1. J Anim Breed Genet. 2006 Jun;123(3):172-9.

Evaluation of genetic diversity in Japanese Brown cattle population by pedigree analysis.

Honda T[1], Fujii T, Nomura T, Mukai F.

Author information:

- [1]Department of Animal Science, Faculty of Agriculture, Kobe University, Kobe, Japan.

Abstract

The Japanese Brown is the second most common domestic beef breed in Japan. However, nowadays this breed is facing reduction in numbers because of pressure from a profitable domestic breed. This breed is uniformly characterized by its brown coat colour, but is comprised of two isolated sub-breeds, Kumamoto and Kouchi, each possessing a different gene pool. Pedigree analyses were carried out for the two sub-breeds using the pedigree records of animals born from 1970 to 2000. The effective population size has been found to be consistently reducing during the last three decades in both sub-breeds. The current effective sizes were estimated to be 25.5 and 6.0 for the Kumamoto and Kouchi sub-breeds, respectively. The estimate of the effective number of founders (N(ef)) in the Kumamoto sub-breed decreased from 152.1 to 74.4; that of non-founders (N(enf)), from 41.7 to 5.3; and that of founder genome equivalents (N(ge)), from 32.7 to 4.9. The corresponding changes in the Kouchi sub-breed were from 108.2 to 79.4, 16.2 to 4.1, and 14.1 to 3.9. Increasing differences between the two genetic diversity indices in the sub-breeds indicate that the greater part of the reduction of genetic diversity can be attributed to genetic drift that accumulated in the non-founder generations. A comparison with published estimates for several cattle breeds suggests the extremely limited genetic diversity of Japanese Brown. In addition to the avoidance of further reduction of genetic diversity, it will be important to counteract the process of breed decline by establishing a production system to efficiently utilize the unique characteristics of this breed and by developing links between the breed and products with market value.