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Symposium review: Novel strategies to genetically improve mastitis resistance in dairy cattle¹

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ABSTRACT

Mastitis is a disease of major economic importance to the dairy cattle sector because of the high incidence of clinical mastitis and prevalence of subclinical mastitis and, consequently, the costs associated with treatment, production losses, and reduced animal welfare. Disease-recording systems compiling data from a large number of farms are still not widely implemented around the world; thus, selection for mastitis resistance is often based on genetically correlated indicator traits such as somatic cell count (SCC), udder depth, and fore udder attachment. However, in the past years, several countries have initiated collection systems of clinical mastitis, based on producers recording data in most cases. The large data sets generated have enabled researchers to assess incidence of this disease and to investigate the genetic background of clinical mastitis itself, as well as its relationships with other traits of interest to the dairy industry. The genetic correlations between clinical mastitis and its previous proxies were estimated more accurately and confirmed the strong relationship of clinical mastitis with SCC and udder depth. New traits deriving from SCC were also studied, with the most relevant findings being associated with mean somatic cell score (SCS) in early lactation, standard deviation of SCS, and excessive test-day SCC pattern. Genetic correlations between clinical mastitis and other economically important traits indicated that selection for mastitis resistance would also improve resistance against other diseases and enhance both fertility and longevity. However, milk yield remains negatively correlated with clinical mastitis, emphasizing the importance

of including health traits in the breeding objectives to achieve genetic progress for all important traits. These studies enabled the establishment of new genetic and genomic evaluation models, which are more efficient for selection to mastitis resistance. Further studies that are potential keys for future improvement of mastitis resistance are deep investigation of the bacteriology of mastitis, identification of novel indicator traits and tools for selection, and development of a larger female reference population to improve reliability of genomic evaluations. These cutting-edge studies will result in a better understanding of the genetic background of mastitis resistance and enable a more accurate phenotyping and genetic selection to improve mastitis resistance, and consequently, animal welfare and industry profitability. **Key words:** mastitis, selection index, clinical mastitis, genetics

INTRODUCTION

Mastitis, inflammation of the mammary gland, is predominantly caused by intramammary invasion of pathogens in the udder. Mastitis is one of the most frequent diseases of dairy cattle, and it has important economic implications for the industry due to costs associated with reduced milk production and milk quality, premature culling of animals, veterinary treatment, and animal welfare (Lescourret and Coulon, 1994; Hogeveen et al., 2011; Siivonen et al., 2011; Heikkilä et al., 2012). A cow is considered to have clinical mastitis (CM) if it presents abnormal milk secretion from one or more quarters, with possible signs of inflammation of the udder tissues (e.g., heat, swelling, or discoloration of the skin; Kelton et al., 1998). A relatively high proportion of dairy cows have subclinical mastitis; that is, inflammation of the udder as indicated by an elevated SCC but no signs of CM. Subclinical mastitis also affects milk production and quality and is characterized by the presence of inflammatory components in the milk (Heringstad et al., 2000).

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The incidence of CM is high in many dairy herds around the world. For example, a mean incidence rate of 23.0% was found among a sample of Canadian herds in 2008 (Olde Riekerink et al., 2008). Furthermore, the incidence of CM has not decreased over time despite great efforts to identify management and cow factors that are associated with it (e.g., Ruud et al., 2010; Richert et al., 2013; Bates and Dohoo, 2016). This is probably partly due to the traditional intensive genetic selection for milk production traits and the genetic antagonism between milk production and mastitis resistance (Strandberg and Shook, 1989; Rupp and Boichard, 2003). In 2013, over 20% of involuntarily culled Canadian cows were culled because of problems with mastitis or high SCC (CDN, 2014).

Since the late 1970s, SCC has been widely used as a phenotypic indicator of mastitis in breeding programs around the world. The increase of milk SCC is mainly due to white blood cell recruitment in response to udder infection, and the evolution of SCC is closely linked to the magnitude of the inflammation process (Coffey et al., 1986). The SCC measurement presents a large economic advantage compared with direct bacteriological assessments. Somatic cell count is also more heritable than the direct record of CM (Rupp and Boichard, 2003) and does not require the implementation of a new system of data recording because milk samples are already routinely collected and analyzed. Furthermore, SCC is genetically both an indicator of subclinical and CM, and indirect selection is considered at least as efficient as direct selection on CM (de Jong and Lansbergen, 1996). Because the trait is not normally distributed (majority of low values), SCC is usually transformed on a logarithm scale to facilitate analysis (Ali and Shook, 1980); the SCS is the result of this logarithmic transformation. Other traits, such as udder depth or milking speed, are also associated with mastitis (Seykora and McDaniel, 1985; Sørensen et al., 2000; Rupp and Boichard, 2003) or have been shown to improve the accuracy of an index for mastitis resistance compared with an index with SCS only (Boettcher et al., 1998). Those traits, associated with SCC, were the basis of selection for mastitis resistance in most countries in past decades when no collection of CM data was implemented. The only exception is the Scandinavian countries, where health data (e.g., treatments) have been recorded by veterinarians for several decades (Heringstad et al., 2000). Health data records are useful for genetic selection; however, highly accurate breeding values are obtained only for bulls with a large number of progeny. More recently, with the development and wide uptake of genomic selection and other cutting-edge technologies in dairy cattle

breeding programs, as well as the increasing demand to accelerate genetic progress for health traits, health data recording has become even more important to accelerate genetic progress for mastitis resistance. The main objectives of this review are to describe the novel phenotypic and genomic strategies to improve mastitis resistance that have been developed and implemented in the dairy industry over time, as well as to assess current studies and challenges. This review will focus on the Canadian dairy industry as an example of these advancements; however, progress in other countries will be mentioned as well.

AN INCREASING COLLECTION OF PHENOTYPES

The Nordic countries (Denmark, Finland, Norway, and Sweden) have had health recording systems for a long time. Denmark first started data collection through veterinary recording by means of a pilot study in 1966, and preliminary recording by the other Nordic countries soon followed. This led to full routine recording on a national scale implemented in Norway, Finland, Sweden, and Denmark in 1975, 1982, 1984, and 1990, respectively, with recording done by veterinarians (Heringstad et al., 2000). Following the initiative from the Nordic countries and the increasing demand for healthier cows, several countries began collecting health data.

In 2007, Canada began a nationwide effort to collect health and disease data through a project titled “National dairy cattle health and disease data management system,” which aimed to provide information to dairy producers and veterinarians about herd management (Koeck et al., 2012a). Another main objective was to develop a genetic evaluation system to improve overall disease resistance in Canadian dairy cattle. As an outcome, 8 health events are voluntarily recorded by producers using on-farm management software or record books: CM, metritis, retained placenta, cystic ovaries, lameness, milk fever, ketosis, and displaced abomasum. To standardize phenotype recording, producers were provided with disease definitions adapted from Kelton et al. (1998) as a guide for identification and recording of diseases.

The data are transferred to DHI technicians at each test-day herd visit and then forwarded to the regional DHI association. Additionally, health data from Québec producers participating in the *Dossier Santé Animale/Animal Health Record* program (Koeck et al., 2012a), which collects health data for herd management and veterinarian use, are also forwarded to the DHI database by the veterinarians. Once all recorded health events are processed within the national DHI database, they

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