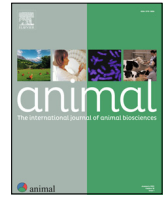




Contents lists available at ScienceDirect

Animal

The international journal of animal biosciences



Review: Opportunities and challenges for the genetic selection of dairy calf disease traits

C. Lynch^a, E.M. Leishman^{a,b}, F. Miglior^{a,c}, D. Kelton^d, F.S. Schenkel^a, C.F. Baes^{a,e,*}

^a Centre for the Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, 50 Stone Road East, Guelph, ON, Canada

^b Centre for Nutrition Modelling, Department of Animal Biosciences, University of Guelph, 50 Stone Road East, Guelph, ON, Canada

^c Lactanet Canada, Guelph, ON N1K-1E5, Canada

^d Department of Population Medicine, University of Guelph, Ontario N1G-2W1, Canada

^e Institute of Genetics, Department of Clinical Research and Veterinary Public Health, University of Bern, Bern 3001, Switzerland

ARTICLE INFO

Article history:

Received 8 October 2023

Revised 14 March 2024

Accepted 15 March 2024

Available online xxx

Keywords:

Dairy calves

Diarrhoea

Genetic selection

Respiratory disease

Calf health

ABSTRACT

Interest in dairy cow health continues to grow as we better understand health's relationship with production potential and animal welfare. Over the past decade, efforts have been made to incorporate health traits into national genetic evaluations. However, they have focused on the mature cow, with calf health largely being neglected. Diarrhoea and respiratory disease comprise the main illnesses with regard to calf health. Conventional methods to control calf disease involve early separation of calves from the dam and housing calves individually. However, public concern regarding these methods, and growing evidence that these methods may negatively impact calf development, mean the dairy industry may move away from these practices. Genetic selection may be a promising tool to address these major disease issues. In this review, we examined current literature for enhancing calf health through genetics and discussed alternative approaches to improve calf health via the use of epidemiological modelling approaches, and the potential of indirectly selecting for improved calf health through improving colostrum quality. Heritability estimates on the observed scale for diarrhoea ranged from 0.03 to 0.20, while for respiratory disease, estimates ranged from 0.02 to 0.24. The breadth in these ranges is due, at least in part, to differences in disease prevalence, population structure, data editing and models, as well as data collection practices, which should be all considered when comparing literature values. Incorporation of epidemiological theory into quantitative genetics provides an opportunity to better determine the level of genetic variation in disease traits, as it accounts for disease transmission among contemporaries. Colostrum intake is a major determinant of whether a calf develops either respiratory disease or diarrhoea. Colostrum traits have the advantage of being measured and reported on a continuous scale, which removes the issues classically associated with binary disease traits. Overall, genetic selection for improved calf health is feasible. However, to ensure the maximum response, first steps by any industry members should focus efforts on standardising recording practices and encouragement of uploading information to genetic evaluation centres through herd management software, as high-quality phenotypes are the backbone of any successful breeding programme.

© 2024 The Authors. Published by Elsevier B.V. on behalf of The Animal Consortium. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Implications

The dairy industry is trending away from conventional calf-rearing practices, meaning alternative methods to control calf disease are needed. Genetic selection can be a valuable tool, and current literature shows the potential for calf disease genetic evaluation. However, large ranges in heritability estimates exist, mostly due to differences in model approach, population structure

and recording practices. Most importantly, emphasis should be placed on encouraging consistent accurate data recording going forward. Furthermore, alternative approaches such as incorporating epidemiological modelling theory with current quantitative genetic approaches, and selection on colostrum traits should be considered as potential avenues to further improve calf health.

Introduction

In recent years, there has been a notable shift towards prioritising animal health, driven by increasing awareness of how diseases

* Corresponding author.

E-mail address: cbaes@uoguelph.ca (C.F. Baes).

<https://doi.org/10.1016/j.animal.2024.101141>

1751-7311/© 2024 The Authors. Published by Elsevier B.V. on behalf of The Animal Consortium.

This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

can negatively impact dairy cattle performance. Additionally, there is a growing interest of the public in agricultural production (Svensson and Hultgren, 2008; Alonso et al., 2020). For example, in Canada, national genetic evaluations for dairy cattle now contain various health-related traits, including mastitis resistance, ketosis, hoof lesions, displaced abomasum, fertility disorders, and more (Koeck et al., 2012; Beavers and Van Doormaal, 2013, 2018; Jamrozik et al., 2016, 2021; Miglior et al., 2016; Malchiodi et al., 2017; Fleming and Van Doormaal, 2020). However, these traits are measured on adult cows; early-life health traits have received comparatively less attention until recently. Several progressive studies have highlighted the potential of genetic selection to improve calf health (Henderson et al., 2011; Gonzalez-Peña et al., 2019, 2020; Haagen et al., 2021; Zhang et al., 2022; van Staaveren et al., 2023; Lynch et al., 2024). Additionally, Zoetis became the first commercial animal health company to include calf disease traits within a genomic test, as part of CLARIFIDE® Plus (Zoetis, 2022). Although these efforts are promising, to our knowledge, there is no national genetic evaluation for calf disease traits to date. Conventional methods to control calf disease have centred on the early removal of the calf from the dam and rearing calves in single pens (Flower and Weary, 2003; Beaver et al., 2019), with consequently limited interaction with conspecifics and reduced disease transmission (Ventura et al., 2013; Pempek et al., 2017). Despite reduced disease transmission, the dairy industry may be encouraged to shift back to group housing and increased cow-calf time for several reasons. These reasons include poor public opinion of calf social isolation and early removal (Hötzel et al., 2017; Placzek et al., 2021), the demonstrated benefits of group housing for social support (Duve and Jensen, 2012; Costa et al., 2016), and improved feeding behaviour of group-housed calves (De Paula Vieira et al., 2012; Costa et al., 2015; Jensen et al., 2015). Additionally, the other conventional method of treating calf diseases with antibiotics is not necessarily desirable long term due to concerns with antibiotic use and antimicrobial resistance, which further underlines the need for other strategies to improve calf health. Therefore, calf health will become an even bigger area of interest and genetic selection may become a valuable tool to reduce disease incidence in dairy calves.

Before discussing potential avenues for enhancing calf health through genetic selection, the fundamental elements of calf health, diseases, and effects on performance should be discussed. Two major calf disease classes are gastrointestinal disease (henceforth referred to as diarrhoea) and respiratory disease. Diarrhoea is characterised by persistent loose stool lasting multiple days, accompanied by signs such as decreased appetite, lethargy, dehydration, and fever (Renaud et al., 2020; Springer and Yost, 2022). This disease primarily affects calves within the 1st 2–3 weeks of life, with the timing of infection often associated with specific pathogens (Blanchard, 2012). Common pathogens implicated in diarrhoea can be viral (e.g., bovine rotavirus, bovine coronavirus, bovine viral diarrhoea virus), parasitic (e.g., *Cryptosporidium parvum*, *Eimeria* spp.) and bacterial (e.g., *Escherichia coli* K99, *Salmonella* spp., *Clostridium perfringens*) (Foster and Smith, 2009; Cho and Yoon, 2014). *Escherichia coli* K99 generally affects calves within the 1st 3 or 4 days after birth, bovine rotavirus is most infectious between 4 and 14 days old, *Cryptosporidium parvum* and bovine coronavirus are commonly observed between the first and 3rd week of life, and *Salmonella* can affect a calf at any point in its early life (McGuirk, 2008; Foster and Smith, 2009; Brunauer et al., 2021).

Respiratory disease encompasses infections that affect both the upper and lower respiratory tracts and can be caused by both viruses and bacteria (Gorden and Plummer, 2010). Respiratory disease commonly occurs before the age of 6 months, especially when maternal antibodies begin to diminish, combined with environmental stressors (Donovan et al., 1998; Taylor et al., 2010). To pro-

vide a practical framework for characterising respiratory disease, it can be split into three distinct groups, as described by (Callan and Garry, 2002). Firstly, respiratory disease encompasses conditions such as shipping fever pneumonia and enzootic calf pneumonia where bacterial and viral agents attack the respiratory tract of the animal. Second is acute interstitial pneumonias which refers to acute inflammatory conditions affecting the interstitial tissue of the lungs more selectively. Lastly, metastatic pneumonia refers to infections that spread to the lungs from a primary site of infection in another part of the body. This can occur when pathogens enter the bloodstream and reach the lungs, leading to secondary pneumonia. As evident, diarrhoea and respiratory disease can be caused by a multitude of pathogens making control of the diseases very difficult on farm. This is apparent when considering the incidence rates for both diseases across the literature, with diarrhoea generally reported between 23 and 44%, while respiratory disease ranged from 12–22% (Windeyer et al., 2014; Urie et al., 2018; USDA, 2018).

Disease expression is further complicated when considering the components that control it: the interaction of the pathogen causing the disease, the host's natural resistance to the pathogen, and the environment in which both live (Leblanc et al., 2006). Management practices can help alleviate pathogen burden in the environment, including management of the calving pen, bedding material, housing dynamics, and feeding (Renaud et al., 2018; Karle et al., 2019). Efforts to enhance host resistance have primarily revolved around vaccine programmes and prophylactic antibiotic treatment (Woolums, 2021; Uyama et al., 2022). Vaccine programmes are commonplace in dairy herds, with approximately 75% of herds vaccinating against bovine viral diarrhoea in the USA (APHIS, 2008). Roughly 25% of calves receive antimicrobial treatment, primarily due to diarrhoea or respiratory disease cases. Among calves diagnosed with diarrhoea or respiratory disease, 69 and 88% receive antimicrobial treatment, respectively (Urie et al., 2018). However, growing global concern around the emergence of antibiotic-resistant bacteria and vaccine-resistant viruses, coupled with their often-limited effectiveness at preventing disease transmission, diminishes the attractiveness of these interventions (Gibson and Bishop, 2005; De Oliveira et al., 2020).

