



Deutscher Tropentag - Bonn, 9-11 October 2001  
Conference on International Agricultural Research for  
Development

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### Polymorphism of porcine C3 Gene in Thai Native Pig

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#### Abstract

The third component (C3) is a major molecule of the complement system. It plays a significant role in inflammation, phagocytosis and immunoregulation processes to destroy microorganism. Therefore the gene for C3 can be regarded as a candidate gene for disease resistance. The aim of this study was to determine the genetic polymorphism of porcine C3 gene in Thai native pigs. Blood samples of 32 Thai native pigs from regions of Northern Thailand were collected and DNA was isolated. The genomic DNA was utilized for a Polymerase Chain Reaction (PCR) and genotyping of the Thai native pigs was performed at the three polymorphic sites of C3 gene. It could be shown that the three polymorphic sites in the C3 gene segregate among the Thai native pigs. The allele frequencies of the three polymorphic sites of the C3 gene in the sample of the Thai native pig population were 0.68 and 0.32 for the C and A alleles of position 1905. For the C and A alleles at position 3,882 the frequencies were 0.80 and 0.20, respectively, and 0.58 and 0.42 for the T and C alleles at position 204 in intron 13. In contrast, no polymorphism was found among 80 commercial pig breeds (German Landrace (n=28), Large White (n=29) and Pietrain (n=23)). The Thai native pigs are highly variable at the C3 locus. The genetic variation detected within the Thai native pigs may be associated to phenotypic variation especially of trait related to fitness and disease resistance. Our results demonstrate that animals of native non-selected tropical origin are valuable resource of genetic polymorphism.

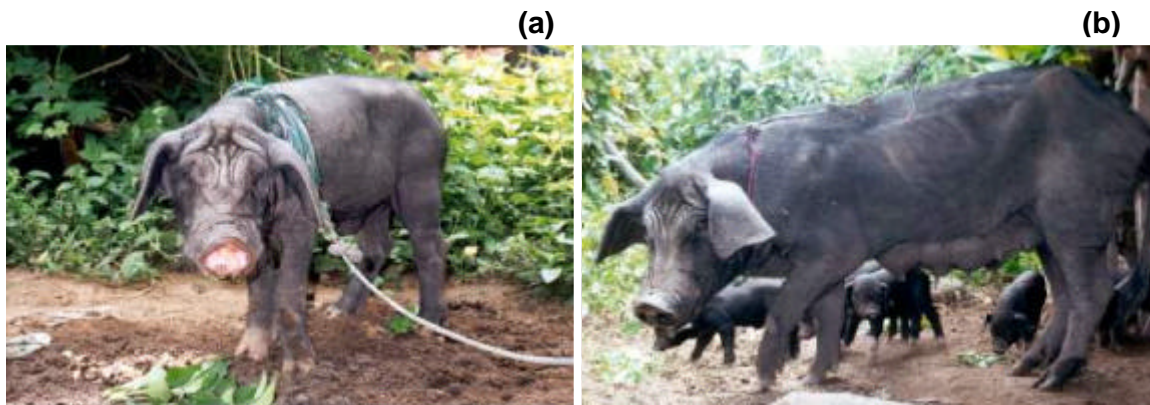
#### Introduction

The complement system is an important host defence mechanism against microbial infections in animals. The third component (C3) is the central molecule of the complement system. Activation of the C3 protein plays a significant role in inflammation, phagocytosis and immunoregulation processes to destroy microorganism. Therefore the gene for C3 can be regarded as a candidate gene for disease resistance. In our previous study, we determined the cDNA sequence of porcine C3 gene (access number AF154933) and detected three polymorphism sites. The first polymorphism is a C→A substitution in exon 15 (position 1905) that can be detected by PCR-RFLP with restriction enzyme Hsp92I. The second polymorphism is a G→A substitution in exon 30 (position 3882) and that can be genotyped by allele-specific PCR. For the third

polymorphism, there is a T→C substitution at nucleotide position 204 of intron 13 that alters the restriction site of Taq I (Wimmers et al. 2000, 2001). The aim of this study was to determine the genetic polymorphism of porcine C3 gene in the Thai native pigs.

