

1.1 Introduction

Kenya's dairy cattle breeding programme aims at increasing milk yield (Bebe et al., 2003). Dairy cattle are reared under variable production systems which based on scale of production can be classified into small-scale and large-scale dairy production systems (Peeler and Omore, 1997). Large-scale production systems have a commercial orientation while small-scale range from mainly subsistence to commercial. Small-scale production systems rear over 80% of the national dairy herd and account for over 85% of total annual milk production and 80% of marketed milk (Staal et al., 2001). By virtue of rearing the bulk of dairy cattle numbers, the small-scale production systems form an important market for dairy bull semen and replacement stock and breeding programmes should be geared towards meeting their needs (Mulder and Bijma, 2006). Currently, semen from locally bred and foreign sires are used.

In developing countries, nucleus breeding schemes (NBS) based on local progeny testing of dairy sires in a section of the population (nucleus) have been recommended (Okeno et al., 2010a,b; Vargas and Van Arendonk, 2004) due to lack of financial and logistical support to implement a population wide progeny testing (Kahi et al., 2004). The nucleus is usually composed of high performing herds since the aim is to increase genetic variability for accurate identification of genotypes (Schierenbeck et al., 2011), apart from ensuring availability of adequate useable data (Meinert et al., 1997). When the genetic correlation for a trait between the nucleus and the rest of the population is not different from unity, NBS lead to sustainable genetic gains to the entire population (König et al., 2008). Recruiting herds into the nucleus based on milk production level (Schierenbeck et al., 2011) can create a performance gradient, with high producing herds forming the nucleus and low producing herds being predominant in the production environment (PE). High milk production levels are associated with higher additive genetic variances (Gernand et al., 2007) and as the milk production gradient widens, genetic variation in low producing herds decreases leading to significant GE for milk yield (Hammami et al., 2009; Cerón-Muñoz et al., 2004b). There are few studies on GE between contrasted herd environments in developing countries for fertility traits and genetic correlations below 0.8 have been reported (Cienfuegos-Rivas et al., 2006; Cerón-Muñoz et al., 2004a).

Low genetic correlations imply that selection in the high opportunity herd environments would lead to substantial genetic losses in the entire population (Mulder and Bijma, 2006). In the absence of performance records in the production environment, genetic losses of up to 20% in the PE occur when genetic correlation differ from unity and 0.8

(Mulder and Bijma, 2005). Considering that most studies have reported severe GE for milk yield and fertility traits between contrasted environments in developing countries (Hammami et al., 2009; Cerón-Muñoz et al., 2004a,b), genetic losses in the PE due to selection of sires in high input environments could be higher, and it is optimal to have environment specific breeding programmes with progeny testing in each environment (Mulder et al., 2006). The losses are likely to be higher when antagonistic relationship between production and fertility traits within and across environments is considered (Miglior et al., 2005).

Herd environments for studying GE can be defined based on country borders (Ojango and Pollott, 2002), regions within a country (Valencia et al., 2008), production systems (Raffrenato et al., 2003), herd production level (Hammami et al., 2009) or herd-year-standard deviation for milk yield (Montaldo et al., 2009). Clustering of herds based on several exogenous and endogenous factors influencing dairy production has been carried out (Zwald et al., 2003). Pedigree data can be used to determine the structure of a population and categorise dairy herds based on whether they contribute breeding animals (nucleus) or use sires bred in other herds (production environment) (Valera et al., 2005). This hierarchy can be used to estimate components of covariances between contrasted herd environments and practical implications of implementing NBS evaluated. In unstructured populations, study of the population structure and demography can also highlight important circumstances affecting the genetic history of the population (Valera et al., 2005). Pedigree analysis has been used to estimate genetic variability of populations by estimating parameters such as inbreeding, effective population size, genetic diversity and other important population parameters in dairy cattle (McParland et al., 2007) revealing a decline in effective population size and increase in inbreeding level of dairy cattle populations (Koenig and Simianer, 2006; Sørensen et al., 2005). Therefore, studying population structure and assessment of within population variability and gene flow (and flow of individuals) is necessary before implementation of selection programmes and long-term management of genetic variability of populations.

Use of dairy sires selected for increased milk yield in the average herd environment can lead to deterioration of fertility traits due to unfavourable genetic correlation between milk yield and fertility (Albarrán-Portillo and Pollott, 2013; Cienfuegos-Rivas et al., 2006). Poor fertility and longevity has been shown to contribute to culling decisions in dairy cattle in dairy cattle herds in the tropics (Menjo et al., 2009; Ojango et al., 2005). Genetic correlation between production and functional traits also vary with herd environment (Windig et al., 2006) and the economic importance of fertility traits can change depending on herd

environment, and may be more important as production circumstances become more limiting (Calus et al., 2005). As breeding programmes change their breeding goals to include functional traits, the number of top common sires is declining (Miglior et al., 2005; Van der Beek, 2003) due to lower correlation between total merit indices. This is because as GE becomes severe, populations in different environments diversify, leading to differentiation in breeding objectives (Banos and Smith, 1991). A number of studies have recommended inclusion of functional traits in breeding goals of dairy cattle breeding programmes to avoid further decline or even to improve the traits (Sewalem et al., 2010), despite most of them having low additive genetic variation. The rationale is that improvement of management leads to increased sensitivity of genotypes to changing environments, thereby limiting the range of environments within which the genotypes are suitable (Kolmodin et al., 2003). When genetic correlations are less than unity, and genetic correlation between production and functional traits vary with herd environment, breeding programmes should be optimized for multiple environments.

Inclusion of fertility traits in genetic evaluation is limited by availability and inadequate quality of data on functional traits. Lactation curve parameters such as peak yield, persistency of lactation and days to peak yield derived from available test day milk yield data can be used to develop a strategy to improve functional traits without sacrificing milk yield or to improve both traits simultaneously (Albarrán-Portillo and Pollott, 2013; Muir et al., 2004b). Reducing peak yield by shifting daily yield from early to late lactation reduces metabolic stress during early lactation (Friggens et al., 2007) leading to reduced occurrence of diseases and reproductive failure (Appuhamy et al., 2009; Harder et al., 2006) and increased lactation milk yield due to improved lactation persistency (Togashi and Lin, 2004). Improvement of persistency is intuitively appealing to dairy cattle farmers in the tropics, where feed quantity and quality, and diseases are major limiting factors to dairy enterprises and lactation curves are characterized by a sharp decline after peak yield or are ever decreasing (King et al., 2006).

1.2 Objectives

The overall goal of this study was to contribute to increased efficiency of dairy enterprises in the presence of imperfect within and between trait genetic correlations across herd production environments in Kenya. To achieve the goal, five specific objectives were formulated: