Analysis of association between a microsatellite at intron 1 of the insulin-like growth factor 1 (IGF1) gene and fat deposition, meat production and quality traits in Italian Large White and Italian Duroc pigs

Luca Fontanesi,1,2 Emilio Scotti,1 Luca Buttazzoni,3 Stefania Dal’Olio,1 Vincenzo Russo1
1Dipartimento di Scienze e Tecnologie Agroalimentari, Università di Bologna, Italy
2Centre for Genome Biology, Università di Bologna, Italy
3Consiglio per la Ricerca e la Sperimentazione in Agricoltura, Roma, Italy

Abstract

A few studies have shown that a microsatellite at intron 1 of the insulin-like growth factor 1 (IGF1) gene is associated with several production traits in a few pig populations. In the current work we evaluated associations between this microsatellite and production traits in Italian Large White and Italian Duroc pigs. Association studies were carried out on a total of 1120 animals using two experimental designs: i) a selective genotyping approach based on extreme and divergent Italian Large White pigs for back fat thickness (BFT) estimated breeding value (EBV) or on extreme and divergent Italian Duroc pigs for visible intermuscular fat (VIF) EBV; and ii) analysis of unselected pigs (random groups) coming from populations of the two breeds. Allele distributions between Italian Large White and Italian Duroc pigs were different (P<0.05) with longer alleles being more frequent in Italian Large White pigs for back fat thickness (BFT) EBV in Italian Duroc pigs using two experimental designs, with potential practical applications in predicting genetic merit of pigs. A conserved dinucleotide (CA)n microsatellite is located in intron 1 of the bovine and porcine IGF1 gene (Kirkpatrick, 1992; Winterton et al., 1994), a region that often contains regulatory elements affecting gene expression (Rowntree et al., 2001; Foti and Reichardt, 2004). This marker has been associated with growth traits in beef cattle, but with inconsistent results (Regitano et al., 1999; Curi et al., 2005; Andrade et al., 2008). In pigs, a few studies investigated this microsatellite in association analyses with production traits. Casas-Carrillo et al. (1997) reported evidence of a QTl for average daily gain (ADG) on Sus scrofa chromosome (SSC) 5 in the interval containing the IGF1 microsatellite. Estany et al. (2007) analysed this microsatellite in Landrace and Duroc populations and reported association between longer alleles and increased plasma IGF1 level in both breeds. Longer alleles were also associated with increased live weight, BFT and intramuscular fat content in Landrace pigs whereas in Duroc pigs a negative substitution effect of a longer allele vs a shorter allele was observed for BFT, leading to leaner carcasses (Estany et al., 2007). Assis de Faria et al. (2009) reported association between the IGF1 microsatellite and several carcass traits in an experimental F2 population obtained crossing Piata boars (Brazilian pigs) and commercial sows. In this study we evaluated association between the intron 1 IGF1 microsatellite and several carcass traits in an experimental F2 population obtained crossing Piata boars (Brazilian pigs) and commercial sows. Materials and methods Animals All procedures involving animals followed Italian and European Union regulations for animal care and slaughtering. The association study was conducted on a total of 1120 animals, divided in four groups of pigs from two different experimental approaches: i) two groups were based on a selective genotyping design and ii) two groups were not selected by any phenotypic or geno-
typic criteria (random groups). All pigs were performance tested at the Test Station of the National Pig Breeder Association (ANAS). Performance test was conducted on triplets of siblings from the same litter (two females and one castrated male). Data are routinely used for the genetic evaluation of a male from the same litter (sib-testing).

