Influence of single nucleotide polymorphisms in the *myostatin* and *myogenic factor 5* muscle growth-related genes on the performance traits of Marchigiana beef cattle


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Influence of single nucleotide polymorphisms in the myostatin and myogenic factor 5 muscle growth-related genes on the performance traits of Marchigiana beef cattle

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ABSTRACT: The Marchigiana is famous for its large body size and favorable dressing percentage. A myostatin (MSTN) gene mutation (a G to T transversion) was identified in the breed. The homozygote “GG” yields a “normal” phenotype, the homozygote “TT” yields a double muscled body shape but sometimes causes survival problems, and the heterozygote genotype produces an extremely muscled body without defects. In practice, Marchigiana “TT” homozygotes are culled from reproduction, but the heterozygotes are chosen as sires. The objective of this study was to assess genes involved in Marchigiana muscle development to improve selection procedures. The effects of the MSTN and myogenic factor 5 (MYF5) genes on the growth and muscle traits in the Marchigiana breed were assessed. The effects of MSTN together with the genotype of the causative mutation (g.874G > T) and the effects of the two SNP in the promoter were studied (g.-371T > A and g.-805G > C). The SNP effects were evaluated in a comparison between the means of the several genotypes or for the average gene substitution and dominance effect. Two hundred forty-nine bullocks were evaluated using a performance test. At the beginning and end of the trial, the animals were weighed and their bodies were measured every 21 d up to 12 mo of age. In addition to these observations, morphological scores and the BLUP indices were estimated at the end of the performance test. The obtained results suggested that the MSTN g.874G > T and MYF5 SNP could be considered in the selection program of the Marchigiana breed. A MSTN g.874G > T genotyping service for the breeders could help to avoid the “TT” genotype and to select for the “GT” genotype. The “AA” MYF5 SNP genotype could also be selected for even if good muscle development yields a certain size reduction.

Key words: animal breeding, candidate genes, Italian beef cattle, molecular markers

INTRODUCTION

Some cattle breeds exhibit the double muscling phenotype, a condition caused by mutations at the myostatin (MSTN) or GDF8 locus (McPherron and Lee, 1997; Grobet et al., 1997; Kambadur et al., 1997; Karim et al., 2000). The homozygote and heterozygote state allows the formation of the enlarged muscular fiber during embryonic development, and it is regulated by the myogenic determination factors (MYOD) gene family that includes 4 genes, 2 of which, the MYF5 in combination with MYOD1, are involved in the determination of the muscular lineage (Braun et al., 1989, 1990). MYF5 is being considered as a suitable candidate gene for growth traits (te Pas et al., 1999; Li et al., 2004).

The Marchigiana is an Italian beef cattle breed and it is renowned for its large body size, high daily gains, and superior carcass dressing percentage (ANABIC, 2013). Due to its excellent performance, this breed can today be found in Canada, the United States, Brazil, and Australia, where it is either reared as a pure breed or integrated in crossbreeding with the local Bos taurus or Bos indicus breeds (Trombetta and Filippini, 2009).
In studying the *MSTN*, the effect of the causative mutation (g.874G > T; *MSTN_1*) and the effects of 2 SNP in the promoter were investigated. The first SNP in the promoter (g.-371T > A; *MSTN_2*) is caused by a T/A transversion at position –371 (relative to the ATG start codon); the other SNP polymorphism in the promoter (g.–805G > C; *MSTN_3*) is due to a G/C transversion (Crisà et al., 2003). The effects of the *MYF5* gene were studied using a SNP (A/G) at the 1,948 bp position of intron II (Li et al., 2004; Table 1).

The objective of this study is to investigate several candidate genes involved in Marchigiana muscle development, such as *MSTN* and *MYF5*, by assessing their effects on growth and muscle traits. The SNP effects were also evaluated both as a comparison between the means of several genotypes and as an average gene substitution (AGS) and dominance effect (D).

**MATERIALS AND METHODS**

**Animal and Data Source**

Breed improvement and selection programs of the Marchigiana breed are mainly based on performance testing using a subset of approximately 20% of the most eligible sires and on the linear morphological ranking of dam cows. Young bulls eligible for reproduction evaluation are identified at 5 mo of age. Ranking is based on pedigree and morphological traits; once selected, the bulllocks are transferred to the performance test station. Biometric measurements are taken at the start and at the end of the 7 mo testing period. Weights are registered twice every 21 d (Sbarra et al., 2009). During the trial period all animals are genotyped at *MSTN_1* SNP (ANABIC, 2013): the genotyping does not affect the final approval but rather gives the breeder more information on the animal that very often is bought at auction. At the end of the trial, each sire is evaluated by 3 aggregated BLUP indices: the growth index (GI), muscle index (MI), and total index (TI). In addition to these genetic indices, 3 morphological aggregate scores are also assessed: the dimension morphological score (DMS), muscle morphological score (MMS), and total morphological score (TMS). The BLUP indices and morphological scores are standardized (mean = 100 and SD = 10).

