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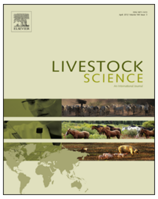

Association study between single nucleotide polymorphisms in candidate genes and reproduction traits in Italian Large White sows

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ABSTRACT

In this study we evaluated the effects of candidate single nucleotide polymorphisms (SNPs) on reproduction traits of Italian Large White (ITLW) purebred sows at first parity. We genotyped DNA samples extracted from hair roots of 1,548 sows distributed across six farms located in Northern Italy. A total of 21 SNPs in 20 genes, selected from literature, were genotyped. Seventeen SNPs showed minor allele frequencies >0.05 in the ITLW breed. Association analyses were performed with the following traits: number of piglets born alive (NBA1), number of stillborn piglets (NSB1), total number born (TNB1), NBA1 estimated breeding values (EBVs) and NBA1 random residuals (RRs). SNPs in *BMPR1B*, *FUT1*, *GPX5*, *RBP4* and *TGFBR1* genes showed significant association (P nominal <0.003) with NBA1 EBVs. Additional three markers (*EPOR*, *GDF9*:c.1806T > C and *STAT5B*) presented suggestive effects (P nominal <0.03) on NBA1 EBVs. The *BMPR1B* SNP showed a trend (P nominal from 0.01 to 0.05) on NBA1, NBA1 RRs and TNB1. This gene could be a promising candidate for additional investigations aiming to confirm evidences reported in this study.

1. Introduction

Reproductive efficiency of sows (measured as piglets weaned per sow per year) is an important factor affecting pig farming productivity and profitability. Reproductive efficiency of sows is determined by the number of piglets born alive (NBA), survival at weaning and the number of farrowings per sow per year. NBA is a complex phenotype influenced by numerous parameters including ovulation rate (OR), number of embryos, embryonic and fetal survival, and uterine capacity (UC) (Vallet et al., 2010). Most of the traits determining litter size variability (i.e., OR and UC) are difficult, time-consuming and expensive to measure on a large number of sows, whereas NBA is easily recorded in pig farms. Estimated Breeding Values for NBA at first parity (NBA1) have been routinely calculated in the Italian Large White (ITLW) breed and used to improve the number of viable offspring since the late 1990s. Other co-selected traits in this heavy pig breed are growth rate, feed conversion efficiency, lean tissue deposition (lean cuts), fatness (back-fat thickness), ham weight and ham salting losses. At present, a specific goal of selection for the ITLW breed is to maintain an appropriate back-fat thickness, as the production of high quality dry-cured hams needs green thighs with at least 2 cm of fat coverage (Bosi and Russo, 2004). In comparison with performance and carcass and meat production traits, genetic progress for NBA as well as other reproduction traits (e.g. number of stillborns piglets, NSB; and total number of piglets born, TNB) is slower, because these traits are sex-limited and have low heritability (Bidanel, 2011).

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Several studies have been carried out to identify markers associated with reproduction traits in different pig breeds and populations in order to use them in marker assisted selection (MAS) programs (Bidanel, 2011; Distl, 2007; Rempel et al., 2010; Sironen et al., 2010; Spötter and Distl, 2006). The first marker resulting to be associated with litter size in pigs was the *ESR1-Pvu*II restriction fragment length polymorphism (RFLP; Rothschild et al., 1994). However, the effects of this polymorphism on litter size were not consistent across populations (Distl, 2007). The *ESR1-Pvu*II RFLP and a single nucleotide polymorphism (SNP) in the *ESR2* gene were recently tested for association with litter size in the ITLW breed (Dall′Olio et al., 2011). The obtained results did not confirm their putative effects on prolificacy, as previously reported in other populations. Because of relevant potential impact of DNA markers, it is important to verify in the target population claimed effects of markers before their implementation in actual breeding plans.

The objective of this study was to investigate 21 candidate SNPs for reproduction traits selected from literature and to evaluate their association with litter size in a large population of first parity ITLW sows.