In addition to respiratory disease and diarrhoea being highly prevalent and difficult to control, previous work has also established that calf disease negatively impacts production efficiency. (Nor et al., 2013) reported a 6% increase in rearing costs in heifers exhibiting disease during calthood. (Sischo et al., 1990) found that calf disease accounted for 4% of total lifetime costs. Estimates for the cost per case of diarrhoea ranged between 73 and 128 USD (Pro Earth Animal Health, 2017; Roche et al., 2020), while the cost per incident of respiratory disease case ranged between 42 and 282 USD (Dubrovsky et al., 2020; Overton, 2020). Cost variability is due to several factors, including the severity of the disease, the age of the calf, and management practices (e.g., disease intervention strategies). The associated costs of these diseases not only arise from medical intervention and labour costs but also from effects on production such as average daily gain and future milk potential. In a meta-analysis of 27 studies, (Buczinski et al., 2021) reported that calthood respiratory disease reduced heifer average daily gain by 0.067 kg/d. For diarrhoea, the literature is less definitive, with studies reporting a decrease of up to 0.03 kg/d (Donovan et al., 1998; Stanton, 2011), while others found no significant effect (Vitala et al., 1996). Concerning production, cows with a single case of diarrhoea when they were calves produced 344 kg less energy-corrected milk than healthy animals during the first lactation (Svensson and Hultgren, 2008). Similarly, heifers experiencing respiratory disease produced 121.2 kg less milk during their first lactation compared to healthy animals (Buczinski et al., 2021). These findings show the influence of calf illnesses on animals mak-

ing the transition from calthood to the milking herd and help explain why respiratory disease and diarrhoea are the primary reasons behind involuntary culling and mortality until first calving (Waltner-Toews et al., 1986; Wathes et al., 2008; Zhang et al., 2019b). Preweaning mortality rates in dairy calves range from 5–11% (Murray, 2011; Urie et al., 2018; Winder et al., 2018; Zhang et al., 2019b), with diarrhoea (53–56%) and respiratory disease (21–23%) accounting for roughly 75% of preweaned calf mortality (NAHMS, 2007; Murray, 2011). For the postweaning period, mortality is between 2 and 7%, of which respiratory disease accounts for roughly 50% of cases (NAHMS, 1996; Winder et al., 2018; Santman-Berends et al., 2019; Zhang et al., 2019b; Peel, 2020).

Clearly, calf disease can have a substantial impact on farm productivity, and that societal concerns regarding current rearing practices of dairy calves need to be addressed. Genetic selection may be a tool to address these issues long term and needs to be further explored. The objective of this review is to examine the current literature on genetic selection for enhancing calf health and to discuss the key opportunities and challenges that are likely to arise in implementing routine genetic selection. This review compares current genetic estimates, exploring the impact of recording practices and calf-specific information on model estimates. Furthermore, alternative approaches to improve calf health via epidemiological modelling approaches, and the potential of indirectly selecting for improved calf health through improving colostrum quality are discussed.

Comparing current genetic approaches

Current genetic parameters in the literature for diarrhoea and respiratory disease are summarised in Table 1. Studies that estimated parameters using a threshold model had their values converted to the observed scale. This transformation was completed

using the method described in the appendix of (Dempster and Lerner, 1950) by Alan Robertson:

$$h_o^2 = \frac{h_l^2 * z^2}{p(1-p)}$$

where h_o^2 is heritability on the observed scale, h_l^2 is heritability on the underlying liability scale, p is the proportion of affected individuals in the population of interest, z is the height of the standard normal curve at the truncation threshold for the corresponding value of p . Theoretically, the threshold model is better for disease traits because it respects the discrete nature of the trait by fitting a non-Gaussian distribution (Roff, 1996). However, with large numbers of records, model fit and animal ranking do not differ significantly between linear and threshold models. This lack of difference means both models are viable options for the genetic evaluation of disease traits (Jamrozik et al., 2005; Koeck et al., 2012). Across the literature, heritability estimates on the observed scale for diarrhoea ranged from 0.03 to 0.20, while those for respiratory disease estimated ranged from 0.02 to 0.24 (Table 1). These large ranges can be attributed to differences in disease prevalence, population structure, data editing and model approach, and/or data collection practices. This section will highlight how each of these points can lead to differences in reported values. Furthermore, the value of incorporating genomic information into genetic evaluations of calf disease traits is discussed.

Effect of prevalence and population structure

The linear model, which estimates parameters on the observed scale, does not account for prevalence. Heritability estimates when using a linear model are maximised when prevalence nears 50%, and approach 0 when prevalence nears 0 or 100%. This is because phenotypic variance of binary disease traits is determined by the

Table 1
Summary of genetic parameters in the literature for diarrhoea and respiratory disease in dairy calves.

Paper	Country	Breed	Diagnosis	Traits	Sample size (# herds)	Prevalence	Minimum disease incidence	Model	h_l^2	h_o^2
Lynch et al., 2024	Canada	Holstein	Producer	RESP	158 273 (288)	19%	1%	Linear	NA	0.03
					102 438 (180)	26%	5%	Threshold	0.05	0.02
								Threshold	0.06	0.03
				DIAR	65 642 (122)	19%	1%	Linear	NA	0.04
					39 965 (61)	28%	5%	Threshold	0.07	0.03
								Linear	NA	0.06
Zhang et al., 2022	China	Holstein	Veterinarian	RESP	184 563 (31)	4%	NA	Linear	NA	0.05
								Threshold	0.08	0.02
								Linear	NA	0.06
Yin et al., 2022	Germany	Holstein	Producer & Veterinarian	DIAR	112 563 (53)	28%	NA	Threshold	0.10	0.06
					176 904 (53)	22%			0.17	0.09
Haagen et al., 2021	USA	Holstein	Producer	RESP	10 527 (16)	12%	1%	Threshold	0.10	0.04
					11 603 (16)	44%			0.08	0.05
Quick et al., 2020	USA	Holstein	Veterinarian	RESP	1 017 (6)	19%	NA	Linear	NA	0.24
Johnston et al., 2020	Ireland	Mixed	Producer	RESP	727 (32)	5%	NA	Linear	NA	0.09
Gonzalez-Peña et al., 2020	USA	Jersey	Producer	DIAR	276 134 (90)	14%	0.5%	Threshold	0.06	0.02
					186 505 (90)	37%			0.08	0.05
Gonzalez-Peña et al., 2019	USA	Holstein	Producer	RESP	1 331 626 (188)	21%	0.5%	Threshold	0.04	0.02
					741 484 (118)	26%			0.05	0.03
Mahmoud et al., 2017	Germany	Holstein	Producer & Veterinarian	RESP	31 396 (43)	28%	NA	Threshold	0.07	0.04
Neiberger et al., 2014	USA	Holstein	Laboratory	RESP	2 763 (NA)	50%	NA	Linear	NA	0.13
Henderson et al., 2011	Canada	Holstein	Veterinarian	RESP	7 372 (36)	38%	NA	Linear	NA	0.10
McCorquodale et al., 2013	Canada	Holstein	Veterinarian	RESP	1 588 (16)	10%	NA	Linear	NA	0.04

RESP = Respiratory disease; DIAR = Diarrhoea; h_l^2 = Heritability on liability scale; h_o^2 = Heritability on observed scale.

prevalence of the disease. If prevalence is close to 0 or 100%, there is limited phenotypic variance, while as prevalence reaches 50% it is maximised, better-enabling prediction of genetic differences between animals. Furthermore, at these extremes in prevalence, genetic variation is largely due to non-additive effects, namely epistatic effects (Dempster and Lerner, 1950). The threshold model estimates parameters on the liability scale, which accounts for prevalence in the population. This explains why liability scale heritability estimates are larger. Observed scale and linear scale estimates will become closer as disease prevalence nears 50% in a study population. For example, (Zhang et al., 2022) had a prevalence of 4% for respiratory disease, and in this study, the difference between the observed scale heritability estimate and the liability scale heritability estimate was 4 times smaller (0.02 vs 0.08) (Table 1). In contrast, (Haagen et al., 2021) had a diarrhoea prevalence of 44%, and the difference between the observed and liability scale estimates was 1.6 times smaller (0.05 vs 0.08). Lynch et al. (2024) further confirmed the impact of prevalence on observed scale estimates when comparing different data inclusion criteria with respect to minimum herd-year disease incidence (1 vs 5%), which in turn impacted the prevalence across analyses. From Table 1, we can see that the magnitude of the difference between observed and liability scale estimates is less when the analysis had a disease prevalence closer to 0.5. Together, this shows the impact that prevalence has on the observed scale estimates, and therefore, should always be considered when comparing heritability estimates across studies.

Population structure is another factor that can impact the size of the heritability estimates. One issue with calf disease traits is that accurate recording of information can be difficult, and as a result, parameters are often estimated on relatively small groups of animals (<3,000) on limited herds (McCorquodale et al., 2013; Neibergs et al., 2014; Johnston et al., 2020; Quick et al., 2020). The issue with small datasets is that sires may be poorly distributed across herds, potentially causing a confounded effect between sires' genetic effects and herds' environmental effect. If a sire only has records from a single herd, it is hard to untangle the environmental influence versus the sire's influence on the phenotype, often resulting in inflated estimates either positively or negatively. As additive variance is directly related to the variance of the estimated breeding values, this can lead to an overestimation of heritability within a population. This effect on heritability estimates was shown by Neibergs et al. (2014) who analysed two datasets from California and New Mexico, using exclusively genomic relationships. The heritability estimate for respiratory disease when locations were analysed separately was 0.21 for both locations. When the locations were analysed together, the heritability estimate dropped to 0.13. Both estimates are high relative to other studies with much larger datasets, which may be partially linked to the aforementioned effect of sire distribution. However, it is essential to acknowledge that other factors, such as genotype-environment interaction and degree of genetic connectedness across contemporary groups within the population, may also contribute to variations in heritability estimates (Roso et al., 2004; Zhang et al., 2019a). Overall, care needs to be given when interpreting heritability estimates on small samples of animals, as it is possible that estimated effects may be biased.

Recording practices

The success of long-term genetic selection programmes is dictated by the recording of accurate and high-quality phenotypes (Coffey, 2020). As mentioned, disease prevalence greatly influences heritability on the observed binary scale, influencing the potential rate of genetic change. Therefore, efforts should be made to help develop a cost-effective data pipeline with standardised protocols

for recording calf disease traits. The first step when adding a new phenotype of interest to genetic evaluations is to define the trait. This is a challenge when it comes to both diarrhoea and respiratory disease, as laboratory testing is required for accurate etiologic diagnosis (Cho and Yoon, 2014). Since this type of analysis is not feasible for most farmers, visual appraisal and clinical examination by either farmers or veterinarians is the common practice (McGuirk and Peek, 2014). Common signs of diarrhoea include watery faeces and lethargy (Renaud et al., 2020), while respiratory disease signs include coughing, fever, nasal discharge, and changes in respiration rate (McGuirk and Peek, 2014). Given the subjective nature of visual appraisal, variation in definition can exist, leading to many cases being misdiagnosed. Producers tend to diagnose cases with relatively low sensitivity (more likely to miss identifying sick animals), but higher specificity (more likely to correctly identify healthy animals) (Sivula et al., 1996). Knauer et al. (2017) reported that producers could identify the health status of group-housed calves with a sensitivity of 26% and a specificity of 97%. Low sensitivity leads to an under-representation of disease prevalence due to a higher amount of false negatives. Therefore, to maximise selection potential, methods to increase recording consistency need to be considered. Possible avenues to help improve the consistency of recording are scoring systems, which help remove the subjectivity of the tester, to provide a more objective evaluation, and to allow for greater consistency across testers (Hayes et al., 2010). Probo and Veronesi (2022) and Wilson et al. (2023) have reviewed current scoring systems. Examples for respiratory disease include the Wisconsin scoring system (WIS score) and the California scoring system (CAL score) (McGuirk, 2008; Love et al., 2014). Buczinski et al. (2015) reported a sensitivity and specificity of 62.4 and 74.1% for the WIS score, respectively. For the CAL score, sensitivity and specificity were reported to be 89.4 and 90.8%, respectively (Love et al., 2014). The Kappa coefficient of agreement between the WIS score and CAL score was estimated to be 0.85, indicating excellent agreement between methods (Aly et al., 2014). For diarrhoea, most methods centre around faecal consistency scoring (Lewis and Heaton, 1997; Lesmeister and Heinrichs, 2004; Renaud et al., 2020). Faecal consistency has been reported to be used currently by dairy farmers as a decision tool regarding treatment for diarrhoea (McGuirk, 2008). Unfortunately, no studies relating to the sensitivity or specificity of faecal consistency scoring were found in the literature by the authors, which would be of great value to the industry. Overall, these methods help improve the diagnosis of disease and provide an opportunity to increase the consistency of recording practices. A concerted effort from industry to encourage the use of these methods will further maximise the potential of genetic selection for calf disease traits.

