

Ranjbar., S., Rabiee, A.R., Ingenhoff, L., House, J.K., 2020. Farmers' perceptions and approaches to detection, treatment and prevention of lameness in pasture-based dairy herds in New South Wales, Australia. *Aust. Vet. J*., 98:264–269. https://doi.org/10.1111/avj.12933

Ring, S.C., Twomey, A.J., Byrne, N., Kelleher, M.M., Pabiou, T., Doherty, M.L., Berry, D.P., 2018. Genetic selection for hoof health traits and cow mobility scores can accelerate the rate of genetic gain in producer-scored lameness in dairy cows. *J. Dairy Sci.* 101(11), 10034–10047. https://doi.org/10.3168/jds.2018-15009

Robinson, P.H. & Juarez, S.T., 2003. Locomotion scoring your cows: use and interpretation. In: *Proc. Mid-South Nutrition Conference*.

Sadiq, M.B., Ramanoon, S.Z, Mossadeq, W.M.S., Mansor, R., Hussain, S.S.S, 2019. Review: Dairy farmers' perceptions of and actions in relation to lameness management. *Anim.* 9(5):270. https://doi.org/10.3390/ani9050270

Sadiq, M.B., Ramanoon, S.Z., Mansor, R., Hussain, S.S.S., Mossadeq, W.M.S., 2020. Claw trimming as a lameness management practice and the association with welfare and production in dairy cows. *Anim.* 10(9):1515. https://doi.org/10.3390/ani10091515

Sahana, G., Guldbrandtsen, B., Thomsen, B., Holm, L.E., Panitz, F., Brøndum, R.F., Bendixen, C., Lund, M.S., 2014. Genome-wide association study using high-density single nucleotide polymorphism arrays and whole-genome sequences for clinical mastitis traits in dairy cattle. *J. Dairy Sci.* 97(11):7258-7275. https://doi.org/10.3168/jds.2014-8141

Sánchez-Molano, E., Bay, V., Smith, R.F., Oikonomou, G., Banos, G., 2019. Quantitative Trait Loci Mapping for Lameness Associated Phenotypes in Holstein–Friesian Dairy Cattle. *Front. Genet.* 10:926. https://doi.org/10.3389/fgene.2019.00926

Sender, G., Korwin-Kossakowska, A., Pawlik, A., Hameed, K.G.A., Oprządek, J., 2013. Genetic basis of mastitis resistance in dairy cattle–a review/Podstawy Genetyczne Odporności Krów Mlecznych Na Zapalenie Wymienia–Artykuł Przeglądowy. *Ann. Anim. Sci.* 13(4):663–673. https://doi.org/10.2478/aoas-2013-0043

Shearer, J.K. & Van Amstel, S.R., 2007. Effect of flooring and/or flooring surfaces on lameness disorders in dairy cattle. In: *Proc. Western Dairy Management Conference.* 7–9 March, Reno, NV, USA.

Shearer, J.K. & Van Amstel, S.R., 2017. Pathogenesis and treatment of sole ulcers and white line disease. *Vet. Clin. North Am. Food Anim. Pract*. 33(2):283–300. https://doi.org/10.1016/j.cvfa.2017.03.001

Shearer, J.K., Belknap, E., Berry, S., Guard, C., Hoblet, K., Hovingh, E., Kirksey, G., Langill, A., Van Amstel, S.R., 2002. The standardization of input codes for capture of lameness data in dairy records. In: *Proc. 12th International Symp. on Lameness in Ruminants*. 9–13 January, Orlando, FL, USA.

Shearer, J., Anderson, D., Ayars, W., Belknap, E., Berry, S., Guard, C., Hoblet, K., Hovingh, E., Kirksey, G., Langill, A., Mills, A., Miskimins, D., Osterstock, J., Price, R., Prigel, D., Roussel, A., Van Amstel,

S., Wallace, R., Wasson, J., Cook, N., Garrett, E. F., Hostetler, D. E., & Schugel, L., 2004. A Record keeping system for capture of lameness and foot-care information in cattle. *The Bovine Practitioner 38*(1):83–92. https://doi.org/10.21423/bovine-vol38no1p83-92

Solano, L., Barkema, H.W., Mason, S., Pajor, E.A., LeBlanc, S.J., Orsel, K., 2016. Prevalence and distribution of foot lesions in dairy cattle in Alberta, Canada. *J. Dairy Sci.* 99(8):6828–6841. https://doi.org/10.3168/jds.2016-10941

Sölzer, N., May, K., Yin, T., König, S., 2022. Genomic analysis of claw disorders in Holstein cows: Genetic parameters, trait associations, and genome-wide associations considering interactions of SNP and heat stress. *J. Dairy Sci.,* 105(10), 8218–8236. https://doi.org/10.3168/jds.2022-22087

Somers, J.G.C.J., Frankena, K., Noordhuizen-Stassen, E.N., Metz, J.H.M., 2005. Risk factors for digital dermatitis in dairy cows kept in cubicle houses in The Netherlands. *Prev. Vet. Med. 71*:11–21. https://doi.org/10.1016/j.prevetmed.2005.05.002

Somers, J. & O'Grady, L., 2015. Foot lesions in lame cows on 10 dairy farms in Ireland. *Ir. Vet. J. 68*:1–7. https://doi.org/10.1186/s13620-015-0039-0

Sprecher, D.E.A., Hostetler, D.E., Kaneene, J.B., 1997. A lameness scoring system that uses posture and gait to predict dairy cattle reproductive performance. *Theriogenology* 47(6):179–1187. https://doi.org/10.1016/S0093-691X(97)00098-8

Swalve, H.H., Alkhoder, H., Pijl, R., 2008. Estimates of breeding values for sires based on diagnoses recorded at hoof trimming: Relationships with EBV for conformation traits. *Interbull Bull.* 38:87–87.

Tellam, R.L., Lemay, D.G., Van Tassell, C.P., Lewin, H.A., Worley, K.C., Elsik, C.G., 2009. Unlocking the bovine genome. *BMC Genomics* 10:193. https://doi.org/10.1186/1471-2164-10-193

Van der Spek, D., Van Arendonk, J.A.M., Vallée, A.A.A., Bovenhuis, H., 2013. Genetic parameters for claw disorders and the effect of preselecting cows for trimming. *J. Dairy Sci.* 96(9):6070–6078. https://doi.org/10.3168/jds.2013-6833

Van der Spek, D., 2015. Genetic background of claw health in dairy cattle. PhD thesis, Wageningen University, The Netherlands.

Van der Waaij, E.H., Holzhauer, M., Ellen, E., Kamphuis, C., de Jong, G., 2005. Genetic parameters for claw disorders in Dutch dairy cattle and correlation with conformation traits. *J. Dairy Sci.* 88(10):3672–3678. https://doi.org/10.3168/jds.S0022-0302(05)73053-8

Van Nuffel, A., Zwertvaegher, I., Pluym, L., Van Weyenberg, S., Thorup, V.M., Pastell, M., Sonck, B., Saeys, W., 2015. Lameness Detection in Dairy Cows: Part 1. How to Distinguish between Non-Lame and Lame Cows Based on Differences in Locomotion or Behavior. *Anim.* 5:838–860. https://doi.org/10.3390/ani5030387

Vukasinovic, N., Bacciu, N., Przybyla, C.A., Boddhireddy, O., DeNise, S.K., 2017. Development of genetic and genomic evaluation for wellness traits in US Holstein cows. *J. Dairy Sci*. 100:428–438. https://doi.org/10.3168/jds.2016-11520

Weber, A., Stamer, E., Junge, W., Thaller, G., 2013. Genetic parameters for lameness and claw and leg diseases in dairy cows. *J. Dairy Sci. 96*(5):3310–3318. https://doi.org/10.3168/jds.2012-6261

Wiggans, G.R. & Carrillo, J.A., 2022. Genomic selection in United States dairy cattle. *Front. Genet.* 13:994466. https://doi.org/10.3389/fgene.2022.994466

Wiggans, G.R., Cole, J.B., Hubbard, S., Sonstegard, T.S., 2017. Genomic Selection in Dairy Cattle: The USDA Experience. *Annu. Rev. Anim. Biosci.* 5:309–327. https://doi.org/10.1146/annurev-animal-021815-111422

Zinpro® Corporation, 2008. *Claw Lesion Identification in Dairy Cattle* (D40-08-30-07). Eden Prairie, MN, USA.

CHAPTER 3

ROUTINE HOOF-TRIMMING DATA PROVIDES INSIGHT INTO THE OCCURRENCE OF CLAW LESIONS IN HOLSTEIN HERDS IN THE CENTRAL REGION OF SOUTH AFRICA

This article was prepared and published in *Tropical Animal Health and Production*.

R.C. Joubert[1], H.F. Strydom[2], E. van Marle-Köster[1]

[1]Department of Animal Science, University of Pretoria, Private Bag X20, Hatfield, Pretoria 0028, South Africa
[2]Department of Statistics, University of Pretoria, Private Bag X20, Hatfield, Pretoria 0028, South Africa

Received: 7 June 2023 / Accepted: 24 October 2023 / Published online: 4 November 2023

Tropical Animal Health and Production (2023) 55:395
https://doi.org/10.1007/s11250-023-03814-x

3 Routine hoof-trimming data provides insight into the occurrence of claw lesions in Holstein herds in the central region of South Africa

3.1 Introduction

Claw lesions are the primary cause of lameness in dairy cattle (Garvey, 2022), with serious implications for animal welfare due to the distress and discomfort experienced by the cows (Oehm *et al.*, 2019; Bell *et al.*, 2022). Claw lesions are classified as either infectious lesions such as digital dermatitis (DD), interdigital dermatitis (ID), heel erosion (HE), and interdigital phlegmon (IP), or non-infectious lesions, including white line disease (WL), sole ulcer (SU), and sole haemorrhage (SH) (Sadiq *et al.*, 2020; Garvey 2022). Infectious lesions are mostly related to environmental hygiene, while non-infectious lesions are generally caused by metabolic and/or mechanical factors (Chapinal *et al.*, 2013; Charfeddine & Pérez-Cabal, 2017; Sadiq *et al.*, 2020). The majority of researchers have reported DD, SH, SU, and WL as the primary causes of dairy cattle lameness (Charfeddine & Pérez-Cabal, 2017; Sölzer *et al.*, 2022; Bell *et al.*, 2022). There are several risk factors that influence the prevalence of claw lesions in dairy cattle, including environmental factors, design of housing facilities, and hygiene and management practices (Cook & Nordlund, 2009; Oehm *et al.*, 2019; Garvey, 2022). In addition to environmental factors, there is a heritable component to claw lesions (Van der Waaij *et al.*, 2005; Chapinal *et al.*, 2013; Heringstad *et al.*, 2018) that has probably been underestimated due to the poor quality of recording (Afonso *et al.*, 2020; Bell *et al.*, 2022).

Despite an increased awareness of lameness, its major causes have remained unchanged over the past 30 years, with a continued increase in the occurrence of lameness in dairy herds (Heringstad *et al.*, 2018; Bell *et al.*, 2022). Minimising the occurrence and impact of lameness is one of the greatest challenges for the dairy industry (Ring *et al.*, 2018; Oehm *et al.*, 2019; Sadiq *et al.*, 2020), but it is complex with regard to accurately defining and recording claw traits, and inconsistencies in the measures and terminology applied in terms of lesion identification and scoring systems (Charfeddine & Pérez-Cabal, 2017; Oehm *et al.*, 2019; Afonso *et al.*, 2020). Lameness and claw lesion recording systems differ between and within countries and data may be collected by a variety of people, including producers, veterinarians, and hoof trimmers (Afonso *et al.*, 2020; Garvey, 2022). In addition, there are large discrepancies between farmer-recorded lameness and the rates of lameness recorded by trained professionals (Sadiq *et al.*, 2019; Bell *et al.*, 2022).

Claw trimming is used as a management tool to control claw lesions (Sadiq *et al.*, 2020; Garvey, 2022). In South Africa (SA), claw data are limited to the use of private hoof trimmers, who record lesions on paper, and data is not necessarily captured in an electronic recording system (Mhlongo, 2019). Traits associated with claw health and lameness are seldom included in goal-driven selection in SA dairy herds (Visser *et al.*, 2020). Except for a review of foot health in housed cattle by Du Plessis (2007) and an investigation of hoof-trimming data for improving claw health by Van Marle-Köster *et al.* (2020), claw health has not been investigated in SA. More accurate diagnosis and recording of claw lesions will provide the data necessary to identify the major lesions expressed in SA dairy cattle so that we can further our understanding of causative factors of significant lesions affecting herd performance (Van Marle-Köster *et al.*, 2020; Garvey, 2022).

The total number of commercial dairy cattle in SA is estimated at approximately 1.6 million (DALRRD, 2022), of which the Holstein breed is by far the most numerous (Banga *et al.*, 2014). Dairy cattle farmers mainly employ one of two production systems, either intensive or extensive management systems. Cows that are managed more intensively in the inland regions are generally housed in free-stall (FS) or dirt-lot (DL) systems and fed a total mixed ration (TMR), while coastal dairy farms are pasture-based with cows receiving

varying degrees of supplementary dairy meal in addition to grazing on planted pastures (Meissner *et al.*, 2013; Ducrocq *et al.*, 2022).
In this study, routine trimming data from five intensively managed dairy farms over a six-year period (2014–2019) were analysed to find the prevalence and distribution of claw lesions in Holstein cattle in the central region of SA in order to inform more effective recording and management thereof.

3.2 Material and methods

Ethical approval for the study was granted by the University of Pretoria Ethics Committee in the Faculty of Natural and Agricultural Sciences (NAS292/2020). The five herds included in this study (Table 3.1) represent the central region of SA and include both DL (farms A and E) and FS (farms C and D) housing systems. Farm B employs a combined DL+FS housing system. As shown in Figure 3.1, farms A, D, and E are geographically within less than 150 km from each other, while farm C is approximately 350 km south of the mid-point between these three farms. Farm D is in the country's northern region, on the border with Botswana. Four of the five farms incorporate routine hoof trimming in their dry cow programme as well as lameness treatment (DC+LT), while farm A only employs hoof trimming as a lameness treatment tool (LT).

Table 3.1 Description of study herds and regional climatic data (CustomWeather, © 2022)

Farm	Region	Housing system[a]	Trimming regularity[b]	Hottest month (avg. temp.)	Coldest month (avg. temp.)	Wettest month (avg. rainfall)	Annual precipitation
A	Gauteng	DL	LT	Feb. (24°C)	July (13 °C)	Jan. (128.3 mm)	583.1 mm
B	Limpopo	DL+FS	DC+ LT	Feb. (24°C)	July (15 °C)	Jan. (134.6 mm)	621.4 mm
C	Mpumalanga	FS	DC+ LT	Jan. (21°C)	July (8 °C)	Jan. (140.2 mm)	687.8 mm
D	Gauteng	FS	DC+ LT	Jan. (20°C)	July (11 °C)	Dec. (74.6 mm)	357.6 mm
E	Free State	DL	DC+LT	Jan. (20°C)	July (10 °C)	Dec. (170.3 mm)	774.0 mm

[a]Housing system: DL = dirt lot, FS = free-stall, DL+FS = combination dirt lot and free-stall housing system
[b]Trimming regularity: DC = dry cow programme only, DC+LT = combination of a preventative dry cow programme and trimming as a treatment for lameness

Figure 3.1 The five herds included in this study represent the central region of South Africa

Hoof trimmers in SA are only allowed to perform basic trimming and management procedures, including placement of blocks, while any medical treatments are performed by veterinarians. It is important to note that farmers in SA subscribe to different schools of thought when it comes to hoof trimming, including the ABC methodology developed by Karl Burgi, Dörte Döpfer, and Nigel B. Cook, the *ICAR Claw Health Atlas* (ICAR, 2020), as well as recommendations by the International Lameness Committee.

Herd size data received from the SA Stud Book Association (SA Stud Book, Bloemfontein, South Africa) refer to all female animals on the farm, including young heifers, first- calving heifers, dry cows, and all milking cows in the herds. Average herd sizes over the six-year period were 696, 1 590, 620, 740, and 1 719 for farms A, B, C, D, and E, respectively.

The hoof trimmer provided on-farm data in hard copy, which included all available hoof-trimming records collected during routine hoof-trimming visits to the five herds between January 2014 and December 2019. The hoof-trimming sheets included general information such as the date of visit, farm ID, and cow ID, as well as information relating to the identification of lesions by limb, foot, and claw, and data regarding the treatment of lesions. The *Claw Lesion Identification in Dairy Cattle* brochure (Zinpro® Corporation, 2008) was used as the reference for lesion identification by a local hoof trimmer. The data manually recorded by the hoof trimmer were electronically captured into Microsoft Excel worksheets (Microsoft Corporation, 2018) by the student team. For the purposes of this study, only information in common between this *Hoof-Trimming Report* and the *Claw Lesion Identification in Dairy Cattle* brochure are included (Table 3.2).

Table 3.2 Claw lesion classification, identification and zone of occurrence as recorded by the hoof trimmer

	Zone of occurrence or point of lesion (POL)												
Classification and identification	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
Infectious lesions													
Digital and interdigital dermatitis, including hairy attack	**0**	-	-	-	-	-	-	-	-	**9**	**10**	-	-
Heel erosion	-	-	-	-	-	-	**6**	-	-	-	-	-	-
Foot rot (also foul/phlegmon)	**0**	-	-	-	-	-	-	-	-	**9**	-	-	-
Non-infectious lesions													
Axial fissure	-	-	-	-	-	-	-	-	-	-	-	**11**	**12**
Corkscrew claw	-	-	-	-	-	-	-	**7**	-	-	-	-	-
Hardship grooves or horizontal fissures	-	-	-	-	-	-	-	**7**	**8**	-	-	-	-
Interdigital hyperplasia	**0**	-	-	-	-	-	-	-	-	-	-	-	-
Sole haemorrhage or bruising	-	-	-	-	**4**	**5**	**6**	-	-	-	-	-	-
Sole ulcer or pododermatitis	-	-	-	-	**4**	-	-	-	-	-	-	-	-
Thin sole	-	-	-	-	**4**	**5**	-	-	-	-	-	-	-
Toe ulcer or necrosis	-	**1**	**2**	-	-	-	-	-	-	-	-	-	-
Vertical fissure or sandcrack	-	-	-	-	-	-	-	**7**	**8**	-	-	-	-
White line lesion and white line separation	-	**1**	**2**	**3**	-	-	-	-	-	-	-	-	-

Trim data were imported into a Microsoft SQL Server database (Microsoft Corporation, 2018) for quality control, data editing, and further analysis, after which views were exported back into Microsoft Excel for visualisation. Data for a total of 8754 trimming events, including repeated trimmings, were input for the five farms (Farm B only started trimming in 2017; no data for the period 2014–2016). This amounts to 262 650 data points, including lesion identification, treatment description, POL data, and other observations by the

hoof trimmer. The total number of trimming events was recorded per farm, together with the number of unique trimming events in order to investigate how many cows were subjected to repeated hoof trimming each year. Trimming data were further subdivided per farm into trimming year, trimming season (spring, summer, autumn, winter), and trimming month for evaluation of trimming practices across these various subdivisions. Only six animals were presented for trimming that showed no lesions and were not trimmed, and were excluded from further analysis. The final data file comprised 8 748 total trimming events for the five farms for the period 2014–2019, amounting to 262 470 data points.

Data analysis was performed using SAS/STAT software version 9.4 (SAS Institute Inc., 2015). A PROC FREQ and a chi-square test for independence were applied to assess whether the prevalence of lesions and foot position, and lesions and housing are independent. The SAS correspondence analysis (Benzécri 1973) was used to analyse and explore the relationships between the categorical variables of lesion occurrence and foot position, and lesion occurrence and housing system.

3.3 Results

The number of lesions identified across all farms over the six-year study period is shown in Table 3.3. There were no recorded incidences of IH or VF , so these were excluded from further discussion. The occurrence of non-infectious lesions SH, SU, and WLDS represented more than 75% of all recorded non-infectious lesions; consequently, non-infectious lesions CC, HG, TU, AX, and TS were excluded from further discussion as their counts were insufficient for statistical analysis. The occurrence of infectious lesions (DD, HE, and IP) per foot and the occurrence of the three most prevalent non-infectious lesions are illustrated per foot and per claw in Figure 3.2.