2. Materials and methods

2.1. Animals and phenotypes

Hair root samples were collected from 1803 ITLW sows registered in the Herd Book held by the National Association of Pig Breeders (Associazione Nazionale Allevatori Suini, ANAS, Italy; http://www.anas.it). These sows were raised in six farms (referred to as farm 1 to farm 6, Table 1) having at least 120 sows each, located in Emilia Romagna and Lombardia regions (North of Italy). For each sow NBA1 and NSB (including mummified fetuses at birth) at first parity (NSB1), pedigree and date of birth were recorded (December, 2010). Then, total number of piglets born at first parity (TNB1) was computed as the sum of NBA1 and NSB1. After data editing (e.g. presence of contemporary sows, age at first farrowing between 280 and 490 d), records of 1548 sows (85.9% of the initial collected samples) were used for all subsequent analyses (Table 1). Means of NBA1 and TNB1 in this dataset were 9.77 ± 2.33 and 10.34 ± 2.34, respectively. NBA1 records were used to calculate NBA1 EBVs using a BLUP-single trait-animal model including environmental effects of herd–year–month at birth (contemporary groups), age at first farrowing, inbreeding coefficient of sows and mating type (artificial insemination or natural service).

In addition, random residuals (RRs) for NBA1 data were calculated by using a linear fixed model including the same environmental factors used to calculate NBA1 EBVs. RRs include genetic factors, permanent environmental factors, unknown environmental factors and measurement errors (Fontanesi et al., 2010a). Both NBA1 EBVs and NBA1 RRs were expressed in standard deviation units around the rolling average of data of sows farrowing since 1990. NBA1 EBVs and NBA1 RR means were +0.69 ± 1.23 (range from −3.25 to +5.39) and 0.00 ± 2.27 (range from −7.20 to +8.54), respectively (Table 1).

Additional hair root samples were collected from Italian Duroc (ITDU, $n=91$) and Italian Landrace (ITLA, $n=50$) pigs for allele frequency evaluation in different breeds.

2.2. Genotypes

Genomic DNA was extracted from hair roots using a standard protocol with proteinase K. Twenty-one candidate SNPs in 20 genes (*ADRB2*, *AFP*, *BMPR1B*, *CTSL*, *CYP21A2*, *EDNRA*, *EPOR*, *FUT1*, *GDF9*, *GNRHR*, *GPX5*, *IGF1R*, *LEPR*, *MAN2B2*, *PIT1*, *PNAS4*, *RBP4*, *SCG2*, *STAT5B* and *TGFBR1*) were selected

Table 1.
Number of samples and descriptive statistics[a] of litter size traits of the first litter/farrowing farm.

Farms	No. of sows sampled	No. of sows after data editing	NBA1[b]			NSB1[c]			TNB1[d]			NBA1 EBV[e]			NBA1 RR[f]		
			Mean	SD	Range	Mean	SD	Range	Mean	SD	Range	Mean	SD	Range	Mean	SD	Range
1	691	674	9.60	2.23	3;16	0.58	0.98	0;6	10.18	2.20	3;17	+0.453	1.243	−3.247; +4.799	0.000	2.218	−6.937; +6.497
2	427	307	10.02	2.13	3;16	0.67	0.99	0;6	10.69	2.33	3;17	+1.091	0.855	−1.040; +4.405	0.000	2.103	−7.199; +5.566
3	102	92	9.71	2.85	3;16	0.96	1.47	0;7	10.66	2.66	3;16	+0.882	1.362	−1.916; +5.395	0.000	2.736	−7.109; +4.852
4	323	228	9.55	2.59	3;18	0.22	0.79	0;7	9.77	2.53	3;18	+0.265	1.403	−2.961; +4.112	0.000	2.575	−7.075; +8.538
5	126	123	9.97	2.43	3;15	0.90	1.46	0;7	10.87	2.49	3;16	+0.951	0.904	−0.939; +4.337	0.000	2.258	−6.435; +4.681
6	134	124	10.30	2.12	3;16	0.33	0.67	0;3	10.63	2.06	3;16	+1.319	1.202	−0.768; +4.469	0.000	2.049	−7.054; +4.869
All	1803	1548	9.77	2.33	3;18	0.57	1.04	0;7	10.34	2.34	3;18	+0.686	1.232	−3.247; +5.395	0.000	2.272	−7.200; +8.538

[a] Mean, standard deviation (SD) and range (minimum;maximum values).

[b] NBA1 = number of piglets born alive at first parity.

[c] NSB1 = number of stillborn piglets at first parity.

[d] TNB1 = total number of piglets born at first parity.

[e] NBA1 EBVs = estimated breeding values for number of piglets born alive at first parity, expressed in standard deviation units around the rolling average of data of sows farrowing since 1990.

[f] NBA1 RRs = random residuals for number of piglets born alive at first parity, expressed in standard deviation units around the rolling average of data of sows farrowing since 1990.