Apart from accurate recording of the disease, collection of specific calf and disease information should also be encouraged. Specific calf information includes colostrum (quality, quantity, and timing of administration), calving difficulties, and calf vitality scoring. Colostrum intake and successful passive transfer is a crucial determinant as to whether a calf exhibits morbidity and will be discussed in detail later in this review (Mee, 2008; Furman-Fratczak et al., 2011). In a meta-analysis, (Raboisson et al., 2016) reported that the adjusted risk in calves with failure of passive transport (FPT) for respiratory disease and diarrhoea were 1.75 and 1.51, respectively. (Lombard et al., 2007) reported that calves born to dams having severe dystocia had greater odds of treatment for respiratory disease (1.7) and digestive disease (i.e., diarrhoea) (1.3). Calf vitality scoring considers characteristics of newborn calves that relate to suckling reflex, standing, time to lift head, and colostrum intake (Barrier et al., 2012). Several methods relating to scoring calf vitality have been proposed (Mee, 2008; Murray-Kerr et al., 2018; Probo and Veronesi, 2022). However, many of these methods

have failed to be adopted on a commercial level, likely due to the complexity of the scores and missing recommendations for intervention (Homerovsky et al., 2017; Probo and Veronesi, 2022). Furthermore, conflicting relationships between calf morbidity and calf vigour have been reported (Sorge et al., 2009; Tora et al., 2021; Alemu et al., 2022). From a genetic selection perspective, calf vitality scoring at this point will not benefit current approaches. However, with the development of better indicators of calf vitality, it may be a resource to consider in the future.

Specific disease information includes the duration of the disease, to enable a classification of the severity of the disease. This will allow for clearer distinctions between the phenotypes and may help improve model performance (Lynch et al., 2024). Throughout this section, we have identified numerous sources of information that may help improve our potential for genetic selection of calf health. It must be noted that it is likely unfeasible to expect producers to collect all information noted above, so a concerted effort from industry is required to identify which information they feel producers can collect routinely and effectively.

Data editing and modelling approach

Across the literature, there are differences in model approaches due to factors such as population structure and recording practices. To highlight the impact of these differences when comparing modelling approaches, we can look at the studies by Gonzalez-Peña et al. (2019) and Henderson et al. (2011). For respiratory disease, these studies had the largest difference in heritability estimates (2 vs 10%) (Table 1) when removing studies with small datasets (<3 000 records). This discrepancy may be because two very different samples of animals were analysed, as we know population structure and the relatedness of animals can have a large impact on variance components. Further reasons for this difference could be due to collection practices, incidence thresholds, and model factors. Gonzalez-Peña et al. (2019) analysed records from 183 herds compared to Henderson et al. (2011) who had phenotypes collected by veterinarians at a single facility that reared calves from 36 farms. Therefore, Henderson et al. (2011) had the advantage of trained professionals for diagnosing respiratory disease, and there was a high level of consistency in diagnosis since all animals were reared in one facility. Gonzalez-Peña et al. (2019) likely had variation in definition and recording practices across herds within their analysis. Gonzalez-Peña et al. (2019) set a minimum herd-year disease incidence of 0.5%, while it was not specified for Henderson et al. (2011) we assume this was because they were all reared at the same facility. The impact of including herds with very low incidence revolves around the impact of prevalence on model estimates. Furthermore, though it is not stated how many herds had very low incidence, it would be very rare for a herd to have an incidence around 1%, with between 5 and 15% reported as the gold standard target for both respiratory disease and diarrhoea (Dairy Calf and Heifer Association, 2019; RSPCA, 2021). In most cases, this would be due to under-recording of cases, due to reasons highlighted in the previous section. Under recording may impact model performance as some sick animals that were not recorded will be assumed healthy. If we compare the model factors between papers, the major difference is that Henderson et al. (2011) incorporated specific calf information, including calf weight upon arrival at the rearing facility and serum total protein information (as an indicator for successful passive transfer). This added information further accounts for environmental variation associated with calf diseases, increasing the heritability estimate of the trait. The aim here is not to suggest superiority in approach from either study but to highlight the possibilities with these traits and to show that with excellent data collection and collection of

further calf information, it is possible to greatly improve our heritability estimates and in turn our potential response to selection.

It must be noted that Henderson et al. (2011) estimated heritability of respiratory disease as part of a multiple trait analysis with umbilical disease and bloat, and therefore may benefit from other trait information within their model. The benefits of multiple trait analysis for respiratory disease and diarrhoea together have been reported, with genetic correlations between the traits ranging from 0.15 to 0.62 (Mahmoud et al., 2017; Gonzalez-Peña et al., 2019; Haagen et al., 2021; Zhang et al., 2022; Lynch et al., 2024). As previously mentioned, these large ranges may be a result of differences in prevalence across traits and population structure within studies. Of these studies, only Lynch et al. (2024) compared heritability estimates between univariate and multivariate analysis, in which they reported increases in estimated heritability for respiratory disease when diarrhoea information was included in the model. Biologically, the positive genetic correlation between respiratory disease and diarrhoea is logical. Dairy calves experiencing a disease are more likely to suffer a second illness later in life (McCorquodale et al., 2013). Diarrhoea can lead to dehydration, anorexia, and impaired immune function (Schinwald et al., 2022), which are all risk factors for developing the respiratory disease (Gorden and Plummer, 2010). Together, these points suggest that respiratory disease and diarrhoea should be analysed together in a multiple-trait analysis, to maximise selection potential.

Genomic information

Genomic information has been incorporated into several studies of calf health throughout the literature (Neiberger et al., 2014; Mahmoud et al., 2017; Gonzalez-Peña et al., 2019, 2020; Johnston et al., 2020; Quick et al., 2020; Haagen et al., 2021; Yin et al., 2022). For variance component estimation, the inclusion of genomic information was found to show little difference compared to conventional pedigree-based methods (Gaddis et al., 2014; Gonzalez-Peña et al., 2019). The value of genomic information is by increasing the accuracy of selection, particularly in low heritability traits, such as calf disease (VanRaden et al., 2009). Conventionally, for low heritability traits, sires required many phenotypes to achieve a high accuracy estimated breeding value. However, through genomics, high accuracies can be achieved when no phenotypic information is available on an animal, provided the reference population is representative of the current population of animals (García-Ruiz et al., 2016; Wiggans et al., 2017). Young sire reliabilities have nearly doubled since the introduction of genomic selection across all traits (Fleming and Van Doormaal, 2022). Selection decisions can therefore be made earlier in life, reducing the generation interval, and leading to an increased response to selection (Scheffers and Weigel, 2012). As a result of genomic selection, the rate of genetic gain has been doubled. For example, the net merit index has increased at 85 USD per year since 2010, compared to 40 USD in the previous 5 years (Wiggans and Carrillo, 2022). In Canada, the Pro\$ index increased at 102 CAD per year prior to genomics, and 246 CAD per year postgenomics (Fleming and Van Doormaal, 2022). Genomics will play a large role in any future genetic evaluation. Therefore, studies should incorporate genomic information if it is available when analysing calf disease traits.

Limitations of current approaches

Throughout this section, we have highlighted current practices that are being suggested and implemented for improving dairy calf health. However, there are several limitations to these current approaches such as: (1) the effect of prevalence and population structure on estimates, leading to inflated genetic parameter values that likely are not representative of the population, (2) the lack

of calf information, such as colostrum intake and dystocia, which are known to play a pivotal role in calf disease expression, and (3) limited recording practices to ensure consistent accurate information is being recorded across herds. Even though there are opportunities to improve each of these challenges, alternative strategies to improve calf health exist, which are discussed in the following section.

Alternative approaches

We have outlined the current genetic approaches to improve calf health. However, as mentioned, there are several limitations with current strategies. A number of intriguing avenues of research have emerged to investigate novel or alternative strategies to improve calf health. We have identified two main areas of interest: (1) epidemiological approaches and (2) investigating the role of colostrum, which are discussed in the following sections.

Epidemiological approach

The ultimate goal of disease control is eradication of the disease whereby all animals remain healthy. However, this is theoretically impossible to achieve from a classical quantitative genetics perspective, as additive genetic variance on the observed binary scale will approach 0 as prevalence approaches 0 (Dempster and Lerner, 1950). As mentioned previously, this is because when prevalence is close to 0, there is limited phenotypic variance, reducing your ability to differentiate between animals genetically (Hulst et al., 2021). Furthermore, current methods focus on the susceptibility of individuals to disease, disregard information from group members (Lipschutz-Powell et al., 2014), and assume that the observed phenotypic differences represent differences in host resistance to a given pathogen (Lipschutz-Powell et al., 2013). This approach is unrealistic though, as it assumes that exposure to a pathogen is constant over time, equal among individuals, and purely due to the environment (Lipschutz-Powell et al., 2013). For this reason, it is likely that conventional genetic methods are capturing only a fraction of genetic variation of disease data (Lipschutz-Powell et al., 2012; Bishop and Woolliams, 2014).

The incorporation of epidemiological theory into quantitative genetics provides an opportunity to better determine the level of genetic variation in disease traits (Bishop and Stear, 1997; Bijma et al., 2022). This stems from the ability to allow for the positive feed-back dynamics of disease transmission to be accounted for (Anche et al., 2014; Bijma et al., 2022). The basis of this positive feed-back dynamic is as follows; if an animal is immune to a pathogen, this has a positive effect on animals around them, as they will not spread the pathogen. If many animals within a group are immune, this positive feedback effect will be compounded, to the point where the pathogen can no longer spread, and thus die out completely. On the other hand, if an animal is very susceptible to a disease, they will become sick and aid in the spread of disease. This increases the likelihood of animals around them becoming sick, potentially resulting in an outbreak within a group of animals (Bijma et al., 2022). An example of this positive feedback effect is seen with herd immunity via vaccination protocols, whereby complete eradication of a disease can be achieved without the full population being vaccinated, as the pathogen is unable to spread (Fine, 1993).