In the present study, 249 bulls were evaluated. The animals were born during the 1989 to 2008 period and, following weaning at 5 mo, were reared in the performance station under stringent standardized conditions. At the beginning of the test, the animals were 180 ± 20 d old. The present study also included the following measurements due to their strong correlation with body dimension and muscularity: withers height (WH), trunk length (TL), chest girth (CG), rump length (RL), and loin length (LW). The weights were recorded every 21 d until animals were 12 mo of age. In addition to these observations, the morphological scores and the BLUP indices were also considered.

**Deoxyribonucleic Acid Preparation and SNP Genotyping**

Blood samples were stored at –20°C until DNA extraction. Genomic DNA was isolated using the GenElute Blood Genomic DNA kit (Sigma Aldrich, St. Louis, MO). The SNP were genotyped by LGC Genomics (Hoddesdon, Herts, UK), using KBioscience Competitive Allele-Specific Polymerase chain reaction (KASPar) assay, where 10% of the samples were genotyped in duplicates to assess genotyping accuracy.

**The SNP**

In the Marchigiana breed, the *MSTN* mutation is a G to T transversion at nucleotide 874 in exon 3, known as E291X (Cappucio et al., 1998), which converts a glutamic acid codon into a stop codon. This mutation is different from the mutations described in other hypertrophied breeds such as Belgian Blue or Piedmontese (Bellinge et al., 2005), while the 2 promoter mutations are the same as those already reported in the other double muscling breeds.

In Marchigiana, as in the other double muscling breeds, the *MSTN* genotypes yield 3 different and distinct phenotypes. The homozygote “GG” induces the “normal” phenotype, whereas the other homozygote, “TT,” is expressed as a double muscled body shape while maintaining its small frame and is frequently selected as sires (Landi et al., 2008). Since the “TT” homozygotes are usually culled, only 4 animals in the study group were found to be “TT” homozygous for

<table>
<thead>
<tr>
<th>Gene</th>
<th>Bovine chromosome</th>
<th>SNP name</th>
<th>Location</th>
<th>Accession number and base position</th>
<th>SNP genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>MSTN_1</td>
<td>2</td>
<td><em>MSTN_1</em></td>
<td>Exon III</td>
<td>AJ794986 and 874</td>
<td>G &gt; T</td>
</tr>
<tr>
<td>MSTN_2</td>
<td>2</td>
<td><em>MSTN_2</em></td>
<td>Promoter</td>
<td>A438578 and –371</td>
<td>T &gt; A</td>
</tr>
<tr>
<td>MSTN_3</td>
<td>2</td>
<td><em>MSTN_3</em></td>
<td>Promoter</td>
<td>A438578 and –805</td>
<td>G &gt; C</td>
</tr>
<tr>
<td>MYF5</td>
<td>5</td>
<td><em>MYF5</em></td>
<td>Intron II</td>
<td>M95684 and 1948</td>
<td>A &gt; G</td>
</tr>
</tbody>
</table>

**Table 1. Information on myostatin (MSTN) and myogenic factor 5 (MYF5) SNP**
MSTN_1; hence, due to the low numbers, this genotype was not included in the association study.

Genetic studies on double muscled Marchigiana have analyzed growth and slaughtering traits (Lasagna et al., 2008), but no information is available for the MSTN5 genetic and genotypic frequencies or its influence on performance traits.

Statistical Analysis

The number of copies of allele and genotype were found directly by summation and divided by their respective totals. The Hardy-Weinberg equilibrium in the studied loci was tested according to Rodriguez et al. (2009).

To estimate the effects of SNP, the following statistical approaches were applied.

Differences between Genotypes

The data were analyzed using the GLM procedure of SAS (SAS Inst. Inc., Cary, NC) according to the model

\[ y_{ij} = \mu + G_i + b(AGE)_{ij} + e_{ij}, \]

in which \( y_{ij} \) is the observed variable (body measures, weights, BLUP indices, and morphological scores), \( \mu \) is the general mean, \( G_i \) is the effect of marker genotype, \( b \) is the regression coefficient of the trait on the covariate AGE (age of the young bulls), and \( e_{ij} \) is the residual effect.