The first group of the selective genotyping approach was constituted by 560 Italian Large White gilts with no common parents, selected among ~12,000 performance tested pigs of this breed in the period 1995-2007 (Fontanesi et al., 2012b). Two hundred eighty pigs had the lowest BFT estimated breeding value (EBV), mean and s.d.=-9.40 ±1.60 mm; and 280 had the highest BFT EBV, mean and s.d.=-8.00± 5.95 mm. Genotyping results were obtained for 275 and 272 pigs, respectively (Table 1). The second group was constituted by 100 Italian Duroc pigs (58 females and 42 castrated males from 62 different sires) selected among 1225 pigs of that breed (evaluated in period 1996-1999; Fontanesi et al., 2009): 50 with the most negative (-2.35±0.27) and 50 with the most positive visible intermuscular fat (VIF) EBV (+2.17±0.34). Estimated breeding values were calculated as described below.

Of the two random groups, one was made up of 261 Italian Large White pigs (172 females and 79 castrated males, from 77 different sires; a subset of the population investigated by Fontanesi et al., 2008, 2010). Pigs of this group were slaughtered over 6 different days in 2002. The other random group was made up by 212 Italian Duroc pigs (139 females and 73 castrated males, from 92 different sires) slaughtered at 33 different days in the years 1995-2003 (Fontanesi et al., 2010).

### Traits

Performance test of the animals included in this study was carried out at the Test Station of ANAS as already described (Fontanesi et al., 2008; 2010; 2012a). Feed intake was recorded daily and body weight was measured bimonthly. Using these data average daily gain (ADG) and feed:gain ratio (FGR) were calculated. At the end of test, animals were transported to a commercial slaughterhouse and slaughtered as previously reported (Fontanesi et al., 2008). Within 3 h post-mortem at the slaughterhouse, BFT at the level ofMusculus glutaeus medius, weight of lean cuts (LC: necks and loins), and weight of hams (HW) were measured. Only for the Italian Duroc pigs visual evaluation of VIF was obtained on leg muscles based on a binary scale (presence/absence). Only for the 261 Italian White gilts of the random group, measures of pH1 (at 2 h post-mortem), pHu (at 24 h post-mortem) and calpastatin B activity (Catb) (24 h post-mortem) were obtained on Musculus semimembranosus as previously described (Fontanesi et al., 2008; Russo et al., 2008).

### Genotyping of the IGF1 microsatellite

Genomic DNA was extracted from blood using standard protocols. PCR amplification was carried out using the following primers designed on GenBank sequence X64400: forward, 5'-GCTTGGATGGACCATGTTG-3'; reverse, 5'-CATATTTTCTGCATAACTTGACCT-3' (Estany et al., 2007). Primer forward was labelled at 5' with 6-FAM. PCR analyses were done in a 10 µL reaction volume, that included 1-2 µL of DNA template (10-30 ng), 2 pmol of each primer, 2.5 mM dNTP mix, 1.5 mM MgCl2 and 0.5 U Taq DNA polymerase EuroTaq (EuroClone, Milano, Italy). PTC-100 (MJ Research, Waltham, MA, USA) thermal cycler was used for PCR reactions that included a first denaturation step at 95°C for 5 min, 35 cycles (30 s at 95°C, 30 s at 58°C, 30 s at 72°C) and a final 8 min extension at 72°C. For size determination, PCR products (0.5-2 µL) were diluted in 5 or 10 µL of Hi-Di formamide (Applied Biosystems, Invitrogen, Carlsbad, CA, USA) and added to 0.1 µL of Rox labelled DNA ladders (500HD Rox; Applied Biosystems) before electrophoresis on an ABI3100 Avant sequencer (Applied Biosystems). Genotyping results were obtained for a total of 1120 pigs.

According to sequence X64400, amplified fragments containing the CA repeat obtained with reported primers should give odd size, thus we adopted an odd nomenclature to describe alleles as also reported by Assis de Faria et al. (2009). This is different from the even nomenclature (1 bp of difference) reported by Estany et al. (2007). Sequencing of the PCR fragment obtained from a homozygous 196/196 Italian Duroc pig was used to confirm allele size and allele nomenclature.

