



*Brief Note*

## **Low diversity of the major histocompatibility complex class II DRA gene in domestic goats (*Capra hircus*) in Southern China**

**L.P. Chen<sup>1\*</sup>, G.X. E<sup>1</sup>, Y.J. Zhao<sup>1</sup>, R.S. Na<sup>1</sup>, Z.Q. Zhao<sup>1</sup>, J.H. Zhang<sup>1</sup>,  
Y.H. Ma<sup>2</sup>, Y.W. Sun<sup>1</sup>, T. Zhong<sup>3</sup>, H.P. Zhang<sup>3</sup> and Y.F. Huang<sup>1\*</sup>**

<sup>1</sup>College of Animal Science and Technology,  
Chongqing Key Laboratory of Forage and Herbivores,  
Chongqing Engineering Research Centre for Herbivores Resource Protection  
and Utilization, Southwest University, Chongqing, China

<sup>2</sup>Key Laboratory of Farm Animal Genetic Resources and Utilization of Ministry  
of Agriculture, Institute of Animal Science,  
Chinese Academy of Agricultural Sciences, Beijing, China

<sup>3</sup>Farm Animal Genetic Resources Exploration and Innovation Key Laboratory  
of Sichuan Province, Sichuan Agricultural University, Chengdu, Sichuan, China

\*These authors contributed equally to this study.

Corresponding author: Y.F. Huang

E-mail: H67738337@swu.edu.cn

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**ABSTRACT.** DRA encodes the alpha chain of the DR heterodimer, is closely linked to DRB and is considered almost monomorphic in major histocompatibility complex region. In this study, we identified the exon 2 of DRA to evaluate the immunogenetic diversity of Chinese south indigenous goat. Two single nucleotide polymorphisms in an

untranslated region and one synonymous substitution in coding region were identified. These data suggest that high immunodiversity in native Chinese population.

**Key words:** Major histocompatibility complex; DRA; Domestic goat; *Capra hircus*

## INTRODUCTION

The major histocompatibility complex (MHC) plays an important role in the adaptive immune response of vertebrates (Trowsdale, 1993). The DRA locus, which encodes the alpha chain of the DR heterodimer, is closely linked to DRB and is considered almost monomorphic (Ballingall et al., 2010). It exhibits low diversity in artiodactyl species (Sena et al., 2003; Sun et al., 2014), including its exon 2 (Sena et al., 2003; Zhou et al., 2007; Shafer et al., 2012). Therefore, investigating the diversity of the 2nd exon in the DRA of domestic goat breeds would help in understanding the specific evolutionary mechanism of the DRA gene, and realize the full breeding potential of Chinese goats.

## MATERIAL AND METHODS

DNA samples were obtained from 247 individuals of 12 domestic goat breeds in southern China (Table 1). Screening for polymorphisms was performed by direct polymerase chain reaction (PCR) product sequencing in both directions. The primers and PCR protocol employed for the DRA exon 2 were the same as those used by Shafer et al. (2012). Linkage disequilibrium (LD) between loci within each population was analyzed by Genepop (Rousset, 2008). The heterozygosity ( $H_E$  and  $H_O$ ) and polymorphism information content (PIC) were estimated using Microsatellite Toolkit (Park, 2001).

## RESULTS

The total length of the aligned sequences was 303 bp, which included two single-nucleotide polymorphisms, the locations of which were based on AB008755: MI, C > T at 2373 bp on the 2nd intron, and one synonymous substitution (MII) in positions C > T (p.Ala) at 2169 bp on the 2nd exon. In all of the populations studied, the MII site exhibited extremely low diversity ( $H_O = 0.057$ ,  $H_E = 0.0685$ , and PIC = 0.0631) in comparison to the MI site ( $H_E = 0.471$ ,  $H_O = 0.405$ , and PIC = 0.3525). We found unlinkage between MI and MII in all of the populations studied (Table 1).

## DISCUSSION

Comparative analysis of the results obtained in our experiments revealed minimal diversity in exon 2 of the DRA gene. It seems to be highly conserved for residues that form the peptide-binding site region in the domestic goat, which is consistent with the fact that the gene is highly conserved in all of the mammalian species studied (Shafer et al., 2012; Sun et

