J. Dairy Sci. 100:1–6
https://doi.org/10.3168/jds.2017-12627

Estimation of genetic parameters and heterosis for longevity in crossbred Danish dairy cattle

J. B. Clasen,*†[1] E. Norberg,* P. Madsen,* J. Pedersen,† and M. Kargo*†
*Department of Molecular Biology and Genetics, Science and Technology, Aarhus University, 20 Blichers Allé, 8830 Tjele, Denmark
†SEGES, 15 Agro Food Park, 8200 Aarhus N, Denmark

ABSTRACT

Crossbreeding has been shown to improve the longevity of dairy cattle in countries across the world. The aim of this study was to estimate heterosis, breed effects, and genetic parameters for longevity in crossbred dairy cattle among Danish Holstein (DH), Danish Red (DR), and Danish Jersey (DJ) breeds. Data were provided from 119 Danish commercial herds that use systematic crossbreeding (i.e., rotational crossbreeding). Additional data from 11 mixed-breed herds with DH and DJ were included to estimate reliable breed effects for DJ. Survival information on 73,741 cows was analyzed with a linear animal model using the artificial insemination–REML algorithm in the DMU package. Five longevity (L) traits were defined: days from first calving until the end of first lactation or culling (L1), days from first calving until the end of second lactation or culling (L2), days from first calving until the end of third lactation or culling (L3), days from first calving until the end of fourth lactation or culling (L4), and days from first calving until the end of fifth lactation or culling (L5). Heritabilities ranged between 0.022 and 0.090. Additive breed effects in units of days were estimated relative to DH for DR as −0.5 (L1), +10.5 (L2), +18.5 (L3), +11.9 (L4), and +28.6 (L5), and corresponding figures for DJ were +2.0, +0.5, +14.2, +27.7, and +44.0. Heterosis effects in L1 were low (1.2%) but favorable in crosses between DH and DR, whereas negative heterosis effects were estimated for crosses between DH and DJ (−2.5%) and DR and DJ (−1.2%). The largest heterosis effects for L2, L3, L4, and L5 were found in DH × DR and were favorable (+3.3, +5.7, +7.7, and +8.5%, respectively). Corresponding figures for heterosis effects in DH × DJ and DR × DJ were favorable as well: +2.3, +4.1, +5.6, and +6.2% in DH × DJ and +3.1, +7.3, +6.9, and +7.2% in DR × DJ. The favorable heterosis effects show that crossbreeding is an efficient tool for improving longevity in Danish dairy cattle.
Key words: dairy cattle, crossbreeding, longevity

INTRODUCTION

During the last decades, the focus on including longevity and functional traits (mainly fertility, health, and conformation) in dairy cattle breeding goals has increased throughout the world (Leitch, 1994; Miglior et al., 2005; Kargo et al., 2014). Longevity is a complex trait that is highly affected by production and functional traits as well as other factors such as herd management and the farmer's decisions (Berry et al., 2005). In Denmark, the average lifetime of dairy cows is approximately 2.5 lactations (SEGES, 2015). Yet studies indicate that the full milk yield potential of a cow is not obtained until the third or fourth lactation (Jairath et al., 1998), assuming that this is when the cow may become most profitable. However, as the cow gets older, the functional traits may deteriorate (Fleischer et al., 2001; Weber et al., 2013), and in many cases the cow will therefore be culled before it reaches its full milk yield potential.

Herd management is a key factor in minimizing the decline in functional traits and improving longevity (de Mello et al., 2014), but longevity is also influenced by genetics. Heritability estimates for longevity are highly dependent on how it is analyzed; reported estimates range from 0.03 to 0.39 (Roxström and Strandberg, 2002; SEGES, 2015). The complexity of longevity makes it hard to define a measurable phenotype and select directly for longevity. However, large genetic correlations between production, functional traits, and longevity exist (Roxström and Strandberg, 2002; Pritchard et al., 2013). This suggests that selection can be based on production and functional traits rather than directly on longevity. Indeed, this is accounted for in the Nordic Total Merit Index, where the largest weights are put on milk yield, udder health, and udder conformation (NAV, 2013).