The key parameter in epidemiology to access this positive feedback mechanism and the impact of disease interventions on epidemic risk is the basic reproductive ratio, which represents the average number of secondary cases caused by an infected individual in a susceptible population (Diekmann et al., 1990). The basic reproductive ratio has a threshold value of one, which dictates if

a disease outbreak can happen. If it is less than one, the epidemic will die out, but if it exceeds one, outbreaks may occur (Diekmann et al., 1990; Anche et al., 2014; Tsairidou et al., 2019). The basic reproductive ratio is controlled by the transmission rate of the disease and the resulting recovery rate from infection. Across the literature, most studies have concentrated on the genetics of the transmission rate, which is determined by two host traits, the host's susceptibility to contracting a disease, and a host's infectivity to transmit the disease (Anche et al., 2014; Lipschutz-Powell et al., 2014; Biemans et al., 2017; Tsairidou et al., 2019). From an epidemiology perspective, both susceptibility and infectivity can be seen as indirect genetic effects (IGEs), which are when the genotype of one individual affects the phenotype of a second individual (Griffing, 1967; Muir, 2005; Bijma, 2014). These IGE can drastically affect the rate and direction of response to selection, which has been shown both theoretically and experimentally (Griffing, 1976; Lipschutz-Powell et al., 2012; Anche et al., 2014). One reason for this is that greater genetic variation may exist in infectivity compared to susceptibility, enabling faster rates of genetic change. Across generations, natural selection has reduced genetic variation in susceptibility, as it is linked to an individual's fitness (Lipschutz-Powell and Woolliams, 2012). However, infectivity is not linked to an individual's own fitness, and therefore, genetic variation would not have been impacted by natural selection (Boddicker et al., 2012).

Epidemiological models unravel the genetic heterogeneity in both susceptibility and infectivity traits, and respect the impact each animal has on its contemporaries compared to conventional quantitative genetic approaches (Nath et al., 2008; Doeschl-Wilson et al., 2011). From a calf health perspective, there is a shift towards group housing of young livestock which increases the interaction of animals from a young age (Costa et al., 2015; Jensen et al., 2015; Placzek et al., 2021). It would be possible to apply epidemiological theory discussed above through the recording of animal groups/pens to determine which animals were exposed to each other at each point of calthood. This of course becomes difficult from a management perspective to continuously track, especially on large enterprises. However, with continuous incorporation of precision livestock technology, such as sensor data, it may be feasible to automatically track calves via ear tags, to record calf location at any point in time, and is already commercially available for adult cows (Wolfger et al., 2017; Costa et al., 2021a).

Colostrum

One of the major determinants for whether a calf develops either respiratory disease or diarrhoea is the quantity and quality of colostrum that they received and when they receive it. Therefore, a possible proactive measure to help reduce calf disease would be genetically selecting for traits related to colostrum quality of the dam and antibody absorption of the calf. The importance of colostrum feeding in calf rearing has been well-documented, as it profoundly influences health and long-term performance (Khan et al., 2011; Ballou, 2012; Hammon et al., 2020). Colostrum is the first milk that a cow releases postcalving, and is rich in antibodies, also known as immunoglobulins (Ig), and other nutrients that provide the calf protection from disease early in life (McGrath et al., 2016). The importance of feeding colostrum stems from dairy cows not having an epitheliochorial placenta, meaning passive immunity cannot be transferred to the neonate during gestation (Robbers et al., 2021). Therefore, calves solely rely on the transfer of immune constituents through initial feedings from the dam via colostrum. Within colostrum, there are three major Ig, IgG (80–90%) is considered the most important, while IgM and IgA make up about 7 and 5%, respectfully (Stilwell and Carvalho,

2011; Godden et al., 2019). Colostrum quality varies among animals (Gilbert et al., 1988) and is determined by numerous factors, including volume, collection time, Ig concentration, and bacterial levels (McGuirk and Collins, 2004; Godden, 2008). Timing of feeding is also important. To ensure successful passive transfer of Ig, the calf must consume colostrum shortly after birth, ideally within 2–3 h (Weaver et al., 2000; Godden, 2008). If colostrum feeding is delayed or is of low quality, FPT can occur (Raboisson et al., 2016). FPT occurs when the calf serum IgG concentration falls below 10 mg/mL (Pritchett et al., 1991; Faber et al., 2005; Beam et al., 2009), and is associated with increased calf mortality and morbidity rates (Mee, 2008; Furman-Fratczak et al., 2011). FPT rates vary across the literature, falling somewhere between 19 and 40% (Beam et al., 2009; Raboisson et al., 2016; Abuelo et al., 2019). Together, this highlights the importance of colostrum in calf disease prevention. Furthermore, it is common practice in many herds to pool colostrum to help reduce labour requirements (King et al., 2020), and therefore, improving colostrum quality at the cow level may have greater effects at the herd level. However, the benefits of pooling colostrum must be weighed against the potential for disease transmission, especially in herds with endemic infectious diseases such as Johne's Disease or Bovine Leukaemia Virus (Godden, 2008; Williams et al., 2014).

To evaluate if a trait is suitable for genetic selection, certain criteria should be considered, as described by (Shook, 1989). This includes that the trait needs to be clearly defined, cost-effective and easy to measure, it must exhibit significant genetic variation and be heritable, and there must be economic value to improving the trait. Colostrum quality can be defined by the concentration of Ig within colostrum, while calf absorption ability can be defined as the level of Ig within calf serum 24 h postfeeding. Colostrum quality and calf absorption ability can be directly determined by radial immunodiffusion (RID), which is considered the gold standard measurement (Bartens et al., 2016; Ahmann et al., 2021). Though RID is highly accurate and repeatable, it is expensive and time-consuming reducing its merit for a potential measure on a large-scale genetic programme (Costa et al., 2021b). For colostrum quality, several other measurement methods have been proposed, including the use of enzyme-linked immunosorbent assay (ELISA) (Gelsinger et al., 2015), near-infrared spectroscopy (NIRS) (Rivero et al., 2012; Costa et al., 2021b), and Brix refractometer (Quigley et al., 2013; Bartier et al., 2015). Like RID, ELISA tests are time-consuming and require lab work. NIRS and Brix provide the most promise, with both being rapid and cost-effective measures for determining colostrum quality. Genetic and phenotypic correlations between NIRS and RID were estimated to be 0.85 and 0.77, respectively (Costa et al., 2021b), while phenotypic correlations between Brix and RID have ranged from 0.64 to 0.75 (Bielmann et al., 2010; Quigley et al., 2013; Gelsinger et al., 2015), showing good potential as indicator traits of RID values. One challenge with calf absorption ability is that it requires a blood sample, making recording more difficult and time-consuming, while also being quite invasive to the animal. For genetic selection on calf absorption ability to be feasible, long-term alternative measures will need to be identified. One area of interest to predicting calf serum Ig concentration is through calf saliva, which is less invasive and easier to record (Johnsen et al., 2019; Silva et al., 2023). Johnsen et al. (2019) reported a strong positive correlation ($r = 0.7$) between saliva IgG and serum IgG. However, all sampled calves in this study had serum IgG levels above 10 g/L, meaning it is unknown how calves with FPT (i.e., serum IgG < 10 g/L) can be predicted by saliva IgG. Therefore, further work is required to determine if saliva can be used as an indicator of FPT.

For selection, traits also need to have genetic variance and be heritable. Though limited, several studies have estimated the heritabilities of colostrum-related traits, including colostrum yield,

IgG concentration, total solids (Brix %), serum total protein, serum IgG, and numerous associated natural antibodies. Heritability estimates for colostrum yield range from 0.04 to 0.21 (Conneely et al., 2013; Soufleri et al., 2019), IgG concentration ranged from 0.10 to 0.40 (Gilbert et al., 1988; Conneely et al., 2013; Cockrum et al., 2016; Martin et al., 2021; Cordero-Solorzano et al., 2022), and total solids (Brix %) ranged from 0.27 to 0.41 (Soufleri et al., 2019; Cordero-Solorzano et al., 2022). For calf absorption ability, the heritability estimate for serum total protein was 0.07 (Cordero-Solorzano et al., 2022), while serum IgG estimates ranged from 0.18 to 0.56 (Gilbert et al., 1988; Burton et al., 1989; Martin et al., 2021; Cordero-Solorzano et al., 2022). The large range in estimates could be due to many factors including differences in population structure, colostrum and serum measurement methods, and phenotyping strategies. However, it is clear that there are much higher heritability estimates for colostrum traits compared to health traits, which are typically below 0.1. Colostrum traits have the advantage of being a continuous variable which removes the issues classically associated with binary disease traits. The advantage of this is due to the clearer distinction between animals phenotypically, which increases the ability to identify genetic differences amongst animals. However, in many cases, heritability estimates were not different from zero, with many studies reporting high SEs. This is likely due to the limited amount of data within certain studies. Therefore, further research is still required to better determine the genetic influence on colostrum-related traits.

The last criterion for genetic selection relates to the economic importance of the trait. When discussing colostrum traits, we are mainly concerned with helping to reduce FPT by maximising the quality of colostrum and the calf's ability to absorb the associated antibodies, so economics should be related to the impact of FPT. (Raboisson et al., 2016) reported that the average marginal cost for FPT ranged from €60 to €121 for dairy calves and €80 to €140 for beef calves. These values stem from the fact that FPT is a leading reason behind preweaning morbidity and in-turn mortality. (Raboisson et al., 2016) also reported that the adjusted risks of FPT (and 95% confidence intervals) for mortality, respiratory disease, diarrhoea and overall morbidity were 2.12 (1.43–3.13), 1.75 (1.50–2.03), 1.51 (1.05–2.17) and 1.91 (1.63–2.24), respectively. Preweaning mortality rates in dairy calves range from 5 to 11% (Murray, 2011; Urie et al., 2018; Winder et al., 2018; Zhang et al., 2019b) and in the UK, it was reported that calf mortality costs roughly 60 million pounds/year (Department for Environment, 2003). Given this large economic impact, reducing FPT is of great interest, showing the value of improving colostrum-related traits through genetic selection.

Genetic selection for colostrum traits has promise for improving overall calf health. Some challenges going forward will include the standardisation of recording methods to measure colostrum traits. For long-term genetic evaluation, one method should be decided upon and encouraged to be used by producers to ensure consistency of testing practices. Another potential challenge is the issue of hypergammaglobulinemia, which refers to the overproduction of immunoglobulin (Beuvon, 2021) and has been related to diseases in numerous species including humans and dogs (Buadi et al., 2011; Colopy et al., 2019). Evidence of hypergammaglobulinemia in dairy cattle were not found by the authors but caution would be suggested when selecting colostrum traits, particularly related to immunoglobulin production to fully understand its impact on the dairy cow.