**Table 1.** Sampling locations, population details, and characteristics of the DRA gene in Chinese domestic goats.

| Population       | Code | Sample size | Location    | MI                   |          |    |           |       |       | MII      |        |     |           |       |        | P (LD) |        |          |
|------------------|------|-------------|-------------|----------------------|----------|----|-----------|-------|-------|----------|--------|-----|-----------|-------|--------|--------|--------|----------|
|                  |      |             |             | Genotype             |          |    | Diversity |       |       | Genotype |        |     | Diversity |       |        |        |        |          |
|                  |      |             |             | CC                   | TT       | CT | $H_o$     | $H_e$ | PIC   | CC       | TT     | CT  | $H_o$     | $H_e$ | PIC    |        |        |          |
|                  |      |             | Breed type  | Longitude            | Latitude |    |           |       |       |          |        |     |           |       |        |        |        |          |
| FuShun Black     | FS   | 18          | Cultivation | 29°17'N <sup>#</sup> | 108°09'E | 5  | 6         | 7     | 0.368 | 0.508    | 0.372  | 17  | 0         | 1     | 0.0526 | 0.0526 | 0.0499 | 0.26203  |
| ChuanZhong Black | CZ   | 22          | Indigenous  | 29°59'N <sup>#</sup> | 106°14'E | 7  | 5         | 10    | 0.476 | 0.511    | 0.374  | 21  | 0         | 1     | 0.0476 | 0.0476 | 0.0454 | 1.00000  |
| ChuanNan Black   | CN   | 23          | Indigenous  | 29°21'N              | 104°46'E | 4  | 13        | 6     | 0.130 | 0.507    | 0.3731 | 23  | 0         | 0     | 0      | 0      | 0      | -        |
| DaZu Black       | DZ   | 24          | Indigenous  | 29°24'N <sup>#</sup> | 105°27'E | 5  | 8         | 11    | 0.458 | 0.503    | 0.3711 | 22  | 1         | 1     | 0.0417 | 0.1197 | 0.1103 | 0.795840 |
| GuangFeng        | GF   | 20          | Indigenous  | 28°21'N              | 118°15'E | 3  | 8         | 9     | 0.450 | 0.481    | 0.3589 | 20  | 0         | 0     | 0      | 0      | 0      | -        |
| GanXi            | GX   | 20          | Indigenous  | 28°02'N              | 114°08'E | 1  | 14        | 5     | 0.300 | 0.328    | 0.2688 | 20  | 0         | 0     | 0      | 0      | 0      | -        |
| HeChuan White    | HC   | 23          | Indigenous  | 29°59'N <sup>#</sup> | 106°14'E | 3  | 6         | 14    | 0.609 | 0.502    | 0.3707 | 20  | 0         | 3     | 0.1304 | 0.1246 | 0.1145 | 0.395840 |
| JianZhou Big Ear | JZ   | 28          | Cultivation | 30°23'N              | 104°31'E | 2  | 16        | 10    | 0.357 | 0.382    | 0.3047 | 26  | 0         | 2     | 0.0714 | 0.0701 | 0.0665 | 1.000000 |
| MeiGu            | MG   | 26          | Indigenous  | 28°02'N              | 102°53'E | 3  | 11        | 12    | 0.500 | 0.449    | 0.3432 | 23  | 0         | 3     | 0.0769 | 0.0754 | 0.0712 | 0.317710 |
| NanJiang Yellow  | NJ   | 16          | Cultivation | 32°20'N <sup>#</sup> | 106°49'E | 5  | 7         | 4     | 0.250 | 0.508    | 0.3711 | 15  | 0         | 1     | 0.0625 | 0.0625 | 0.0587 | 1.000000 |
| Tibetan          | TG   | 27          | Indigenous  | 32°53'N              | 101°46'E | 5  | 8         | 14    | 0.556 | 0.498    | 0.3695 | 22  | 1         | 4     | 0.1481 | 0.2013 | 0.178  | 0.423670 |
| All              |      | 247         |             |                      |          | 43 | 102       | 102   | 0.405 | 0.471    | 0.3525 | 229 | 2         | 16    | 0.0574 | 0.0685 | 0.0631 | 0.913429 |

$H_e$  = expected heterozygosity;  $H_o$  = observed heterozygosity; PIC = polymorphism information content; P (LD) = P value for linkage disequilibrium between loci within populations; (-) = no data; # sampling location; and without any label reflect the main productive location which reference as the China National Commission of Animal Genetic Resources (2011).

al., 2014). Directional selection appears to have conserved these specific functional regions (antigens that are specific to infectious xenobiotics) in the DRA gene of ruminant animals. In comparison to the monomorphic allele in the North American mountain goat (*Oreamnos americanus*) (Shafer et al., 2012), a weak but valuable variant of exon 2 in DRA indicates great potential to improve goat varieties and promote animal husbandry development in the Chinese domestic goat.

### Conflicts of interest

The authors declare no conflict of interest.

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