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Short Commentary

Short Commentary on: Absence of Genetic Variation in the Coding Sequence of Myostatin Gene (*MSTN*) in New Zealand Cattle Breeds

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ABSTRACT

The objective of this short commentary is to elaborate on some of the main themes identified in the previously published article entitled Genetic variation and haplotypic diversity in the myostatin gene of New Zealand cattle breeds .The absence of genetic variation in the coding sequences of myostatin gene in the New Zealand cattlebreeds likely suggests one or more of the effects of selection pressure, cross-breeding and inbreeding and genetic drift.

Keywords: Myostatin gene (*MSTN*); Selection; Genetic variation; Exon; Cattle

ABOUT THE STUDY

The myostatin gene *MSTN*, sometimes called the Growth and Differentiation Factor 8 (GDF8) gene encodes the myostatin protein MSTN. The protein is a circulating factor secreted by muscle cells whose function is to regulate the pre-natal proliferation of muscle fibres [1,2]. At least 20 different genetic variants (deletions, insertions and nucleotide substitutions) have been described for cattle *MSTN* [3].

In their recent investigation of genetic variation and haplotypic diversity in *MSTN* of 10 New Zealand (NZ) cattle breeds (Charolais, Hereford, Angus, South Devon, Simmental, Red Poll, Composite, Murray Grey, Shorthorn and cross bred Holstein-Friesian × Jersey-cross cows), Haruna et al. [4] did not identify any genetic variation in the coding sequence of *MSTN* in any of the NZ breeds investigated. This was in contrast to previous reports about European cattle breeds, and since the NZ breeds investigated originated from Europe, Haruna et al. [4] suggested this may be attributed to test sample size, founder effects, selection, and other cross-breeding and in-breeding practices. The focus of this commentary is to elaborate more on some of these factors, as we compare the NZ results with their European parent breeds.

In an investigation of haplotypic diversity in *MSTN* of European cattle breeds, Dunner et al. [5] identified five nucleotide variations in the coding region of bovine *MSTN* in nine European cattle breeds (Charolais, Maine-Anjou, Aubrac, Salers, Parthenaise, Bazadaise, Ayrshire, Galloway cattle and the Intr95 sire-line). Two of these nucleotide variations brought about amino acid change (p.S105C and p.D182N), whereas three (c. 267A/G, c.324C/T and c.387G/A) were silent. The c.324C/T was identified in exon 1 in the Charolais, Maine-Anjou, Aubrac, Salers and Intr95 sire-line cattle breeds. Haruna et al. [4] also investigated the Charolais breed, but found no variation in the exons. This could have been for a number of reasons as outlined above. Reports from the NZ Charolais cattle society [5,6] reveal that between 1969 and 1981, 61 bulls and 302 Charolais cows were imported into NZ from Great Britain and bred, which included bulls mated to Angus, Friesian and Hereford cows over five successive generations. In this way, the 'NZ Charolais' was developed, with it still having the typical Charolais growth rate and muscle development, but being better suited to the pasture-based beef production systems used in NZ. Thus, selection pressure and cross breeding strategy may have contributed to the differences between the NZ Charolais and the European Charolais cattle investigated by Dunner et al.[5].

Introgression from other populations may result in the loss of original genetic variants, hence, breeds can not only be threatened by extinction due to breed replacement, but also by the genetic erosion of native populations [7]. In this context, although the NZ Charolais might have originated from Europe, the longer the time that populations have remained isolated, the greater will be the genetic differentiation due to random genetic drift, particularly if the effective population size has been small.

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In an investigation of genetic differences between Hereford cattle from Britain, NZ, Canada, Ireland and Sweden, Blott et al. [7], suggested that founder effects and genetic drift may have played a significant part in the differentiation of national populations. Also, while varied selection objectives may have promoted genetic divergence of the different population, intense selection within a population may have further reduced levels of genetic variation in some populations. Studies on the effect of introgression of Holstein genes into European populations of black-and-white cattle have found that while the performance of production traits (milk yield and protein) was improved, there was an unfavourable effect on fertility traits [8-10].

Even though the NZ and European cattle breeds are likely to have originated from a common ancestor, as suggested by Edwards et al. [9], a number of different effects such as selection objectives, cross-breeding and inbreeding, genetic drift and founder effects may have contributed to the physical and physiological differences within this species, which are reflected in their coding sequences. This is supported by the observation that variation within coding and non-coding sequences produces phenotypic variation between both individuals in a species, and between different species.

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