Table 3.3 Total lesion count per foot, and the percentage occurrence of each lesion as a percentage of total lesions recorded and as a percentage of total observations by the hoof trimmer

	Left front (LF)	Right front (RF)	Left rear (LR)	Right rear (RR)	Total	Occurrence (% of total lesions)	Occurrence (% of total observations)
None	25 968	25 918	24 329	24 473	100 688		
DD	213	228	1 428	1 224	3 093	64,02%	2,93%
HE[a]					543	11,24%	0,51%
IP	7	20	27	27	81	1,68%	0,08%
SU	8	6	191	210	415	8,59%	0,39%
WLDS	25	41	94	143	303	6,27%	0,29%
SH	5	2	96	104	207	4,28%	0,20%
Total lesions					4 831		4,58%
Total observations					105 519		

[a]Heel erosion data were not split by POL by the hoof trimmer

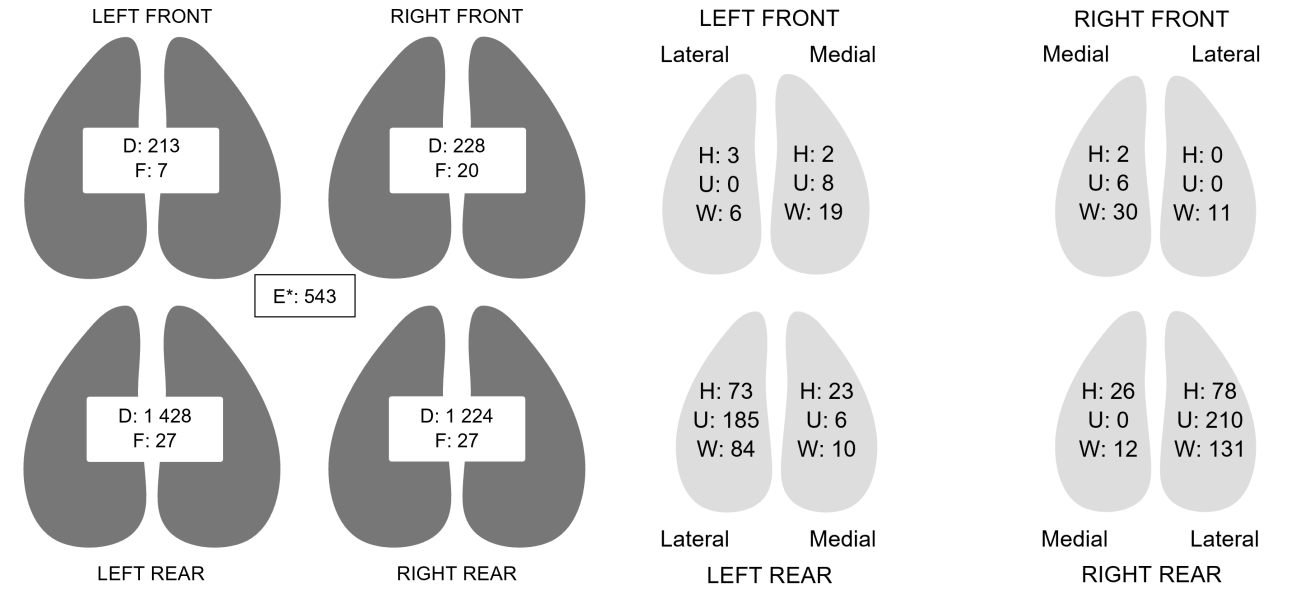


Figure 3.2 Left: Total count of infectious claw lesions (digital and interdigital dermatitis, DD; interdigital phlegmon, IP; and heel erosion, HE) per foot for the six-year study period (note that heel erosion data were not split per point of lesion by the hoof trimmer). Right: Total count of the most common non-infectious claw lesions (sole haemorrhage, SH; sole ulcer, SU; white line lesion and/or separation, WLDS) per foot and per claw position for the six-year study period

The SAS frequency procedure output for lesion by foot (location) and lesion by housing system are given in Addenda 3A1 and 3A2. Independence of both the prevalence of lesions and foot (location) and the prevalence of lesion and housing were confirmed using chi-square analysis ($P < 0.0001$). CA was performed between lesions and foot (location) (Figure 3.3) and lesion and housing system (Figure 3.4) in order to further explore the dependencies identified by the frequency procedure (Addenda 3A3 and 3A4).

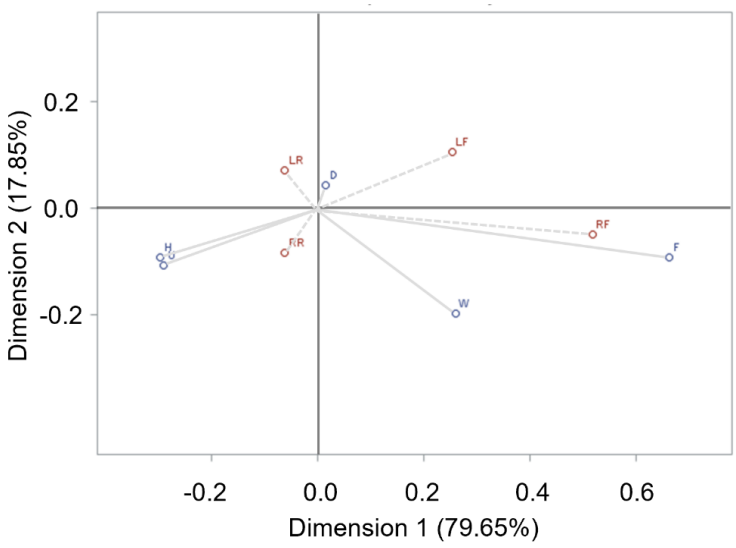


Figure 3.3 Correspondence analysis between lesion and foot (location)

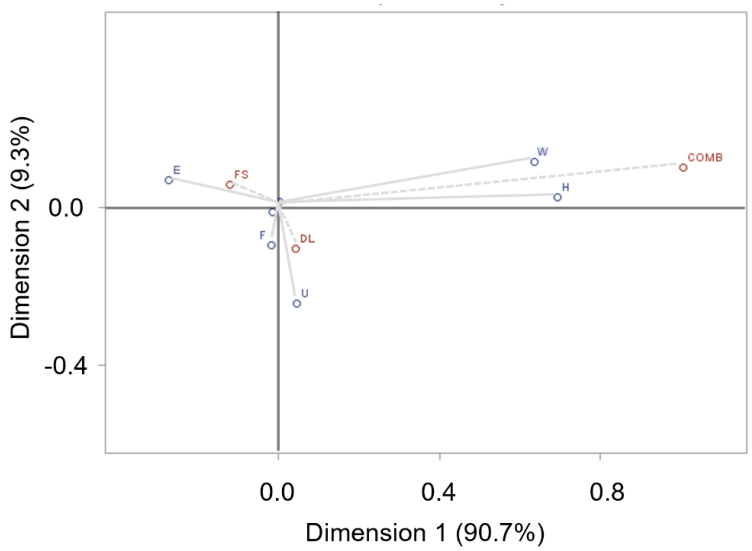


Figure 3.4 Correspondence analysis between lesion and housing system

3.4 Discussion

The recording, identification, and management of claw lesions add to the complexity of finding sustainable solutions to reduce the occurrence of lameness in dairy cattle. In this study, hoof-trimming data from five intensively managed dairy farms in the central region of SA were analysed, including both DL and FS systems. The system for identification and classification of claw lesions was based on hoof- trimming data received in the form of a local hoof trimmer's *Hoof-Trimming Report* that was also common to the *Claw Lesion Identification in Dairy Cattle* brochure.

Infectious lesions were the most common claw disorder, accounting for 77% of all recorded lesions on farms between 2014 and 2019. These results are similar to reports on Dutch and Canadian dairy cattle, where infectious lesions were also more prevalent compared to non-infectious lesions (Van der Waaij *et al.*, 2005; Chapinal *et al.*, 2013). Of infectious lesions recorded in this study, DD accounted for 64% of all recorded lesions, followed by HE (11%) and IP (1.7%). Numerically, SU (8.59%), WLD (6.27%), and SH (4.28%) accounted for most of the non-infectious lesions. This agrees with previous research in which digital dermatitis was consistently recorded as the most prevalent lesion (DeFrain *et al.*, 2013; Solano *et al.*, 2016; Charfeddine & Pérez-Cabal, 2017). These authors also noted SU and WL as the most prevalent non-infectious claw lesions recorded, similar to this study, while DeFrain *et al.* (2013) and Solano *et al.* (2016) recorded TU as another significant lesion. In a study on German Holstein Friesian cows using the official ICAR nomenclature, Stock *et al.* (2013) reported DD as the most prevalent infectious lesion, with SU and IH as the most prevalent non- infectious lesions (Sölzer *et al.*, 2022), which agrees with the results of the current study. Despite using different claw classification systems and lesion descriptions, most studies confirmed DD and EH, and SH and SU, respectively, as the two most prevalent lesions (Buch *et al.*, 2011; Chapinal *et al.*, 2013; Charfeddine & Pérez-Cabal, 2017; Afonso *et al.*, 2020).

In studies that made the distinction between lesions occurring in rear and front feet, lesions occurred more frequently in the rear feet (Van der Waaij *et al.*, 2005; Chapinal *et al.*, 2013; Solano *et al.*, 2016), similar to results in the current study. This is likely due to rear claws being more exposed to manure and urine, which,

in FS housing systems, may be attributed to the front feet being placed in the stall and the rear feet in the aisle. Additionally, claw horn lesions (SU, SH, WL, and TU) tend to develop more regularly in the rear claws because of overloading of the lateral hind claws (Sadiq *et al.*, 2020).

Results from the SAS frequency procedure, which included chi-square tests for independence between lesion and foot (location) and between lesion and housing, in both cases were highly significant ($P < 0.0001$), indicating potential associations. In the first CA, lesions SU and SH showed high similarity for foot and lesion association. In addition, the occurrence of these two associated lesions is more highly associated with rear than front feet. SU is a continuous break in the epidermis of the sole horn that exposes the corium, of which SH is regarded as an early sign (Van der Waaij *et al.*, 2005; Van Amstel & Shearer, 2006; Solano *et al.*, 2016), which may explain the association between these two lesions here.

DD and IP are important infectious claw diseases, with bacteria often entering the tissue as a result of mechanical injury and/or softening of the skin and claw horn, which may occur as a result of a non-infectious lesion and/or mechanical damage to the claw and foot tissues. DD is manifested as an ulceration on the planar surface of the foot, often extending into the interdigital space, while interdigital phlegmon is defined as a necrotic infectious disease that results in decay of the foot tissues (Abubakar & Manzoor, 2018; Garvey, 2022). In cases of IP, the bacterium often isolated is *Fusobacterium necrophorum* (Abubakar & Manzoor, 2018). In this study, the infectious lesion DD showed the greatest association with non-infectious lesions SH and SU in terms of lesion by foot (location), while infectious lesion IP differed from this group. The weak association between IP and the other claw lesions under study may be a result of its low prevalence recorded (only 1.68% of total lesions recorded, compared to 64% for DD). IP was also more closely associated with the front feet, which was opposite to the higher association of DD with the rear feet. According to Garvey (2022), approximately 90% of DD is found in the rear feet, similar to the current study.

Globally, dairy cattle are managed under a wide variety of housing systems, including tie-stall barns, cubicle or FS housing systems, DL, and on pastures (Shearer & Van Amstel, 2007; Cook & Nordlund, 2009; Garvey, 2022). Indoor systems offer animals improved protection from extreme weather, improved access to feed and water, and a comfortable place for cows to lie down (Shearer & Van Amstel, 2007), but do expose cows to more concrete walkways, which predispose claws to non-infectious lesions (Somers *et al.*, 2005; Garvey, 2022). Excess manure and moisture have been shown to predispose cows to infectious lesions (Chapinal *et al.*, 2013; Garvey, 2022), and indoor housing systems generally show the highest rate of lameness (Shearer & Van Amstel, 2007; Cook & Nordlund, 2009).

In this study, the CA between lesion and housing system showed higher associations between DD, IP, and SU, while HE differed, while the categories of lesions expressed as a percentage were similar for both the DL and FS housing systems for all four of these lesions. Somers *et al.* (2005) noted that the presence of HE may predispose cows to other infectious claw lesions (e.g. DD and IP). In the current study, DD, IP, and HE were not highly associated in the lesion by housing CA. The foot (location) of HE was, however, not recorded and it was excluded from the lesion by foot (location) CA. It has previously been reported that the odds of DD occurring are two times higher in cows housed indoors with access to an exercise area, but an outdoor area that is wet or unhygienic could lead to increased prevalence (Solano *et al.*, 2016). In general, DD, SU, and WL are reported as the three most frequently recorded disorders indoors, and shared risk factors included the presence of other non-infectious lesions and housing type (Solano *et al.*, 2016).

Non-infectious lesions WL and SH showed a higher association with each other than with other lesions under study, and these were more highly associated with the combination housing system (DL+FS). The

white line forms the flexible junction between the hard claw wall and the softer sole horn. It is the softest part of the claw and is susceptible to mechanical damage due to its location on the weight-bearing surface (Shearer & Van Amstel, 2007; Van der Spek, 2015). The prevalence of foot lesions has been reported to differ among housing types, but DD remains the most common lesion, followed by SU and WL (Buch *et al.*, 2011; Solano *et al.*, 2016; Garvey, 2022).

The data included in this study were captured in hard copy with over 30 different lesion identification codes recorded by the hoof trimmer. Given these results, it seems that this number may be drastically reduced. In terms of infectious lesions, DD was by far the most prevalent in the current study, and, based on the correspondence analyses, one could argue that infectious lesions may be broadly recorded as present or absent. The three non-infectious lesions that were numerically the most prevalent were SH, SU, and WL, albeit each at very low rates (less than 0.5% of all observations recorded). It is important to note that, compared to the total number of cows subjected to hoof trimming, the overall occurrence of lesions was only 4.58%, with DD at 2.93%, E at 0.51%, SU at 0.39%, and WL at 0.29%. This suggests that the identification of specific claw lesions might be a heavy-handed approach to the management of lameness in dairy herds. Infectious and non-infectious lesions have different risk factors and, hence, different strategies for prevention and management (Buch *et al.*, 2011; Chapinal *et al.*, 2013; Garvey, 2022). Dividing the recording sheet simply into two sections, infectious versus non-infectious lesions, may provide sufficient information for the hoof trimmer and the farmer to effectively manage the risk factors associated with each lesion category.

Researchers agree that prevention, early diagnosis, and prompt, effective treatment are the cornerstones of effective lameness management (Afonso *et al.*, 2020; Bell *et al.*, 2022; Garvey, 2022). The results of this study indicate that claw recording remains an early detection tool for an infectious versus a non-infectious problem in the herd.

Electronic record-keeping will be more convenient from a practical perspective and allows faster, more accurate recording by hoof trimmers, while facilitating the creation of a practical summary for the farmer to promptly address lameness issues (DeFrain *et al.*, 2013). From a data analysis perspective, electronic record-keeping is useful for benchmarking and genetic improvement (Chapinal *et al.*, 2013), as well as increasing efficiency and accuracy of data collection for research purposes (Shearer & Van Amstel, 2007). The results of this study indicate that recording in the South African dairy system may be simplified, which might facilitate more routine trimming and a larger database for subsequent studies and potential inclusion in selection.

In conclusion, results of this study not only highlighted the complexity of lesion data but also indicated that specific associations between different lesions could lead to simplifying the recording thereof. It is important that the description and recording of claw lesions are made as easy as possible for accurate and consistent recording. Consolidating the most informative claw lesions into categories will aid in the practical prevention, management, and treatment of lameness on-farm.

References

Abubakar, M., Manzoor, S., 2018. *Animal Welfare*. https://doi.org/10. 5772/intechopen.70919

Afonso, J.S., Bruce, M., Keating, P., Raboisson, D., Clough, H., Oikonomou, G., Rushton, J., 2020. Profiling detection and classification of lameness methods in British dairy cattle research: A systematic review and meta-analysis. *Front. Vet. Sci.* 7:542. https://doi.org/10.3389/fvets.2020.00542

Banga, C.B., Neser, F.W.C, Garrick, D.J., 2014. Breeding objectives for Holstein cattle in South Africa. *S. Afr. J. Anim. Sci.* 44(3):199–214. http://dx.doi.org/10.4314/sajas.v44i3.1

Bell, N., Bacon, D., Craven, E., Crowe, S., Newsome, R., Oikonomou, G., Pedersen, S., Reader J., Wilson, J., 2022. Dairy cattle lameness: A roundtable discussion. L*ivestock* 27(Sup3):S1–S11. https://doi.org/10.12968/live.2022.27.S1.115

Benzécri, J.P., 1973. *L'analyse des données: T. 2, l'analyse des correspondances* [Data analysis: T. 2, Correspondence analysis]. Paris: Dunod.

Buch, L.H., Sørensen, A.C., Lassen, J., Berg, P., Eriksson, J-Å., Jakobsen, J.H., Sørensen, M.K., 2011. Hygiene-related and feed-related hoof diseases show different patterns of genetic correlations to clinical mastitis and female fertility. *J. Dairy Sci.* 94(3):1540–1551. https://doi.org/10.3168/jds.2010-3137

Chapinal, N., Koeck, A., Sewalem, A., Kelton, D.F., Mason, S., Cramer, G., Miglior, F., 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. *J. Dairy Sci.* 96(4):2596–2604. http://dx.doi.org/10.3168/jds.2012-6071

Charfeddine, N. & Pérez-Cabal, M.A., 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100(1):653–665. https://doi.org/10.3168/jds.2012-6017

Cook, N.B. & Nordlund, K.V., 2009. The influence of the environment on dairy cow behavior, claw health and herd lameness dynamics. *Vet. J.* 179(3):360–369. https://doi.org/10.1016/j.tvjl.2007.09.016

DALRRD, 2022. Livestock Production. In: *Animal Production. Department of Agriculture, Land Reform, and Rural Development of the Republic of South Africa*. http://www.old.dalrrd.gov.za/Branches/ Agricultural-Production-Health-Food-Safety/Animal-Production/ Livestock-Production. Accessed 1 April, 2023.

DeFrain, J.M., Socha, M.T., Tomlinson, D.J., 2013. Analysis of foot health records from 17 confinement dairies. *J. Dairy Sci.* 96(11):7329–7339. https://doi.org/10.3168/jds.2012-6017

Ducrocq, V., Cadet, A., Patry, C., Van der Westhuizen, L., Van Wyk, J.B., Neser, F.W.C., 2022. Two approaches to account for genotype-by-environment interactions for production traits and age at first calving in South African Holstein cattle. *Genet. Sel. Evol.* 5443. https://doi.org/10.1186/s12711-022-00735-5

Du Plessis, I., 2007. Foot health in housed cattle: A review. *S. Afr. J. Anim. Sci.* 8:11–17.

Garvey, M., 2022. Review: Lameness in dairy cow herds: Disease aetiology, prevention and management. *Dairy* 2022(3):199–210. https://doi.org/10.3390/dairy3010016

Heringstad, B., Egger-Danner, C., Charfeddine, N., Pryce, J.E., Stock, K.F., Kofler, J., Sogstad, A.M., Holzhauer, M., Fiedler, A., Müller, K., Nielsen, P., Thomas, G., Gengler, N., de Jong, G., Ødegård, C., Malchiodi, F., Miglior, F., Alsaaod, M., Cole, J.B., 2018. Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *J. Dairy Sci.* 101(6):4801–4821. https://doi.org/10.3168/jds.2017-13531

ICAR Claw Health Atlas. In: *ICAR Technical Series* (ISSN: 92-95014-14-6 and ISBN: 92-95014-18). International Committee on Animal Recording (ICAR). 2020. https://www.icar. org/index.php/publications-technical-materials/technical-series- and-proceedings/atlas-claw-health-and-translations/. Accessed 21 February 2023

Meissner, H.H., Scholtz, M.M., Palmer, A.R., 2013. Sustainability of the South African Livestock Sector towards 2050. Part 1: Worth and impact of the sector. *S. Afr. J. Anim. Sci.* 43(3):282–297. http://dx.doi.org/10.4314/sajas.v43i3.5

Mhlongo, N.L., 2019. Evaluation of claw health of dairy cattle housed in dirt lot vs free stall in TMR systems in the central region of South Africa. Dissertation (MSc (Agric)), University of Pretoria.