Average Gene Substitution Effect

The AGS estimates for body measurements and weights were computed by MTDFREML (Boldman et al., 1995) according to an individual animal model that takes into account the relationship matrix of 2,573 animals.

Three models were used:

\[ y_{ijk} = \mu + G_i + G_1 + G_2 + a_{ijk} + e_{ijk}, \]

in which \( y_{ijk} \) is the observed trait (body measures and weights); \( \mu \) is the general mean; \( b \) is the AGS, the regression coefficient of a trait on the covariate number of alleles at a SNP locus; \( G_1 \) and \( G_2 \) are the fixed effects of the genotypes at the other 2 loci; and \( e_{ijk} \) is the residual effect.

The results of the association analysis indicated that except for LL, all the other body measurements taken at the beginning of the performance test showed no significant differences between the 3 polymorphic SNP genotypes \((P < 0.05)\) for the “AT” MSTN_2 genotype and for the “GG” MYF5 genotype (data not shown).

The AGS estimates for the BLUP indices and morphological scores were also computed according to the 3 models using the GLM procedure of SAS (SAS Inst. Inc.):

\[ y_{ijk} = \mu + b(SNP)_{ijk} + G_1 + G_2 + e_{ijk}, \]

in which \( y_{ijk} \) is the observed variable (BLUP indices and morphological scores); \( \mu \) is the general mean; \( b \) is the AGS, the regression coefficient of a trait on the covariate number of alleles at a SNP locus; \( G_1 \) and \( G_2 \) are the fixed effects of the genotypes at the other 2 loci; and \( e_{ijk} \) is the residual effect.

Dominance Effect

The dominance effect was estimated by subtracting the average homozygous estimate from the heterozygous estimate. The dominance effect was not estimated for MSTN_1 since the “TT” homozygotes were excluded.

RESULTS

The genotype and allele frequencies for the MSTN gene (MSTN_1), MSTN promoters (MSTN_2 and MSTN_3), and MYF5 are reported in Table 2.

For the 2 SNP in the MSTN promoter, the MSTN_2 polymorphism indicated that the “T” frequency was the highest \((P = 0.84)\), and “TT” was the most represented genotype \((0.72)\). In the Marchigiana sample, the SNP MSTN_3 was monomorphic and therefore was not considered in the association analysis.

The frequencies of the 2 MYF5 alleles were 0.53 (A) and 0.47 (G), whereas the “GG” genotype was less frequent \((0.23)\) than the other genotypes.

No significant deviation from the Hardy-Weinberg equilibrium was observed in the studied loci.

By the end of the performance testing period (Table 3), the “GT” genotype was significantly larger than the “GG” genotype in MSTN_1 for RW \((55.0 vs. 53.2 \text{ cm}; P \leq 0.01)\) and SW \((53.5 vs. 52.4 \text{ cm}; P \leq 0.05)\).

In the case of the MSTN_2 genotypes, the only significant effect on the measurements at the end of the performance test was on LW, whereas the “AT” hetero-
zygote was larger than either of the homozygotes states (35.7 vs. 34.9 cm “AA” and 35.0 cm “TT”).

The MYF5 SNP genotype exhibited a greater effect on the morphological measurements of Marchigiana bulls, whereas the smallest sizes were observed in the “AA” genotype. Overall, statistical differences were recorded in WH (130.4 cm for “AA”, 132.6 cm for “AG”, and 131.6 cm for “GG”), TL (146.3 cm for AA, 148.6 cm for “AG”, and 147.7 cm for “GG”), CG (190.6 cm for “AA”, 192.0 cm for “AG”, and 193.0 cm for “GG”), and SW (52.1 cm for “AA”, 52.6 cm for “AG”, and 436.2 kg for “GG”), 310 d of age (454.5 kg –0.1 TL) to –0.5 cm (SW) in the genotype. The AGS effect on the measurements ranged from 2.3 cm (TL) to –1.16 cm (RW) and from 0.07 (LL) to –4.30 to –11.36 kg in BWd. The dominance effect of the MYF5 gene. The AGS was significant only in the BWd for MYF5. The dominance effect on the measurements ranged from 2.3 cm (TL) to –0.1 cm (RW) in the MYF5 _MSTN_2_ and from 1.6 cm (WH and TL) to –0.5 cm (SW) in the MYF5. The gene substitution effects at the _MSTN_1 SNP was less than 1 cm for all of the measurements and were completely negligible in the RL (0.07 cm) and LL (0.02 cm). The AGS effect of the _MSTN_2 ranged from 1.84 (TL) to –1.38 cm (RW) and from 0.07 (LL) to –1.16 cm (TL) for the MYF5 gene. The AGS was significant only in the BWd for MYF5. The dominance effect on the measurements ranged from 2.3 cm (TL) to –0.1 cm (RW) in the _MSTN_2 and from 1.6 cm (WH and TL) to –0.5 cm (SW) in the MYF5.