Sequencing was carried out as previously described (Fontanesi et al., 2010). It is worth to mention that a true comparative determination of microsatellite allele size and nomenclature would be possible if a common DNA sample was analysed in the different studies mentioned. This was not the case. However, comparison with allele size and nomenclature is, to some extent, possible between our work and that of Estany et al. (2007). These authors investigated a Duroc population in which allele indicated with size 197 was the most frequent (0.57) among the allelic series reported in this breed that included only other 4 alleles. In our study, the most frequent allele in the Duroc popula-

### Table 1. Distribution of IGF1 alleles and genotypes in Italian Large White and Italian Duroc investigated populations.

| N of pigs | N of alleles | 182 | 184 | 190 | 192 | 194 | 196 | 198 | 200 | 202 | 204 | N of genotypes |
|-----------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|
| EBV Negative | EBV Positive | Random Group | Total | EBV Negative | EBV Positive | Random Group | Total | EBV Negative | EBV Positive | Random Group | Total |
| 275        | 272         | 261 | 808 |      | 50         | 212 | 312 |
| 9          | 7           | 9   | 9   | 9   | 4          | 7   | 7   |
| 2          | 0           | 2   | 2   | 0   | 0          | 0   | 0   |
| 1          | 0           | 1   | 3   | 0   | 0          | 0   | 0   |
| 1          | 2           | 3   | 5   | 0   | 4          | 24  | 28  |
| 0          | 0           | 0   | 0   | 0   | 0          | 0   | 0   |
| 1          | 6           | 7   | 6   | 0   | 1          | 1   | 1   |
| 136        | 147         | 120 | 385 | 57  | 63         | 196 | 318 |
| 33         | 38          | 32  | 98  | 7   | 0          | 27  | 34  |
| 302        | 290         | 282 | 829 | 35  | 28         | 152 | 215 |
| 59         | 47          | 63  | 169 | 1   | 1          | 11  | 13  |
| 10         | 14          | 12  | 36  | 0   | 2          | 13  | 15  |
| 18         | 16          | 17  | 21  | 6   | 7          | 16  | 16  |
tion was allele 196 (0.51) among a series that accounted other 6 alleles (Table 1). Therefore, it seems possible that allele named 197 in Estany et al. (2007) correspond to allele that we indicated with size 196.

**Data analysis**

Difference in allele distribution between the Italian Large White and Italian Duroc pigs was evaluated by t-test and a box plot was used to obtain a graphical representation (Figure 1; SAS release 9.2; SAS Inst. Inc., Cary, NC, USA).

Estimated Breeding Values for ADG (g), BFT (mm), FGR (units), HW (kg) and LC (kg) were calculated by a BLUP-Multiple Trait-Animal Model with different models for each trait. Depending on the trait, models included the fixed effects of sex, batch on trial, inbreeding coefficient of the animal, interaction of sex by age at slaughtering, date of slaughtering and the random effects of litter and animal. Random Residuals (RRs) were calculated for all considered traits using linear fixed models including the same factors used for each trait in the BLUP-Multiple Trait Animal Model (Fontanesi et al., 2010; 2012a). Reasons for using both EBVs and RRs in association analyses has been discussed in details in Fontanesi et al. (2012a).

Association analyses were carried out grouping pigs according to the length of their alleles as already proposed by Estany et al. (2007), e.g. alleles with size ≤198 bp were considered as short alleles, alleles >198 bp were considered as long alleles. In the group of pigs of the selective genotyping experiments, we also considered size ≤196 bp to define the short alleles and size >196 bp to define long alleles as Estany et al. reported significant results using also this way of grouping IGF1 alleles (please note that we used odd allele size as indicated above). Association analyses were carried out in different ways according to the two different experimental approaches and groups of pigs.

For the two random groups of pigs (Italian Large White and Italian Duroc) association between the IGF1 microsatellite and EBVs and RRs was carried out using the procedure GLM of SAS release 9.2. The models included only the fixed effects of individual marker genotypes (three genotype classes: homozygous for any short alleles; heterozygous including any short and any long alleles; homozygous for any long alleles) as all other factors contributing to variability of the investigated traits were considered as random effects.