Microsoft Corporation, 2018. *Microsoft Excel*, available at: https:// office.microsoft.com/excel

Oehm, A.W., Knubben-Schweizer, G., Rieger, A., Stoll, A., Hartnack, S., 2019. A systematic review and meta-analyses of risk factors associated with lameness in dairy cows. *BMC Vet. Res.* 15:346. https://doi.org/10.1186/s12917-019-2095-2

Ring, S.C., Twomey, A.J., Byrne, N., Kelleher, M.M., Pabiou, T., Doherty, M.L., Berry, D.P., 2018. Genetic selection for hoof health traits and cow mobility scores can accelerate the rate of genetic gain in producer-scored lameness in dairy cows. *J. Dairy Sci.* 101(11):10034–10047. https://doi.org/10.3168/jds.2018-15009

Sadiq, M.B., Ramanoon, S.Z., Mossadeq, W.M.S., Mansor, R., Hussain, S.S.S, 2019. Review: Dairy farmers' perceptions of and actions in relation to lameness management. *Anim.* 9(5):270. https://doi.org/10.3390/ani9050270

Sadiq, M.B., Ramanoon, S.Z., Mansor, R., Hussain, S.S.S., Mossadeq, W.M.S., 2020. Claw trimming as a lameness management practice and the association with welfare and production in dairy cows. *Anim.* 10(9):1515. https://doi.org/10.3390/ani10091515

SAS Institute Inc. 2015. SAS/STAT® 14.1 User's Guide. Cary, NC: SAS Institute Inc.

Shearer, J.K. & Van Amstel, S.R., 2007. Effect of flooring and/or flooring surfaces on lameness disorders in dairy cattle. In: *Proc. of the Western Dairy Herd Management Conference*. 7–9 March, Reno, NV, USA. http://www.wdmc.org/2007/shearer.pdf

Solano, L., Barkema, H.W., Mason, S., Pajor, E.A., LeBlanc, S.J., Orsel, K., 2016. Prevalence and distribution of foot lesions in dairy cattle in Alberta, Canada. *J. Dairy Sci.* 99(8):6828–6841. https://doi.org/10.3168/jds.2016-10941

Sölzer, N., May, K., Yin, T., König, S., 2022. Genomic analysis of claw disorders in Holstein cows: Genetic parameters, trait associations, and genome-wide associations considering interactions of SNP and heat stress. *J. Dairy Sci.* 105(10):8218–8236. https://doi.org/10.3168/jds.2022-22087

Somers, J.G.C.J., Frankena, K., Noordhuizen-Stassen, E.N., Metz, J.H.M., 2005. Risk factors for digital dermatitis in dairy cows kept in cubicle houses in The Netherlands. *Prev. Vet. Med. 71*:11–21. https://doi.org/10.1016/j.prevetmed.2005.05.002

Stock, K.F., Cole, J., Pryce, J., Gengler, N., Bradley, A., Andrews, L., Heringstad, B., Egger-Danner, C., 2013. Standardization of health data. ICAR guidelines including health key. In: C. Egger-Danner, O.K. Hansen, K. Stock, J.E. Pryce, J. Cole, N. Gengler, B. Heringstad (eds), ICAR Technical Series (Challenges and benefits of health data recording in the context of food chain quality, management and breeding), ICAR, Via G. Tomasseti, Rome, Italy. https://hdl.handle.net/2268/216992

Van Amstel, S.R. & Shearer, J.K., 2006. Review of pododermatitis circumscripta (ulceration of the sole)in dairy cows. *J. Vet. Intern. Med.* 20:805–811. https://doi.org/10.1111/j.1939-1676.2006.tb01789.x

Van der Spek, D., 2015. Genetic background of claw health in dairy cattle. PhD thesis, Wageningen University, The Netherlands.

Van der Waaij, E.H., Holzhauer, M., Ellen, E., Kamphuis, C., de Jong, G., 2005. Genetic parameters for claw disorders in Dutch dairy cattle and correlation with conformation traits. *J. Dairy Sci.* 88(10):3672–3678. https://doi.org/10.3168/jds.S0022-0302(05)73053-8

Van Marle-Köster, E., Mhlongo, N.L., Tucker, J., 2020. Hoof trimming data for improving claw health in South African dairy cattle: Understanding claw health can improve cow comfort and welfare. In:

IDF Animal Health Report N° 14. International Dairy Federation. https://shop.fil-idf.org/products/idf-animal- health-report-n-14. Accessed 25 March 2023

Visser, C., Van Marle-Köster, E., Myburgh, H., de Freitas, A., 2020. Phenomics for sustainable production in the South African dairy and beef cattle industry. *Animal Front.* 10(2):12–18. https://doi.org/10.1093/af/vfaa003

Zinpro® Corporation, 2008. *Claw Lesion Identification in Dairy Cattle* (D40-08-30-07). Eden Prairie, MN, USA.

ADDENDA TO CHAPTER 3

ROUTINE HOOF-TRIMMING DATA PROVIDES INSIGHT INTO THE OCCURRENCE OF CLAW LESIONS IN HOLSTEIN HERDS IN THE CENTRAL REGION OF SOUTH AFRICA

Addendum 3A1: SAS output: Cross-tabulation of lesion and foot position

Table of lesion by location

Frequency / Percent / Row Pct / Col Pct	location				
lesion	LF	LR	RF	RR	Total
D	213	1428	228	1224	3093
	5.20	34.84	5.56	29.86	75.46
	6.89	46.17	7.37	39.57	
	82.56	77.78	76.77	71.66	
F	7	27	20	27	81
	0.17	0.66	0.49	0.66	1.98
	8.64	33.33	24.69	33.33	
	2.71	1.47	6.73	1.58	
H	5	96	2	104	207
	0.12	2.34	0.05	2.54	5.05
	2.42	46.38	0.97	50.24	
	1.94	5.23	0.67	6.09	
U	8	191	6	210	415
	0.20	4.66	0.15	5.12	10.12
	1.93	46.02	1.45	50.60	
	3.10	10.40	2.02	12.30	
W	25	94	41	143	303
	0.61	2.29	1.00	3.49	7.39
	8.25	31.02	13.53	47.19	
	9.69	5.12	13.80	8.37	
Total	258	1836	297	1708	4099
	6.29	44.79	7.25	41.67	100.00

Addendum 3A2: SAS output: Cross-tabulation of lesion and housing

Frequency Expected Deviation Cell Chi-Square Percent Row Pct Col Pct	Table of lesion by housing lesion housing			
		COMB	**DL**	**FS**	**Total**
	D	91	671	1042	1804
		97.622	663.94	1042.4	
		-6.622	7.0595	-0.438	
		0.4491	0.0751	0.0002	
		2.88	21.23	32.97	57.09
		5.04	37.20	57.76	
		53.22	57.70	57.06	
	E	0	237	509	746
		40.369	274.56	431.07	
		-40.37	-37.56	77.925	
		40.369	5.1373	14.087	
		0.00	7.50	16.11	23.61
		0.00	31.77	68.23	
		0.00	20.38	27.88	
	F	2	19	25	46
		2.4892	16.93	26.581	
		-0.489	2.0703	-1.581	
		0.0962	0.2532	0.094	
		0.06	0.60	0.79	1.46
		4.35	41.30	54.35	
		1.17	1.63	1.37	
	H	29	56	56	141
		7.6301	51.893	81.477	
		21.37	4.1066	-25.48	
		59.852	0.325	7.9662	
		0.92	1.77	1.77	4.46
		20.57	39.72	39.72	
		16.96	4.82	3.07	
	U	11	113	108	232
		12.554	85.385	134.06	

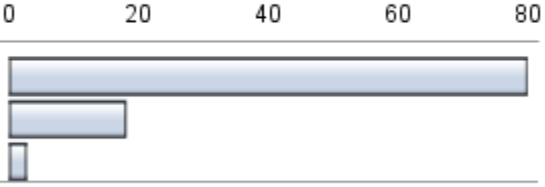
		-1.554	27.615	-26.06	
		0.1925	8.9313	5.0661	
		0.35	3.58	3.42	7.34
		4.74	48.71	46.55	
		6.43	9.72	5.91	
	W	38	67	86	191
		10.336	70.295	110.37	
		27.664	-3.295	-24.37	
		74.045	0.1545	5.3806	
		1.20	2.12	2.72	6.04
		19.90	35.08	45.03	
		22.22	5.76	4.71	
	Total	171	1163	1826	3160
		5.41	36.80	57.78	100.00

Addendum 3A3: SAS output: Correspondence analysis of lesion by foot (location)

The CORRESP Procedure

Inertia and Chi-Square Decomposition

Singular Value	Principal Inertia	Chi-Square	Percent	Cumulative Percent
0.16384	0.02684	110.028	79.65	79.65
0.07756	0.00602	24.657	17.85	97.50
0.02902	0.00084	3.451	2.50	100.00
	0.03370	138.136	100.00	



Pr > Chisq < .0001 DF = 12

Row Coordinates

	Dim1	Dim2
D	0.0157	0.0424
F	0.6633	-0.0924
H	-0.2968	-0.0912
U	-0.2892	-0.1080
W	0.2612	-0.1978

Column Coordinates

	Dim1	Dim2
LF	0.2536	0.1058
RF	0.5185	-0.0488
LR	-0.0626	0.0707
RR	-0.0612	-0.0835

Addendum 3A4: SAS output: Correspondence analysis of lesion by housing

Inertia and Chi-Square Decomposition

Singular Value	Principal Inertia	Chi-Square	Percent	Cumulative Percent	0 20 40 60 80
0.25269	0.06385	201.773	90.70	90.70	
0.08094	0.00655	20.700	9.30	100.00	
	0.07040	222.473	100.00		Pr > Chisq < .0001 DF = 10

Row Coordinates

	Dim1	Dim2
D	-0.0139	-0.0099
E	-0.2737	0.0707
F	-0.0186	-0.0964
U	0.0465	-0.2429
W	0.6349	0.1162
H	0.6947	0.0268

Column Coordinates

	Dim1	Dim2
DL	0.0415	-0.1052
FS	-0.1207	0.0574
COMB	1.0064	0.1029

CHAPTER 4

PHENOTYPIC AND GENETIC ANALYSES OF CLAW LESIONS IN TMR HOLSTEIN HERDS IN SOUTH AFRICA

This article has been prepared and submitted for publication in *Archives Animal Breeding*.

R.C. Joubert[1], B.E. Mostert[1], A.Masenge[2], E. van Marle-Köster[1]

[1]Department of Animal Science, University of Pretoria, Private Bag X20, Hatfield, Pretoria 0028, South Africa
[2]Department of Statistics, University of Pretoria, Private Bag X20, Hatfield, Pretoria 0028, South Africa

4 Phenotypic and genetic analyses of claw lesions in TMR Holstein herds in South Africa

4.1 Introduction

Claw lesions in dairy cattle have been widely reported as the primary cause of lameness (Huxley, 2013; Solano *et al*., 2016), which raises animal welfare concerns (Oehm *et al*., 2019; Sadiq *et al*., 2019) and affects the profitability of dairy herds due to losses incurred from reduced milk yield and reproduction, and premature culling (Chapinal *et al*., 2013; Afonso *et al*., 2020). Among the types of lesions reported, digital dermatitis (DD), sole ulcers (SU), and white line (WL) lesions tend to be the most significant lesions reported in dairy herds all over the world (Christen *et al*., 2015; Solano *et al*., 2016; Shearer & Van Amstel, 2017), as well as in South Africa (Joubert *et al*., 2023).

Breeding strategies to improve functional traits such as udder health and fertility have proven to be successful (Heringstad *et al*., 2012; Fleming *et al*., 2018), but the same progress has not been made in claw conformation and lesions (Egger-Danner *et al*., 2015). Selection for claw traits presents a more permanent solution to the problem and researchers agree that hoof-trimming data can be used for genetic evaluations (Koenig *et al*., 2005; Chapinal *et al*., 2013; Ødegård *et al*., 2013). However, the use of different sources of data, different classification systems, and a multitude of definitions in the reference groups limits the comparison across herds and decreases the usability of the recordings for phenotypic and genetic analyses (Charfeddine & Pérez-Cabal, 2017; Heringstad *et al*., 2018; Afonso *et al*., 2020). Despite guidelines by the International Lameness Committee (ILC) and the International Committee for Animal Recording (ICAR), different recording systems are used by hoof trimmers within and between countries (Oehm *et al*., 2019; Afonso *et al*., 2020). Different countries collect vastly different amounts of data on claw lesions, collecting information on up to 20 different traits, with the level of information also varying widely, with several countries also recording information on the severity grades of the lesions observed (Christen *et al*., 2015). In addition to the difficulty and effort of performing routine claw trimming, data sets often lack complete pedigrees and tend to be limited in size for genetic evaluations (Heringstad *et al*., 2018). Accurate genetic analysis requires regular, consistent phenotypic recording, which means that simplifying the description and recording of claw lesions is important to facilitate farmer compliance (Egger-Danner *et al*., 2015; Zavadolová *et al*., 2021). In addition, specific phenotypic associations between individual claw lesions and categories may provide valuable information for hoof trimmers regarding the easiest and most effective way to record data on the farm to help prevent, manage, and treat lameness (Joubert *et al*., 2023).

Several researchers have estimated phenotypic correlations between individual claw lesions and lesion categories, which often show significant variability. This variability can be attributed to a number of factors, including the methods used for recording, the completeness of the data, and the qualifications of the person conducting the recording, i.e. whether it's a farmer, hoof trimmer, or veterinarian. Weak, positive correlations were found by Van der Waaij *et al.* (2005) between sole haemorrhage (SH) and WL (+0.10), WL and SU (+0.09), and SH and SU (+0.08), while Häggman & Juga (2013) found mostly weak, negative correlations between the same lesions: -0.24, -0.12, and -0.18, respectively. Stronger, positive phenotypic correlations of +0.18 between SH and both DD and heel horn erosion (HE), +0.35, +0.38 and +0.42 between WL and HE, DD, and SH, respectively, and +0.38 and +0.51 between HE and DD were reported by Capion *et al.* (2009). In addition, the combined trait analysis of double sole, interdigital hyperplasia and sole ulcers reported by Capion *et al*. (2009) showed positive correlations with both DD and HE (+0.14 and +0.26).

Claw disorders may be defined as binary traits for genetic evaluations, and analysed using linear, logistic, or threshold models, with estimates of heritability being slightly lower from linear models than from the other two (Malchiodi *et al*., 2017; Heringstad *et al*., 2018). Among the infectious lesions, DD (0.07–0.16) and interdigital hyperplasia, or IH, (0.01–0.39) tend to have the highest heritability and interdigital phlegmon, or IP, (0.01–0.06) tends to have the lowest, while SU generally has the highest estimated heritability under the non-infectious lesions (0.03–0.17), with the estimated heritability of SH tending to be the lowest, at between 0.02 and 0.09 (Van der Spek *et al*., 2013; Pérez-Cabal & Charfeddine, 2015; Malchiodi *et al*., 2017; Oliveira Junior *et al*., 2021). Genetic correlations between specific claw disorders tend to be low, ranging from -0.18 between DD and SU to +0.18 between SU and IH (Van der Waaij *et al*., 2005). Categorising claw diseases into two groups, Buch *et al.* (2011) found genetic correlations between traits within groups to be higher than correlations between traits from different groups (≤ +0.23). In particular, the low correlation (+0.08) between infectious and non-infectious lesions was confirmed by Chapinal *et al.* (2013). Digital dermatitis has been shown to have positive correlation with all the other claw diseases, with the largest correlation being with IH at +0.57 (Malchiodi *et al*., 2017).

Despite the low heritability of claw traits, researchers agree that the genetic variability is satisfactory and that genetic selection is a viable option for improving these in dairy cattle (Van der Waaij *et al*., 2005; Van der Spek *et al.*, 2013; Pérez-Cabal & Charfeddine, 2015). A number of European and Scandinavian countries, including the Netherlands, Denmark, Finland, Sweden and Norway, routinely carry out genetic evaluations for claw health and results indicate that it is possible to produce reliable breeding values using data currently available (Heringstad *et al*., 2018). In South Africa, hoof trimmers are among the only sources of data regarding claw lesions, as producers do not routinely collect this information. In addition, local participation in the South African National Milk Recording Scheme does not compare favourably with other countries globally. In 2018, only approximately 13% of the national herd participated in official milk recording with either the Agricultural Research Council (ARC) or SA Stud Book (https://my.icar.org/stats/list). This has resulted in limited pedigrees and small complete datasets being available for genetic analysis.

In this study, the aim was to analyse phenotypic and genetic associations among (a) total lesions (TL), (b) infectious lesions (IL), (c) non-infectious lesions (NL) and (d) digital and interdigital dermatitis (DD) in South African Holstein cattle managed under a total mixed ration (TMR) feeding system.

4.2 Material and methods

The study received ethical clearance (NAS292/2020) from the Ethics Committee at the University of Pretoria within the Faculty of Natural and Agricultural Sciences. Five herds of Holstein cattle under a TMR management system were selected for this study, based on the availability of hoof-trimming data, pedigree information, and participation in the South African National Milk Recording Scheme. These five farms used hoof trimming as part of their management protocol. The local hoof trimmer based their assessments on the claw lesion identification brochure that was co-developed by Zinpro® Corporation (D40-08-30-07; Eden Prairie, MN, USA) and the International Lameness Committee (2008). Herd size data (Table 4.1) was received from the SA Stud Book Association (SA Stud Book, Bloemfontein, South Africa) and represented all female animals on the farm.

Table 4.1 Total herd size per farm per year over the 10-year study period

Farm	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	Average
A	708	734	757	665	543	769	998	1 046	1 105	1 088	841
B	1 111	1 380	1 626	1 735	1 701	1 985	2 008	1 959	1 649	1 715	1 833
C	526	510	614	633	608	826	1 012	979	1 478	1 052	824
D	472	365	793	813	770	1 225	1 306	1 385	1 378	1 421	967
E	1 509	1 545	1 628	1 690	1 724	2 215	2 149	-[a]	-[a]	-[a]	2 149

[a]Farm E stopped milk recording in 2021; therefore, herd size data is not available for 2021, 2022, or 2023

Records of the most common claw diseases scored by the hoof trimmer between 2014 and 2023 were used in the present study. Claw lesions were recorded per cow as the presence or absence of infectious lesions (combined digital and interdigital dermatitis, DDID; interdigital phlegmon, IP; and heel erosion, HE) or non-infectious lesions (combined white line disease and white line separation, WLDS; sole ulcer, SU; and sole haemorrhage, SH). Three additional categories (the totals of all lesions, infectious lesions, and non-infectious lesions) were also evaluated, as was the presence of individual total lesions in front and rear feet.

Many cows were trimmed more than once within a lactation and also trimmed in more than one lactation. However, for this analysis, only the information from the first recorded trimming was used (Uggla *et al*., 2008; Laursen *et al*., 2009). The edited dataset included 23 334 hoof-trimming records collected from five Holstein dairy herds between 2014 and 2023. Of these, 11 283 records were associated with cows that could be identified as registered animals at SA Stud Book.

The final dataset used for phenotypic analyses consisted of 3 650 unique cows with only their first trimming records per year included. Some cows had more than one disorder, leading to a mismatch in the total of prevalence records and the percentage of cows with a claw disorder. The non-parametric Spearman correlation was performed using SAS® 9.4 (SAS Institute Inc., 2018) to test for correlations between the various lesions and lesion categories. The Spearman rho is equivalent to the phi coefficient used to measure association between dichotomous data. The Spearman rho coefficient ranges between -1 and 1 with phi $\phi = 1$ implying a perfect positive association in which the presence of one variable perfectly predicts the presence of the other variable, while phi=-1 indicates that the presence on one variable perfectly predicts the absence of another variable (Table 4.2). In addition, the odds ratios were calculated to investigate the probability of specific lesions influencing the occurrence of each other.

Table 4.2 Phi coefficient categories (Akoglu, 2018)

Phi coefficient	Strength of association
$\lvert\phi\rvert < 0.1$	Negligible
$0.01 \leq \lvert\phi\rvert < 0.3$	Weak
$0.03 \leq \lvert\phi\rvert < 0.5$	Moderate
$0.5 \leq \lvert\phi\rvert < 0.7$	Strong
$\lvert\phi\rvert \geq 0.7$	Very strong

The final study population used to estimate genetic parameters amounted to 3 650 animals with repeated trimming measurements (11 283 records). The pedigree file included the relationships of 7 921 animals,

representing the three-generations lineage of these cows. Genetic parameters were estimated for claw lesions (TL, IL, NL and DD) with the restricted maximum likelihood (REML) procedure using analytical gradients, fitting single-trait linear animal models using the VCE 6.0 software package (Groeneveld *et al*., 2008). The model (Equation 1) included linear regression of age in months and the fixed effect of herd-year-season. The number of repeated records did not warrant the inclusion of a permanent environmental effect, so only the additive genetic effect (animal) was included as a random effect.

$$y_{ijklm} = \mu + hys_{jk} + age_{jl} + animal_{ij} + e_{ijklm} \quad (1)$$

where y_{ijklm} = observation of trait t on animal i (t=total, infectious, non-infections claw, or digital dermatitis), μ = overall mean, hys_{jk} =fixed effect for trait t of the contemporary group k constructed as animals measured in the same herd, year, and season, age_{jl} = linear regression modelling the effect of age at measurement on trait t, $animal_{ij}$ = random direct additive genetic effect of animal i and e_{ijklm} = random residual error.