With regards to the periodic weights taken along the test period (Table 4), the _MSTN_1 genotypes “GG” (normal) were heavier than the “GT” (double muscled carrier), but these differences were not significant. The differences in weights between the _MSTN_2 genotype were significant (P < 0.05) only at 290 d; however, the “AA” genotype exhibited consistently lower values at all of the 9 weighing days.

The weights of the MYF5 were always the highest in the “GG” genotype, the lowest in “AA” genotype, and intermediate in the heterozygote “AG” state. For _MSTN_2, the differences between the MYF5 genotypes were significant (P ≤ 0.05) at the last 3 measuring episodes: 290 d of age (420.1 kg for “AA”, 429.1 kg for “AG”, and 436.2 kg for “GG”), 310 d of age (454.5 kg for “AA”, 465.6 kg for “AG”, and 472.0 kg for “GG”), and 330 d of age (485.3 kg for “AA”, 496.7 kg for “AG”, and 506.0 kg for “GG”). The AGS effect on weights ranged from 2.75 to 9.02 kg in _MSTN_1, from 2.08 to 8.19 kg in _MSTN_2, and from –4.30 to –11.36 kg in MYF5. The dominance effects ranged from 5.2 to 17.7 kg in _MSTN_2 and from 0.9 to 6.1 kg in MYF5. As expected, these results give evidence suggesting that the effect of both AGS and D increases with age.

The association between the _MSTN_1 and _MSTN_2 and MYF5 SNP, the BLUP indices, and the morphological scores are reported in Table 5. In _MSTN_1, the “GG” is, as expected, higher in GI (101.0 vs. 100.6) and “GT” is significantly higher in MI (105.1 vs. 100.9) and in TI (103.6 vs. 101.2). With regards to morphology, the heterozygote sires displayed significantly higher scores (P ≤ 0.01) in DMS (103.3), MMS (108.9), and TMS (104.5). Significant differences were not observed in _MSTN_2; however, it is possible to highlight the higher MI (104.3 vs. 101.2 and 102.7) and, as a consequence, the higher TI (103.0 vs. 101.5 and 101.3) in the “AA” genotype. The morphological scores of MMS and TMS are extremely close in the 3 genotypes, but a considerably lower DMS value in the “AA” was observed. The lower values recorded for “AA” animals were previously noted in results reported in Table 4. In MYF5, as already observed for several previously analyzed traits, the “AA” genotype was more advantageous (P ≤ 0.01) in the BLUP indices, mainly for MI (104.3) and TI (103.5). On the other hand, the “AA” genotype revealed a lower DMS (107.5) than that observed for “AG” (108.4) and lower MMS (99.8) and TMS (101.5) than the ones recorded for the 2 other genotypes (102.9–102.0 and 103.0–102.8, respectively, for “AG” and “AA”).

The AGS estimated using the BLUP indices and the morphological scores were never significant and rather different for the _MSTN_1 and _MSTN_2 and MYF5 SNP. _MSTN_1 had a stronger effect on MI and MMS than on GI and DMS, while the AGS in _MSTN_2 seems to be negligible based on all of the indices and scores obtained in this study. The MYF5 AGS was somewhat difficult to interpret: positive values are obtained in the indices, mainly in MI; conversely, the AGS value is negative in MMS (~1.09) as well as in TMS. The dominance effects were rather low, and they displayed an absolute value greater than 1% only in _MSTN_2 (MI = –2.3 and DMS = 1.4) and in MYF5 (DMS = 1.5 and MMS = 2.0).

**DISCUSSION**

**Polymorphism/Allele Frequencies**

Marker-assisted selection plans have to use SNP that are polymorphic. In the present study, one SNP in the _MSTN_ promoter (_MSTN_3) was monomorphic and therefore was useless for selection.

