

SNP g.1007A>G within the Porcine DNAL4 Gene Affects Sperm Motility Traits

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Abstract : A requirement for sperm motility is a morphologically intact flagellum with a central axoneme. The flagellar beating is caused by the varying activation and inactivation of dynein molecules which are located in the axoneme. DNAL4 (dynein, axonemal, light chain 4) is regarded as a possible functional candidate gene encoding a small subunit of the dyneins. In the present study, 5814bp of the porcine DNAL4 (GenBank Acc. No. AM284696.1, 6097 bp, 4 exons) were comparatively sequenced using three boars with a high motility (>68%) and three with a low motility (<60%). Primers were self-designed except for those covering exons 1, 2 and 3. Prior to sequencing, the PCR products were purified. Sequencing was performed with an ABI PRISM 3100 Genetic Analyzer using the BigDye™ Terminator v3.1 Cycle Sequencing Reaction Kit. Finally, 23 SNPs were described and genotyped for 82 AI boars representing the breeds Piétrain, German Large White and German Landrace. The genotypes were used to assess possible associations with standard spermatological parameters (ejaculate volume, density, and sperm motility (undiluted (Motud), 24h (Mot1) and 48h (Mot2) after semen collection) that were regularly recorded on the AI station. The analysis included a total of 8,833 spermatological data sets which ranged from 2 to 295 sets per boar in five years. Only SNP g.1007A>G had a significant effect. Finally, the gene substitution effect using the following statistical model was calculated: $Y_{ijk} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + b_1 S_{ijk} + b_2 A_{ijk} + b_3 T_{ijk} + b_4 V_{ijk} + b_5 (\alpha * A)_{ijk} + b_6 (\beta * A)_{ijk} + b_7 (A * T)_{ijk} + U_{ijk} + e_{ijk}$ where Y_{ijk} is the semen characteristics, μ is the general mean, α is the main effect of breed, β is the main effect of season, S is the effect of SNP (g.1007A > G), A is the effect of age at semen collection, V is the effect of diluter, $\alpha\beta$, $\alpha * A$, $\beta * A$, $A * T$ are interactions between the fixed effects, b_1 - b_7 are regression coefficients between y and the respective covariate, U is the random effect of repeated observation on animal and e is the random error. The results from the single marker regression analysis revealed highly significant effects ($p < 0.0001$) of SNP g.1007A > G on Mot1 resp. on Mot2, resulting in a marked reduction by 11.4% resp. 15.4%. Furthermore a loss of Motud by 4.6% was detected ($p < 0.0178$). Considering the SNP g.1007A > G as a main factor (dominant-recessive model), significant differences between genotypes AA and AG as well as AA and GG for Mot1 and Mot2 exist. For Motud there was a significant difference between AA and GG.

Keywords : association, DNAL4, porcine, sperm traits

Conference Title : ICAFAS 2015 : International Conference on Agricultural, Food and Animal Sciences

Conference Location : Zurich, Switzerland

Conference Dates : July 29-30, 2015