4.3 Results

Across 3 650 unique records, 56.32% of cows in this study exhibited at least one claw lesion (whether infectious or non-infectious) (Table 4.3). The majority of lesions recorded were infectious (40.87%) versus only 9.74% non-infectious lesions. The highest incidence was for DDID, with almost 40% of records indicating the occurrence of digital or interdigital dermatitis in at least one foot.

Table 4.3 Cow-level prevalence (number and percentage) of the claw disorders recorded on five TMR Holstein farms in South Africa between 2014 and 2023

Claw disorder	No. lesions present	Lesion presence (%)
Total lesions	1 315	56.32
Total infectious lesions	1 059	40.87
Digital and interdigital dermatitis (DDID)	1 035	39.58
Heel erosion (HE)	410	12.65
Interdigital phlegmon (IP)	36	0.99
Total non-infectious lesions		9.74
Sole ulcer (SU)	102	2.87
Sole haemorrhage (SH)	63	1.76
White line disease and separation (WLDS)	111	3.14

Spearman correlation coefficients between the different lesions and categories of lesions are presented in Table 4.4. Negligible negative correlations were observed between total individual infectious and non-infectious lesions ($P < 0.05$), while within the infectious lesions category, total DDID was weakly positively associated with total HE ($|\phi| = 0.240$, $P < 0.01$). Total HE and total IP were weakly positively associated with total infectious lesions (($|\phi| = 0.235$, $P < 0.01$ and ($|\phi| = 0.156$, $P < 0.01$), while DDID was almost perfectly associated with the occurrence of total infectious lesions (($|\phi| = 0.984$, $P < 0.01$). Within the non-infectious lesions, SH was moderately positively associated with total non-infectious lesions ($|\phi| = 0{,}425$, $P < 0.01$) and the occurrence of SU and WLDS were both strongly positively associated with total non-infectious lesions ($|\phi| = 0.543$, $P < 0.01$ and $|\phi| = 0.576$, $P < 0.01$, respectively). While the association between DDID and HE within infectious lesions is weak, the relationships observed among non-infectious lesions (SH, SU, and WLDS) are moderate to strong.

Table 4.4 Spearman correlation coefficients between total lesion categories

	HE (total)	IP (total)	DDID (total)	IL (total)	SU total)	SH (total)	WLDS (total)
HE (total)							
IP (total)	0.008						
DDID (total)	**0.240**[a]	0.011					
IL (total)	**0.235**[a]	**0.156**[a]	**0.984**[a]				
SU (total)	-0.034[b]	-0.017	0.015	0.012			
SH (total)	-0.034[a]	-0.013	-0.065[a]	-0.066[a]	0.016		
WLDS (total)	-0.043[a]	-0.018	-0.041[a]	-0.043[a]	-0.020	0.001	
NL (total)	-0.062[a]	-0.021	-0.053[a]	-0.055[a]	**0.543**[a]	**0.425**[a]	**0.567**[a]

[a]$P < 0.01$; [b]$P < 0.05$

In Table 4.5, the Spearman correlations indicate that HE was weakly positively associated with the occurrence of DDID in both front and rear feet ($|\phi| = 0.112$, $P < 0.01$ and $|\phi| = 0.238$, $P < 0.01$, respectively). Furthermore, the occurrence of DDID was moderately positively associated with the occurrence of infectious lesions in the front feet ($|\phi| = 0.390$, $P < 0.01$) and strongly with the rear feet ($|\phi| = 0.893$, $P < 0.01$), while IP was weakly correlated with total infectious lesions in both front and rear feet ($|\phi| = 0.129$, $P < 0.01$ and $|\phi| = 0.159$, $P < 0.01$, respectively).

The occurrence of WLDS was moderately positively associated with the occurrence of total non-infectious lesions in the front feet ($|\phi| = 0.373$, $P < 0.01$), with a stronger correlation with the occurrence of non-infectious lesions in the rear feet ($|\phi| = 0.455$, $P < 0.01$). The occurrence of SU was moderately associated with the occurrence of non-infectious lesions in the rear feet ($|\phi| = 0.415$, $P < 0.01$), while SH was strongly associated with the occurrence of non-infectious lesions in the rear feet ($|\phi| = 0.573$ $P < 0.01$).

Table 4.5 Spearman correlation coefficients between individual lesions in front and rear feet and totals on lesion categories

	HE	IP (front)	IP (rear)	DDID (front)	IL front (total)	IL rear (total)	NL front (total)	NL rear (total)
HE								
IP (front)	0.060[a]							
IP (rear)	- 0.030	-0.005						
DDID (front)	**0.112**[a]	-0.013	0.009					
DDID (rear)	**0.238**[a]	0.073[a]	-0.040[b]	0.038[b]				
IP (total)					**0.129**[a]	**0.159**[a]		
DDID (total)					**0.390**[a]	**0.893**[a]		
SU (total)							0.022	**0.573**[a]
SH (total)							0.092[a]	**0.415**[a]
WLDS (total)							**0.373**[a]	**0.455**[a]

[a]$P < 0.01$; [b]$P < 0.05$

Heritability estimates were computed for total lesions (TL), infectious lesions (IL), non-infectious lesions (NL), and digital and interdigital dermatitis (DDID), but only traits with a significant value are reported in Table 4.6.

Table 4.6 Heritability estimates and standard errors (SE) for lesion categories based on single-trait linear animal models using VCE 6.0 (n=3 650)

Lesion category	h^2	SE
Total lesions	0.0083	0.01
Total non-infectious lesions	0.0498	0.04
Digital and interdigital dermatitis	0.0164	0.02

4.4 Discussion

This study aimed to investigate phenotypic and genetic associations between individual claw lesions and categories of claw lesions in South African Holstein herds in order to gain a greater insight into the occurrence of lesions and propose recommendations for improving the recording of claw lesions in South Africa.

A wide range of prevalence of between 40% and 70% has been reported in the literature for cows exhibiting at least one claw lesion, and this is also the case for this study, with more than 50% of cows having at least one claw lesion (Manske *et al*., 2002; Sogstad *et al*., 2005; Buch *et al*., 2011). Studies by Van der Spek *et al.* (2013) and Croué *et al.* (2017) reported a prevalence of 55% and up to 80% incidence of at least one claw lesion being present in dairy cows in France. In the current study, infectious lesions were found to be prevalent at a rate five times higher than non-infectious lesions, with DDID being the most prevalent lesion overall, and WLDS, SU, and SH being the most prevalent non-infectious lesions, as has been reported by other researchers (Machiodi *et al*., 2017; Van Huyssteen *et al*., 2020). Despite increased awareness, repeated findings of a high prevalence of claw lesions indicate that adoption of prevention and control strategies by producers remains low (Heringstad *et al*., 2018; Van Huyssteen *et al*., 2020). This may be due to underestimation of the problem, ambiguity regarding different scoring and reporting systems, or information overload on the part of the producer when too many individual lesions are reported on, or a combination thereof.

Phenotypic correlations between individual and combined claw lesion scores have been estimated by a number of researchers and tend to be highly variable due to differences in the study population size, lesion scoring methodology (i.e. present versus absent, or ordinal scoring according to severity), as well as lesion categorisation (Capion *et al*., 2009; Häggman & Juga, 2013). The study of Van der Waaij *et al.* (2005) categorised interdigital dermatitis with heel erosion (IDHE) as a combined trait and evaluated DD and IH as individual traits, while both Capion *et al*. (2009) and Häggman & Juga (2013) evaluated DD and ID separately, and Häggman & Juga (2013) did not evaluate IH at all. In addition, while both Van der Waaij *et al.* (2005) and Häggman & Juga (2013) scored lesions as present or absent, Van der Waaij *et al.* (2005) only reported on lesions occurring in the rear legs, and Capion *et al.* (2009) scored lesion severity on two different scales for different lesions. This emphasises the complexity of comparing research results across studies.

As a result of this study's limited sample size, only total lesion categories were evaluated, together with DDID due to its high prevalence. The combined trait of DDID was very strongly associated with the occurrence of total infectious lesions, which probably reflects the prevalence of the infectious lesion

recorded; DDID and HE, and HE and IP were also weakly positively correlated. While the phenotypic association between individual infectious lesions were weak, the relationships observed among non-infectious lesions (SH, SU, and WLDS) were moderate to strong, suggesting that the non-infectious lesions are more highly associated with each other than infectious lesions are. However, a large, statistically significant odds ratio of 4.39 was found between DDID and HE (95% confidence interval: 3.55 to 5.43, $P < 0.0001$), indicating that the presence of one of these infectious lesions is associated with approximately a four-fold increase in the odds of the other occurring. In the literature, it is common to group claw disorders into categories, especially those with low frequencies and similar biological basis, to increase the sample size (Heringstad *et al*., 2018). Researchers have differed in their categorisation over the years: Buch *et al.* (2011) grouped lesions related to hygiene- (dermatitis and heel erosion) separately from those related to feed (SU and SH) together due to higher genetic correlations within groups than between groups; Johansson *et al.* (2011) added an additional category called malformation (CC) traits; Ødegård *et al.* (2013) suggested adding WL to the feed-related category and relabelling it laminitis-related lesions, and then grouped infectious lesions together (HE, DD, and IP); Chapinal *et al.* (2013) also defined three categories as infectious, horn, and other lesions; and Dhakal *et al.* (2015) suggested simply categorising groups as either infectious and non-infectious. Given the distinct management actions required for intervention regarding infectious versus non-infectious lesions, the categorisation of Dhakal *et al.* (2015) seems to be the simplest and most relevant for practical reasons.

Claw data are usually recorded as binary or categorical traits and, in theory, threshold models are the most suitable to analyse these kinds of response variables (Chapinal *et al*., 2013; Pérez-Cabal & Charfeddine, 2015; Malchiodi *et al*., 2017). Threshold models tend to return higher heritability estimates from threshold models than linear models, ranging from 0.05 to 0.20 (Van der Waaij *et al*., 2005; Swalve *et al*., 2008; Malchiodi *et al.*, 2017), respectively. However, linear models are easier to implement (Malchiodi *et al*., 2017) and previous research has not indicated relevant differences in results from the two models (Weller *et al*., 1988; Van der Waaij *et al*., 2005; Malchiodi *et al*., 2017).

The low heritability of combined digital and interdigital dermatitis (0.016) reported for this study is similar to that found by Pérez-Cabal & Charfeddine (2015) at 0.02 using linear modelling, although they found a higher heritability using a threshold model (0.14). Previous researchers found a higher heritability for the combined digital and interdigital dermatitis trait than the present study: 0.073 using logistic modelling (Koenig *et al*., 2005) and 0.04 using linear modelling (Van der Spek *et al*., 2013). In their study, Van der Waaij *et al.* (2005) categorised two traits: interdigital dermatitis and heel horn erosion (IDHE) as a combination versus DD individually, and found heritabilities of 0.05 and 0.10, respectively. Other researchers that categorised DD and ID as two separate traits found a similar estimated heritability for DD (0.08 and 0.07, respectively), while the estimated heritability of ID was not similar in these two studies: 0.09 versus 0.01, respectively (Swalve *et al*., 2008; Malchiodi *et al*., 2017). Similarly, the Canadian Dairy Network has published heritability estimates of 0.08 for DD and 0.05 for ID (Butty *et al*., 2021).

The heritability of the total lesions category (representing the existence of at least one claw lesion on any foot) was found to be 0.008. In their respective studies, Van der Spek *et al.* (2013) and Pérez-Cabal & Charfeddine (2015) also included a combined claw disorder trait and found the heritability to be 0.05. Chapinal *et al.* (2013) performed a similar study to the current experiment using a linear animal model and found an estimated heritability for any lesion as $h^2 = 0.075$. The higher heritability estimates found in the literature are probably a reflection of the smaller sample size of this study.

The estimated heritability of total non-infectious lesions in the current study is 0.05, comparing favourably with previous research. Combining laminitis, interdigital hyperplasia and white line disease records into a category called non-purulent claw disorders, Gernand *et al.* (2012) reported an estimated heritability of 0.07 using threshold modelling. The category of horn lesions (SH, SU, and WL) as defined by Chapinal *et al.* (2013) had a heritability of 0.015, while Dhakal *et al.* (2015) reported a heritability of 0.08 for total non-infectious lesions.

While genetic correlations were not investigated in this study due to the small sample size, estimated correlations in the literature tend to vary widely (Johansson *et al*., 2011; Van der Spek *et al*., 2013) with a trend towards lower correlations between the two categories (infectious versus non-infectious) than within them, underlining the distinct genetic foundation of these two categories (Croué *et al*., 2017).

It has been shown that both specific claw lesions and categories of lesions are heritable and can be improved by selection. However, this requires regular, consistent phenotypic recording, so it is vital that the description and recording of claw lesions are made as easy as possible (Zavadolová *et al*., 2021; Joubert *et al*., 2023). Claw-trimming records can be used to improve our understanding of lesion occurrence and prevalence in South African Holstein herds in order to develop procedures that accommodate the most common circumstances in the field. Using data relating to phenotypic correlations between specific lesions and grouping lesions into categories based on their aetiology and management interventions, trimmers can simplify their recording sheets to encourage increased producer participation.

4.5 Conclusions

Claw lesions seem to occur relatively as often in South African Holstein cattle as in dairy cows elsewhere in the world. Similar issues are reported regarding accurate, consistent, and comparable phenotypic recording of lesion data by hoof trimmers. The phenotypic correlations and heritability estimates found in this and other studies indicate that incorporating some measure of claw health into breeding programmes has merit, but it is important that combined traits be used instead of individual lesions in order to maximise the amount of phenotypic data available. In addition, in order to make a real difference on the farm, producers need to be empowered with only the most relevant information to enable practical management interventions. Hoof lesion data can be used to genetically improve hoof health; therefore, it should be encouraged that the collection of this data be simplified and standardised.

References

Afonso, J.S., Bruce, M., Keating, P., Raboisson, D., Clough, H., Oikonomou, G., Rushton, J., 2020. Profiling detection and classification of lameness methods in British dairy cattle research: A systematic review and meta-analysis. *Front. Vet. Sci*. 7:542. https://doi.org/10.3389/fvets.2020.00542

Akoglu, H., 2018. User's guide to correlation coefficients. *Turk. J. Emerg. Med*. 18(3):91–93. https://doi.org/10.1016/j.tjem.2018.08.001

Buch, L.H., Sørensen, A.C., Lassen, J., Berg, P., Eriksson, J.-Å., Jakobsen, J.H., Sørensen, M.K., 2011. Hygiene-related and feed-related hoof diseases show different patterns of genetic correlations to clinical mastitis and female fertility. *J. Dairy Sci.* 94(3):1540–1551. https://doi.org/10.3168/jds.2010-3137

Butty, A.M., Chud, T.C.S., Cardoso, D.F., Lopes, L.S.F., Miglior, F., Schenkel, F.S., Cánovas, A, Häfliger, I.M., Drögemüller, C., Stothard, P., Malchiodi, F., Baes, C.F., 2021. Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. *J. Dairy Sci.* 104:8050–8061. https://doi.org/10.3168/jds.2020-19879

Capion, N., Thamsborg, S.M., Enevoldsen, C., 2009. Prevalence and severity of foot lesions in Danish Holstein heifers through first lactation. *Vet. J.* 182:50–58 https://doi.org/10.1016/j.tvjl.2008.05.026

Chapinal, N., Koeck, A., Sewalem, A., Kelton, D.F., Mason, S., Cramer, G., Miglior, F., 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. *J. Dairy Sci*. 96:2596–2604. https://doi.org/10.3168/jds.2012-6071

Charfeddine, N. & Pérez-Cabal, M.A., 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100(1):653–665. https://doi.org/10.3168/jds.2016-11434

Christen, M., Bergsten, C., Burgstaller, J., Capion, N., Charfeddine, N., Clarke, J., Daniel, V., Döpfer, D., Fiedler, A., Fjeldaas, T., Heringstad, B., Cramer, G., Kofler, J., Mueller, K.R., Nielsen, P., Oakes, E., Ødegård, C., O'Driscoll, K.J., Pryce, J.E., Steiner, A., Stock, K.F., Thomas, G., Ulvshammar, K., Holzhauer, M., Cole, J.B., Egger-Danner, C., Kowalski, Z., Petreny, N., Burke, M., Buček, P., Journaux, L., Coffey, M., Hunlun, C., Radzio, D., 2015. Recording of claw and foot disorders in dairy cattle: Current role and prospects of the international harmonization initiative of ICAR. *ICAR Tech. Series* 19:157–165, 2015.

Croué, I., Fikse, F., Johansson, K., Carlén, E., Thomas, G., Leclerc, H., Ducrocq, V., 2017. Genetic evaluation of claw health traits accounting for potential preselection of cows to be trimmed. *J. Dairy Sci.* 100(10)8197–8204. https://doi.org/10.3168/jds.2017-13002

Dhakal, K., Tiezzi, F., Clay, J.S., Maltecca, C., 2015. Short communication: Genomic selection for hoof lesions in first-parity US Holsteins. *J. Dairy Sci.* 98, 3502–3507. https://doi.org/10.3168/jds.2014-8830

Egger-Danner, C., Cole, J.B., Pryce, J.E., Gengler, N., Heringstad, B., Bradey, A, Stock, K.F., 2015. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Anim.* 9(2): 191–207. https://doi.org/10.1017/S1751731114002614

Fleming, A., Abdalla, E.A., Maltecca, C., Baes, C.F., 2018. Invited review: Reproductive and genomic technologies to optimize breeding strategies for genetic progress in dairy cattle. *Arch. Anim. Breed.* 61:43–57. https://doi.org/10.5194/aab-61-43-2018

Gernand, E., Rehbein, P., von Borstel, U.U., König, S., 2012. Incidences of and genetic parameters for mastitis, claw disorders, and common health traits recorded in dairy cattle contract herds. *J. Dairy Sci.* 95:2144–2156. https://doi.org/10.3168/jds.2011-4812

Groeneveld, E., Kovac, M., Mielenz, N., 2008. VCE 6.0.2, Co-variance components estimation package, Institute of Farm Animal Genetics, Mariensee, Germany.

Häggman, J. & Juga, J., 2013. Genetic parameters for hoof disorders and feet and leg conformation traits in Finnish Holstein cows. *J. Dairy Sci.* 96(5):3319–3325. https://doi.org/10.3168/jds.2012-6334

Heringstad, B., Klemetsdal, G., Steine, T., 2012. Selection responses for disease resistance in two selection experiments with Norwegian Red Cows. *J. Dairy Sci.* 90(5):2419–2426. https://doi.org/10.3168/jds.2006-805

Heringstad, B., Egger-Danner, C., Charfeddine, N., Pryce, J.E., Stock, K.F., Kofler, J., Sogstad, A.M., Holzhauer, M., Fiedler, A., Müller, K., Nielsen, P., Thomas, G., Gengler, N., de Jong, G., Ødegård, C., Malchiodi, F., Miglior, F., Alsaaod, M., Cole, J.B.: Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *J. Dairy Sci.* 101(6):1–21. https://doi.org/10.3168/jds.2017-13531

Huxley, J.N., 2013. Impact of lameness and claw lesions in cows on health and production. *Livest. Sci.* 156:64–70. https://doi.org/10.1016/j.livsci.2013.06.012

International Committee for Animal Recording (ICAR) statistics, https://my.icar.org/stats/list, last access: 20 September 2024.

Johansson, K., Eriksson, J.-Å., Nielsen, U.S., Pösö, J., Aamand, G.P., 2011. Genetic evaluation of claw health in Denmark, Finland and Sweden. *Interbull Bull.* 44:224–228.

