Breeding potential of the Slovak Pinzgau cattle: seeking biochemical and molecular biologic traits

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SUMMARY
Slovak Pinzgau cattle belong to the low populous, endangered breeds. In our study we tested 53 healthy steers for the single nucleotide polymorphism T/C at the nucleotide position 878 of the bovine stearoyl-CoA desaturase gene (SCD1) together with the cholesterol metabolites (HDL-cholesterol, LDL-cholesterol, total cholesterol). The group comprehends 33 extensive pastured and 20 corn-fattened animals.

We revealed presence of the genetic equilibrium in the population (p=0.93), significant higher values of HDL-cholesterol (p=0.03) and total cholesterol (p=0.01), but not LDL-cholesterol in pastured steers and non-significant lower concentrations of cholesterol metabolites in A/A homozygotes for T878C SCD1 polymorphism carriers.

Keywords: Slovak Pinzgau cattle, SCD1 gene, cholesterol metabolites

INTRODUCTION
Slovakian Pinzgau cattle belongs to the traditional livestock breeds, mainly in upland regions in Slovakia. Nowadays, this breed belongs to the endangered populations (Kadlecik et al., 2004) due to drastic decreasing of the animal counts. On the other hand, there are available advanced laboratory methods that could help in seeking new suitable benefiting traits for the next breeding.

In our study we applied a complex approach involving genotyping for the single nucleotide polymorphism T/C at the nucleotide position 878 of the bovine stearoyl-CoA desaturase gene (SCD1) together with the cholesterol metabolites (HDL-cholesterol, LDL-cholesterol, total cholesterol) analysis in animal serum.

Previous studies (Taniguchi et al. 2004) revealed association of T/C 878 SCD1 polymorphism (associated with the V-valine or A-alanine variant, respectively) with the higher portion of the mono-unsaturated fatty acids in the adipocytes, with a favorable influence on the beef meat quality.

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The concentration of cholesterol and its derivates is of increasing importance in human nutrition and metabolomics (Kaput et al., 2006), so the logical antipode is the validation of these parameters in animal production, especially with the fatty acids metabolism.

The aims of our study were:
• to reveal the genetic parameters of T878C SCD1 polymorphism in the population of the Slovak Pinzgau cattle
• to verify the concentrations of the selected cholesterol metabolites in the tested samples, with regard to SCD1-genotypes and nutrition of the animals
• to propose following necessary analyses in the future

MATERIAL AND METHODS

Animals:
53 healthy steers of the Slovakian Pinzgau cattle, 33 of them extensive pastured and the 20 remaining ones corn-fattened in stall.

Samples:
Whole blood samples for the DNA analyses were collected in tubes containing EDTA (S-Monovette® EDTA 2.7mL tubes, Sarstedt Nümbrecht, Germany), transported at the temperature of 4 - 6 °C, stored at -20°C. For the analyses of the cholesterol and it metabolites in serum were used glass tubes without anticoagulant, filled with 3ml of the whole blood.

Methods:
T878C SCD1 polymorphism was analyzed via the polymerase chain reaction (Taniguchi et al., 2004), with the SatI restriction endonuclease cleavage (PCR-RFLP). Resulting fragments were separated and visualized electrophoretically on the 12% polyacrylamide gel containing 1x TBE buffer. Cholesterol metabolites were analyzed in serum samples on the automatic biochemical analyzer AU640 (Olympus, UK) with the tests: OSR6216 for total cholesterol (mmol/l), OSR6287 for HDL-cholesterol (mmol/l) and OSR6283 for LDL-cholesterol (mmol/l), all based on enzymatic colorimetric method. For the calibrations were used: Olympus System Calibrator Cat. No. 66300 (for total cholesterol), Olympus HDL-cholesterol Calibrator ODC0011 (for HDL-cholesterol), and ODC1104 for LDL-cholesterol. For the internal quality control were used control samples ODC0005 (Olympus).

Statistics:
Basic statistics is given as an arithmetical mean ( \( \bar{x} \) ), with sample size (n) and standard deviation (S.D.) Genetic parameters were tested toward Hardy-Weinberg principle (chi-square test based on the Pearson’s distribution).
Differences between compared categories were tested with the non-parametrical Mann-Whitney test, as the counts in the particular categories were $5 \leq n < 30$.

**RESULTS AND DISCUSSION**

We found tested population to be in genetic equilibrium ($p=0.96$) with the allelic frequencies $A=0.74$ and $V=0.26$ (exact numbers in tables 1, 2). The substantial question is, however, the relations of the polymorphism with other metabolites, associated with final meat quality and influence of the epigenetic factors, such nutrition.

Table 1 Cholesterol parameters in steers

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Extensive pastured</th>
<th>Fattened</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>$\bar{x}$</td>
<td>SD</td>
</tr>
<tr>
<td>Tch</td>
<td>23</td>
<td>3.00</td>
<td>0.58</td>
</tr>
<tr>
<td>HDLch</td>
<td>23</td>
<td>2.29</td>
<td>0.40</td>
</tr>
<tr>
<td>LDLch</td>
<td>23</td>
<td>1.00</td>
<td>0.25</td>
</tr>
</tbody>
</table>

Legend: n-sample size, $\bar{x}$ - arithmetical mean, S.D.- standard deviation, p- level of significance for Mann-Whitney test, Tch- total cholesterol, HDLch- HDL-cholesterol, LDLch- LDL cholesterol, all concentrations are given in mmol/l.

In general, the palette of the fodder, its amount, composition and quality are determining for the resulting quality of the particular animal products (Archibeque et al., 2005, Lehnert et al., 2006). Our findings are all the more interesting, that revealed significantly higher serum concentration of both total – and- HDL cholesterol in the extensive pastured steers (table 1), as compared with engrossed animals. Merely LDL- cholesterol is weaker significant.

When divided into six categories (each cholesterol derivate with- and-without at least one V-allele), it can be seen that in the case of the extensive pastured steers, the presence of the V-allele slightly increases the cholesterol concentrations, especially for LDL-cholesterol.

Table 2 Cholesterol parameters in steers with regard to SCD1 genotypes

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Genotype</th>
<th>Extensive pastured</th>
<th>Fattened</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>$\bar{x}$</td>
<td>SD</td>
<td>N</td>
</tr>
<tr>
<td>TCH</td>
<td>V/V+V/A 11</td>
<td>3.11</td>
<td>0.60</td>
<td>0.46</td>
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<td></td>
<td>A/A   12</td>
<td>2.90</td>
<td>0.56</td>
<td>0.19</td>
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<td>HDLCH</td>
<td>V/V+V/A 11</td>
<td>2.36</td>
<td>0.40</td>
<td>0.44</td>
</tr>
<tr>
<td></td>
<td>A/A   12</td>
<td>2.23</td>
<td>0.41</td>
<td>0.19</td>
</tr>
<tr>
<td>LDLCH</td>
<td>V/V+V/A 11</td>
<td>1.07</td>
<td>0.28</td>
<td>0.19</td>
</tr>
<tr>
<td></td>
<td>A/A   12</td>
<td>0.94</td>
<td>0.21</td>
<td>0.19</td>
</tr>
</tbody>
</table>

Legend: n-sample size, $\bar{x}$ - arithmetical mean, S.D.- standard deviation, p- level of significance for Mann-Whitney test, Tch- total cholesterol, HDLch- HDL-cholesterol, LDLch- LDL cholesterol, all concentrations are given in mmol/l.
ACKNOWLEDGEMENTS
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REFERENCES