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# A novel single nucleotide polymorphism (SNP) of the *IGF1R* gene and the association with growth traits in yak (Brief Report)

## Ein neuer Einzelnukleotid-Polymorphismus (SNP) des *IGF1R* Gens und die Assoziation mit Wachstumsmerkmalen beim Yak (Brief Report)

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## Background

The insulin-like growth factor-I (IGF1) is a peptide growth factor that exerts mitogenic and metabolic activities, which are regulators of growth, survival and cell differentiation in a number of cell and tissue types. To elicit its effects, IGF1 must bind its receptors. The insulin-like growth factor 1 receptor (IGF1R) is similar to insulin receptor (INSR) and it mediates the growth-promoting effect of IGF1. The *IGF1R* gene, therefore, was selected as a biological candidate gene for growth, body composition, metabolic, and skeletal traits in animals (ROTHSCHILD *et al.* 1997). By now, no polymorphism of yak (*Bos grunniens*) *IGF1R* gene is reported. In the present paper, the partial exon 1 region of IGF1R was screened to detect the SNPs in Chinese yak breeds. Associations of SNP of IGF1R with growth traits were analysed.

## Procedure

*Primer sequences*

As any of yak *IGF1R* gene sequences was not available, the primer pairs were designed based on bovine partial *IGF1R* gene (acc. no. NM174305).

5′-ACC CGC CAA GAA ATT GTT TC-3′
5′-GGC TCC TCC ATA CTT CCT GTA-3′

*PCR conditions*

50 ng of genomic DNA in a 20 µl reaction containing 1.5 mM MgCl2, 0.2 mM of each dNTP, 0.5 U of Taq DNA polymerase (TaKaRa, China) and 0.4 µM of each primer. The cycling protocol conditions included an initial denaturation cycle at 94 °C for 5min, followed by 30 cycles of denaturation at 94 °C for 1 min, annealing at 57.5 °C for 30 s, 72 °C for 45 s. Then, the amplified products were subjected to a final extension at 72 °C for 10 min. Polymorphism of *IGF1R* was detected by SSCP in 12 % PAGE in constant voltage (200V) for 12-15 h after its PCR products was denatured 10 min at 98 °C. The gel was stained with silver nitrate and visualized with 2 %

NaOH solution (supplied with 0.1 % formaldehyde) (PAN *et al.* 2007). The PCR fragments from different SSCP patterns were subcloned and sequenced.

## Result

A novel SNP was discovered in the exon 1 region of the *IGF1R* gene among 404 unrelated one-year-old animals which belonged to five yak breeds in China (Datong yak, 72; Tianzhu White yak, 111; Gannan yak, 133; Qinghai Plateau yak, 70; Xingjiang yak, 50). Gene and genotype frequencies of the discovered SNP were shown in Table 1. According to acc. no. BTU33122, the SNP was at nt437 within exon 1 of the coding sequence, but caused no amino acids exchange.

Table 1
Allele and genotype frequencies of PCR-SSCP at exon 1 region of *IGF1R* gene in five populations
*Relative Häufigkeit von Allelen und Genotypen einer PCR-SSCP im Exon 1 des IGF1R Gens in fünf Yak-Populationen*

| Breed | N | N of each genotype | | | Genotypic frequencies | | | Allelic frequencies | | HW equilibrium |
|---|---|---|---|---|---|---|---|---|---|---|
| | | AA | AB | BB | AA | AB | BB | A | B | $x^2$-test |
| Datong yak | 72 | 30 | 33 | 9 | 0.4166 | 0.4583 | 0.1250 | 0.6458 | 0.3542 | 0.0012 |
| Tianzhu White yak | 111 | 50 | 51 | 10 | 0.4505 | 0.4595 | 0.0901 | 0.6802 | 0.3198 | 0.2250 |
| Gannan yak | 101 | 59 | 33 | 9 | 0.5842 | 0.3267 | 0.0891 | 0.7475 | 0.2525 | 1.8240 |
| Qinghai Plateau yak | 70 | 18 | 42 | 10 | 0.2570 | 0.6000 | 0.1429 | 0.5571 | 0.4429 | 3.2561 |
| Xingjiang yak | 50 | 14 | 33 | 3 | 0.2800 | 0.6600 | 0.0600 | 0.6100 | 0.3900 | 7.497 |

The SNP found in the yak *IGF1R* gene enable to conduct association analyses in order to evaluate the SNP as a genetic marker for breeding. As IGF1R binds IGFs which has effects on growth and reproduction, the association of genotypes (the C>A of exon I) with growth traits were analysed in yak (Table 2). The associations were analysed by the least-squares method as applied in the general linear model (GLM) procedure of SPSS according to the following statistical model:

$$y_{ijk}=\mu+B_i+S_j+M_k+e_{ijk} \quad (1)$$

with $y_{ijk}$ is the studied traits, $\mu$ is the overall mean; $B_i$ is the fixed effect of breed, $S_j$ is the fixed effect of sex, $M_k$ is the *IGF1R* genotype effect, $e_{ijk}$ is the random residual effect. The result indicated the different genotype of *IGF1R* exon 1 had a significant effect on traits including of body weight, body height, body slanting length ($P<0.05$), but the genotype did not affected on cannon circumference and heart girth. This result provoked the *IGF1R* gene as important candidate gene for production trait.

Table 2
Effects of different genotypes of the exon 1 SNP of *IGF1R* Gene on production traits
*Effekte verschiedener Genotypen des Exon 1 SNP im IGF1R Gen auf Produktionsmerkmale*

| Traits | AA | AB | BB | *P*-value |
|---|---|---|---|---|
| Body height, cm | 93.83 ± 2.95 | 90.18 ± 3.10 | 90.34 ± 3.43 | 0.046 |
| Heart girth circumference, cm | 121.91 ± 2.53 | 120.69 ± 2.38 | 121.67 ± 3.19 | 0.756 |
| Cannon circumference, cm | 13.01 ± 0.09 | 12.98 ± 0.10 | 13.07 ± 0.31 | 0.644 |
| Body slanting length, cm | 91.32 ± 2.13 | 88.77 ± 2.15 | 88.67 ± 2.48 | 0.044 |
| Body weight, kg | 119.29 ± 2.67 | 115.32 ± 1.92 | 113.68 ± 4.02 | 0.031 |

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