Joubert, R.C., Strydom, H.F., Van Marle-Köster, E., 2023. Routine hoof-trimming data provides insight into the occurrence of claw lesions in Holstein herds in the central region of South Africa. *Trop. Anim. Health Prod.* 55:395, https://doi.org/10.1007/s11250-023-03814-x

Koenig, S., Sharifi, A.R., Wentrot, H., Landmann, D., Eise, M., Simianer, H., 2005. Genetic parameters of claw and foot disorders estimated with logistic models. *J. Dairy Sci.* 88:3316–3325. https://doi.org/10.3168/jds.S0022-0302(05)73015-0

Laursen, M.V., Boelling, D., Mark., T., 2009. Genetic parameters for claw and leg health, foot and leg conformation, and locomotion in Danish Holsteins. *J. Dairy Sci.* 92(4):1770–1777. https://doi.org/10.3168/jds.2008-1388

Malchiodi, F., Koeck, A., Mason, S., Christen, A.M., Kelton, D.F., Schenkel, F.S., Miglior, F., 2017. Genetic parameters for hoof health traits estimated with linear and threshold models using alternative cohorts. *J. Dairy Sci.* 100(4):2828–2836. https://doi.org/10.3168/jds.2016-11558

Manske, T., Hultgren, J., Bergsten, C., 2002. Prevalence and interrelationships of hoof lesions and lameness in Swedish dairy cows. *Prev. Vet. Med.* 54(3):247–263. https://doi.org/10.1016/S0167-5877(02)00018-1

Microsoft Corporation, Microsoft Excel, available at: https://office.microsoft.com/excel, 2018.

Ødegård, C., Svendsen, M., Heringstad, B., 2013. Genetic analyses of claw health in Norwegian Red cows. *J. Dairy Sci.* 96(11):7274–7283. https://doi.org/10.3168/jds.2012-6509

Oehm, A.W., Knubben-Schweizer, G., Rieger, A., Stoll, A., Hartnack, S., 2019. A systematic review and meta-analyses of risk factors associated with lameness in dairy cows. *BMC Vet. Res.* 15:346. https://doi.org/10.1186/s12917-019-2095-2, 2019

Oliveira Junior, G.A., Schenkel, F.S., Alcantara, L., Houlahan, K., Lynch, C., Baes, C.F., 2021. Estimated genetic parameters for all genetically evaluated traits in Canadian Holsteins. *J. Dairy Sci.* 104(8):9002–9015. https://doi.org/10.3168/jds.2021-20227

Pérez-Cabal, M.A & Charfeddine, N., 2015. Models for genetic evaluations of claw health traits in Spanish dairy cattle. *J. Dairy Sci.* 98:8186–8194. http://dx.doi.org/10.3168/jds.2015-9562

Sadiq, M.B., Ramanoon, S.Z., Mossadeq, W.M.S., Mansor, R., Hussain, S.S.S., 2019. Dairy farmers' perceptions of and actions in relation to lameness management. *Anim.* 9(5):270. https://doi.org/10.3390/ani9050270

SAS Institute Inc.: SAS User's Guide, Version 9.4. SAS Institute, Cary, United States of America, 2018.

Shearer, J.K. & Van Amstel, S.R., 2017. Pathogenesis and treatment of sole ulcers and white line disease. *Vet. Clin. North Am. Food Anim. Pract*. 33(2):283–300. https://doi.org/10.1016/j.cvfa.2017.03.001

Sogstad, A.M., Fjeldaas, T., Østerås, O., Forshell, K.P., 2005. Prevalence of claw lesions in Norwegian dairy cattle housed in tie stalls and free stalls. *Prev. Vet. Med.* 70:191–209. https://doi.org/10.1016/j.prevetmed.2005.03.005

Solano, L., Barkema, H.W., Mason, S., Pajor, E.A., LeBlanc, S.J., Orsel, K., 2016. Prevalence and distribution of foot lesions in dairy cattle in Alberta, *Canada. J. Dairy Sci.* 99(8):6828–6841. https://doi.org/10.3168/jds.2016-10941

Swalve, H., Alkhoder, H., Pijl, R., 2008. Estimates of breeding values for sires based on diagnoses recorded at hoof trimming: Relationships with EBV for conformation traits. *Interbull Bull.,*38:87–90.

Uggla, E., Jakobsen, J.H., Bergsten, C., Eriksson, J.-Å., Strandberg, E., 2008. Genetic correlations between claw health and feet and leg conformation traits in Swedish dairy cows. *Interbull Bull.* 38:91–95.

Van der Spek, D., Van Arendonk, J.A.M., Vallée, A.A.A., Bovenhuis, G., 2013. Genetic parameters for claw disorders and the effect of preselecting cows for trimming. *J. Dairy Sci.* 96(9):6070–6078. http://dx.doi.org/10.3168/jds.2013-6833

Van der Waaij, E.H., Holzhauer, M., Ellen, E., Kamphuis, C., de Jong, G., 2005. Genetic parameters for claw disorders in Dutch dairy cattle and correlation with conformation traits. *J. Dairy Sci.* 88(10):3672–3678. https://doi.org/10.3168/jds.S0022-0302(05)73053-8

Van Huyssteen, M., Barkema, H., Mason, S., Orsel, K., 2020. Association between lameness risk assessment and lameness and foot lesion prevalence on dairy farms in Alberta, Canada. *J. Dairy Sci.* 103:11750–11761. https://doi.org/10.3168/jds.2019-17819

Weller, J., Misztal, I., Gianola, D., 1988. Genetic analysis of dystocia and calf mortality in Israeli-Holsteins by threshold and linear models. *J. Dairy Sci.* 71:2491–2501. https://doi.org/10.3168/jds.S0022-0302(88)79836-7

Zavadilová, L., Kašná, E., Krupová, Z., Klímová, A., 2021. Health traits in current dairy cattle breeding: A review. *Czech J. Anim. Sci.* 66:235–250. https://doi.org/10.17221/163/2020-CJAS

CHAPTER 5

APPLICATION OF GENOMIC INFORMATION FOR THE ANALYSIS OF CLAW LESIONS IN SOUTH AFRICAN HOLSTEIN CATTLE

A short communication will be prepared from this chapter for publication.

5 Application of genomic information for the analysis of claw lesions in South African Holstein cattle

5.1 Introduction

Livestock genetic improvement programmes have been revolutionised by genomics, specifically due to the accessibility of a wide variety of high-density single nucleotide polymorphism (SNP) arrays, increasingly sophisticated statistical techniques, and a continuous decline in the cost of genotyping (Berry & Spangler, 2023; Hossein-Zadeh, 2024), Widespread use of artificial insemination in the dairy industry means that biological repositories are widely available. This, together with access to phenotypic information through milk recording databases, enabled the dairy industry to be at the forefront of this revolution (Erasmus & Van Marle-Köster, 2021). It has been over a decade since genomic prediction strategies have been implemented in the genetic evaluation of dairy cattle on a routine basis for over a decade, facilitated by GWAS that have identified significant variants related to economically important traits (Gutierrez-Reinoso *et al*., 2021; Sahana *et al*., 2023). As a result, significant progress has been made for yield traits in dairy cattle (milk, fat, and protein) and the rate of improvement in daughter pregnancy rate in American Holstein bulls has doubled since the implementation of genomic selection (Guinan *et al*., 2023; Sahana *et al*., 2023). The advances in molecular genetics and genomics have created unique opportunities to increase the rate of genetic improvement of especially health traits in farm animals (Vukasinovic *et al*., 2022). Genomic information offers a great opportunity to develop a more comprehensive understanding of the genetic mechanisms involved in difficult-to-measure traits and those with low heritability, and more recent studies have started including health and welfare traits in such analyses (Hossein-Zadeh, 2024; Krupová *et al*., 2024).

Cow lameness caused by claw lesions represents one of the more challenging cases for genetic and genomic improvement (Garvey, 2022; Bell *et al*., 2024). Claw health traits are generally difficult to measure, have low heritability, and differences in definition, identification, and recording practices. Furthermore, validation criteria for claw health data vary among countries, which makes achieving collective genetic improvement very difficult (Heringstad *et al*., 2018; Croué *et al*., 2019). Despite these difficulties, reducing the incidence of claw lesions is high on the priority list of dairy farmers, as they present a major issue, both from a welfare point of view and in terms of profitability (Malchiodi *et al*., 2018; Croué *et al*., 2019). Claw lesions are ranked third in cost among health disorders in dairy cattle (Charfeddine & Pérez-Cabal, 2017, Heringstad *et al*., 2018). In addition, lame cows also suffer from mastitis, metabolic disorders, and reduced fertility more often than non-lame cows (Garvey, 2022). In a recent study in South African Holstein cattle, approximately 30% of cows had at least one claw lesion (Mhlongo, 2019), which is in agreement with previous studies reporting a prevalence of between 10% and 80% (Chapinal *et al*., 2013; Croué *et al*., 2019).

When it comes to complex traits, one of the challenges experienced with GWAS is that the power depends on both the number of animals and the total number of SNP, as well as the heritability of the trait in question (Barden, 2022). In order to increase study power, many researchers have grouped individual lesions under a single composite trait (Dhakal *et al*., 2015; Malchiodi *et al*., 2018).

The main objective of this study was to use a genomic approach together with functional analysis to identify genomic regions and potential candidate genes associated with four categories of claw health traits in South African Holstein cattle managed under a TMR system.

5.2 Material and methods

The Faculty of Natural and Agricultural Sciences at the University of Pretoria granted ethical approval for the study (NAS292/2020) through its Ethics Committee. Phenotypic data were collected from five South African Holsten herds between January 2014 to December 2023 by a local hoof trimmer using a modified version of the *Claw Lesion Identification Guide* (Zinpro® Corporation). Genotypes were extracted from the Dairy Genomic Programme (DGP) database, where animals were genotyped over a three-year period using the Illumina Bovine SNP50 BeadChip® (Illumina Inc., San Diego, CA, USA) as part of a state-funded project by the Technology Innovation Agency (Van Marle-Köster & Visser, 2018).

Four traits were evaluated: Total lesions (TL), total non-infectious lesions (NL), total infectious lesions (IL), and a combined trait representing the occurrence of digital and interdigital dermatitis (DDID). These traits were recorded as binary traits, i.e. recorded as 1 if the trimmer observed the lesion during trimming and 0 if not present (Table 5.1).

Table 5.1 Distribution of lesions in the four trait categories: Total lesions, total non-infectious lesions, total infectious lesions, and digital and interdigital dermatitis (n = 3 650)

Trait	Lesions present	Lesions absent
Total lesions (TL)	1 550	2 100
Total non-infectious lesions (NL)	247	3 403
Total infectious lesions (IL)	1 105	2 545
Digital and interdigital dermatitis (DDID)	898	2 752

The GWAS was performed using EMMAX (Kang *et al*., 2010). Due to the limited size of the dataset, the first step included testing different parameters in EMMAX to find the best fit. Quality control (QC) included removing non-autosomal SNPs and duplicates in PLINK 1.9 (Purcell *et al*., 2007), which retained 1 318 animals and removed 1 969 variants. Thereafter, 20 animals and 1 452 SNP with individual call rate < 90% (Wiggans *et al*., 2010) and SNP call rate < 95% (Berry & Kearney, 2011) were filtered out, respectively (Table 5.2.

Table 5.2 GWAS quality control (QC) steps

QC step	PLINK command	No. of animals	No. of variants
Original dataset		1 318	53 218
Remove non-autosomal SNP	--chr 1-29	1 318	51 278
Remove duplicates	--exclude file.dupvar	1 318	51 249
Individual call rate (90%)	--mind 0.10	1 298	51 249
SNP call rate (95%)	--geno 0.05	1 298	49 797

PLINK 1.9 was used to generate the input files for EMMAX, with the final input files containing either 230 or 1 298 animals and between 40 735 and 49 797 variants, depending on the methodology applied (Table 5.3).

Dataset A is the original dataset based on the first level of QC described above. Rare alleles are often removed in GWAS; however, they may contribute to genetic variability and therefore were not removed in this dataset (Berry & Spangler, 2023). In datasets B and C, SNP with minor allele frequences of < 1% and <

5%, respectively, were removed. Datasets D and E included covariates for herd, year, and season based respectively on the mean and median values of these, and dataset E retained only animals with both genotypes and phenotypes for the trait under evaluation together with the true covariates for herd, year, and season.

Table 5.3 EMMAX input for parameter testing

Method	No. of genotypes	No. of phenotypes	No. of variants	Covariates for HYS* included
A (original)	1 298	230	49 797	No
B (maf1)	1 298	230	44 344	No
C (maf5)	1 298	230	40 735	No
D (mean of covariates)	1 298	230	49 797	Yes
E (median of covariates)	1 298	230	49 797	Yes
F (actual covariates)	230	230	49 797	Yes

*HYS: herd-year-season

The original dataset (A) of total non-infectious lesions provided the best fit (Table 5.4). This is indicated by the highest log-likelihood when accounting for variance components. The likelihood ratio test (LRT) showed that including variance components significantly improved model fit. In addition, the p-value of 0.091 was also the lowest among the different categories and methodologies tested, indicating a stronger association compared to others and suggesting a notable association worth further investigation, despite not reaching conventional significance thresholds ($P < 0.05$). With the exception of the category of non-infectious lesions, the addition of variance components in the analyses did not improve the fit of the model. Therefore, the results from applying the original dataset (A) on non-infectious lesion data are presented and discussed.

Population structure was accounted for using the Balding–Nichols kinship matrix in EMMAX, and the qqman package in R (Turner, 2014) was used to create Manhattan and quantile-quantile (qq) plots to visualise results. The genome-wide significance level for the dataset under study according to Bonferroni (pBF = 0.05/NSNP = 49 797) was set at $1 \, x \, 10^{-6}$ and a less conservative normative significance threshold was defined as $pCD = 1x10^{-4}$ (Kurz *et al*., 2018; Sölzer *et al*., 2022).

Version 113 of the Ensembl database (Harrison *et al*., 2024) was used to identify potential candidate genes based on the *Bos taurus* ARS-UCD1.3 genome assembly and assign them to the corresponding significant or suggestive SNP. Specifically, the BiomaRt package in R (Turner, 2014) was employed to query the dataset for cattle genes (Ensembl, 2024). A gene was considered as a candidate gene if at least one significantly associated or suggestive SNP was located in the gene or within a window size of 200 kb up- and downstream (Sölzer *et al*., 2022).

Finally, physiological functions and/or associated mammalian phenotypes of potential candidate genes were inferred based on information from the Ensembl (Harrison *et al*., 2024) database, the Mouse Genome Informatics batch query database (Smith & Eppig, 2009; Sahana *et al*., 2023), the UniProtConsortium (UnitProt), and the Human Protein Atlas (Uhlen *et al*., 2010).

Table 5.4 EMMAX output for parameter testing

Methodology and trait	No. SNP	p-value computation	Log-likelihood with variance component	Log-likelihood without variance component	δ ($\sigma e^2/\sigma g^2$)	σg^2	σe^2	Pseudo-heritability estimate	LRT*
A (original_nomaf)									
TL	49 797	0.141	-161.606	*-161.606*	2 2026.466	0.000	0.240	0.00002	-0.00017
NL	49 797	0.091	-43.695	-45.188	1.336	0.048	0.064	0.26594	2.98662
IL	49 797	0.172	-131.730	*-131.730*	2 2026.466	0.000	0.185	0.00002	-0.00042
DDID	49 797	0.109	-113.710	*-113.709*	2 2026.466	0.000	0.158	0.00002	-0.00047
B (maf1)									
TL	44 344	0.133	-161.606	*-161.606*	2 2026.466	0.000	0.240	0.00002	-0.00019
NL	44 344	0.172	-43.441	-45.188	1.160	0.053	0.061	0.29910	3.49479
IL	44 344	0.181	-131.730	*-131.730*	2 2026.466	0.000	0.185	0.00002	-0.00040
DDID	44 344	0.152	-113.709	*-113.709*	2 2026.466	0.000	0.158	0.00002	-0.00044
C (maf5)									
TL	40 735	0.125	-161.606	*-161.606*	2 2026.466	0.000	0.240	0.00002	-0.00020
NL	40 735	0.114	-43.381	-45.188	1.143	0.053	0.061	0.30174	3.61404
IL	40 735	0.169	-131.730	*-131.730*	2 2026.466	0.000	0.185	0.00002	-0.00041
DDID	40 735	0.120	-113.709	*-113.709*	2 2026.466	0.000	0.158	0.00002	-0.00045
D (mean of covariates)									
TL	49 797	0.054	-159.756	*-159.756*	2 2026.466	0.000	0.241	0.00002	-0.00006
E (median of covariates)									
TL	49 797	0.041	-159.756	*-159.756*	2 2026.466	0.000	0.241	0.00002	-0.00006
F (actual covariates)									
TL	49 797	0.338	-159.756	*-159.756*	2 2026.466	0.000	0.241	0.00002	-0.00007

*LRT = Likelihood ratio test = 2 × (log-likelihood full – log-likelihood reduced)

TL: total lesions; NL: total non-infectious lesions; IL: total infectious lesions; DDID: digital and interdigital dermatitis

5.3 Results

The Manhattan and qq plots for the non-infectious lesions GWAS are shown in Figure 5.1 (a) and (b).

(a) (b)

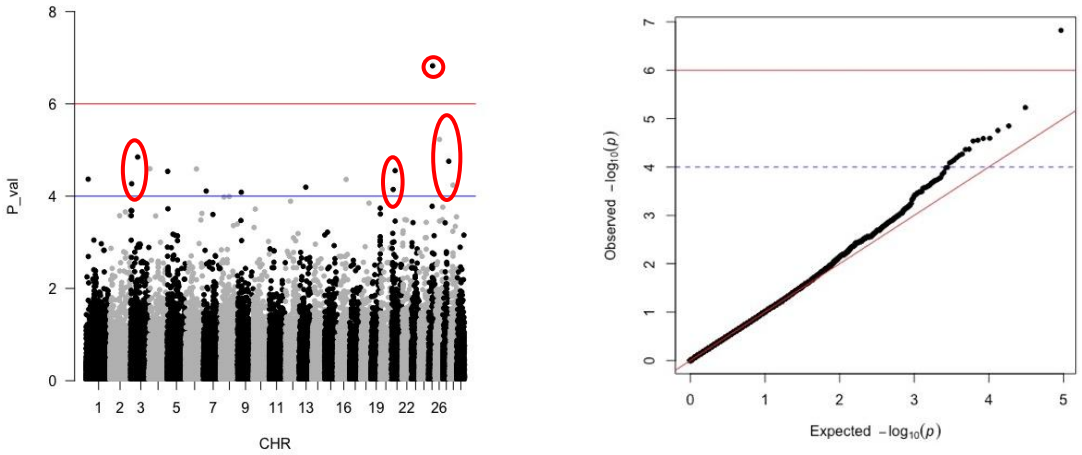


Figure 5.1 (a) Manhattan plot of SNP effects for non-infectious lesions with the genome-wide significance threshold set at 1×10^{6} and suggestive line set at 1×10^{4}; (b) qq plot of observed and expected p-values with significant and suggestive lines indicated

One genome-wide significant SNP and 15 genome-wide suggestive SNP were detected in the GWAS (Table 5.5). These SNP were further investigated by gene annotation in R (Turner, 2014) using *Bos taurus* data in the Ensembl database (version 113). Results are shown in Table 5.6 and Addendum 5A1.