Received January 23, 2017.
Accepted April 2, 2017.
[1]Corresponding author: julieclasen@mbg.au.dk

Crossbreeding between purebred lines or populations is known to produce offspring with better economic and phenotypic abilities compared with the parental breeds. Systematic crossbreeding (i.e., rotational crossbreeding) has been used successfully within beef cattle, poultry, and pig production systems for a long time but is less common in dairy cattle. However, interest in systematic crossbreeding has been increasing throughout the world during the last decade (Sørensen et al., 2008). An experiment conducted in Denmark in the 1980s showed that longevity can be improved in Danish dairy cattle by using a crossbreeding scheme (Sørensen et al., 2008). Additionally, other studies such as those in Sweden (Jönsson, 2015), Canada (Vesely et al., 1986), the United States (Heins et al., 2011, 2012), and New Zealand (Lopez-Villalobos et al., 2000) have found improvement in longevity by crossbreeding. The use of systematic crossbreeding in Danish dairy herds is of increasing interest, and reliable estimates of the effect of crossbreeding under Danish circumstances will be of great value for both breeding organizations and dairy farmers. The aim of this study was to estimate heterosis, breed effects, and genetic parameters for longevity in crossbred dairy cattle among Danish Holstein (**DH**), Danish Red (**DR**), and Danish Jersey (**DJ**) breeds.

MATERIALS AND METHODS

Data

Data and information on survival, breed proportion, and relationships between animals were provided by the Danish Cattle Registry (SEGES) on 73,741 animals with a total of 188,678 calvings from November 10, 1999, to October 1, 2016. All animals had at least the first calving registered within that period. Data were extracted from 119 Danish commercial herds that use systematic crossbreeding and 11 mixed-breed herds with purebred DH and DJ. The herds using crossbreeding were selected by Danish breeding consultants. The mixed-breed herds were included to estimate breed effects between DJ and the other breeds, as the number of pure DJ represented in the herds using systematic crossbreeding was limited. The pedigree was traced back 4 generations and included 262,027 animals.

The data set exclusively contained data that met the following requirements: (1) the individual cow had a minimum age of 450 d and a maximum age of 1,280 d at first calving, (2) cows did not change herds during the observation period, and (3) unknown breed proportions did not exceed 12.5%. Registration of breed proportion was not a standard procedure in Denmark until the late 1990s; thus, some cows may have proportions of unknown breed. Instead of removal, for the 2,994 cows with less than 12.5% unknown breed, the unknown proportion was substituted with the breed (DH, DR, or DJ) representing the largest proportion. This was done to keep as many crossbred animals in the data as possible.

It is important to note that the breeds DH, DR, and DJ contain more lines. Danish Holstein consists mainly of Holstein-Friesian, but it also contains a small proportion of Original Danish Black and White. Danish Jersey is a mixture of Danish, New Zealand, and American Jersey. Danish Red is the most heterogeneous breed because it contains a small proportion of Original Danish Red, whereas the remaining part is a mixture of Swedish Red, Norwegian Red, Canadian Ayrshire, Finnish Ayrshire, American Brown Swiss, and Red Holstein Friesian (SEGES, 2015). For our analysis, we wanted to keep the 3 breeds as distinct as possible. We therefore chose to include Red Holstein Friesian in DH instead of DR, as Red Holstein Friesian is more genetically related to DH than DR.

Longevity Traits

Five longevity traits were constructed to reflect productive longevity, which is described as the number of days survived from first calving until culling, without correction for any production or functional traits. These 5 traits correspond to the traits used for evaluating longevity in the Nordic Cattle Genetic Evaluation (**NAV**; NAV, 2013). The longevity (**L**) traits are defined as follows: days from first calving until the end of first lactation or culling (**L1**), days from first calving until the end of second lactation or culling (**L2**), days from first calving until the end of third lactation or culling (**L3**), days from first calving until the end of fourth lactation or culling (**L4**), and days from first calving until the end of fifth lactation or culling (**L5**). A specific trait is the sum of days in all previous lactations plus the number of days until culling in the current lactation. Thus, an observation on L5 can be considered as the total longevity. To avoid penalizing particularly fertile cows, the number of days in lactation was set to 365 d if the cow was culled in a later lactation. Hence, the maximum observation was 365, 730, 1,095, 1,460, and 1,825 for L1, L2, L3, L4, and L5, respectively. However, in the lactation in which the cow was culled, the observation was set to the exact number of productive days (although a maximum of 365 d). Furthermore, no censored data were included; thus, all cows with data had finished or had the opportunity to finish the current lactation number.