Conclusions

Management of dairy calf health is likely to become a greater area of interest as conventional methods of disease control (e.g.,

early removal from the dam, single housing) become less attractive due to societal pressure and the apparent impact on overall calf development. One result of this shift will be group housing, which will expose young calves to higher levels of pathogen. To combat the potential impact of this exposure, genetic selection may be a valuable asset. Throughout this review, we have detailed current genetic practices to help improve calf health and highlighted the areas where we see opportunities and challenges, most notably with respect to improving data recording practices. Furthermore, we have detailed alternative approaches, such as incorporating epidemiological modelling to better understand disease transmission, and reviewed the potential of selection on colostrum traits as a proactive measure to improve calf health. Overall, enhancing calf health through genetic selection is attainable. However, to optimise response, initial actions by industry stakeholders should prioritise the standardisation of recording practices and the promotion of data uploads to herd management software, as high-quality phenotypes are the backbone of any successful breeding programme.

Ethics approval

Not applicable.

Data and model availability statement

Not applicable. Information can be made available from the authors upon request.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author(s) did not use any AI and AI-assisted technologies.

Author ORCIDs

CL: <https://orcid.org/0000-0002-0524-3939>.
EL: <https://orcid.org/0000-0003-1739-3915>.
FM: <https://orcid.org/0000-0003-2345-8842>.
DK: <https://orcid.org/0000-0001-9606-7602>.
FS: <https://orcid.org/0000-0001-8700-0633>.
CB: <https://orcid.org/0000-0001-6614-8890>.

CRedit authorship contribution statement

C. Lynch: Writing – review & editing, Writing – original draft, Conceptualization. **E.M. Leishman:** Writing – review & editing, Writing – original draft. **F. Miglior:** Writing – review & editing. **D. Kelton:** Writing – review & editing. **F.S. Schenkel:** Writing – review & editing. **C.F. Baes:** Writing – review & editing, Conceptualization.

Declaration of interest

None.

Acknowledgements

None.

Financial support statement

This review was conducted as part of the Resilient Dairy Genome Project (RDGP). We gratefully acknowledge all funding and support for the Resilient Dairy Genome Project from the organisations listed at <http://www.resilientdairy.ca/funders-and-partners/>, as administered by Genome Canada, Genome Alberta, Ontario Genomics, Genome Quebec, and Genome British Columbia. Dr. Christine Baes also gratefully acknowledges support from the Natural Sciences and Engineering Research Council of Canada (NSERC) Canada Research Chair and Discovery programmes. As per the research agreement, the funders had no role in the design and conduct of the study as well as the decision to publish.

References

- Abuelo, A., Havrlant, P., Wood, N., Hernandez-Jover, M., 2019. An investigation of dairy calf management practices, colostrum quality, failure of transfer of passive immunity, and occurrence of enteropathogens among Australian dairy farms. *Journal of Dairy Science* 102, 8352–8366.
- Ahmann, J., Steinhoff-Wagner, J., Büscher, W., 2021. Determining immunoglobulin content of bovine colostrum and factors affecting the outcome: a review. *Animals* 11, 1–29.
- Alemu, Y.F., Jemberu, W.T., Mekuriaw, Z., Abdi, R.D., 2022. Incidence and predictors of calf morbidity and mortality from birth to 6-months of age in dairy farms of Northwestern Ethiopia. *Frontiers in Veterinary Science* 9, 1–12.
- Alonso, M.E., González-Montaña, J.R., Lomillos, J.M., 2020. Consumers' concerns and perceptions of farm animal welfare. *Animals* 10, 1–13.
- Aly, S.S., Love, W.J., Williams, D.R., Lehenbauer, T.W., Van Eenennaam, A., Drake, C., Kass, P.H., Farver, T.B., 2014. Agreement between bovine respiratory disease scoring systems for pre-weaned dairy calves. *Animal Health Research Reviews* 15, 148–150.
- Anche, M.T., De Jong, M.C.M., Bijma, P., 2014. On the definition and utilization of heritable variation among hosts in reproduction ratio R0 for infectious diseases. *Heredity* 113, 364–374.
- APHIS 2008. Bovine Viral Diarrhea (BVD) Management practices and detection in bulk tank milk in the United States, 2007. Animal & Plant Health Inspection Service- Veterinary Services. Retrieved on 9 January 2023 from https://www.aphis.usda.gov/animal_health/nahms/dairy/downloads/dairy07/Dairy07_is_BVD_1.pdf.
- Ballou, M.A., 2012. Immune responses of Holstein and Jersey calves during the preweaning and immediate postweaned periods when fed varying planes of milk replacer. *Journal of Dairy Science* 95, 7319–7330.
- Barrier, A.C., Ruelle, E., Haskell, M.J., Dwyer, C.M., 2012. Effect of a difficult calving on the vigour of the calf, the onset of maternal behaviour, and some behavioural indicators of pain in the dam. *Preventive Veterinary Medicine* 103, 248–256.
- Bartens, M.-C., Drillich, M., Rychli, K., Iwersen, M., Arnholdt, T., Meyer, L., Klein-Jöbstl, D., 2016. Assessment of different methods to estimate bovine colostrum quality on farm. *New Zealand Veterinary Journal* 64, 263–267.
- Bartier, A.L., Windeyer, M.C., Doepel, L., 2015. Evaluation of on-farm tools for colostrum quality measurement. *Journal of Dairy Science* 98, 1878–1884.
- Beam, A.L., Lombard, J.E., Kopral, C.A., Garber, L.P., Winter, A.L., Hicks, J.A., Schlater, J. L., 2009. Prevalence of failure of passive transfer of immunity in newborn heifer calves and associated management practices on US dairy operations. *Journal of Dairy Science* 92, 3973–3980.
- Beaver, A., Meagher, R.K., von Keyserlingk, M.A.G., Weary, D.M., 2019. Invited review: a systematic review of the effects of early separation on dairy cow and calf health. *Journal of Dairy Science* 102, 5784–5810.
- Beavers L and Van Doormaal B 2013. Official Genetic evaluation for mastitis resistance. Canadian Dairy Network. Retrieved on 9 January 2023 from <https://www.cdn.ca/document.php?id=333>.
- Beavers L and Van Doormaal B 2018. Genetic selection for improved hoof health is now possible | Canadian Dairy Network. Retrieved on 9 January 2023 from <https://www.cdn.ca/document.php?id=513>.
- Beuvon, C., 2021. Etiologies of polyclonal hypergammaglobulinemia: a scoping review. *European Journal of Internal Medicine* 90, 119–121.
- Bielmann, V., Gillan, J., Perkins, N.R., Skidmore, A.L., Godden, S., Leslie, K.E., 2010. An evaluation of brix refractometry instruments for measurement of colostrum quality in dairy cattle. *Journal of Dairy Science* 93, 3713–3721.
- Biemans, F., De Jong, M.C.M., Bijma, P., 2017. A model to estimate effects of SNPs on host susceptibility and infectivity for an endemic infectious disease. *Genetics Selection Evolution* 49, 1–13.
- Bijma, P., 2014. The quantitative genetics of indirect genetic effects: a selective review of modelling issues. *Heredity* 112, 61–69.
- Bijma, P., Hulst, A.D., de Jong, M.C.M., 2022. The quantitative genetics of the prevalence of infectious diseases: hidden genetic variation due to indirect genetic effects dominates heritable variation and response to selection. *Genetics* 220, iyab141.
- Bishop, S.C., Stear, M.J., 1997. Modelling responses to selection for resistance to gastro-intestinal parasites in sheep. *Animal Science* 64, 469–478.