Table 5.5 Significant (bold) and suggestive SNP names, rsID numbers, chromosome, and position

SNP name	rsID	chr	bp
ATP2A1_2		25	26 197 204
ARS-BFGL-BAC-12976	rs109130929	1	14 762 256
BTA-88009-no-rs	rs41595711	3	7 391 544
BTB-01537076	rs42653868	3	47 254 544
BTA-72294-no-rs	rs41651662	4	6 822 285
BTB-00214944	rs43424770	5	3 928 512
BTA-76807-no-rs	rs41654332	6	72 587 575
ARS-BFGL-NGS-118401	rs110757459	7	18 257 573
BTB-01072905	rs42233228	9	24 573 723
ARS-BFGL-NGS-119393	rs108978029	13	43 458 932
Hapmap44069-BTA-39354	rs41639636	16	58 677 757
Hapmap41293-BTA-53465	rs41639425	21	12 712 258
BTB-00811262	rs41973273	21	25 482 576
BTB-01430967	rs42555606	26	29 896 827
DIAS-336	rs110557450	27	39 204 962
BTB-01171634	rs42329096	28	21 516 493

Table 5.6 Gene annotations, position, and functional information for candidate genes on chromosome 25 associated with significant SNP ATP2A1_2

Ensembl gene ID	Gene	Start position	End position	Function
ENSBTAG00000006543	EIF3CL	26 008 727	26 028 899	Polydactyly, postnatal growth retardation, abnormal limb morphology
ENSBTAG00000018000	CLN3	26 043 076	26 055 242	Decreased body weight, impaired coordination, abnormal gait, short stride length, abnormal macrophage physiology
ENSBTAG00000018015	IL27	26 061 018	26 066 743	Abnormal T cell differentiation, increased susceptibility to parasitic infection induced morbidity/ mortality, impaired inflammation
ENSBTAG00000016883	SGF29	26 082 046	26 123 452	
ENSBTAG00000018016	NUPR1	26 082 047	26 086 316	Abnormal cell cycling and death
ENSBTAG00000008635	SULT1A1	26 123 609	26 126 047	Abnormal morphology of skeletal muscles, skin, and lymph nodes
ENSBTAG00000008633	SLX1A	26 125 933	26 131 638	DNA repair and recombination
ENSBTAG00000008631	CORO1A	26 134 793	26 139 202	Impaired macrophage phagocytosis, abnormal T cell activation and physiology, decreased T cell number and proliferation, increased T cell apoptosis
ENSBTAG00000016156	MAPK3	26 178 352	26 186 189	Abnormal cytokine secretion, decreased T cell production
ENSBTAG00000016155	GDPD3	26 186 549	26 191 906	
ENSBTAG00000009047	YPEL3	26 192 889	26 197 088	Decreased body length, short tibia, hyperactivity, abnormal startle reflex
ENSBTAG00000009046	TBX6	26 197 455	26 202 361	Abnormal vertebrae morphology and development, enlarged tail bud
ENSBTAG00000012928	PPP4C	26 202 220	26 210 323	Apoptosis, DNA repair, DNA damage checkpoint signalling, and cell migration
ENSBTAG00000012927	ALDOA	26 212 566	26 217 280	Decreased leukocyte cell number
ENSBTAG00000005033	TLCD3B	26 230 395	26 247 628	Decreased length, decreased startle reflex
ENSBTAG00000048797	C16orf92	26 247 838	26 248 727	Male infertility, female infertility
ENSBTAG00000005031	DOC2A	26 255 007	26 260 480	
ENSBTAG00000005030	INO80E	26 259 541	26 268 086	Increased body weight
ENSBTAG00000005028	HIRIP3	26 267 918	26 271 508	Increased neutrophil cell number, hyperactivity, abnormal behaviour
ENSBTAG00000017422	TAOK2	26 268 068	26 289 860	Decreased body size
ENSBTAG00000021785	TMEM219	26 290 035	26 342 937	Increased eosinophil cell number, increased susceptibility to injury
ENSBTAG00000015982	KCTD13	26 343 322	26 356 561	Reduced male fertility
ENSBTAG00000026319	ASPHD1	26 356 460	26 360 506	Abnormal digit morphology
ENSBTAG00000007955	SEZ6L2	26 362 158	26382 374	May contribute to specialised neuron functions
ENSBTAG00000007954	CDIPT	26 388 343	26 391 768	

Figure 5.2 indicates the relative positions of the candidate genes associated with significant SNP ATP2A1_2 located at base-pair position 26 197 204 on chromosome 25, indicating that 14 of these are close to or overlap this SNP.

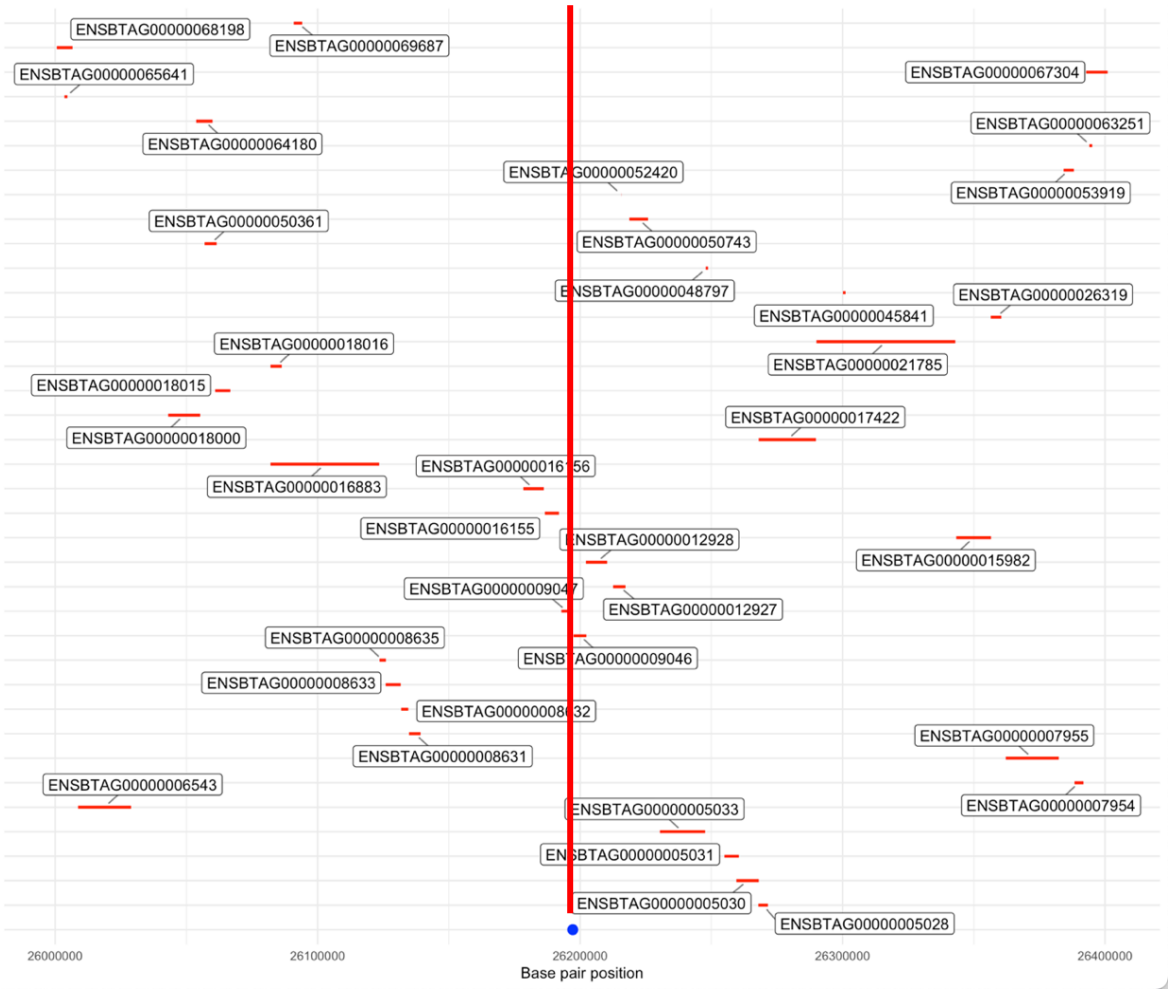


Figure 5.2 Comparative positions of candidate genes to the significant SNP ATP2A1_2 on chromosome 25; the red line indicates where these genes overlap with the significant SNP

In Figure 5.3, the results of this study were compared with candidate genes identified in GWAS studies between 2018 and 2023 (Malchiodi *et al*., 2018; Butty *et al*., 2021; Lai *et al*., 2021; Sánchez-Molano *et al*., 2021; Sölzer *et al*., 2022; Li *et al*., 2023). Despite the identification of a number of suggestive SNP on various chromosomes in this study that are similar to the literature, only BTA25 contained candidate genes related to the significant SNP identified.

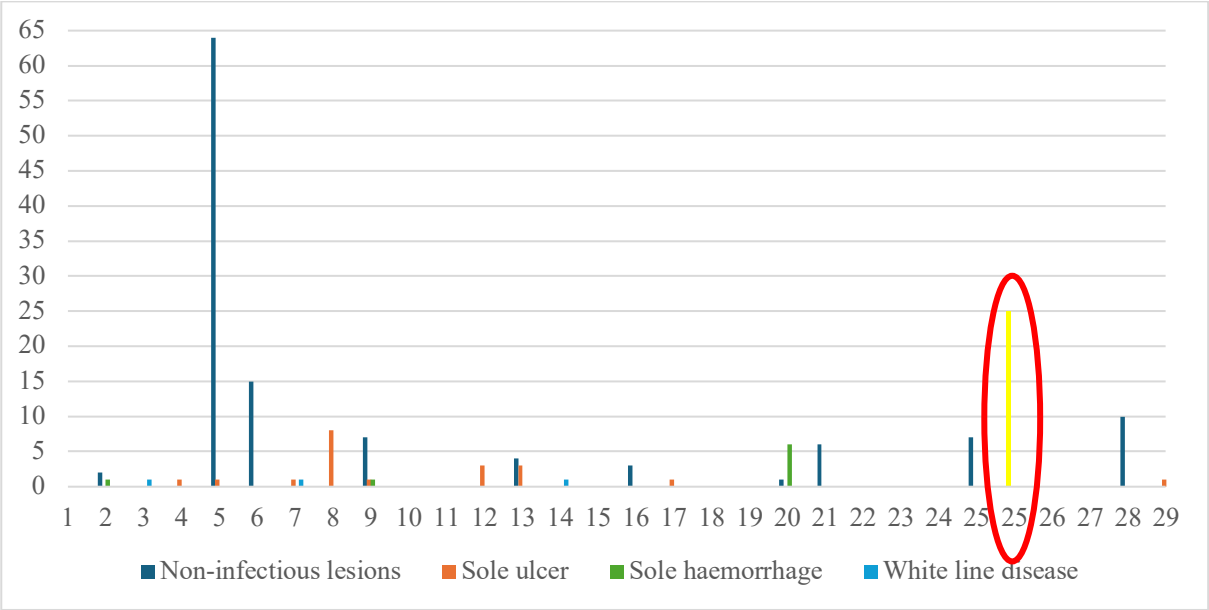


Figure 5.3 Number of candidate genes identified per chromosome for non-infectious claw lesions in dairy cattle compared to the current study highlighted circled in red (BTA25)

5.4 Discussion

A number of researchers have attempted to investigate claw lesion traits using a genomic approach, although, as is the case in defining and recording claw lesions, here, too, trait definition and the ways of estimating the accuracy of genomic evaluation approaches varies widely among authors (Croué *et al*., 2019; Lai *et al*., 2020).

In the present study, a genomic approach was used to detect possible candidate genes affecting non-infectious claw lesions in South African Holstein cattle. Based on the aetiology of claw lesions, infectious lesions are expected to be related to immune-related genes, while non-infectious lesions are expected to be related to structural abnormalities and metabolic processes (Heringstad *et al*., 2018). In this study, candidate genes related to skeletal or bone abnormalities, inflammation, immunity, skin abnormalities, and metabolic processes were considered functionally relevant.

Previous studies have reported candidate genes for non-infectious claw lesions on 20 different chromosomes, with the highest number (64) being located on chromosome 5, followed by eight on chromosome 25 (Malchiodi *et al*., 2018; Croué *et al*., 2019; Butty *et al*., 2021; Lai *et al*., 2021). The current study identified 25 candidate genes on chromosome 25 related to abnormal skin morphology (SULTIA1), abnormal digit and limb morphology (ASPHD1, EIF3CL), and inflammatory and immune response (ALDOA, CLN3, CORO1A, HIRIP3, IL27, MAPK3, SULTIA1, TMEM219). Other candidate genes have been identified on chromosome 25 by Malchiodi *et al.* (2018), including two for abnormal bone structure or morphology (CUX1, PLOD3) and three for immunity (CUX1, ORAI2, SH2B2), as well as by Sölzer *et al.* (2022), who reported candidate genes related to body size (AUTS2, CUX1, ZNHIT1, CLN3, INO80E, TAOK2, TLCD3B, YPEL3) and fertility (CUX1, C16orf92, KCTD13). Of the 14 candidate genes identified here on

chromosome 25 that are close to or overlap with the significant SNP ATP2A1_2 as indicated in Figure 5.2, five have been previously identified (C16orf92, MAPK3, ALDOA, CORO1A, and INO8E).

In addition to the candidate genes identified on chromosome 25 with known functions in animals that have been described in Table 5.6 (Smith & Eppig, 2009; Harrison *et al*., 2024), the SGF29, CDIPT, and GDPD3 have been identified in humans as a prognostic marker for a number of carcinomas. Furthermore, various candidate genes related to the suggestive SNP identified in this study (Addendum 5A1) have also been reported as prognostic markers for cancer in humans (Human Protein Atlas; Uhlen *et al*., 2010). These include OLFML2B, POLR2B, IGFBP7, GTF2F1, ALKBH7, CLPP, MLLT1, RFX2, RANBP3, AKR1C4, TMED3, and NAT1. Genes that are implicated in cancer progression often play roles in tissue repair and inflammation (Trinchieri, 2012), which may have relevance for the development of claw lesions.

In this study, only one suggestive SNP was observed on chromosome 5, although several candidate genes have been reported in literature. These are related to inflammatory and immune response (ANO2, CBY1, CERK, DDX23, GUCY2C, KLRK1, PLCZ1, TSPAN9, VWF), skeletal or bone abnormalities (APAF1, CHST11, LRP6, PTPRO, TULP3), and impaired glucose tolerance or insulin resistance (GUCY2C, LRP6, PIK3C2G, PPARA, TULP3) (Malchiodi *et al*., 2018; Lai *et al*., 2021). Candidate genes have been reported to be associated with abnormal gait and motor coordination or balance: Seven genes on chromosome 5 (BAIAP2L2, CERK, GRIN2B, KMT2D, PLCZ1, SOX10, TXNRD1), one on chromosome 9 (ADGRG6), two on chromosome 25 (AUTS2, CLN3) and two on chromosome 28 (CDH23, PSAP) (Malchiodi *et al*., 2018; Lai *et al*., 2021). In this study, only suggestive SNP were found on these chromosomes. These candidate genes may be related to the development of non-infectious claw lesions due to uneven or uncoordinated weight-bearing on individual feet and the genomic architecture of this trait warrants further research attention. It is clear that potential candidate genes are widely spread across the genome, demonstrating that the inheritance of this trait is polygenic, involving multiple genes across various loci that collectively influence its expression and variability.

While some researchers have performed GWAS on non-infectious claw lesions as a group or category, others investigated each of these individually (Butty *et al*., 2021; Lai *et al*., 2021; Sánchez-Molano *et al*., 2021; Sölzer *et al*., 2022; Li *et al*., 2023). Results differ regarding the location of candidate genes for non-infectious claw lesions, which is not surprising given their complex genetic background (Barden, 2022). However, differences in trait definition and categorisation, study design, data analysis, and the population under investigation may also contribute to a lack of replicability (Croué *et al*., 2019). The interplay of genetic variability, methodological differences, and diverse definitions of claw lesions complicates the landscape of research, making it challenging to draw definitive comparisons across studies.

5.5 Conclusion

This study serves a as a starting point for the collection of genomic information related to non-infectious claw lesions in South African Holstein cattle. The candidate genes found in this study on BTA25, as well as suggestive SNP related to inflammation, immune function, and bone abnormalities, should be investigated further. Identifying the causal variants that contribute to claw lesions is challenging because they are likely affected by numerous genes that each only explain a very small portion of the variation observed. Future GWAS based on larger datasets containing accurate phenotypic data may be useful to increase our knowledge of the underlying pathology of these traits.

References

Barden, M., 2022. Genetic and metabolic aspects of claw horn lesion aetiopathogenesis in Holstein cows. PhD thesis, University of Liverpool.

Bell, N.J., Pedersen, S.I.L., Randall, L.V., Remnant, J.G., Wilson, J.P., 2024. Lameness in Cattle. In: Gross, J.J. (eds) *Production Diseases in Farm Animals*. Springer, Cham. https://doi.org/10.1007/978-3-031-51788-4_17

Berry, D.P. & Kearney, J.F., 2011. Imputation of genotypes from low- to high-density genotyping platforms and implications for genomic selection. *Anim.* 5(8):1162–1169. https://doi.org/10.1017/S1751731111000309

Berry, D.P. & Spangler, M.L., 2023. Animal board invited review: Practical applications of genomic information in livestock. *Anim.* 17(11):100996. https://doi.org/10.1016/j.animal.2023.100996

Butty, A.M., Chud, T.C.S, Cardoso, D.F., Lopes, L.S.F., Miglior, F., Schenkel, F.S., Cánovas, A, Häfliger, I.M., Drögemüller, C., Stothard, P., Malchiodi, F., Baes, C.F., 2021. Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. *J. Dairy Sci.* 104:8050–8061. https://doi.org/10.3168/jds.2020-19879

Chapinal, N., Koeck, A., Sewalem, A., Kelton, D.F., Mason, S., Cramer, G., Miglior, F., 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. *J. Dairy Sci.* 96:2596–2604. https://doi.org/10.3168/jds.2012-6071

Charfeddine, N. & Pérez-Cabal, M.A., 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100(1):653–665. https://doi.org/10.3168/jds.2016-11434

Croué, I., Michenet, A., Leclerc, H., Ducrocq, V., 2019. Genomic analysis of claw lesions in Holstein cows: Opportunities for genomic selection, quantitative trait locus detection, and gene identification. *J. Dairy Sci.* 102(7):6306–6318. https://doi.org/10.3168/jds.2018-15979

Dhakal, K., Tiezzi, F., Clay, J.S., Maltecca, C., 2015. Short communication: Genomic selection for hoof lesions in first-parity US Holsteins. *J. Dairy Sci.* 98:3502–3507. https://doi.org/10.3168/jds.2014-8830

Erasmus, L. & Van Marle-Köster, E., 2021. Moving towards sustainable breeding objectives and cow welfare in dairy production: a South African perspective. *Trop. Anim. Health Prod.* 53: 470. https://doi.org/10.1007/s11250-021-02914-w

Garvey, M., 2022. Review: Lameness in dairy cow herds: Disease aetiology, prevention and management. *Dairy* 2022(3):199–210. https://doi.org/10.3390/dairy3010016

Guinan, F.L., Wiggans, G.R., Norman, H.D., Dürr, J.W., Cole, J.B., Van Tassel, C.P., Misztal, I., Lourenco, D., 2023. Changes in genetic trends in US dairy cattle since the implementation of genomic selection. *J. Dairy Sci.* 106(2): 1110–1129. https://doi.org/10.3168/jds.2022-22205

Gutierrez-Reinoso, M.A., Aponte, P.M., Garcia-Herrer, M., 2021. Genomic Analysis, Progress and Future Perspectives in Dairy Cattle Selection: A Review. *Anim.* 11:599. https://doi.org/10.3390/ani11030599

Harrison, P.W., Amode, M.R., Austine-Orimoloye, O., Azov, A.G., Barba, M., Barnes, I., Becker, A., Bennett, R., Berry, A., Bhai, J., Bhurji, S.K., Boddu, S., Lins, P.R.B., Brooks, L., Ramaraju, S.B., Campbell, L.I., Martinez, M.C., Charkhchi, M., Chougule, K., Cockburn, A., Davidson, C., De Silva, N.H., Dodiya, K., Donaldson, S., El Houdaigui, B., El Naboulsi, T., Fatima, R., Giron, C.G., Genez, T., Grigoriadis, D., Ghattaoraya, G.S., Martinez, J.G., Gurbich, T.A., Hardy, M., Hollis, Z., Hourlier, T., Hunt, T., Kay, M., Kaykala, V., Le, T., Lemos, D., Lodha, D., Marques-Coelho, D., Maslen, G., Merino, G.A., Mirabueno, L.P., Mushtaq, A., Hossain, S.N., Ogeh, D.N., Sakthivel,

M.P., Parker, A., Perry, M., Piližota, I., Poppleton, D., Prosovetskaia, I., Raj, S., Pérez-Silva, J.G., Salam, A.I.A., Saraf, S., Saraiva-Agostinho, N., Sheppard, D., Sinha, S., Sipos, B., Sitnik, V., Stark, W., Steed, E., Suner, M., Surapaneni, L., Sutinen, K., Tricomi, F.F., Urbina-Gómez, D., Veidenberg, A., Walsh, T.A., Ware, D., Wass, E., Willhoft, N.L., Allen, J., Alvarez-Jarreta, J., Chakiachvili, M., Flint, B., Giorgetti, S., Haggerty, L., Ilsley, G.R., Keatley, J., Loveland, J.E., Moore, B., Mudge, J.M., Naamati, G., Tate, J., Trevanion, S.J., Winterbottom, A., Frankish, A., Hunt, S.E., Cunningham, F., Dyer, S., Finn, R.D., Martin, F.J., Yates, A.D., 2024. Ensembl 2023. *Nucleic Acids Res.* 52(D1): 891–899. https://doi.org/10.1093/nar/gkad1049

Heringstad, B., Egger-Danner, C., Charfeddine, N., Pryce, J.E., Stock, K.F., Kofler, J., Sogstad, A.M., Holzhauer, M., Fiedler, A., Müller, K., Nielsen, P., Thomas, G., Gengler, N., de Jong, G., Ødegård, C., Malchiodi, F., Miglior, F., Alsaaod, M., Cole, J.B., 2018. Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *J. Dairy Sci.* 101(6):1–21. https://doi.org/10.3168/jds.2017-13531

Hossein-Zadeh, N.G., 2024. An overview of recent technological developments in bovine genomics. *Vet. Anim. Sci.* 25:100382. https://doi.org/10.1016/j.vas.2024.100382

Human Protein Atlas. www.proteinatlas.org. Accessed 11 November, 2024.

