The STAT (signal transducers and activators of transcription) protein family was identified as proteins which are involved in signal transduction from cytokine receptors to the cell nucleus and thus activate the transcription of appropriate genes [1]. Eight STAT transcription factors have been identified so far, namely: STAT1, STAT2, STAT3, STAT4, STAT5A, STAT5B, STAT6 and STAT-D [2]. The function of STAT transcription factors is to regulate gene expression in response to the signals from cytokine receptors. Three of the known STAT proteins (STAT2, STAT4 and STAT6) are activated only by particular ligands, whereas transcription factors, such as STAT1, 3, 5A or 5B are activated by a large number of different ligands [3].

Initially, STAT5 protein was referred to as MGF (mammary gland factor) as it had been discovered in the sheep mammary gland where, being a transcription factor, it participates in the signal transduction pathway of prolactin promoting milk protein gene expression [4]. The STAT5 transcription factor has two isoforms: A and B, which are encoded by two different genes. Both isoforms possess tyrosine 694 which, phosphorylated by JAK kinases, is essential for the activation of both proteins [2].

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In cattle, the STAT5A gene was localized at position 17 (19q17) on the long arm of chromosome 19 [5]. It is located within the 40 kbp “STAT” locus, which also contains STAT3 and STAT5B genes [6, 7]. The bovine STAT5A gene is 15947 bp long and contains 19 exons [8]. Using the PCR-RFLP method and Aval restrictase, the following mutation was detected within exon 7 of the bovine STAT5A gene: C→T nucleotide substitution at position 6853. It is a so-called “silent mutation” in the proline (CCC) codon as it does not result in a change to the amino acid in a protein [9].

The study on polymorphism within the STAT5A gene (transition C6853T) was conducted using the PCR-RFLP method and Aval restrictase. The study covered a herd of 723 cows of the Polish Red-and-White variety of Holstein Friesian breed, kept for dairy purposes in the Opole region, Poland. Two alleles (C and T) of the analyzed STAT5A polymorphism were found in the studied herd. The alleles determined the occurrence of two genotypes: CC and CT. The homozygous TT genotype was not found. The STAT5A/Aval allele frequencies were as follows: C—88.31% and T—11.69%, whereas the genotype frequencies were 76.6% for CC and 23.4% for CT. The analysis of associations between the STAT5A/Aval polymorphism and milk utility traits considered in the study showed that these traits were different in animals with different STAT5A/Aval genotypes.

The study on associations between the STAT5A/Aval gene polymorphism and meat production traits conducted by Flisikowski et al. (2003) [9, 10] showed a significant influence of this polymorphism on meat production traits in Black-and-White cattle. Furthermore, Brym et al. [11] reported that SSCP (A→G) polymorphism within intron 9 affects milk utility traits in Jersey cows. The results obtained by those researchers may suggest that the STAT5A gene is a candidate marker of quantitative traits (QTL) in cattle.

The aim of this study was to identify STAT5A/Aval mutation in a selected gene fragment, determine the genetic structure of the herd of Red-and-White cows under study and find possible associations between the STAT5A/Aval genotypes and the analyzed milk utility traits.

MATERIALS AND METHODS

The study covered 723 cows of the Polish Red-and-White variety of Holstein Friesian breed, kept in seven barns in the Opole region, Poland. The share of Holstein Friesian genes in all the animals was above 70%. The DNA used in the analysis was isolated from 3 ml samples of whole blood collected into vacuum test tubes containing K3EDTA as anticoagulant. DNA iso-
The PCR-RFLP analysis for bovine \( STAT5A/Avai \) polymorphism; M—pUC19/MspI; 1 to 3—genotype CC; 4 to 5—genotype CT.

RESULTS AND DISCUSSION

The primer sequences used in the study allowed amplification of a 215 bp fragment of the \( STAT5A \) gene (Fig. 1), which was digested with \( Avai \) restriction enzyme. After the PCR product had been incubated at 37°C with endonuclease \( Avai \), Electrophoresis was performed on the 2% agarose gel containing Ethidium Bromide with pUC19/MspI as a DNA fragment size marker and the obtained restriction fragments were separated. Visualization of the restriction fragments revealed the existence of 181 and 34 bp fragments of the CC genotype and 215, 181 and 34 bp fragments of the CT genotype (Fig. 2).

Two out of three possible \( STAT5A/Avai \) genotypes determined by two alleles were found in the herd of 723 dairy cows: CC and CT. No homozygous \( TT \) gene...