- Bishop, S.C., Woolliams, J.A., 2014. Genomics and disease resistance studies in livestock. *Livestock Science* 166, 190–198.
- Blanchard, P.C., 2012. Diagnostics of Dairy and Beef Cattle Diarrhea. *Veterinary Clinics of North America: Food Animal Practice* 28, 443–464.
- Boddicker, N., Waide, E.H., Rowland, R.R.R., Lunney, J.K., Garrick, D.J., Reedy, J.M., Dekkers, J.C.M., 2012. Evidence for a major QTL associated with host response to porcine reproductive and respiratory syndrome virus challenge. *Journal of Animal Science* 90, 1733–1746.
- Brunauer, M., Roch, F.F., Conrady, B., 2021. Prevalence of worldwide neonatal calf diarrhoea caused by bovine rotavirus in combination with bovine coronavirus, *escherichia coli* k99 and *cryptosporidium* spp.: a meta-analysis. *Animals* 11, 1–23.
- Buadi, F., Hsing, A.W., Katzmann, J.A., Pfeiffer, R.M., Waxman, A., Yeboah, E.D., Biritwum, R.B., Tettey, Y., Adjei, A., Chu, L.W., Demarzo, A., Netto, G.J., Dispenzieri, A., Kyle, R.A., Rajkumar, S.V., Landgren, O., 2011. High prevalence of polyclonal hypergamma-globulinemia in adult males in Ghana, Africa. *American Journal of Hematology* 86, 554–558.
- Buczinski, S., Ollivett, T., Dendukuri, N., 2015. Bayesian estimation of the accuracy of the calf respiratory scoring chart and ultrasonography for the diagnosis of bovine respiratory disease in pre-weaned dairy calves. *Preventive Veterinary Medicine* 119, 227–231.
- Buczinski, S., Achard, D., Timsit, E., Cliniques, S., Vétérinaire, F.D.M., De, M.U., Js, C., 2021. Effects of calfhood respiratory disease on health and performance of dairy cattle: a systematic review and meta-analysis. *Journal of Dairy Science* 104, 8214–8227.
- Burton, J.L., Kennedy, B.W., Burnside, E.B., Wilkie, B.N., Burton, J.H., 1989. variation in serum concentrations of immunoglobulins G, A, and M in Canadian Holstein-Friesian Calves. *Journal of Dairy Science* 72, 135–149.
- Callan, R.J., Garry, F.B., 2002. Biosecurity and bovine respiratory disease. *Veterinary Clinics of North America - Food Animal Practice* 18, 57–77.
- Cho, Y. il, Yoon, K.J., 2014. An overview of calf diarrhoea - infectious etiology, diagnosis, and intervention. *Journal of Veterinary Science* 15, 1–17.
- Cockrum, R.R., Speidel, S.E., Salak-Johnson, J.L., Chase, C.C.L., Peel, R.K., Weaver, R.L., Loneagan, G.H., Wagner, J.J., Boddhireddy, P., Thomas, M.G., Prayaga, K., Denise, S., Enns, R.M., 2016. Genetic parameters estimated at receiving for circulating cortisol, immunoglobulin G, interleukin 8, and incidence of bovine respiratory disease in feedlot beef steers. *Journal of Animal Science* 94, 2770–2778.
- Coffey, M., 2020. Dairy cows: in the age of the genotype, #phenotypeisking. *Animal Frontiers* 10, 19–22.
- Colopy, L.J., Rout, E.D., Laura, K.S., Anne, A.S., Moore, A.R., 2019. Immunoglobulin G4-related disease in a dog. *Journal of Veterinary Internal Medicine* 33, 2732–2738.
- Conneely, M., Berry, D.P., Sayers, R., Murphy, J.P., Lorenz, I., Doherty, M.L., Kennedy, E., 2013. Factors associated with the concentration of immunoglobulin G in the colostrum of dairy cows. *Animal* 7, 1824–1832.
- Cordero-Solorzano, J., de Koning, D.J., Tráven, M., de Haan, T., Jouffroy, M., Larsson, A., Myrthe, A., Arts, J.A.J., Parmentier, H.K., Bovenhuis, H., Wensman, J.J., 2022. Genetic parameters of colostrum and calf serum antibodies in Swedish dairy cattle. *Genetics Selection Evolution* 54, 1–18.
- Costa, J.H.C., Cantor, M.C., Neave, H.W., 2021a. Symposium review: precision technologies for dairy calves and management applications. *Journal of Dairy Science* 104, 1203–1219.
- Costa, A., Franzoi, M., Visentin, G., Goi, A., De Marchi, M., Penasa, M., 2021b. The concentrations of immunoglobulins in bovine colostrum determined by the gold standard method are genetically correlated with their near-infrared prediction. *Genetics Selection Evolution* 53, 1–14.
- Costa, J.H.C., Meagher, R.K., von Keyserlingk, M.A.G., Weary, D.M., 2015. Early pair housing increases solid feed intake and weight gains in dairy calves. *Journal of Dairy Science* 98, 6381–6386.
- Costa, J.H.C., von Keyserlingk, M.A.G., Weary, D.M., 2016. Invited review: effects of group housing of dairy calves on behavior, cognition, performance, and health. *Journal of Dairy Science* 99, 2453–2467.
- Dairy Calf & Heifer Association 2019. DCHA Gold Standards. Retrieved on 9 January 2023 from https://calfandheifer.org/wp-content/uploads/2020/09/DCHA_GoldStandards_2020_En_WEB-final.pdf.
- De Oliveira, D.M.P., Forde, B.M., Kidd, T.J., Harris, P.N.A., Schembri, M.A., Beatson, S. A., Paterson, D.L., Walker, M.J., 2020. Antimicrobial resistance in ESKAPE pathogens. *Clinical Microbiology Reviews* 33, 1–49.
- De Vieira Paula, A., von Keyserlingk, M.A.G., Weary, D.M., 2012. Presence of an older weaned companion influences feeding behavior and improves performance of dairy calves before and after weaning from milk. *Journal of Dairy Science* 95, 3218–3224.
- Dempster, E., Lerner, I., 1950. Heritability of threshold characters. *Genetics* 35, 212–236.
- Department for Environment F and RA (DEFRA) 2003 2003. Improving calf survival. Retrieved on 9 January 2023 from <http://www.veeru.reading.ac.uk/comp2/Comcomp/adobe/calfsurv.pdf>.
- Diekmann, O., Heesterbeek, A.P., Metz, J.A.J., 1990. Mathematical biology. *Journal of Mathematical Biology* 28, 365–382.
- Doeschl-Wilson, A.B., Davidson, R., Conington, J., Roughsedge, T., Hutchings, M.R., Villanueva, B., 2011. Implications of host genetic variation on the risk and prevalence of infectious diseases transmitted through the environment. *Genetics* 188, 683–693.
- Donovan, G.A., Dohoo, I.R., Montgomery, D.M., Bennett, F.L., 1998. Calf and disease factors affecting growth in female Holstein calves in Florida, USA. *Preventive Veterinary Medicine* 33, 1–10.
- Dubrovsky, S.A., Van Eenennaam, A.L., Aly, S.S., Karle, B.M., Rossitto, P.V., Overton, M.W., Lehenbauer, T.W., Fadel, J.G., 2020. Preweaning cost of bovine respiratory disease (BRD) and cost-benefit of implementation of preventative measures in calves on California dairies: the BRD 10K study. *Journal of Dairy Science* 103, 1583–1597.
- Duve, L.R., Jensen, M.B., 2012. Social behavior of young dairy calves housed with limited or full social contact with a peer. *Journal of Dairy Science* 95, 5936–5945.
- Faber, S.N., Faber, N.E., McCauley, T.C., Ax, R.L., 2005. Case study: effects of colostrum ingestion on lactational performance. *The Professional Animal Scientist* 21, 420–425.
- Fine, P.E.M., 1993. Herd immunity: history, theory, practice. *Epidemiologic Reviews* 15, 265–302.
- Fleming A and Van Doormaal B 2020. New Genetic Evaluations Coming in December 2020. Lactanet. Retrieved on 9 January 2023 from <https://www.cdn.ca/document.php?id=544>.
- Fleming A and Van Doormaal B 2022. Lactanet: The Impact of Genomics. Lactanet. Retrieved on 9 January 2023 from <https://lactanet.ca/en/impact-genomics/?print=enabled&id=175313>.
- Flower, F.C., Weary, D.M., 2003. The effects of early separation on the dairy cow and calf. *Animal Welfare* 12, 339–348.
- Foster, D.M., Smith, G.W., 2009. Pathophysiology of diarrhoea in calves. *Veterinary Clinics of North America - Food Animal Practice* 25, 13–36.
- Furman-Fratczak, K., Rzaa, A., Stefaniak, T., 2011. The influence of colostral immunoglobulin concentration in heifer calves' serum on their health and growth. *Journal of Dairy Science* 94, 5536–5543.
- Gaddis, K.L.P., Cole, J.B., Clay, J.S., Maltecca, C., 2014. Genomic selection for producer-recorded health event data in US dairy cattle. *Journal of Dairy Science* 97, 3190–3199.
- García-Ruiz, A., Cole, J.B., VanRaden, P.M., Wiggans, G.R., Ruiz-López, F.J., Van Tassel, C.P., 2016. Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. *Proceedings of the National Academy of Sciences* 113, E3995–E4004.
- Gelsing, S.L., Smith, A.M., Jones, C.M., Heinrichs, A.J., 2015. Technical note: comparison of radial immunodiffusion and ELISA for quantification of bovine immunoglobulin G in colostrum and plasma. *Journal of Dairy Science* 98, 4084–4089.
- Gibson, J.P., Bishop, S.C., 2005. Use of molecular markers to enhance resistance of livestock to disease: a global approach Utilising and improving genetic resistance to disease. *Revue Scientifique et Technique (International Office of Epizootics)* 24, 343–353.
- Gilbert, R.P., Gaskins, C.T., Hillers, J.K., Brinks, J.S., Denham, A.H., 1988. Inbreeding and immunoglobulin G concentrations in cattle. *Journal of Animal Science* 66, 2490–2497.
- Godden, S., 2008. Colostrum management for dairy calves. *Veterinary Clinics of North America - Food Animal Practice* 24, 19–39.
- Godden, S.M., Lombard, J.E., Woolums, A.R., 2019. Colostrum management for dairy calves. *Veterinary Clinics of North America: Food Animal Practice* 35, 535–556.
- Gonzalez-Peña, D., Vukasinovic, N., Brooker, J.J., Przybyla, C.A., Denise, S.K., 2019. Genomic evaluation for calf wellness traits in Holstein cattle. *Journal of Dairy Science* 102, 2319–2329.
- Gonzalez-Peña, D., Vukasinovic, N., Brooker, J.J., Przybyla, C.A., Baktula, A., Denise, S. K., 2020. Genomic evaluation for wellness traits in US Jersey cattle. *Journal of Dairy Science* 103, 1735–1748.
- Gorden, P.J., Plummer, P., 2010. Control, management, and prevention of bovine respiratory disease in dairy calves and cows. *Veterinary Clinics of North America: Food Animal Practice* 26, 243–259.
- Griffing, B., 1967. Selection in reference to biological groups I. Individual and group selection applied to populations of unordered groups. *Australian Journal of Biological Sciences* 20, 127–139.
- Griffing, B., 1976. Selection in reference to biological groups V. Analysis of full-sib groups. *Genetics* 82, 703–722.
- Haagen, I.W., Hardie, L.C., Heins, B.J., Dechow, C.D., 2021. Genetic parameters of calf morbidity and stayability for US organic Holstein calves. *Journal of Dairy Science* 104, 11770–11778.
- Hammon, H.M., Liermann, W., Fretien, D., Koch, C., 2020. Review: importance of colostrum supply and milk feeding intensity on gastrointestinal and systemic development in calves. *Animal* 14, s133–s143.
- Hayes, G., Mathews, K., Kruth, S., Doig, G., Dewey, C., 2010. Illness severity scores in veterinary medicine: what can we learn? *Journal of Veterinary Internal Medicine* 24, 457–466.
- Henderson, L., Miglior, F., Sewalem, A., Wormuth, J., Kelton, D., Robinson, A., Leslie, K.E., 2011. Short communication: genetic parameters for measures of calf health in a population of Holstein calves in New York State. *Journal of Dairy Science* 94, 6181–6187.
- Homerovsky, E.R., Caulkett, N.A., Timsit, E., Pajor, E.A., Kastelic, J.P., Windeyer, M.C., 2017. Clinical indicators of blood gas disturbances, elevated L-lactate concentration and other abnormal blood parameters in newborn beef calves. *The Veterinary Journal* 219, 49–57.
- Hötzel, M.J., Cardoso, C.S., Roslindo, A., Von, K.M., 2017. Citizens' views on the practices of zero-grazing and cow-calf separation in the dairy industry: does providing information increase acceptability? *Journal of Dairy Science* 100, 4150–4160.
- Hulst, A.D., de Jong, M.C.M., Bijma, P., 2021. Why genetic selection to reduce the prevalence of infectious diseases is way more promising than currently believed. *Genetics* 217, iyab024.

