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1 **Genome-wide analysis of bull sperm quality and fertility traits**

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12

13 Running title: GWAS of bull fertility traits

14

15 **Keywords:** high-density panel, genome-wide association study, chromatin status,

16

17 **Abstract**

18 Because the priority of AI industry is to identify sub fertile bulls, a predictive model that allowed for
19 the prediction of 91% bulls of low fertility was implemented based on seminological (motility)
20 parameters and DNA status assessed both as DNA fragmentation index (DFI) and by TUNEL assay
21 using sperm of 105 Holstein Friesian bulls (4 batches per bull) selected based on *in vivo* estimated
22 relative conception rates (ERCR). Thereafter, sperm quality and male fertility traits of bulls were
23 explored by GWAS using a high density (777K) Illumina chip.

24 After data editing, 85 bulls and 591,988 SNPs were retained for GWAS. Out of 12 SNPs with false
25 discovery rate < 0.2, four SNPs located on BTA28 and BTA18 were significantly associated (LD
26 adjusted Bonferroni < 0.05) with the non-compensatory sperm parameters DFI and TUNEL. Other
27 SNPs of interest for potential association with TUNEL were found on BTA3, in the same
28 chromosome where associations with non-compensatory *in vivo* bull fertility were already reported.
29 Further suggestive SNPs for sperm membrane integrity were located on BTA28, the chromosome
30 where QTL studies previously reported associations with sperm quality traits. Suggestive SNPs for
31 ERCR were found on BTA18 in the vicinity of a site already associated with *in vivo* bull fertility.
32 Additional SNPs associated with ERCR and sperm kinetic parameters were also identified. In contrast
33 to other, but very few GWAS on fertility traits in bovine spermatozoa, which reported significant
34 SNPs located on BTX, we have not identified SNPs of interest in this sexual chromosome.

35

36 **Introduction**

37

38 Numerous authors investigating the genetic basis of fertility suggest that genome-wide association
39 studies (GWAS) are more effective in detecting causal variants associated to complex fertility traits
40 when compared to traditional quantitative trait loci (QTL) mapping (Zhang et al. 2012). However,
41 only few GWAS have focused on bull fertility (Fortes et al. 2013). Although the accurate estimate of
42 fertility allows to identify the critical number of viable sperm required to obtain adequate pregnancy

43 rates, there are some uncompensable characteristics, such as the state of nuclear chromatin, which
44 cannot be overcome by simply increasing the sperm number (Evenson and Wixon 2006). Because
45 the priority of AI industry is to identify hypofertile bulls, which require more sperm in the dose to
46 reach maximum fertility, a predictive model for the low level of fertility as estimated *in vivo* was
47 developed in the present work based on standard seminological and DNA status assessments.
48 Furthermore, sperm quality and male fertility traits were explored by GWAS using a high density
49 Illumina chip.
50
51 **Materials and methods**
52
53 **Estimate of *in vivo* bull fertility**
54 Four batches of commercial frozen sperm (years 2002-2014; 13 AI centres) of 105 Holstein Friesian
55 bulls were selected according to their fertility, based on 56-day non-return to oestrus adjusted for
56 environmental effects, calculated as the random effect of service sire (estimated relative conception
57 rates, ERCR; 90% reliability) using the model described in Puglisi et al. (2012). Fifteen bulls were of
58 low fertility (ERCR < -2.46; mean = -3.8 ± 0.8) and 90 bulls were of middle-high fertility (ERCR >
59 -2.46; mean = +0.4 ± 1.7), based on the threshold fixed at 3 standard deviations below the mean
60 ERCR calculated on a dataset of 4989 bulls (mean ERCR = 0.0005 ± 0.82).
61
62 **Sperm analysis**
63 Sperm quality parameters of the 105 bulls were assessed as follows: membrane integrity (MI) was
64 evaluated by the NucleoCounter SP100 (ChemoMetec A/S, Allerød, Denmark); motility (total, TM;
65 progressive, PM; average path velocity, VAP) was evaluated by CASA System-HTM IVOS v.12
66 (Hamilton Thorne); DNA status, assessed both as DNA fragmentation index (DFI) implemented in
67 the sperm chromatin structure assay (SCSA©) and by the TUNEL assay, was determined using the

flow cytometer Guava EasyCyte Plus® (IMV Technologies, l'Aigle, France) as described (Evenson and Wixon 2006).