Kang, H.M., Sul, J.H., Service, S.K., Zaitlen, N.A., Kong, S., Freimer, N.B., Sabatti, C., Eskin, E., 2010. Variance component model to account for sample structure in genome-wide association studies. *Nat. Genet.* 42:348–354. https://doi.org/10.1038/ng.548

Krupová, Z., Kašná, E., Zavadilová, L., Krupa, E., Bauer, J., Wolfová, M., 2024. Udder, Claw, and Reproductive Health in Genomic Selection of the Czech Holstein. *Anim.* 14(6):864. https://doi.org/10.3390/ani14060864

Kurz, J.P., Yang, Z., Weiss, R.B., Wilson, D.J., Roodl, K., Liu, G.E., Wang, Z., 2018. A genome-wide association study for mastitis resistance in phenotypically well-characterized Holstein dairy cattle using a selective genotyping approach. *Immunogenetics* 71:35–47. https://doi.org/10.1007/s00251-018-1088-9

Lai, E., Danner, A.L., Famula, T.R., Oberbauer, A.M., 2020. Genome-Wide Association Studies Reveal Susceptibility Loci for Digital Dermatitis in Holstein Cattle. *Anim.* 10:11. https://doi.org/10.3390/ani10112009

Lai, E., Danner, A.L., Famula, T.R., Oberbauer, A.M., 2021. Genome-wide association studies reveal susceptibility loci for noninfectious claw lesions in Holstein dairy cattle. *Front. Genet.* 12:657375. https://doi.org/10.3389/fgene.2021.657375

Li, B., Barden, M., Kapsona, V., Sánchez-Molano, E., Anagnostopoulos, A., Griffiths, B.E., Bedford, C., Dai, X., Coffey, M., Psifidi, A., Oikonomou, G., Banos, G., 2023. Single-step genome-wide association analyses of claw horn lesions in Holstein cattle using linear and threshold models. *Genet. Sel. Evol*. 55:16. https://doi.org/10.1186/s12711-023-00784-4

Malchiodi, F., Brito, L.F., Schenkel, F.S., Christen, A.M., Kelton, D.F., Miglior, F., 2018. Genome-wide association study and functional analysis of infectious and horn type hoof lesions in Canadian Holstein cattle. In: *Proc. of the World Congress on Genetics Applied to Livestock Production.* 11–16 February, 2018, Auckland, New Zealand.

Mhlongo, N.L., 2019. Evaluation of claw health of dairy cattle housed in dirt lot vs free stall in TMR systems in the central region of South Africa. MSc dissertation, University of Pretoria.

Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M. A., Bender, D., Maller, J., de Bakker, P.I.W., Daly, M.J., Sham, P.C., 2007. PLINK: A toolset for whole-genome association and population-based linkage analysis. *Am. J. Hum. Genet.* 81:559–575. https://doi.org/10.1086/519795

Sahana, G., Cai, Z., Sanchez, M.P., Bouwman, A.C., Boichard, D., 2023. Invited review: Good practices in genome-wide association studies to identify candidate sequence variants in dairy cattle. *J. Dairy Sci.* 106(8):5218–5241. https://doi.org/10.3168/jds.2022-22694

Sánchez-Molano, E., Bay, V., Smith, R.F., Oikonomou, G., Banos, G., 2019. Quantitative Trait Loci Mapping for Lameness Associated Phenotypes in Holstein–Friesian Dairy Cattle. *Front. Genet.* 10:926. https://doi.org/10.3389/fgene.2019.00926

Smith, C.L., Eppig, J.T., 2009. The mammalian phenotype ontology: enabling robust annotation and comparative analysis. *Wiley Interdiscip. Rev. Syst. Biol. Med.* 1(3):390-–399. https://doi.org/10.1002/wsbm.44

Sölzer, N., May, K., Yin, T., König, S., 2022. Genomic analysis of claw disorders in Holstein cows: Genetic parameters, trait associations, and genome-wide associations considering interactions of SNP and heat stress. *J. Dairy Sci.,* 105(10), 8218–8236. https://doi.org/10.3168/jds.2022-22087

Trinchieri, G., 2012. Cancer and Inflammation: An Old Intuition with Rapidly Evolving New Concepts. *Annu. Rev. Immunol.* 30:677–706. https://doi.org/10.1146/annurev-immunol-020711-075008

Turner, S.D., 2014. qqman: an R package for visualizing GWAS results using Q-Q and manhattan plots. bioRxiv. https://doi.org/10.1101/005165

Uhlen, M., Oksvold, P., Fagerberg, L., Lundberg, E., Jonasson, K., Forsberg, M., Zwahlen, M., Kampf, C., Wester, K., Hober, S., Wernerus, H., Björling, L., Ponten, F., 2010. Towards a knowledge-based Human Protein Atlas. *Nat. Biotechnol*. 28:1248–1250. https://doi.org/10.1038/nbt1210-1248

Van Marle-Köster, E. & Visser, C., 2018. Genetic improvement in South African livestock: can genomics bridge the gap between the developed and developing sectors? *Front. Genet.* 9:331. https://doi.org/10.3389/fgene.2018.00331

Vukasinovic, N., Gonzalez, D., Przybyla, C., Brooker, J., Kulkarni, A., Passafaro, T., McNeel, A., 2022. Genetic Control of Wellness in Dairy Cattle. *Anim. Husb.* IntechOpen. http://dx.doi.org/10.5772/intechopen.103819

Wiggans, G.R., Van Raden, P.M., Bacheller, L.R., Tokker, M.E., Hutchison, J.L., Cooper, T.A., Sonstegard, T.S., 2010. Selection and management of DNA markers for use in genomic evaluation. *J. Dairy Sci.* 93(5):2287–2292. https://doi.org/10.3168/jds.2009-2773

The UniProtConsortium, 2023. UniProt: the Universal Protein Knowledgebase in 2023. *Nucleic Acids Res*. 51(D1):523–531. https://doi.org/10.1093/nar/gkac1052

Zinpro® Corporation, 2008. *Claw Lesion Identification in Dairy Cattle* (D40-08-30-07). Eden Prairie, MN, USA.

ADDENDA TO CHAPTER 5

APPLICATION OF GENOMIC INFORMATION FOR THE ANALYSIS OF CLAW LESIONS IN SOUTH AFRICAN HOLSTEIN CATTLE

Addendum 5A1: Suggestively associated SNP and annotated potential candidate genes for non-infectious claw lesions in Holstein cattle

BTA	SNP ID	Ensembl gene ID	Gene
3	BTA-88009-no-rs	ENSBTAG00000010158	NOS1AP
		ENSBTAG00000045173	SNORA70
		ENSBTAG00000034147	OLFML2B
5	BTB-00214944	ENSBTAG00000035083	ATXN7L3B
6	BTA-76807-no-rs	ENSBTAG00000019366	POLR2B
		ENSBTAG00000019368	IGFBP7
7	ARS-BFGL-NGS-118401	ENSBTAG00000021016	GTF2F1
		ENSBTAG00000025540	ALKBH7
		ENSBTAG00000014712	CLPP
		ENSBTAG00000008095	ACER1
		ENSBTAG00000002277	MLLT1
		ENSBTAG00000009105	ACSBG2
		ENSBTAG00000017661	RFX2
		ENSBTAG00000006070	RANBP3
7	ARS-BFGL-NGS-119393	ENSBTAG00000058245	AKR1C4
16	Hapmap44069-BTA-39354	ENSBTAG00000013715	BRINP2
21	Hapmap41293-BTA-53465	ENSBTAG00000013689	MCTP2
		ENSBTAG00000043663	U4
21	BTB-00811262	ENSBTAG00000019940	RASGRF1
		ENSBTAG00000036380	MIR184
		ENSBTAG00000062558	ANKRD34C
		ENSBTAG00000000807	TMED3
		ENSBTAG00000007094	MINAR1
27	DIAS-336	ENSBTAG00000016473	NAT1
		ENSBTAG00000033140	LRRC3B

CHAPTER 6

CRITICAL REVIEW AND RECOMMENDATIONS

6 Critical review and recommendations

6.1 Introduction

There are approximately 600 000 commercial dairy cows in South Africa, producing 3.35 million tonnes of milk (Van Heerden, 2024), making this industry a major contributor to food security and employment. Milk consumption is driven by population growth and growth in per capita consumption, which increased by 23% over the past decade (Milk SA, 2023). Despite the number of dairy farmers decreasing steadily over the past 10 years, annual milk production has increased as producers embrace modern housing, nutrition, and genetic technologies. The increases in yield traits have placed an additional burden on these dairy cows farmed under intensive production systems, which is resulting in an increase in health- and welfare-related issues. Of these, lameness stemming from claw lesions is one of the top welfare priorities within the dairy industry (FVE, 2019; Roche *et al*., 2024). Despite several research studies, as have been reviewed in Chapter 2 of this thesis, the prevalence of lameness among dairy cows remains high with limited improvements over the past 20 to 30 years (Bell *et al*., 2024; Roche *et al*., 2024).

Most of the research conducted regarding the significance, prevalence, and management of claw lesions originates from Europe and North America (Thomsen *et al*., 2023), with very few studies conducted in South Africa (Mhlongo, 2019; Van Marle-Köster *et al*., 2020; Erasmus & Van Marle-Köster, 2021; Matshetsheni & Jaja, 2024). This study was the first attempt to integrate existing phenotypic, genetic, and genomic data to enhance our understanding of claw lesions in South African Holstein cattle raised in total mixed ration (TMR) management systems.

6.2 Claw lesions: Phenotypes and recording

Two of the objectives of this study focused on hoof-trimming data and, similar to the majority of studies, the digital dermatitis (DD) was found most often, followed by sole ulcer (SU), sole haemorrhage (SH), and white line disease (WL). All the lesions showed a greater tendency to occur in the rear feet, possibly due to greater weight-bearing on the hind claws as well as behavioural adaptations in intensive housing systems.

In this study, the hoof-trimming data originated from one trimmer using the *Claw Lesion Identification in Dairy Cattle* brochure, co-developed by Zinpro® Corporation and the International Lameness Committee (ILC) (D40-08-30-07; Eden Prairie, MN, USA), for recording. Of interest, are the relationships between different lesions, feet, and the housing system. In this study, the prevalence of DD and interdigital phlegmon (IP) was strongly associated, and closely associated with SU. These three lesions were associated with both dirt lot and free-stall housing systems, while WL and SH were observed to be associated when cattle were housed in a combination of the two systems.

The data collection sheet used by the trimmer, while broadly based on the ILC methodology, allows for over 40 different observations per cow. These include observations regarding the presence and positions of lesions and treatment interventions applied, as well as comments on foot and hock anatomy and injuries. Data is recorded by hand, and only observations related to treatment interventions are used to calculate the amount invoiced to the farmer and to inform the farmer about relevant management interventions. While this hoof-trimming methodology was the source of information for the current study, dairy farmers in South Africa make use of different trimmers who employ different claw lesion definitions, trimming methodologies, and treatments. It is clear, based on the correspondence analyses, that the identification and recording of so many data points for claw lesions for individual cows may be an overly stringent method to improving claw health

in South African dairy herds. Furthermore, recording data by hand poses the additional threats of losing historic records, errors in data capture, and misinterpretation of observations due to poor handwriting, none of which is in keeping with the level of technology applied elsewhere in dairy cattle breeding.

Lameness is a multifaceted and complex issue, which makes prevention and control challenging, at best (Garvey, 2022; Bell *et al*., 2024). Unfortunately, dairy farmers and farm workers have different perceptions and levels of understanding of the disease, mainly due to vague, poor, and/or misleading definitions (Olmos *et al*., 2018; Matshetsheni & Jaja, 2024). Farmers often relate the term 'lameness' to only severely lame cows, meaning that cows that are not visibly lame and those presenting with mild gait changes are less likely to be presented for trimming or treatment (Bruijnis *et al*., 2013; Sadiq *et al*., 2019; Roche *et al*., 2024). Furthermore, successful treatment also requires understanding of the underlying causes of claw lesions, and Horseman *et al.* (2013) reported that many farmers cannot differentiate between several of the individual lesions. Olmos *et al.* (2018) also reported that some farmers group lameness, claw lesions, and laminitis under separate health categories. Although farmer perception was beyond the scope of this study, the use of hoof trimming and participation in national milk recording among South African dairy farmers are limited and an indication of the priority given to claw lesions.

While these five herds only represent a small percentage of Holstein herds in the country that are managed under a TMR system, they were chosen based on the availability of both phenotypic and genetic data, as well as participation in the South African National Milk Recording Scheme. Unfortunately, there are very few herds in South Africa that qualify under these parameters, and the number is continually decreasing. The fragmentation of milk recording and the closure of the country's only local bull breeding station, together with the advent of genomic selection elsewhere in the world, has resulted in the local dairy industry being less and less interested in participating in national phenotypic recording. It seems that South African dairy farmers significantly underestimate the pervasive nature of claw lesions that lead to lameness in their herds as well as the effect thereof on animal welfare, which is generally the case elsewhere in the world as well. There is also a general perception among dairy farmers that lameness is a so-called 'TMR problem'; therefore, to date, no research studies have been performed in pasture-based herds.

Researchers agree that effective lameness management relies on early diagnosis, and timely, efficient treatment. (Bell *et al*., 2022; Garvey, 2022) and routine hoof trimming represents one of the major strategies for the prevention of lameness and improvement of welfare in these animals (Thomsen *et al*., 2019; Roche *et al*., 2024). Hoof trimmers are trained in the identification and treatment of different lesions, albeit within different schools of thought, and their expertise should be utilised better, together with input from dairy consultants and veterinarians, to inform dairy farmers' decisions regarding prevention and treatment options tailored to their specific farm circumstances (Olmos *et al*., 2018; Bell et *al*., 2024). In addition, implementation of electronic record-keeping will allow easier and more accurate recording of these lesions, as well as being useful for both genetic improvement and individual benchmarking exercises for producers (Chapinal *et al*., 2013; Heringstad *et al*., 2018).

Risk factors, preventative actions, and management intervention strategies differ between infectious and non-infectious claw lesions (Olmos *et al*., 2018; Garvey, 2022). The question is whether the farmer needs to know the prevalence of each individual claw lesion on their farm in order to more successfully address a lameness issue, or if this information overload rather contributes to the confusion surrounding the issue. It is suggested that the hoof trimmer consolidates recording data into easy-to-use information in order advise the producer as to the risk factors that need to be managed in each case.

6.3 Phenotypic and genetic analyses

A number of researchers have estimated phenotypic correlations between individual and combined claw lesions, but results tend to vary widely, again as a result of differences in lesion identification and scoring methods, and depending on who is doing the recording. This makes it difficult to compare previous results with the current study, which found the strongest phenotypic correlation between DDID and total infectious lesions, confirming that DDID was the most prevalent lesion recorded here. Furthermore, the occurrence of DDID was also very strongly correlated with the rear feet. Within the non-infectious lesions, the relationships observed between SH, SU, and WLDS were moderate to strong, SU and WLDS were both strongly positively associated with total non-infectious lesions, and SU was strongly associated with the occurrence of non-infectious lesions in the rear feet. Previous research has noted that claw lesions occur more frequently in the rear than in the front feet (Manske *et al.*, 2002; Sogstad *et al.*,2005; Chapinal *et al.*, 2013), and this was also the case here.

In this study, the combined incidence of non-infectious lesions was below 10%, and SH, SU, and WLDS were the most common lesions identified, while the infectious lesion DDID was the most highly prevalent at almost 40%. This is consistent with studies across the world (Roche *et al.*, 2024). Given the fact that, in most of the literature, DD is the most prevalent lesion overall, with the most prevalent non-infectious lesions being SH, SU, and WL, as well as these results that indicate a strong correlations between DDID and total infectious lesions and strong correlations between SH, SU, and WL, the recommendation to simplify the claw lesion recording system in South Africa is further underscored.

In addition to management interventions, genetic selection could also contribute to reducing the incidence of claw lesions in dairy herds. Although inconsistent, estimates of heritability for claw lesions do indicate sufficient genetic variation for successful selection strategies to be implemented (Pérez-Cabal & Charfeddine, 2015) and that claw-trimming data provides suitable phenotypic information for this purpose (Barden, 2022). In this study, the heritability of the combined trait DDID (0.016) is similar to that reported by Pérez-Cabal & Charfeddine (2015), but lower than those reported by Koenig *et al.* (2005) and Van der Spek *et al.* (2013). The higher heritability estimates found in the literature are probably a reflection of the smaller sample size of this study. However, the estimated heritability of total non-infectious lesions in the current study is 0.05, comparing favourably with previous research (Gernand *et al.*, 2012; Chapinal *et al.*, 2013; Dhakal *et al.*, 2015).

Although it is not feasible to directly compare or extrapolate the heritability estimates reported here to other populations, these results are useful to highlight the potential of selective breeding to reduce claw lesions. Additionally, developing infrastructure to compile national claw-trimming data would greatly benefit the South African dairy industry.

6.4 Genomics

Notwithstanding the limited sample size here, a GWAS was attempted in Chapter 5 with the aim of identifying potential candidate genes associated with different categories of claw lesions. Based on model fit, only the total non-infectious lesions category was included in the analysis which led to the detection of one significant SNP (BTA25) and 15 suggestive SNP'. The significant SNP was associated with several candidate genes on chromosome 25, confirming the heterogeneity of the trait.

The genetic background of claw lesion traits has been studied by a number of researchers, who have identified candidate genes on at least 20 different chromosomes (Malchiodi *et al.*, 2018; Croué *et al.*, 2019; Butty *et al.*, 2021; Lai *et al.*, 2021). In the current study, functional analysis indicated that most of these are related to inflammatory and immune-related functions, with some being related to skeletal or bone abnormalities, which is both expected and in agreement with the literature.

Even after launching a three-year, state-funded dairy genomic programme in 2016 to establish reference populations for the three most common dairy breeds, routine genotyping has progressed slowly in South Africa, likely because the dairy industry relies on semen companies to provide genetic material in the form of internationally genomic-tested dairy bulls (Van Marle-Köster & Visser, 2018).

Globally, GWAS have been used to investigate claw lesion traits, although the same issue arises regarding the comparison of research results due to inconsistent trait definition, methodology, and analysis (Croué *et al.*, 2019; Lai *et al.*, 2020). To date, GWAS in South African cattle have, for the most part, been limited to investigations of genetic diversity and population structure in indigenous breeds like Nguni and Bonsmara cattle, and very few studies have been published for Holstein cattle (Makina *et al.*, 2014; Mapholi *et al.*, 2016; Van der Westhuizen *et al.*, 2019; Kooverjee *et al.*, 2022; Visser *et al*., 2023).

This study is in agreement with previous researchers that claw lesions definitely show quantitative inheritance, which will require large and complete hoof-trimming data sets for genomic selection. This is in addition to the layer of complexity that arises in consolidation of global GWAS results due to differences in recording and nomenclature. Therefore, leveraging transcriptomics may provide a more nuanced understanding of the biological mechanisms underlying claw lesions in dairy cattle, ultimately offering greater potential for effective selection compared to traditional GWAS approaches.

6.5 Conclusions and future direction

Research on claw lesions in dairy cattle is crucial for understanding their causes, risk factors, genetic architecture, and for enhancing lameness management on farms (Thomsen *et al.*, 2023; Mülling, 2024). Despite a century of study, knowledge remains fragmented and poorly disseminated, leaving many in the dairy industry uninformed. The prevalence of lameness has seen little change over the past 30 years, despite extensive literature that is often inconsistent or contradictory. Current prevention and treatment practices for claw lesions have proven largely ineffective, highlighting the need for re-evaluation and supplementation (Roche *et al*., 2024). Surprisingly, though, there seems to be a notable lack of scientific evidence regarding the widely used Dutch claw-trimming methods, developed over 50 years ago, necessitating further investigation into optimal techniques (Mülling, 2024). Efforts to standardise the nomenclature of claw lesions began in 1976 but have not resolved the ongoing diversity in definitions and methodologies across studies, which hampers effective communication and progress in addressing this costly issue. In South Africa, research on claw lesions is limited but indicates comparable prevalence and challenges to those observed globally.