- Jamrozik, J., Fatehi, J., Kistemaker, G.J., Schaeffer, L.R., 2005. Estimates of genetic parameters for Canadian Holstein female reproduction traits. *Journal of Dairy Science* 88, 2199–2208.
- Jamrozik, J., Kistemaker, G.J., Van, D.B.J., Fleming, A., Koeck, A., Miglior, F., 2016. Genetic evaluation for resistance to metabolic diseases in Canadian dairy breeds. *Interbull Bulletin* 50, 9–16.
- Jamrozik, J., Kistemaker, G., Van, D.B., Baes, C., Miglior, F., 2021. Genomic evaluation for resistance to fertility disorders in Canadian dairy breeds. *Interbull Bulletin* 56, 102–110.
- Jensen, M.B., Duve, L.R., Weary, D.M., 2015. Pair housing and enhanced milk allowance increase play behavior and improve performance in dairy calves. *Journal of Dairy Science* 98, 2568–2575.
- Johnsen, J.F., Chincarini, M., Sogstad, Å.M., Sølverød, L., Vatne, M., Mejdell, C.M., Hänninen, L., 2019. Salivary IgG levels in neonatal calves and its association to serum IgG: an observational pilot study. *Translational Animal Science* 3, 589–593.
- Johnston, D., Mukiibi, R., Waters, S.M., McGee, M., Surlis, C., McClure, J.C., McClure, M.C., Todd, C.C., Earley, B., 2020. Genome wide association study of passive immunity and disease traits in beef-suckler and dairy calves on Irish farms. *Scientific Reports* 10, 1–10.
- Karle, B.M., Maier, G.U., Love, W.J., Dubrovsky, S.A., Williams, D.R., Anderson, R.J., Van Eenennaam, A.L., Lehenbauer, T.W., Aly, S.S., 2019. Regional management practices and prevalence of bovine respiratory disease in California's preweaned dairy calves. *Journal of Dairy Science* 102, 7583–7596.
- Khan, M.A., Weary, D.M., Von, K.M., 2011. Invited review: effects of milk ration on solid feed intake, weaning, and performance in dairy heifers. *Journal of Dairy Science* 94, 1071–1081.
- King, A., Chigerwe, M., Barry, J., Murphy, J.P., Rayburn, M.C., Kennedy, E., 2020. Short communication: effect of feeding pooled and nonpooled high-quality colostrum on passive transfer of immunity, morbidity, and mortality in dairy calves. *Journal of Dairy Science* 103, 1894–1899.
- Knauer, W.A., Godden, S.M., Dietrich, A., James, R.E., 2017. The association between daily average feeding behaviors and morbidity in automatically fed group-housed preweaned dairy calves. *Journal of Dairy Science* 100, 5642–5652.
- Koeck, A., Miglior, F., Kelton, D.F., Schenkel, F.S., 2012. Health recording in Canadian Holsteins: data and genetic parameters. *Journal of Dairy Science* 95, 4099–4108.
- Leblanc, S.J., Lissimore, K.D., Kelton, D.F., Duffield, T.F., Leslie, K.E., 2006. Major advances in disease prevention in dairy cattle. *Journal of Dairy Science* 89, 1267–1279.
- Lesmeister, K.E., Heinrichs, A.J., 2004. Effects of corn processing on growth characteristics, rumen development, and rumen parameters in neonatal dairy calves. *Journal of Dairy Science* 87, 3439–3450.
- Lewis, S.J., Heaton, K.W., 1997. Stool form scale as a useful guide to intestinal transit time. *Scandinavian Journal of Gastroenterology* 32, 920–924.
- Lipschutz-Powell, D., Woolliams, J.A., 2012. Bias, accuracy, and impact of indirect genetic effects in infectious diseases. *Frontiers in Genetics* 3, 215.
- Lipschutz-Powell, D., Woolliams, J.A., Bijma, P., Doeschl-wilson, A.B., 2012. Indirect genetic effects and the spread of infectious disease: are we capturing the full heritable variation underlying disease prevalence? *PLoS One* 7, e39551.
- Lipschutz-Powell, D., Woolliams, J.A., Doeschl-Wilson, A.B., 2013. A unifying theory for genetic epidemiological analysis of binary disease data. *Genetics Selection Evolution* 46, 1–12.
- Lipschutz-Powell, D., Woolliams, J.A., Doeschl-Wilson, A.B., 2014. A unifying theory for genetic epidemiological analysis of binary disease data. *Genetics Selection Evolution* 46, 1–12.
- Lombard, J.E., Garry, F.B., Tomlinson, S.M., Garber, L.P., 2007. Impacts of dystocia on health and survival of dairy calves. *Journal of Dairy Science* 90, 1751–1760.
- Love, W.J., Lehenbauer, T.W., Kass, P.H., Van Eenennaam, A.L., Aly, S.S., 2014. Development of a novel clinical scoring system for on-farm diagnosis of bovine respiratory disease in pre-weaned dairy calves. *PeerJ* 2, e238.
- Lynch, C., Schenkel, F.S., van Staaveren, N., Miglior, F., Kelton, D., Baes, C.F., 2024. Investigating the potential for genetic selection of dairy calf disease traits using management data. *Journal of Dairy Science* 107, 1022–1034.
- Mahmoud, M., Yin, T., Brügemann, K., König, S., 2017. Phenotypic, genetic, and single nucleotide polymorphism marker associations between calf diseases and subsequent performance and disease occurrences of first-lactation German Holstein cows. *Journal of Dairy Science* 100, 2017–2031.
- 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. *Journal of Dairy Science* 100, 2828–2836.
- Martin, P., Vinet, A., Denis, C., Grohs, C., Chanteloup, L., Dozias, D., Maupetit, D., Sapa, J., Renand, G., Blanc, F., 2021. Determination of immunoglobulin concentrations and genetic parameters for colostrum and calf serum in Charolais animals. *Journal of Dairy Science* 104, 3240–3249.
- McCorquodale, C.E., Sewalem, A., Miglior, F., Kelton, D., Robinson, A., Koeck, A., Leslie, K.E.E., 2013. Short communication: analysis of health and survival in a population of Ontario Holstein heifer calves. *Journal of Dairy Science* 96, 1880–1885.
- McGrath, B.A., Fox, P.F., Mcsweeney, P.L.H., Kelly, A.L., 2016. Composition and properties of bovine colostrum: a review. *Dairy Science & Technology* 96, 133–158.
- McGuirk, S.M., 2008. Disease management of dairy calves and heifers. *Veterinary Clinics of North America - Food Animal Practice* 24, 139–153.
- McGuirk, S.M., Collins, M., 2004. Managing the production, storage, and delivery of colostrum. *Veterinary Clinics of North America - Food Animal Practice* 20, 593–603.
- McGuirk, S.M., Peek, S.F., 2014. Timely diagnosis of dairy calf respiratory disease using a standardized scoring system. *Animal Health Research Reviews* 15, 145–147.
- Mee, J.F., 2008. Newborn dairy calf management. *Veterinary Clinics of North America - Food Animal Practice* 24, 1–17.
- Miglior, F., Finocchiaro, R., Malchiodi, F., Fleming, A., Brito, L., Baes, C.F., Jamrozik, J., Martin, P., Chesnais, J. and Schenkel, F.S., 2016. Enhancing the data pipeline for novel traits in the genomic era: from farms to DHI to evaluation centres. In S. Niklitschek, J. Lama, C. Trejo, B. Wickham, M. Burke, and C. Mosconi, eds. *Proceedings of the 40th ICAR Biennial Session, Puerto Varas, Chile*. ICAR, Puerto Varas, Chile, pp. 23–30.
- Muir, W.M., 2005. Incorporation of competitive effects in forest tree or animal breeding programs. *Genetics* 170, 1247–1259.
- Murray B 2011. Optimizing Calf Survival at Birth. Ontario Ministry of Agriculture, Food and Rural Affairs. Retrieved on 22 November 2022, from <http://www.omafra.gov.on.ca/english/livestock/dairy/facts/optbirth.htm>.
- Murray-Kerr, C.F., Leslie, K.E., Godden, S.M., Knauer, W.A. and McGuirk, S.M., 2018. Development of a newborn calf vigor scoring system. In: *Proceedings of the 51st Annual Conference of the American Association of Bovine Practitioners*, 13–15 September 2018, Phoenix, AZ, p. 283.
- NAHMS 1996. Part I: Reference of 1996 Dairy Management Practices. USDA:APHIS:VS, Fort Collins, CO, USA.
- NAHMS National Animal Health Monitoring System 2007. Dairy 2007 Heifer Calf Health and Management Practices on U.S. Dairy Operations, 2007. USDA:APHIS:VS:CEAH, Fort Collins, CO, USA.
- Nath, M., Woolliams, J.A., Bishop, S.C., 2008. Assessment of the dynamics of microparasite infections in genetically homogeneous and heterogeneous populations using a stochastic epidemic model. *Journal of Animal Science* 86, 1747–1757.
- Neibergs, H.L., Seabury, C.M., Wojtowicz, A.J., Wang, Z., Scraggs, E., Kiser, J.N., Neupane, M., Womack, J.E., Van, E.A., Hagevoort, G.R., Lehenbauer, T.W., Aly, S., Davis, J., Taylor, J.F., Bovine, T., Disease, R., Coordinated, C., 2014. Susceptibility loci revealed for bovine respiratory disease complex in pre-weaned Holstein calves. *BMC Genomics* 15, 1164.
- Nor, N.M., Steeneveld, W., Van, W.T., Mourits, M.C.M., Hogeveen, H., 2013. First-calving age and first-lactation milk production on Dutch dairy farms. *Journal of Dairy Science* 96, 981–992.
- Overton, M.W., 2020. Economics of respiratory disease in dairy replacement heifers. *Animal Health Research Reviews* 21, 143–148.
- Peel, D.S., 2020. The effect of market forces on bovine respiratory disease. *Veterinary Clinics of North America - Food Animal Practice* 36, 497–508.
- Pempek, J., Trearchis, D., Masterson, M., Habing, G., Proudfoot, K., 2017. Veal calf health on the day of arrival at growers in Ohio. *Journal of Animal Science* 95, 3863–3872.
- Placzek, M., Christoph-Schulz, I., Barth, K., 2021. Public attitude towards cow-calf separation and other common practices of calf rearing in dairy farming—a review. *Organic Agriculture* 11, 41–50.
- Pritchett, L.C., Gay, C.C., Besser, T.E., Hancock, D.D., 1991. Management and production factors influencing immunoglobulin G1 concentration in colostrum from Holstein cows. *Journal of Dairy Science* 74, 2336–2341.
- Pro Earth Animal Health 2017. Part III: Calf Scours The Economic Impact. Pro Earth Animal Health. Retrieved on 9 January 2023 from <https://proearthanimalhealth.com/wp-content/uploads/2018/02/Calf-Scours-Economic-ImpactsPDF.pdf>.
- Probo, M., Veronesi, M.C., 2022. Clinical scoring systems in the newborn calf: an overview. *Animals* 12, 3013.
- Quick, A.E., Ollivett, T.L., Kirkpatrick, B.W., Weigel, K.A., 2020. Genomic analysis of bovine respiratory disease and lung consolidation in preweaned Holstein calves using clinical scoring and lung ultrasound. *Journal of Dairy Science* 103, 1632–1641.
- Quigley, J.D., Lago, A., Chapman, C., Erickson, P., Polo, J., 2013. Evaluation of the Brix refractometer to estimate immunoglobulin G concentration in bovine colostrum. *Journal of Dairy Science* 96, 1148–1155.
- Raboisson, D., Trillat, P., Cahuzac, C., 2016. Failure of passive immune transfer in calves: a meta-analysis on the consequences and assessment of the economic impact. *PLoS ONE* 11, 1–19.
- Renaud, D.L., Kelton, D.F., LeBlanc, S.J., Haley, D.B., Duffield, T.F., 2018. Calf management risk factors on dairy farms associated with male calf mortality on veal farms. *Journal of Dairy Science* 101, 1785–1794.
- Renaud, D.L., Buss, L., Wilms, J.N., Steele, M.A., 2020. Technical note: is fecal consistency scoring an accurate measure of fecal dry matter in dairy calves? *Journal of Dairy Science* 103, 10709–10714.
- Rivero, M.J., Valderrama, X., Haines, D., Alomar, D., 2012. Prediction of immunoglobulin G content in bovine colostrum by near-infrared spectroscopy. *Journal of Dairy Science* 95, 1410–1418.
- Robbers, L., Jorritsma, R., Nielen, M., Koets, A., 2021. A scoping review of on-farm colostrum management practices for optimal transfer of immunity in dairy calves. *Frontiers in Veterinary Science* 8, 1–16.
- Roche, S.M., Von Massow, M., Renaud, D., Shock, D.A., Jones-Bitton, A., Kelton, D.F., 2020. Cost-benefit of implementing a participatory extension model for improving on-farm adoption of Johne's disease control recommendations. *Journal of Dairy Science* 103, 451–472.