**Table 2. Association results between the IGF1 microsatellite and carcass, performance, meat production and quality traits in Italian Large White and Italian Duroc pigs obtained in the random groups. Animals were grouped according to the number (0, 1 or 2 copies) of long alleles (≥198 bp).**

| Traits | Genotypic classes | P       |
|--------|-------------------|---------|
|        | (least square means±SD) |         |
|        | 0 | 1 | 2 |       |
| ILW    | EBV ADG, g | 29.040±2.216 | 28.745±2.533 | 37.333±2.323 | 0.034* |
|        | EBV LC, kg | 1.715±0.370 | 1.676±0.180 | 2.274±0.165 | 0.039* |
|        | EBV BFT, mm | -1.664±0.758 | -1.387±0.368 | -2.700±0.334 | 0.029* |
|        | EBV HW, kg | 0.545±1.129 | 0.560±0.058 | 0.663±0.054 | 0.825 |
|        | EBV FGR | -0.125±0.030 | -0.134±0.015 | -0.163±0.013 | 0.264 |
|        | RR ADG, g | -17.645±15.920 | -6.352±7.575 | 2.652±6.948 | 0.428 |
|        | RR LC, kg | -0.560±0.550 | -0.312±0.262 | 0.264±0.240 | 0.170 |
|        | RR BFT, mm | -0.571±1.038 | 0.754±0.494 | -0.664±0.453 | 0.096 |
|        | RR HW, kg | -0.213±0.260 | -0.045±0.124 | 0.062±0.113 | 0.584 |
|        | RR FGR | 0.046±0.066 | 0.026±0.031 | 0.014±0.029 | 0.879 |
|        | pH at 2 h post-mortem | 3.85±0.048 | 5.91±0.024 | 5.94±0.022 | 0.250 |
|        | pH at 24 h post-mortem | 5.6±0.041 | 5.67±0.022 | 5.67±0.020 | 0.453 |
|        | Glycogen, µmol | 44.83±4.609 | 50.72±2.461 | 47.49±2.276 | 0.384 |
|        | Lactate, µmol | 57.19±3.181 | 50.01±1.580 | 55.49±1.441 | 0.443 |
|        | GP, µmol | 102.44±4.648 | 108.77±2.468 | 103.38±2.278 | 0.132 |
|        | Catb, nmol | 1.19±0.047 | 1.13±0.025 | 1.17±0.024 | 0.301 |

| ID     | EBV ADG, g | 26.895±2.794 | 29.194±2.358 | 34.658±4.839 | 0.380 |
|        | EBV LC, kg | 1.635±0.193 | 1.932±0.163 | 2.533±0.334 | 0.064 |
|        | EBV BFT, mm | -1.247±0.372 | -1.781±0.314 | -3.326±0.644 | 0.021* |
|        | EBV FGR | -0.150±0.015 | -0.152±0.013 | -0.181±0.026 | 0.569 |
|        | EBV VIF | -0.071±0.128 | -0.193±0.108 | -0.557±0.222 | 0.168 |
|        | RR ADG, g | 7.287±6.531 | 1.83±5.512 | 3.84±11.311 | 0.816 |
|        | RR LC, kg | 0.129±0.231 | -0.06±0.195 | 0.298±0.400 | 0.661 |
|        | RR BFT, mm | 0.515±0.474 | 0.167±0.49 | -1.37±0.822 | 0.136 |
|        | RR HW, kg | 0.062±0.100 | 0.025±0.080 | 0.083±0.173 | 0.893 |
|        | RR FGR | -0.028±0.027 | 0.005±0.025 | -0.005±0.046 | 0.641 |
|        | RR VIF | 0.027±0.041 | 0.007±0.034 | -0.039±0.072 | 0.588 |