The first recommendation, therefore, is employing standardised systems to monitor the prevalence and severity of lameness. As the International Committee for Animal Recording (ICAR) is the global provider of independent guidelines, standards, and certifications for animal identification, recording, and evaluation, the obvious choice is the *ICAR Claw Health Atlas* (ICAR, 2020), of which the second edition was published in January of 2020 and has been translated into 20 languages. The sole focus of this publication was on the standardisation and harmonisation of data recording based on interdisciplinary collaboration among a diverse

group of experts, including health practitioners, hoof trimmers, and geneticists. Descriptive trait definitions ensure accurate classification and supports the collection of high-quality phenotypic data, both for lameness improvement and genetic evaluation purposes.

While South Africa participates in both ICAR and Interbull committees, participation in national phenotypic recording systems is at an all-time low. In order to continue improving the genetic merit of the national herd, something needs to be done to stimulate a revival of interest among South African dairy farmers. Producers need to be encouraged to record claw lesions regularly as this is crucial for genetic evaluation and selection, enabling the implementation of long-term preventive measures (Sadiq *et al.*, 2020). A number of hoof trimmers provide this service in South Africa based on the requirements of the producer, i.e. some herds are trimmed only during the cows' dry period, while others are trimmed twice a year. However, these trimmers have not been uniformly trained and they use various trimming methods and base their assessments on different claw lesion classification systems. In order for producers to accept the additional effort required to record claw lesion, they must be able to see an immediate benefit such as a tool that can assist them with more efficient herd management by detecting problems early on for prompt intervention (Egger-Danner, 2015). The FVE believes that a facilitated, participatory approach should be taken between multiple role players, including the producer, hoof trimmer, nutritionist, dairy consultant, veterinarian, and performance recording organisations. Herd health plans that are co-created between these role players and are tailored to a specific farm will actively encourage a process of continuous improvement. In addition, this could also be supported by quality assurance schemes and tangible requirements from dairy companies to improve hoof health (FVE, 2019; Wynands *et al.*, 2021). Unfortunately, South Africa is lagging behind the rest of the world in this regard, with very few farmers allowing real collaboration between their different advisers. In some cases, a dairy consultant may be able to partially fulfil this role, but it will take a concerted effort to shift the focus from individual to national benchmarking and collaboration.

Simplification of the recording process is necessary in order not to overwhelm producers with too much informational 'noise'. Knowledge regarding previously identified phenotypic and genetic correlations should be used to limit the number of lesions on the recording sheet. As only one example, the strong positive genetic correlation between sole haemorrhage and sole ulcer estimated by Barden (2022) means that these may practically be regarded as a single trait. The identification and recording of claw lesions may also be made easier by utilising available technologies, e.g. automated lameness detection and the use of artificial intelligence monitor lameness over time (Afonso *et al.*, 2020; Barden, 2022). Many of these technologies are still being refined and require validation studies to prove their accuracy in detecting individual claw lesions or lesion categories (Barden, 2022). In terms of genomic research, the main limiting factor at the moment is the collection and availability of useful phenotypes, and automation of phenotypic collection is an urgent need if we want to make fundamental advances in lowly heritable traits (Rexroad *et al.*, 2019).

The recommendation is for farm personnel to assess the prevalence and severity of lameness and foot lesions at least once a month, while ensuring that a qualified hoof trimmer performs regular preventive trimming every six months (FVE, 2019; Ranjbar *et al.*, 2020). Regular trimming has been proven to reduce the incidence of lameness by between 25% and 34% (Ranjbar *et al.*, 2020). The FVE also advises that the quality of hoof trimming should be assured by a process of licensing hoof trimmers by an official body (FVE, 2019). More than 80% of US dairy herds employ a professional hoof trimmer (Wynands *et al.*, 2021), and while this figure is not officially known in South Africa, it is expected to be much lower. In addition, there is no national certification body that evaluates hoof trimmer competence or training in South Africa.

A national database for on-farm lesion recording is essential to enhance genetic evaluations for lameness. In the UK, the newly established Hoof Health Registry encourages stakeholders to share hoof health records, which can facilitate benchmarking and comparisons between farms over time, motivating producers to improve performance (Wilson *et al.*, 2024). Benchmarking also provides rapid feedback on the impact of management interventions, further promoting participation in data collection programs. To ensure effective data sharing, it is crucial to harmonise trait definitions across systems and enable on-farm computers to communicate with external databases, preventing data from being stranded in isolated systems.

In order to facilitate comparison between studies, as well as enable generalisation of results across various target populations, it is important for researchers to clearly describe their definition of lameness and describe each individual claw lesion, define their inclusion or exclusion criteria, and report on all relevant herd and cow characteristics in their scientific publications. The review by Thomsen *et al.* (2023) excluded over 90% of relevant articles identified based on the lack of clarity – and thus comparability – regarding research methodology.

The literature indicates that, despite increased awareness, many herds worldwide still experience a significant occurrence of claw lesions (Mülling, 2024), and this also seems to be the case in South Africa, as more than 50% of cows in this study suffered from at least one claw lesion. Research has shown that farmers and farmworkers consistently underestimate lameness, with the true prevalence often actually being between two and four times higher (Sadiq *et al.*, 2019; Ranjbar *et al.*, 2020). This contributes both to delayed treatment and a lack of implementation of prophylactic or prevention strategies (Ranjbar *et al.*, 2020). In addition to the welfare implications of delayed treatment, the farmer is also likely to suffer additional economic losses related to lower milk yield, delayed reproduction, and additional management interventions needed to treat lame cows (Sadiq *et al.*, 2019; Garvey, 2022). At the end of the day, the global dairy industry's failure to meaningfully lower the incidence of claw lesions and maintain appropriate hoof health indicates that current best practices need to be reevaluated (Roche *et al.*, 2024).

The increasing emphasis on animal welfare and United Nations Sustainable Development Goals highlights the critical need for the dairy industry to address challenges related to overall sustainability. As consumers and stakeholders become more aware of the ethical implications of animal husbandry, issues such as lameness and claw lesions in dairy cattle emerge as significant concerns that must be tackled. Addressing these health issues is not only vital for the well-being of the animals but also essential for ensuring the long-term viability and sustainability of dairy farming practices. By prioritising animal welfare, the dairy industry can contribute to broader sustainability objectives while enhancing productivity and consumer trust. According to the World Organization for Animal Health, research clearly demonstrates that top-performing dairy farms can lower lameness rates to just 5%. It is time that the South African dairy industry accepts this challenge and it is incumbent upon us as the scientific community to work together to help producers reach this very attainable goal.

References

Afonso, J.S., Bruce, M., Keating, P., Raboisson, D., Clough, H., Oikonomou, G., Rushton, J., 2020. Profiling detection and classification of lameness methods in British dairy cattle research: A systematic review and meta-analysis. *Front. Vet. Sci*. 7:542. https://doi.org/10.3389/fvets.2020.00542

Barden, M., 2022. Genetic and metabolic aspects of claw horn lesion aetiopathogenesis in Holstein cows. PhD thesis, University of Liverpool.

Bell, N., Bacon, D., Craven, E., Crowe, S., Newsome, R., Oikonomou, G., Pedersen, S., Reader J., Wilson, J., 2022. Dairy cattle lameness: A roundtable discussion, *Livestock* 27(Sup3):S1–S11. https://doi.org/10.12968/live.2022.27.S1.115

Bell, N.J., Pedersen, S.I.L., Randall, L.V., Remnant, J.G., Wilson, J.P., 2024. Lameness in Cattle. In: Gross, J.J. (eds) *Production Diseases in Farm Animals.* Springer, Cham. https://doi.org/10.1007/978-3-031-51788-4_17

Bruijnis, M., Hogeveen, H., Garforth, C., Stassen, E., 2013. Dairy farmers' attitudes and intentions towards improving dairy cow foot health. *Livest. Sci.* 155(1):103–113. https://doi.org/10.1016/j.livsci.2013.04.005

Butty, A.M., Chud, T.C.S, Cardoso, D.F., Lopes, L.S.F., Miglior, F., Schenkel, F.S., Cánovas, A, Häfliger, I.M., Drögemüller, C., Stothard, P., Malchiodi, F., Baes, C.F., 2021. Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. *J. Dairy Sci.* 104:8050–8061. https://doi.org/10.3168/jds.2020-19879

Chapinal, N., Koeck, A., Sewalem, A., Kelton, D.F., Mason, S., Cramer, G., Miglior, F., 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. *J. Dairy Sci.* 96:2596–2604. https://doi.org/10.3168/jds.2012-6071

Chapinal, N., Weary, D.M., Collings, L., von Keyserlingk, M.A.G., 2014. Lameness and hock injuries improve on farms participating in an assessment program. *Vet. J.* 202(3):646–648. https://doi.org/10.1016/j.tvjl.2014.09.018

Charfeddine, N. & Pérez-Cabal, M.A., 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100(1):653–665. https://doi.org/10.3168/jds.2016-11434

Croué, I., Michenet, A., Leclerc, H., Ducrocq, V., 2019. Genomic analysis of claw lesions in Holstein cows: Opportunities for genomic selection, quantitative trait locus detection, and gene identification. *J. Dairy Sci.* 102(7):6306–6318. https://doi.org/10.3168/jds.2018-15979

Dhakal, K., Tiezzi, F., Clay, J.S., Maltecca, C., 2015. Short communication: Genomic selection for hoof lesions in first-parity US Holsteins. *J. Dairy Sci.* 98, 3502–3507. https://doi.org/10.3168/jds.2014-8830

Egger-Danner, C., Cole, J.B., Pryce, J.E., Gengler, N., Heringstad, B., Bradley, A., Stock, K.F., 2015. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Anim.* 9(2):191–207. https://doi.org/10.1017/S1751731114002614

Erasmus, L. & van Marle-Köster, E., 2021. Moving towards sustainable breeding objectives and cow welfare in dairy production: a South African perspective. *Trop. Anim. Health Prod.* 53: 470. https://doi.org/10.1007/s11250-021-02914-w

FVE, 2019. FVE Position on Welfare and Dairy Cows: Lameness. https://www.fve.org/cms/wp-content/uploads/002-FVE-position-cattle-lameness_adopted.pdf. Accessed 23 October 2024.

Garvey, M., 2022. Review: Lameness in dairy cow herds: Disease aetiology, prevention and management. *Dairy* 2022(3):199–210. https://doi.org/10.3390/dairy3010016

Gernand, E., Rehbein, P., von Borstel, U.U., König, S., 2012. Incidences of and genetic parameters for mastitis, claw disorders, and common health traits recorded in dairy cattle contract herds. *J. Dairy Sci.* 95:2144–2156. https://doi.org/10.3168/jds.2011-4812

Heringstad, B., Egger-Danner, C., Charfeddine, N., Pryce, J.E., Stock, K.F., Kofler, J., Sogstad, A.M., Holzhauer, M., Fiedler, A., Müller, K., Nielsen, P., Thomas, G., Gengler, N., de Jong, G., Ødegård, C., Malchiodi, F., Miglior, F., Alsaaod, M., Cole, J.B., 2018. Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *J. Dairy Sci.* 101(6):1–21. https://doi.org/10.3168/jds.2017-13531

Horseman, V., Whay, H.R., Huxley, J.N., Bell, N.J., Mason, C.S., 2013. A survey of the on-farm treatment of sole ulcer and white line disease in dairy cattle. *Vet. J.* 197(2):461–467. https://doi.org/10.1016/j.tvjl.2013.02.027

International Committee for Animal Recording (ICAR), 2020. *ICAR claw health atlas*. https://www.icar.org/index.php/publications-technical-materials/technical-series-and-proceedings/atlas-claw-health-and-translations/. Accessed 1 November 2024.

Koenig, S., Sharifi, A.R., Wentrot, H., Landmann, D., Eise, M., Simianer, H., 2005. Genetic parameters of claw and foot disorders estimated with logistic models. *J. Dairy Sci.* 88(9):3316–3325. https://doi.org/10.3168/jds.S0022-0302(05)73015-0

Kooverjee, B.B., Soma, P., van der Nest, M.A., Scholtz, M.M., Neser, F.W.C., 2022. Selection Signatures in South African Nguni and Bonsmara Cattle Populations Reveal Genes Relating to Environmental Adaptation. *Front. Genet.* 13. https://doi.org/10.3389/fgene.2022.909012

Lai, E., Danner, A.L., Famula, T.R., Oberbauer, A.M., 2020. Genome-Wide Association Studies Reveal Susceptibility Loci for Digital Dermatitis in Holstein Cattle. *Anim.* 10:11. https://doi.org/10.3390/ani10112009

Lai, E., Danner, A.L., Famula, T.R., Oberbauer, A.M., 2021. Genome-wide association studies reveal susceptibility loci for noninfectious claw lesions in Holstein dairy cattle. *Front. Genet.* 12:657375. https://doi.org/10.3389/fgene.2021.657375

Makina, S.O., Muchadeyi, F.C., van Marle-Köster, E., MacNeil, M.D., Maiwashe, A., 2014. Genetic diversity and population structure among six cattle breeds in South Africa using a whole genome SNP panel. *Front. Genet.* 5:333. https://doi.org/10.3389/fgene.2014.00333

Malchiodi, F., Brito, L.F., Schenkel, F.S., Christen, A.M., Kelton, D.F., Miglior, F., 2018. Genome-wide association study and functional analysis of infectious and horn type hoof lesions in Canadian Holstein cattle. In: *Proc. of the World Congress on Genetics Applied to Livestock Production.* 11–16 February, 2018, Auckland, New Zealand.

Manske, T., Hultgren, J., Bergsten, C., 2002. Prevalence and interrelationships of hoof lesions and lameness in Swedish dairy cows. *Prev. Vet. Med.* 54(3):247–263. https://doi.org/10.1016/S0167-5877(02)00018-1

Mapholi, N.O., Maiwashe, N., Matika, O., Riggio, V., Bishop, S.C., MacNeil, M.D., Banga, C., Taylor, J.F., Dzama, K., 2016. Genome-wide association study of tick resistance in South African Nguni cattle. *Ticks Tick Borne Dis.* 7(3):487–497. https://doi.org/10.1016/j.ttbdis.2016.02.005

Matshetsheni S. & Jaja, I.F., 2024. Dairy farmworkers' knowledge of the causes, risk factors, and clinical signs of bovine lameness. *Vet. World* 17(8):1789–1797. https://doi.org/10.21203/rs.3.rs-3221672/v1

Mhlongo, N.L., 2019. Evaluation of claw health of dairy cattle housed in dirt lot vs free stall in TMR systems in the central region of South Africa. Dissertation (MSc (Agric)), University of Pretoria.

Milk SA, 2023. *Lacto Data* 26, June 2023.

Mülling, C.K.W., 2024. Looking at their feet: A long and ongoing journey towards understanding lameness. In: *Proceedings of the 22nd International Symposium and 14th International Conference on Lameness in Ruminants*, 16–20 September 2024, Venice.

Olmos, G., Bran, J.A., von Keyserlingk, M.A.G., Hötzel, M.J., 2018. Lameness on Brazilian pasture based dairies – Part 2: Conversations with farmers and dairy consultants. *Prev. Vet. Med.* 157:115–124. https://doi.org/10.1016/j.prevetmed.2018.06.009

Pérez-Cabal, M.A & Charfeddine, N., 2015. Models for genetic evaluations of claw health traits in Spanish dairy cattle. *J. Dairy Sci.* 98:8186–8194. http://dx.doi.org/10.3168/jds.2015-9562

Ranjbar., S., Rabiee, A.R., Ingenhoff, L., House, J.K., 2020. Farmers' perceptions and approaches to detection, treatment and prevention of lameness in pasture-based dairy herds in New South Wales, Australia. *Aust. Vet. J*., 98:264–269. https://doi.org/10.1111/avj.12933

Rexroad, C., Vallet, J., Matukumalli, L.K., Reecy, J., Bickhart, D., Blackburn, H., Boggess, M., Cheng, H., Clutter, A., Cockett, N., Ernst, C., Fulton, J.E., Liu, J., Lunney, J., Neibergs, H., Purcell, C., Smith, T.P.L., Sonstegard, T., Taylor, J., Telugu, B., van Eenennaam, A., van Tassel, C., Wells, K., 2019. Genome to Phenome: Improving Animal Health, Production, and Well-Being – A New USDA Blueprint for Animal Genome Research 2018–2027. *Front. Genet*. 10:327. https://doi.org/10.3389/fgene.2019.00327

Roche, S.M., Renaud, D.L., Saraceni, I.J., Kelton, D.F., DeVries, T.J., 2024. Invited review: Prevalence, risk factors, treatment, and barriers to best practice adoption for lameness and injuries in dairy cattle. *J. Dairy Sci.* 107:3347–3366. https://doi.org/10.3168/jds.2023-23870

Sadiq, M.B., Ramanoon, S.Z., Mossadeq, W.M.S., Mansor, R., Hussain, S.S.S, 2019. Review: Dairy farmers' perceptions of and actions in relation to lameness management. A*nim.* 9(5):270. https://doi.org/10.3390/ani9050270

Sadiq, M.B., Ramanoon, S.Z., Mansor, R., Hussain, S.S.S., Mossadeq, W.M.S., 2020. Claw trimming as a lameness management practice and the association with welfare and production in dairy cows. *Anim.* 10(9):1515. https://doi.org/10.3390/ani10091515

Sogstad, A.M., Fjeldaas, T., Østerås, O., Forshell, K.P., 2005. Prevalence of claw lesions in Norwegian dairy cattle housed in tie stalls and free stalls. *Prev. Vet. Med.* 70:191–209. https://doi.org/10.1016/j.prevetmed.2005.03.005

Thomsen, P.T., Shearer, J.K., Houe, H., 2023. Prevalence of lameness in dairy cows: A literature review. *Vet. J.* 295:105975. https://doi.org/10.1016/j.tvjl.2023.105975

Van der Spek, D., Van Arendonk, J.A.M., Vallée, A.A.A., Bovenhuis, H., 2013. Genetic parameters for claw disorders and the effect of preselecting cows for trimming. *J. Dairy Sci.* 96(9):6070–6078. https://doi.org/10.3168/jds.2013-6833

Van der Westhuizen, R.R., Mostert, B E., van der Westhuizen, J., 2019. Implementing Genomic Selection following a Single-Step Approach for South African Jersey Cattle. In: *Proc. of the SALHC 2019*. 2–5 June 2019 Port Elizabeth, South Africa.

Van Heerden, B., 2024. MPO Dairy Market Trends. https://www.mpo.co.za/wp-content/uploads/2024/02/Dairy-Market-Trends-Feb-2024.pdf. Accessed 9 November, 2024.

Van Marle-Köster, E., Mhlongo, N.L, Tucker, J., 2020. Hoof trimming data for improving claw health in South African dairy cattle: Understanding claw health can improve cow comfort and welfare. In: *IDF Animal Health Report N° 14*. International Dairy Federation. https://shop.fil-idf.org/products/idf-animal-health-report-n-14. Accessed 25 March 2023

Van Marle-Köster, E. & Visser, C., 2018. Genetic improvement in South African livestock: can genomics bridge the gap between the developed and developing sectors? *Front. Genet.* 9:331. https://doi.org/10.3389/fgene.2018.00331

Visser, C., Lashmar, S.F., Reding, J., Berry, D.P., van Marle-Köster, E., 2023. Pedigree and genome-based patterns of homozygosity in the South African Ayrshire, Holstein, and Jersey breeds. *Front. Genet.* 14:1136078. https://doi.org/10.3389/fgene.2023.1136078

Wilson, J.P., Higgins, H.M., Tulloch, J., O'Grady., L., Green, M.J., Coffey, M., Banos, G., Oikonomou, G., 2024. The UK Hoof Health Registry: Establishing better genetic evaluations for lameness traits in UK dairy cows. In: *Proceedings of the 22nd International Symposium and 14th International Conference on Lameness in Ruminants*, 16–20 September, 2024, Venice.

Wynands, E.M., Roche, S.M., Cramer, G., Ventura, B.A., 2021. Dairy farmer, hoof trimmer, and veterinarian perceptions of barriers and roles in lameness management. *J. Dairy Sci.* 104(11)11889–11903. https://doi.org/10.3168/jds.2021-20603

Zinpro® Corporation, 2008. *Claw Lesion Identification in Dairy Cattle* (D40-08-30-07). Eden Prairie, MN, USA.