Genomic analysis

Sperm genomic DNA of bulls was genotyped with the Illumina BovineHD chip (777K) (Illumina, San Diego, CA). Both SNPs and bulls with call rate < 95% and < 97.5%, respectively, were discharged. SNPs were removed if the Minor Allele Frequency (MAF) was lower than 0.02, or if they statistically deviated from the Hardy Weimberg equilibrium ($p < 0.0001$).

Statistical analysis

Statistical analysis was implemented by R procedures (R Core Team, 2012).

At first, seminological data were evaluated by general linear mixed model (GLMM) using bull and batch as random effects and semen production centres as fixed effect. Thereafter, in order to implement the model for the identification of the bulls of low fertility, the variable LowFERT was defined as follows: LowFERT = 1 for ERCR < -2.46 and LowFERT = 0 for ERCR > -2.46.

A first logistic model was implemented with the continuous seminal variables and the discrete variable BATCH, as follows:

$$LowFERT = \beta 0 + \beta 1\ TM + \beta 2\ PM + \beta 3\ VAP + \beta 4\ MI + \beta 5\ DFI + \beta 6\ TUNEL + BATCHi + e$$

A second model was, then, implemented including only the effects identified in the first model as significant, as follows:

$$LowFERT = \beta 0 + \beta 1\ PM + \beta 2\ MI + \beta 3\ DFI + \beta 4\ TUNEL + e$$

Results were validated by bootstrapping with nonparametric resampling (1000 trials) using package “boot”.

For GWAS, sperm parameters were pre-corrected for the effect of production batch. The GWAS was carried out with the Grammar genomic control (GC)approach, that account for genetic substructure

94 in the population (Aulchenko et al. 2007), implemented in the GenABLE R package (*polygenic* and
95 *grammar* functions).
96 At first, data were analysed with the following linear mixed model:

97 $$y_{jk} = AI_cent_j + a_k + e_{jk}$$

98 where y_{jk} is the sperm parameter for the k-th bull; AI_cent is the fixed effect of the j-th AI centre; a_k
99 is the random polygenic additive effect of the k-th bull~N(0, $\mathbf{G}\sigma^2_a$); e_{jk} is the random residual~N(0,
100 $I\sigma^2_e$), where G and I are the genetic (co)variance and identity matrices, respectively. The genetic
101 (co)variance between animals was structured using the genomic relationship matrix. Residual of the
102 model were, then, analysed with a linear model that included the fixed effect of the SNP genotype.
103 Given that Bonferroni is the simplest and more conservative correction for multiple testing assuming
104 independence of performed test, and that its application largely ignores the correlation between
105 markers due to linkage disequibrium, the genome wide significance was assessed by LD adjusted
106 Bonferroni (Sun et al. 2014; Wu et al. 2014). To discover SNPs potentially associated to seminal
107 parameters the threshold was fixed at $8.06*10^{-7}$ (0.05/N), where N is the number of haplotype blocks
108 estimated with –blocks flag in plink (N = 62,062). False discovery rate (FDR) and q-values were also
109 calculated: SNPs with FDR < 0.20 are discussed.
110

111 **Results and discussion**

112 Results of seminological and DNA status assessments are presented in Table 1. Statistical analysis
113 shown high variability among bulls for all the parameters, and a moderate variability among batches
114 for TM, PM and MI (Table 2). Differently, for DFI and TUNEL a negligible variability was reported
115 among sperm batches, thus confirming these parameters as intrinsic-not compensable characteristics
116 of individual bulls (Evenson 1999). The effect of the semen production centre was not significant.
117 The statistical model implemented for the identification of hypofertile bulls allowed for the prediction
118 of 91% (n = 14) bulls of low fertility and data was further validated by bootstrapping (89-91%; 95%
119 CI).