- Roff, D.A., 1996. The evolution of threshold traits in animals. *The Quarterly Review of Biology* 71, 3–35.
- Roso, V.M., Schenkel, F.S., Miller, S.P., 2004. Degree of connectedness among groups of centrally tested beef bulls. *Canadian Journal of Animal Science* 84, 37–47.
- RSPCA 2021. RSPCA welfare standards for Dairy cattle. RSPCA. Retrieved on 21 November 2022, from <https://science.rspca.org.uk/documents/1494935/9042554/RSPCA+Dairy+Standards.pdf/bb1a2971-8018-b325-8dcc-d6b590fcd955?t=1625822966824>.
- Santman-Berends, I.M.G.A., Schukken, Y.H., van Schaik, G., 2019. Quantifying calf mortality on dairy farms: challenges and solutions. *Journal of Dairy Science* 102, 6404–6417.
- Schepers, J.M., Weigel, K.A., 2012. Genomic selection in dairy cattle: integration of DNA testing into breeding programs. *Animal Frontiers* 2, 4–9.
- Schinwald, M., Creutzinger, K., Winder, C.B., Haley, D., Renaud, D.L., 2022. Predictors of diarrhea, mortality, and weight gain in male dairy calves. *Journal of Dairy Science* 105, 5296–5309.
- Shook, G.E., 1989. Selection for disease resistance. *Journal of Dairy Science* 72, 1349–1362.
- Silva FG, Lamy E, Pedro S, Azevedo I, Caetano P, Ramalho J, Martins L, Pereira AMF, Cerqueira JOL, Silva SR and Conceição C 2023. Assessing passive immune transfer in newborn calves: salivary and serum IgG association. Proceedings of the 74th EAAP Annual Meeting, 26 August – 1 September 2023, Lyon, France, p. 77.
- Sischo, W.M., Hird, D.W., Gardner, I.A., Utterback, W.W., Christiansen, K.H., Carpenter, T.E., Danaye-Elmi, C., Heron, B.R., 1990. Economics of disease occurrence and prevention on California dairy farms: a report and evaluation of data collected for the national animal health monitoring system, 1986–87. *Preventive Veterinary Medicine* 8, 141–156.
- Sivula, N.J., Ames, T.R., Marsh, W.E., Werdin, R.E., 1996. Descriptive epidemiology of morbidity and mortality in Minnesota dairy heifer calves. *Preventive Veterinary Medicine* 27, 155–171.
- Sorge, U., Kelton, D., Staufenbiel, R., 2009. Neonatal blood lactate concentration and calf morbidity. *Veterinary Record* 164, 553–554.
- Soufferi, A., Banos, G., Panousis, N., Fletouris, D., Arsenos, G., Valergakis, G.E., 2019. Genetic parameters of colostrum traits in Holstein dairy cows. *Journal of Dairy Science* 102, 11225–11232.
- Springer, H., Yost, H., 2022. Penn state extension: neonatal calf diarrhea (Scours). The Pennsylvania State University, State College, PA, USA.
- Stanton A 2011. An evaluation of the impact of management practice on the health and welfare of dairy Heifer calves. University of Guelph. Retrieved on 21 November 2022, from <https://atrium.lib.uoguelph.ca/xmlui/handle/10214/2856>.
- Stilwell, G., Carvalho, R.C., 2011. Clinical outcome of calves with failure of passive transfer as diagnosed by a commercially available IgG quick test kit. *Canadian Veterinary Journal* 52, 524–526.
- Svensson, C., Hultgren, J., 2008. Associations between housing, management, and morbidity during rearing and subsequent first-lactation milk production of dairy cows in Southwest Sweden. *Journal of Dairy Science* 91, 1510–1518.
- Taylor, J.D., Fulton, R.W., Lehenbauer, T.W., Step, D.L., Confer, A.W., 2010. The epidemiology of bovine respiratory disease: what is the evidence for predisposing factors? *Canadian Veterinary Journal* 51, 1095–1102.
- Tora, E., Abayneh, E., Seyoum, W., Shurbe, M., 2021. Longitudinal study of calf morbidity and mortality on smallholder farms in southern Ethiopia. *PLoS ONE* 16, 1–18.
- Tsairidou, S., Anacleto, O., Woolliams, J.A., Doeschl-Wilson, A., 2019. Enhancing genetic disease control by selecting for lower host infectivity and susceptibility. *Heredity* 122, 742–758.
- Urie, N.J., Lombard, J.E., Shivley, C.B., Koprak, C.A., Adams, A.E., Earleywine, T.J., Olson, J.D., Garry, F.B., 2018. Preweaned heifer management on US dairy operations: part I. descriptive characteristics of preweaned heifer raising practices. *Journal of Dairy Science* 101, 9168–9184.
- USDA 2018. Dairy 2014: Health and Management Practices on U.S. Dairy Operations, 2014. Retrieved on 22 November 2022, from https://www.aphis.usda.gov/animal_health/nahms/dairy/downloads/dairy14/Dairy14_dr_PartIII.pdf.
- Uyama, T., Renaud, D.L., Morrison, E.I., McClure, J.T., LeBlanc, S.J., Winder, C.B., de Jong, E., McCubbin, K.D., Barkema, H.W., Dufour, S., Sanchez, J., Heider, L.C., Kelton, 2022. Associations of calf management practices with antimicrobial use in Canadian dairy calves. *Journal of Dairy Science* 105, 9084–9097.
- van Staaveren, N., Hyland, E., Houlihan, K., Lynch, C., Miglior, F., Kelton, D.F., Schenkel, F.S., Baes, C.F., 2023. Recording of calf diseases for potential use in breeding programs: a case study on calf respiratory illness and diarrhea. *Canadian Journal of Animal Science* 103, 192–203.
- VanRaden, P.M., Van Tassell, C.P., Wiggans, G.R., Sonstegard, T.S., Schnabel, R.D., Taylor, J.F., Schenkel, F.S., 2009. Invited review: reliability of genomic predictions for North American Holstein bulls. *Journal of Dairy Science* 92, 16–24.
- Ventura, B.A., Von, K.M., Schuppli, C.A., Weary, D.M., 2013. Views on contentious practices in dairy farming: the case of early cow-calf separation. *Journal of Dairy Science* 96, 6105–6116.
- Virtala, A.K., Mechor, G.D., Grohn, Y.T., 1996. The effect of calfhood diseases on growth of female dairy calves during the first 3 months of life in New York state. *Journal of Dairy Science* 79, 1040–1049.
- Waltner-Toews, D., Martin, S., Meek, A., 1986. The effect of early calfhood health status on survivorship and age at first calving. *Canadian Journal of Veterinary Research* 50, 314–317.
- Wathes, D.C., Brickell, J.S., Bourne, N.E., Swali, A., Cheng, Z., 2008. Factors influencing heifer survival and fertility on commercial dairy farms. *Animal* 2, 1135–1143.
- Weaver, D.M., Tyler, J.W., Vanmetre, D.C., Hostetler, D.E., Barrington, G.M., 2000. Passive transfer of colostrum immunoglobulins in calves. *Journal of Veterinary Internal Medicine* 14, 569–577.
- Wiggans, G.R., Carrillo, J.A., 2022. Genomic selection in United States dairy cattle. *Frontiers in Genetics* 13, 1–7.
- Wiggans, G.R., Cole, J.B., Hubbard, S.M., Sonstegard, T.S., 2017. Genomic selection in dairy cattle: the USDA experience. *Annual Review of Animal Biosciences* 5, 309–329.
- Williams, D.R., Pithua, P., Garcia, A., Champagne, J., Haines, D.M., Aly, S.S., 2014. Effect of three colostrum diets on passive transfer of immunity and preweaning health in calves on a California dairy following colostrum management training. *Veterinary Medicine International* 2014, 1–9.
- Wilson, D.J., Habing, G., Winder, C.B., Renaud, D.L., 2023. A scoping review of neonatal calf diarrhea case definitions. *Preventive Veterinary Medicine* 211, 105818.
- Winder, C.B., Bauman, C.A., Duffield, T.F., Barkema, H.W., Keefe, G.P., Dubuc, J., Uehlinger, F., Kelton, D.F., 2018. Canadian national dairy study: heifer calf management. *Journal of Dairy Science* 101, 10565–10579.
- Windeyer, M.C., Leslie, K.E., Godden, S.M., Hodgins, D.C., Lissemore, K.D., LeBlanc, S. J., 2014. Factors associated with morbidity, mortality, and growth of dairy heifer calves up to 3 months of age. *Preventive Veterinary Medicine* 113, 231–240.
- Wolfer, B., Jones, B.W., Orsel, K., Bewley, J.M., 2017. Technical note: evaluation of an ear-attached real-time location monitoring system. *Journal of Dairy Science* 100, 2219–2224.
- Woolums, A., 2021. Vaccination protocols for dairy calves. *American Association of Bovine Practitioners* 54, 178–180.
- Yin, T., Halli, K., König, S., 2022. Direct genetic effects, maternal genetic effects, and maternal genetic sensitivity on prenatal heat stress for calf diseases and corresponding genomic loci in German Holsteins. *Journal of Dairy Science* 105, 6795–6808.
- Zhang, W., Chang, L., Brito, D., Shi, W., Dong, L., 2019b. Mortality-Culling rates of dairy calves and replacement heifers and its risk factors in Holstein Cattle. *Animals* 9, 730.
- Zhang, Z., Kargo, M., Liu, A., Thomasen, J.R., Pan, Y., Su, G., 2019a. Genotype-by-environment interaction of fertility traits in Danish Holstein cattle using a single-step genomic reaction norm model. *Heredity* 123, 202–214.
- Zhang, H., Wang, K., An, T., Zhu, L., Chang, Y., Lou, W., Liu, A., Su, G., Brito, L.F., Wang, Y., 2022. Genetic parameters for dairy calf and replacement heifer wellness traits and their association with cow longevity and health indicators in Holstein cattle. *Journal of Dairy Science* 105, 6749–6759.
- Zoetis 2022. Dairy Wellness Profit Index® enhancements for profitable genetic selection and helping sustainable practices. Zoetis. Retrieved on 9 January 2023 from <https://www.zoetis.com/content/pages/Solutions/Dairy/Dairy-Genetics/Dairy-genetics-resources/Documents/Genetics-edetailer.pdf>.