The effect of the F94L substitution in myostatin on the live weight of cattle raised on the pasture

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Aim

Identification of F94L mutation in slovak populations.

Evaluation of F94L effect on live weight and muscle thickness of animals raised in extensive conditions.

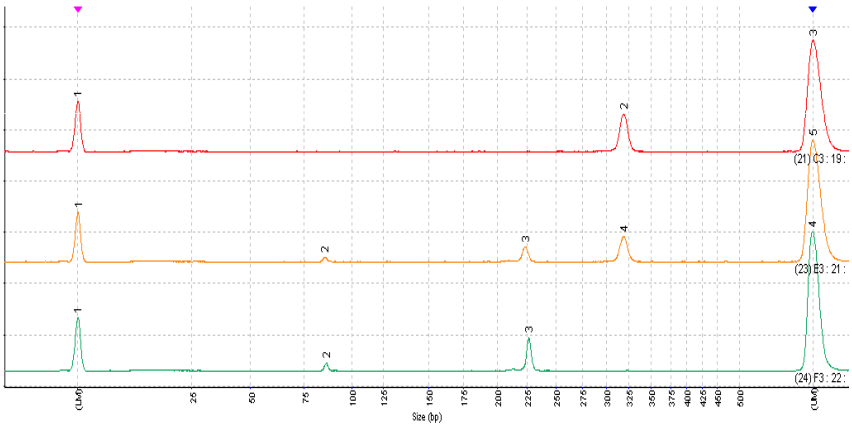


Table 1

Genotype	n	LS means±SE (kg)
LL	65	515.28 ± 56.97
FL	8	658.59 ± 28.48
FF	2	870.94 ± 10.17

Table 2

Genotype	n	LS means±SE (cm)
LL	65	6.03 ± 0.44
FL	8	6.59 ± 0.22
FF	2	6.12 ± 0.08

Results

Significant differences between genotypes were found within live weight (Table 1). Differences (not significant) in the muscle thickness measured at 1st lumbar vertebra site and rump site are shown in Table 2 and 3.

Table 3

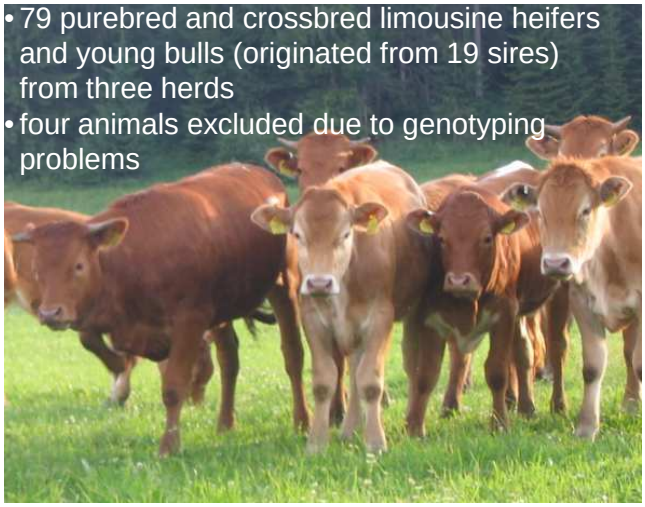
Genotype	n	LS means±SE (cm)
LL	65	11.95 ± 0.72
FL	8	12.88 ± 0.36
FF	2	11.79 ± 0.13

Comments

1. **Frequency of L allele in agreement with published papers.**
2. **Results in contrast with published papers where L allele associated with higher live weight.**
3. **Results not changed significantly after inclusion of age and herd effect.**

Animals

- 79 purebred and crossbred limousine heifers and young bulls (originated from 19 sires) from three herds
- four animals excluded due to genotyping problems



Analyses

1. **Genetic analysis**
   - DNA extraction - from hairy roots (Maxwell purification kit (Promega, USA))
   - PCR-RFLP - 10-50 ng genomic DNAas template, 1x GoTaq Colorless buffer, 1.5 mM $MgCl_2$, 0.2 mmol.l -1 of each dNTP, 0.8 U GoTaq DNA polymerase (Promega, USA) and 0.4 μM of each primer (forward: 5'- TTG CTG GCC CAG TGG ATC TG -3'; reverse: 5'- CTC CGT GGG CAT GGT AAT GAC -3')
   - Restriction endonuclease *Taq* I (Fermentas, Germany)
   - automated microchip electrophoresis system MCE®-2020 MultiNA(Shimadzu, Japan)
2. **Statistical analysis**
   - linear model with genotype effect - effect of sex included

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