120 For GWAS, 85 bulls and 591,988 SNPs were retained, while 130,462 SNPs were discarded because
121 did not reach the MAF threshold. Table 3 lists the top 12 significant SNPs with FDR < 20%, among
122 which, four SNPs located on BTA28 and BTA18 were also significantly associated (Bonferroni-LD)
123 with DFI and TUNEL. Further SNPs for DFI were found on BTA1-4-16-23-28. With respect to
124 BTA28, in this chromosome QTL were previously detected for several semen quality traits (Valour
125 et al. 2015). The complete list of suggestive SNPs for seminological traits and ERCR is presented as
126 supplemental Table 4. Of interest, suggestive SNPs (p-value $< 1.61*10^{-5}= 1/62,062$; Sun et al. 2014)
127 for ERCR were found on BTA18 in the vicinity of the site were Peñagaricano et al. (2012) found
128 association with *in vivo* bull fertility. Other SNPs, ranked by their values of nominal significance,
129 were found on BTA3 for TUNEL, in the chromosome where associations with noncompensatory bull
130 fertility were reported (Blaschek et al. 2011). Similarly, GWAS was successfully used for identifying
131 candidate genes associated with several sperm traits in bulls (Fortes et al. 2013; Hering et al. 2014).
132 In contrast to other studies reporting significant SNPs located on BTX (Suchocki and Szyda 2015),
133 our work has not identified SNPs of interest on this sexual chromosome.
134

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139

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188 Table 1

189 Sperm quality parameters of 105 bulls.

Parameter	Low fertility		Medium-high fertility	
	Mean ± SD	Range	Mean ± SD	Range
Total Motility (%)	46.2 (14.8)[a]	11.0-72.0	53.2 (15.5)[b]	8.0-88.0
Progressive Motility (%)	34.9 (13.7)[a]	6.0-63.0	42.2 (13.8)[b]	6.0-70.0
Average Path Velocity (µm/sec)	90.5 (14.4)	59.0-120	92.5 (16.4)	11.0-138.0
Membrane Integrity (%)	50.0 (11.2)	25.0-71	52.0 (15.2)	0.0-89.0
DNA fragmentation Index (%)	9.8 (4.2)[a]	3.0-25.0	5.8 (5.5)[b]	1.0-96.0
TUNEL (%)	8.11 (4.4)[a]	2.0-22.0	5.6 (3.3)[b]	1.0-32

190 [a,b] Different superscripts within rows indicate statistical difference at the ANOVA test ($p < 0.001$)

191

192 Table 2

193 Random (bull and batch) and fixed (production centre) effects by general linear mixed model.

Parameter	Variance		Centre
	Bull	Batch	
Total Motility (%)	64.88 (27.49%)	20 (8.47%)	< 0.0001
Progressive Motility (%)	70.76 (37.69%)	15.46 (8.24%)	< 0.0001
Average Path Velocity (µm/sec)	96 (44.20%)	8 (3.50%)	< 0.0001
Membrane Integrity (%)	89.24 (46.05%)	19.4 (10.01%)	< 0.0001
DNA fragmentation Index (%)	11 (35.62%)	0.30 (1.00%)	0.0571
TUNEL (%)	9 (20.91%)	0.38 (0.89%)	< 0.0001

194

195 Table 3

196 Top significant SNPs from GWAS with false discovery rate < 0.2.

Trait	SNP	BTA	bp	p-Bonf-LD	q-value
DFI	BovineHD2800009025	28	33,677,489	0.001	0.006
DFI	BovineHD2800009027	28	33,682,118	0.008	0.020
TUNEL	BovineHD0800005232	18	16,773,834	0.016	0.149
DFI	BovineHD2800008609	28	32,601,290	0.026	0.050
DFI	BovineHD2800006900	28	26,638,772	0.100	0.135
DFI	BovineHD1600001050	16	3,700,646	0.191	0.139
DFI	ARS-BFGL-NGS-117941	16	4,095,536	0.254	0.150
DFI	BovineHD2600011042	26	40,124,425	0.327	0.150
DFI	BovineHD0400022506	4	81,577,828	0.383	0.150
DFI	BovineHD1600000982	16	3,486,636	0.428	0.150
DFI	BovineHD2300001056	23	4,581,363	0.483	0.157
DFI	BovineHD0100016322	1	57,604,927	0.712	0.192

197

198 DFI, DNA fragmentation index; p-Bonf-LD = nominal p-value/62,062.

199