*Number of animals for the different genotypic classes were: ILW, 0=27, 1=106, 2=128; ID, 0=70, 1=108, 2=34 (considering only the random group: dataset used to evaluate VIF); ID, 0=114, 1=153, 2=45 (considering the random group + the pigs of the selective genotyping approach: dataset used to evaluate all traits excluding VIF). IGF1, Italian Large White; ID, Italian Duroc; ADG, average daily gain; LC, lean cuts; BFT, back fat thickness; HW, ham weight; FGR, feed gain ratio; Catb, cathepsin B activity (nmol of 7-amino-4-methylcoumarin released/min/g muscle); EBV, estimated breeding value; RR, random residuals. P<0.05.

Figure 1. Box plot distribution of IGF1 microsatellite alleles in Italian Large White (ILW) and Italian Duroc (ID) genotyped pigs.
already considered in the calculation of EBV or RR. Analysis of association in the Italian Duroc pigs for BFT, ADG, LC, HW and FGR was carried out merging the random group and the animals from the selective genotyping approach based on extreme and divergent VIF EBV. This was possible because these animals were normally distributed for the traits indicated above, which were not used as criterion in the selection of the extreme animals (Fontanesi et al., 2012a). A total of 312 Italian Duroc pigs was used in these analyses. Association study for VIF in the Italian Duroc population was carried out using only the random group of pigs (212 pigs) to avoid biases deriving from the selection of extreme animals for a part of the dataset (Fontanesi et al., 2012a). The procedure MIXED of SAS was used to evaluate association between the IGF1 microsatellite marker and meat quality traits (pH1, pH2, lactate and glycogen content, GP and CatB) in the random group of Italian Large White pigs. The model included the random effect of sire and the fixed effects of date of slaughtering, sex and IGF1 genotypes (three classes defined as indicated above).

Association analyses in the selective genotyping groups were carried out as it follows: i) genotype and allele frequency distributions between the two extreme BFT EBV tails in the Italian Large White population and the two extreme VIF EBV tails in the Italian Duroc population were compared by using Chi-square (or Fisher’s exact test two tailed, when appropriate) and Cochran-Armitage trend tests (alleles were defined as indicated above); ii) In the Italian Large White pigs selected on the basis of extreme BFT EBV, association analyses between the IGF1 microsatellite and ADG, FGR, HW and LC, with both EBVs and RRs were carried out by using the procedure GLM of SAS on a model that included the tail as fixed effect and the genotype effect nested within tail to avoid biases derived by the correlation between BFT EBV and all other parameters.

**Results and discussion**

**Allele frequencies and genotypes**

Nine IGF1 microsatellite alleles, ranging from 182 bp to 204 bp, were identified in Italian Large White pigs. Seven alleles, ranging from 190 bp to 204 bp, were observed among the Italian Duroc genotyped animals (Table 1). The larger number of alleles in the Italian Large White breed gave a larger number of genotypes (n=21) as compared to those observed in Italian Duroc pigs (n=16). These differences could be due, at least in part, to the different number of genotyped animals from the two breeds (808 Italian Large White; 312 Italian Duroc; Table 1). However, first and second most frequent alleles were exchanged across the two breeds: allele 200 was the predominant one in the Italian Large White breed (0.513) and the second most frequent in the Italian Duroc pigs (0.345), whereas allele 196 was the predominant one in Italian Duroc pigs (0.510) and the second one in Italian Large White pigs (0.238). The average genotype was longer in Italian Large White than in Italian Duroc pigs (+0.76 CA repeats; P<0.05) (Figure 1). No deviation from Hardy-Weinberg equilibrium was observed in any breed and breed x group combination.