### Materials and methods

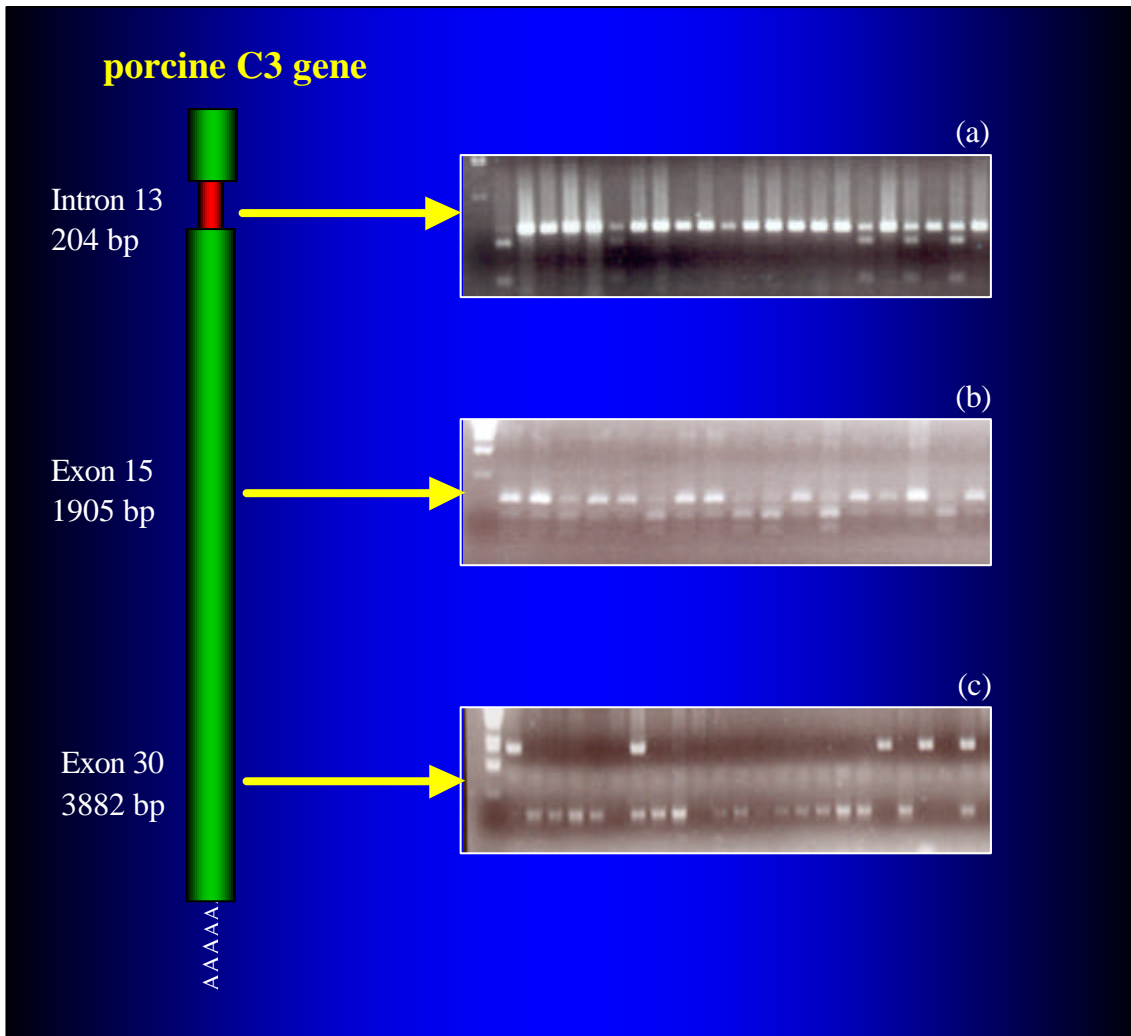
Blood samples were collected from 32 Thai native pigs (figure 1) from regions of Northern Thailand. DNA was isolated from leucocytes. The genomic DNA was utilized for a Polymerase Chain Reaction (PCR) and genotyping of the Thai native pigs at the three polymorphic sites of C3 gene was performed as described by Wimmers et al. (2000; 2001).



**Figure 1:** Thai native pigs (a) boar and (b) sow and piglets form Lumphun province

### Results

Genotypes of the Thai native pigs at the three polymorphic sites of C3 gene were identified. It could be shown that the three polymorphic sites in the C3 gene segregate among the Thai native pigs (figure 2). The allele frequencies of the three polymorphic sites in the sample of the Thai native pig population were 0.68 and 0.32 for the C and A alleles of position 1905 of the C3 gene, 0.80 and 0.20 for the C and A alleles at position 3,882 of the C3 gene and 0.58 and 0.42 for the T and C alleles at position 204 in intron 13 of the C3 gene. The polymorphic information content (PIC) of three polymorphic sites at position 204 in intron 13, 1905 and 3882 were 0.369, 0.341 and 0.269 respectively (table1).



**Figure 2:** Polymorphism of three sites of the porcine *C3* gene in Thai native pigs (a) polymorphism site at 204 bp T→C in intron 13, (b) polymorphism site at 1905 bp exon 15 transition C→A, (c) polymorphism site 3882 bp at exon 30 transition G→A.

**Table 1:** Allele frequency of wild type and variant allele of three polymorphic sites in Thai native pig *C3* gene.

Position	Wild allele	Variant allele	PIC*
204 Intron 13	0.580	0.420	0.369
1905 exon 15	0.680	0.320	0.341
3882 exon 30	0.800	0.200	0.269

\* PIC = polymorphic information content

## **Discussion**

Thai native pigs are found only in very remote areas of northern and north-eastern Thailand. These breeds are known to be well adapted to hot and humid climatic condition, tolerant to low feed quality and housing conditions (FAO, <http://dad.fao.org>). In this study, it could be shown that the three polymorphic sites in the C3 gene segregate among the Thai native pigs. However, in our previous study, no polymorphism was found among 80 commercial breed of pigs e.g. German Landrace (n=28), Large White (n=29) and Pietrain (n=23) (Wimmers et al. 2000, 2001).

## **Conclusion**

The Thai native pigs are highly variable at the C3 locus. The genetic variation detected within the Thai native pigs may be associated to phenotypic variation especially of trait related to robustness, fitness and disease resistance. Our results demonstrate that animals of native non-selected tropical origin are a valuable resource of genetic polymorphism.

## **Acknowledgment**

We express our great appreciation to Prof. Dr. S. Rattanaronchart of the Department of Animal Science, Faculty of Agriculture, Chiang Mai University, Thailand, for providing us with the blood samples for this work. We would also like to thank the German research Council (DFG), and the German Academic Exchange Service (DAAD) for the financial aid.

## **References**

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