The allele and genotypic frequencies at the 3 polymorphic loci studied have revealed the following: in _MSTN_1, a negligible frequency was observed for the
Table 3. Least squares means ± SE, average gene substitution (AGS), and dominance effects (D) for the myostatin (MSTN_1 and MSTN_2) and myogenic factor 5 (MYF5) SNP on body measures at the end of performance test

<table>
<thead>
<tr>
<th>Trait</th>
<th>Genotypes</th>
<th>MSTN_1</th>
<th>MSTN_2</th>
<th>MYF5</th>
<th>AGS ± SE</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weight</td>
<td>AA</td>
<td>115.9 ± 0.4</td>
<td>113.5 ± 0.6</td>
<td>113.4 ± 0.4</td>
<td>113.6 ± 0.7</td>
<td>-0.37 ± 0.2</td>
</tr>
<tr>
<td></td>
<td>GT</td>
<td>113.0 ± 0.4</td>
<td>112.8 ± 0.7</td>
<td>113.4 ± 0.4</td>
<td>113.6 ± 0.7</td>
<td>-0.37 ± 0.2</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>113.4 ± 0.4</td>
<td>113.5 ± 0.6</td>
<td>113.4 ± 0.4</td>
<td>113.6 ± 0.7</td>
<td>-0.37 ± 0.2</td>
</tr>
</tbody>
</table>

Table 4. Least squares means ± SE, average gene substitution (AGS), and dominance effects (D) for the myostatin (MSTN_1 and MSTN_2) and myogenic factor 5 (MYF5) SNP on weights during performance test

<table>
<thead>
<tr>
<th>Weight</th>
<th>Genotypes</th>
<th>MSTN_1</th>
<th>MSTN_2</th>
<th>MYF5</th>
<th>AGS ± SE</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AA</td>
<td>30.5 ± 2.9</td>
<td>306.3 ± 4.3</td>
<td>305.5 ± 2.9</td>
<td>305.7 ± 4.3</td>
<td>2.75 ± 5.3</td>
</tr>
<tr>
<td></td>
<td>GT</td>
<td>300.2 ± 13.3</td>
<td>307.1 ± 4.7</td>
<td>305.7 ± 4.3</td>
<td>305.9 ± 4.3</td>
<td>2.71 ± 5.6</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>299.7 ± 4.3</td>
<td>305.6 ± 3.6</td>
<td>308.1 ± 5.1</td>
<td>308.3 ± 5.1</td>
<td>-4.30 ± 3.3</td>
</tr>
</tbody>
</table>

The high frequencies estimated in this study for the “T” allele and “TT” genotype in the MSTN promoter (MSTN_2) are similar to those obtained by Han et al. (2012), where “T” frequencies were equal to 0.972, 0.781, and 0.878, respectively, in Holstein, Jeju Black, and Hanwoo cattle.

The allele frequencies of MYF5 SNP were both close to 0.5; similar values (A = 0.42 and G = 0.58) were esti-
Association of Polymorphisms with Growth Traits, Genetic Indices, and Morphological Scores

This study showed that the analyzed polymorphic SNP had a varying effect associated with the growth traits, genetic indices, and the morphological scores. The differences in \textit{MSTN\_1} do not suggest a preferred genotype since the body parameters and weights in the two observed genotypes were rather similar. The same observations were reported by Landi et al. (2008), who observed differences in body measures between the “GG” and “GT” \textit{MSTN\_1} genotypes, but the “TT” (not included in this study) genotype differed strongly because of its small size. Additionally, Lasagna et al. (2005), in a small scale experimental trial, did not observe any significant differences between the two \textit{MSTN\_1} genotypes on live weight at slaughtering, body measures, and slaughtering traits, although the “GG” animals were slightly larger.

The effect of the \textit{MSTN\_1} genotype on the BLUP indices and morphological scores was similar to that already discussed with regards to body measurements and weights. In fact, the “GT” genotype yielded a better muscle definition and carcass conformation. Moreover, the high morphological score translates in the popularity of the “GT” animals in the final performance test auction and, as a consequence, their rather high frequency in the population.

The \textit{MSTN\_2} genotypes show similar weights and measurements that seldom reach significant differences. This SNP confirms that the “AA” genotype yields the lowest measurements. The same trend was also observed by Han et al. (2012), where Hanwoo cattle exhibited a lighter weight at slaughter, a lighter carcass weight, and generally a worse meat organoleptic quality for the “AA” genotype.

The effect of the \textit{MSTN\_2} genotype on the BLUP indices and morphological scores was negligible; therefore, this locus should not be incorporated into the selection criteria.