Two other studies reported information on IGF1 microsatellite allele distribution in different pig populations. In particular, Estany et al. (2007) identified a higher frequency of allele 196 (indicated with size 197 in their work) in Duroc pigs, confirming results we obtained in the Italian Duroc breed. In the same study, only 5 alleles (ranging from 190 to 204 bp) were identified in the investigated Duroc population (Estany et al., 2007). Allele 198 (indicated with size 199) was the predominant in Landrace pigs (Estany et al., 2007). Assis de Faria et al. (2009) used this microsatellite in a QTL mapping experiment involving a Piau boars x commercial sows reference population. Allele size in the parental animals ranged from 194 to 208 bp, the largest size so far reported for this microsatellite, not observed in the two investigated Italian pig breeds.

**Association analyses in Italian Large White and Italian Duroc pigs**

Association analysis in the random group of Italian Large White pigs carried out using the GLM procedure and grouping genotypes according to allele sizes (≤198 bp = short alleles; >198 bp = long alleles) into three classes (homozygous for any short alleles; heterozygous including any short and any long alleles; homozygous for any long alleles) showed associations between the IGF1 microsatellite and ADG EBV, LC EBV, and BFT EBV (P<0.05). Homozygous genotypes for longer alleles showed higher ADG, higher LC and lower BFT as compared to both heterozygous or homozygous genotypes for the shorter alleles (Table 2). These results were partially confirmed by the analysis of BFT RR where the association was just below the suggestive significant threshold (P=0.096). However, least square means were not in the same direction as for BFT EBV (Table 2).

Association analysis in the random group of Italian Duroc pigs carried out using the same procedure showed a significant result for BFT EBV (P<0.05). Lower BFT was observed in the homozygous genotypes for longer alleles, as reported in the Italian Large White pigs. Suggestive association was observed for LC EBV (P<0.10), whereas all other traits were not significant (Table 2). Only BFT RR was close to this threshold (P=0.13). No other way of grouping alleles and genotypes based on their size or using other statistical procedures gave any significant association (data not shown).

Genotyping results from the Italian Large White pigs from the selective genotyping design were the following:

- among the animals from the positive BFT EBV tail: i) 23 and 34 pigs were homozygous for alleles ≤196 bp or homozygous for alleles ≤198 bp; ii) 98 and 112 animals carried at least an allele with size ≤196 bp or ≤198 bp; iii) and 129 and 105 pigs carried only alleles with size >196 bp or >198 bp respectively;
- among the animals of the negative tail: i) 21 and 29 pigs carried at least 2 alleles ≤196 bp or two alleles ≤198 bp; ii) 90 and 106 pigs were those with just one allele with size ≤196 bp or ≤198 bp; 142 and 118 pigs did not carry any allele with size ≤196 bp or ≤198 bp.

Considering these data, allele frequencies differences between the two extreme tails for BFT EBV were not significant (for allele frequency distribution: P=0.595, considering size ≤196 bp; P=0.519, considering size ≤198 bp). The same not significant results were obtained considering genotype frequencies (data not shown). Thus, these results did not confirm association between the IGF1 microsatellite and BFT observed in the random group of Italian Large White pigs. Association analysis for other traits (ADG, LC, HW and FGR, using both EBV and RR) carried out in this group of pigs including the tail as fixed factor in the GLM procedure did not show any significant result (data not shown).

Genotyping results obtained in the Italian Duroc pigs from the selective genotyping approach were as follows:

- among the animals of the positive VIF EBV tail: i) 23 were homozygous for alleles ≤196 bp (the same number of the animals homozygous for alleles ≤198 bp); ii) 23 animals carried at least an allele with size ≤196 bp (the same if we considered ≤198 bp); iii) and 4 pigs carried only alleles with size >198 bp;
- among the animals of the negative VIF EBV tail: i) 21 and 26 pigs carried at least 2 alle-
les ≤196 bp or two alleles ≤198 bp; ii) 21 and 22 pigs were those with just one allele with size ≤196 bp or ≤198 bp; iii) 11 and 7 pigs did not carry any allele with size ≤196 bp or ≤198 bp.

