Identifying genetic cause of Dwarfism in American Angus cattle

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Summary and Implications

Dwarfism in American Angus was a major cause of concern in the 1970's. Until recently when several calves from some sire x dam crosses resulted in phenotypically dwarf calves not cases have been observed since then. Six affected calves from 3 sire and 5 dam matings and unrelated normal Angus animals were genotyped for the presence of known mutations, which have been reported in Japanese brown and Australian Dexter cattle. We detected only wild-type alleles in dwarf and phenotypically normal Angus cattle, indicating that known mutations associated with Japanese brown cattle or Dexter dwarfism are not responsible for dwarfism in the American Angus breed. However, this does not preclude the possibility that novel mutations may have arisen in American Angus cattle. In order to begin to identify the causative mutation(s) for dwarfism, a whole genome scan of the affected American Angus pedigree is being pursued.

Introduction

Disproportionate dwarfism has been reported in many cattle breeds including Dexter, Holstein, Aberdeen Angus, Hereford, Japanese brown and Shorthorn breeds. Known mutations of dwarfism have been reported in Japanese Brown and Australian Dexter cattle. To begin to investigate the genetic cause of dwarfism in American Angus, affected and normal Angus animals were investigated for the presence of known mutations.

Materials and Methods

Six affected Angus calves and unrelated normal Angus animals were genotyped for the presence of known mutations, which have been reported in Japanese Brown and Australian Dexter cattle.

PCR Genotyping

Polymerase chain reaction (PCR) was employed to amplify both *limbin* mutations in Angus animals. Amplified fragments were sequenced and compared with known mutations. Similarly, genotyping was carried out for known Dexter mutation . Linked markers were also genotyped on affected and normal Angus animals.

Results and Discussion

Affected and normal Angus animals were screened by PCR for known *limbin* mutations, which revealed only the presence if wild-type *limbin* alleles. The nucleotide sequence around position 1356 indicated no C to T substitutions in any Angus sample as reported for Japanese brown cattle. Also analysis for the second *limbin* mutation at position 2054/2055 showed CA in all Angus animals instead of G reported in dwarf animal. Thus, only wild-type *limbin* alleles were observed in all Angus sample (both dwarf and phenotypically normal), indicating that *limbin* gene mutations associated with Japanese brown cattle dwarfism are not responsible for dwarfism in the American Angus breed. In addition, all Angus animals were observed as homozygous normal for both Dexter bulldog mutations. Furthermore, genotyping for 3 linked markers indicated no loss of heterozygosity. Thus, Dexter mutations are also not associated with dwarfism in American Angus breed. However, this does not preclude the possibility that novel mutations may have arisen in American Angus cattle.

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Table 1. Mutation analysis of American Angus breed for known dwarf mutations

	Affected Angus	Normal Angus	Mutant Allele
limbin mutation in Japanese brown			
C1356T	Wild type (C)	Wild type (C)	Mutant (T)
CAInsG	Wild type (CA)	Wild type (CA)	Mutant (G)
Dexter bulldog mutation			
Mutation 1	Homozygous normal	Homozygous normal	Affected Dexter dwarf must have 2 copies of either mutation in any combination.
Mutation 2	Homozygous normal	Homozygous normal	