The study tends to suggest that the \textit{MYF5} genotype may affect the studied traits, indices, and scores. The “AA” genotype was observed to yield a smaller body frame, which was in agreement with work done by Zhang et al. (2007) on Nanyang cattle, namely for the RW, CG, and TL measures; however, Lisa et al. (2013) did not observe any \textit{MYF\_5} effect on Piedmontese cattle.

For the same SNP, the “GG” genotype was associated with the heaviest weights. Li et al. (2004) observed that this genotype was associated with most favorable birth weights, preweaning ADG, and ADG in \textit{Bos taurus} commercial lines. Chung and Kim (2005) observed heavier weights from birth to 12 mo of age in the “GG” genotype of Korean cattle. The AGS in \textit{MYF5} is always found to be negative on the weights; this finding was also observed by Li et al. (2004), where an additive effect ranging from –1.196 to –0.008 in birth weight and daily gains of beef cattle commercial lines was estimated. Additionally, Chung and Kim (2005) reported AGS from –1.13 to –0.04 for weights and daily gains in Korean cattle.

Based on this study, some relevant suggestions can be proposed on the suitability of the studied loci for incorporation into the selection practice in Marchigiana cattle.

The \textit{MSTN\_1} was already known to influence the productive traits; however, the bull genotype is not included in the official selection procedure (even if, as already

Table 5. Least squares means ± SE, average gene substitution (AGS), and dominance effects (D) for the myostatin (\textit{MSTN\_1} and \textit{MSTN\_2}) and myogenic factor 5 (\textit{MYF5}) SNP on genetic indices

<table>
<thead>
<tr>
<th>Trait</th>
<th>\textit{MSTN_1}</th>
<th>\textit{MSTN_2}</th>
<th>\textit{MYF5}</th>
<th>\textit{AGS ± SE}</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td>GI</td>
<td>101.0 ± 0.6</td>
<td>100.6 ± 0.9</td>
<td>–</td>
<td>–1.05 ± 1.5</td>
<td>–</td>
</tr>
<tr>
<td>AA</td>
<td>101.3 ± 0.9</td>
<td>101.3 ± 0.7</td>
<td>99.4 ± 1.0</td>
<td>0.62 ± 0.8</td>
<td>0.9</td>
</tr>
<tr>
<td>MI</td>
<td>100.9 ± 0.7</td>
<td>105.1 ± 1.0</td>
<td>–</td>
<td>–2.57 ± 1.4</td>
<td>–</td>
</tr>
<tr>
<td>MMS</td>
<td>101.2 ± 0.7</td>
<td>103.6 ± 1.0</td>
<td>–</td>
<td>0.86 ± 1.0</td>
<td>–</td>
</tr>
<tr>
<td>DMS</td>
<td>101.2 ± 0.9</td>
<td>103.3 ± 1.3</td>
<td>–</td>
<td>0.95 ± 1.2</td>
<td>0.9</td>
</tr>
<tr>
<td>MTS</td>
<td>101.6 ± 0.4</td>
<td>104.5 ± 0.6</td>
<td>–</td>
<td>–2.41 ± 1.2</td>
<td>–</td>
</tr>
</tbody>
</table>

\(^{A,B} P \leq 0.01.\ ^{a,b} P \leq 0.05.\}

G = growth index; MI = muscle index; TI = total index; DMS = dimension morphological score; MMS = muscle morphological score; TMS = total morphological score.

SE = standard error.
reported, all the young bulls are genotyped during the performance test), and many breeders are aware of a genotyping service that helps them define a correct mating plan to improve the muscularity without compromising the survivability of the calf (e.g., to increase the frequency of the double muscled “GT” genotype and avoid the “TT” genotype). No reports have analyzed the effects of MYF5 on the Marchigiana breed. This study demonstrated that this gene is polymorphic and can affect productivity traits. Therefore, the “AA” genotype can be selected for because Associazione Nazionale Allevatori Bovini Italiani da Carne is also associated with a reduced size.

Since the SNP in the promoter, the MSTN_3, was monomorphic and the MSTN_2 had low differences between genotypes and the low AGS and D, these 2 may not be useful to be considered in the selection criteria.

LITERATURE CITED


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<td>This article cites 21 articles, 4 of which you can access for free at: <a href="http://www.journalofanimalscience.org/content/92/9/3804#BIBL">http://www.journalofanimalscience.org/content/92/9/3804#BIBL</a></td>
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</tbody>
</table>