The selective genotyping approach in Italian Duroc pigs based on VIF EBV showed that this trait is not associated with any IGF1 microsatellite allele or genotype (P>0.10), confirming results obtained in the Italian Duroc random group. The results obtained in the two Italian breeds support only partially results shown by Estany et al. (2007). These authors reported association between the IGF1 microsatellite and BFT and lean content in a Spanish population of Duroc barrows in the same direction as we identified in the Italian Duroc pigs, e.g. longer alleles are associated with lower BFT and higher carcass lean content. Effects on BFT were not convincingly confirmed in Italian Large White pigs, as the two experimental designs we used did not give the same evidences. Estany et al. (2007) reported also association with early growth rate and weight of hams in Landrace boars that we could not completely confirm with the data obtained in the Italian breeds. Those results probably depended on an effect on circulating IGF1 content in growing pigs, that in turn, was correlated to performance and carcass traits (Estany et al., 2007). Unfortunately we could not analyse the level of circulating IGF1 in the investigated Italian heavy pigs and, for this reason, we could not evaluate if this microsatellite marker would have an effect on this parameter or not. The lack of consistent effects on carcass and meat production traits we observed in Italian Large White and Italian Duroc pigs might be due to the different genetic background of these breeds. Also, it could depend on the absence of segregating QTL alleles in the SSC5 region in which the IGF1 microsatellite is mapped, or on effects which the implemented experimental designs could not detect (derived by the incomplete power of the different experiments). Studies of Casas-Carrillo et al. (1997) and Assis de Faria et al. (2009) based on microsatellite analyses (including the IGF1 short tandem repeat marker) indicated that this chromosome region harbours QTL for growth and carcass traits. However, previous genome wide association studies we conducted on Italian Large White pigs by using single nucleotide polymorphisms in a few hundred candidate genes and the Illumina PorcineSNP60 BeadChip tool did not show any marker significantly associated with BFT in the region of SSC5 located around IGF1 (Fontanesi et al., 2012b, 2012c). These results would indicate that no important segregating SSC5QTL, at least for BFT, might be present in this breed.

This study highlights difficulties in using a microsatellite in association studies in out-bred populations. Grouping alleles according to the size might take into account a stepwise mutation model of microsatellite markers. However, homoplasy would be a problem in defining a common origin of long and short alleles. A large literature has been published on the problems related to the high mutation rate and mutation models of short tandem repeats that may affect interpretations of the results for different purposes (Bhargava and Fuentes, 2010), therefore obtained data should be critically evaluated and compared with results obtained in other studies.

Conclusions

To our knowledge, the present study is the first to investigate associations between the IGF1 microsatellite and production traits in Italian heavy pigs. As this marker includes several alleles that could be difficult to consider separately in association studies (due to the large number of genotypes) we followed the approach proposed by Estany et al. (2007), who grouped IGF1 alleles into two classes, long and short alleles. This approach could have a biological meaning considering the potential regulatory role of repeated sequences as also reported for the microsatellite located in the promoter region of the human IGF1 gene (Rosen et al., 1998; Vaessen et al., 2002). However, a direct effect of the repeated region on intron 1 of the porcine IGF1 gene still needs to be demonstrated.

Our study suggested that variability in the IGF1 microsatellite might be associated with BFT in finishing Italian Duroc and weakly associated in Italian Large White, even if such association is doubtful due to the inconsistent results obtained in the selective genotyping approach. Additional studies should evaluate the effects of this polymorphic microsatellite on performance traits at early ages. Effects of this polymorphism on circulating IGF1 content, that was reported to be correlated with several production traits in growing pigs (Lamberson et al., 1995; Cameron et al., 2003) should also be investigated. In addition, the implementation of a selective genotyping approach on other traits, e.g. ADG, could be useful to further evaluate if the IGF1 microsatellite affects growth efficiency in Italian heavy pigs.

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