Sheep *FecB* Gene Polymorphism Role In Thai Meat Goat Proliferation Rate

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Introduction

The *FecB* (Booroola fecundity) gene is the first major gene to be described that affects ovulation rate and proliferation in sheep. It was first identified in 1980s. In addition, this gene has been to shown to be involved in *FecB*, $FecX^1$, $FecX^H$, $FecX^B$ and $FecX^G$ (Davis (2004)). In recent years, *FecB* gene has been shown to be associated with several phenotypes including reproductive endocrinology, ovarian development, litter size, organ development and body measurement (Guan, F., Liu, S.R., Shi, G.Q. et al. (2007); Hua and Yang (2009)). A study of *FecB* as a genetic marker could lead to breeding goats with more desirable phenotypes.

In Thailand, the major meat source for the Muslim people is goat. Therefore, not only growth traits but also an increase in proliferation is important for improvement of the goat's performance. Unfortunately, the genetic mechanism and genetic markers for caprine proliferation gene has yet to be explored.

This goat population consists of purebred and several types of crossbred goats. Moreover, both purebreds and crossbreds were selected as parent of the next generation. These characteristics had similarities with commercial goat production. Thus, the objective of this study was to identify and characterize a genetic polymorphism for the *FecB* gene in Thai multi-breed meat goats as preliminary information for a more in-depth study in the future.

Material and methods

Animal selection and DNA extraction: The whole blood samples were collected from 63 unrelated individuals from 4 different breeds, Thai Native, Boer, Anglo-Nubian and Saanen meat goats. Crossbred animals had several types of breed differences. They were utilized to extract DNA in this study. Genomic DNA protocols were described by Wuthisuthimethavee (1999).

DNA amplification and Detection genetic polymorphisms: The primers were designed as follows:

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Forward primer: 5'-GTCGCTATGGGGAAGTTTGGATG-3'

Reward primer: 3'-CAAGATGTTTTCATGCCTCATCAACAGGTC-3'

These primers deliberately introduced a point mutation resulting in PCR products with *FecB* in sheep (Kumar, S., Kolte, A.P., Mishra, A.K. et al. (2006); Hua G.H., Chen, S.L., Ai, J.T. et al. (2008)). Genomic DNA (20 ng) was used in a 20 µl of reaction volume. The amplification was carried out using 40 cycles at 95^{o}C for 30 seconds, 58^{o}C for 30 seconds and 72^{o}C for 30 seconds followed by 72^{o}C for 7 minutes. The PCR products of *FecB* gene were 140 bp. The PCR products were validated by the SSCP (Single Strand Conformation Polymorphism) analysis after optimization of non-denaturing polyacrylamide gel concentration and other running conditions.

Results and discussion

Genetic variability in *FecB* gene was assessed by using the SSCP technique which shows the detection of changes in the nucleotide sequence as a PCR product affected by single base substitution. Figure 1 represents the SSCP band pattern for *FecB* gene. All of the 63 individuals were homozygotes, hence none of the samples carried the *FecB* mutation. This detection was similar with Hua G.H., Chen, S.L., Ai, J.T. et al. (2008). Therefore, this gene was not associated with a high proliferation rate in goat. Furthermore, this finding indicated that there were differences DNA sequences in proliferation inheritance phenotypes between sheep and goat and possibly other species. Producers should not consider *FecB* in their breeding programs. Research needs to continue to find other possible candidate proliferation genes or markers for future selection in order to achieve optimum progress for this phenotype. In this study, the sample size of this population was small and therefore, the present finding needs further confirmation using substantially larger multi-breed dataset.

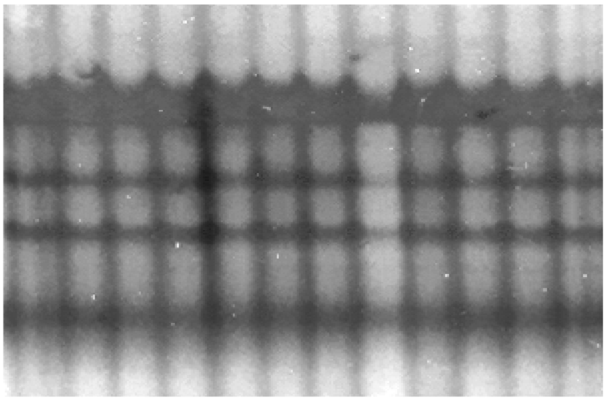

Figure 1: PCR-SSCP band pattern of *FecB* gene on 12% non-denaturing polyacrylamide gel after 12 hours of thev run at 4^{o}C.

Conclusion

Sheep *FecB* gene polymorphism was not found in the Thai multi-breed meat goat population. This result is still an introduction leading to a more in-depth investigation in the different prolific mechanism between goats and sheeps.

References

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