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Lecture conference of the DGfZ and GfT on September 25/26, 2025 in Rostock

Sample title

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1 Introduction

Following the detection of QTL for performance traits, functional traits, including calving traits, have become the focus of scientific research in recent years. These are primarily characterized by low heritabilities and a low influence on the overall breeding value. Furthermore, both the direct effect of the calf and the effect of the dam must be taken into account for these traits. As direct and maternal effects are negatively correlated, this causes problems for breeding using conventional breeding methods. With the knowledge of QTL, these traits could be specifically processed using marker-assisted selection and integrated into an existing breeding program. In recent years, QTL have been mapped for the birth history of cattle in almost all Holstein populations (e.g. Kühn et al. 2003, Schnabel et al. 2005, Thomasen et al. 2008). In a previous study (Seidenspinner et al. 2007) it was shown that the distribution of breeding values by parity for calving traits is of great importance for the detection of QTL. In further studies, the QTL for the course of birth on BTA10 by Kühn et al. (2003) were confirmed and further families segregating at the QTL were identified. The aim of this work was to minimize the confidence interval for a possible QTL on BTA10 for the course of birth in cattle and to derive positional candidate genes. Based on this, comparative sequencing of the candidate genes is planned to identify polymorphisms that will subsequently be used for association studies.

2 Material and methods

The study was based on a granddaughter design (GDD) consisting of 18 paternal half-sib families with a maximum of 1072 sons, whereby the number of sons varied. Due to the usual mating of test bulls to multi-calf cows in Germany, the data set for the direct effects in the first parity had to be reduced to 359 sons. Furthermore, the entire data set could not be used for the third parity, as not enough information was available for all bulls. Table 1 provides a more detailed overview.

Table 1: Results of the QTL analyses in the callipygeal region of the pig.

Feature	F-value$^{(1)}$ $^{())}$	LOD	Additive $^{(2)\,())}$	Dominance$^{(2)}$ $^{())}$	Imprinting$^{(2)}$ $^{())}$
Bacon thickness (comb)	2,31	1,504	0,029±0,016	-0,031±0,023	0,027±0,019
Fat thickness (center of back)	2,86	1,857	0,033 ±0,014	-0,031±0,020	0,009±0,017
Bacon thickness (loin)	1,07	0,694	-0,020±0,015	0,019±0,024	0,017±0,019
Side fat thickness	4,87**	3,163	0,072±0,022	-0,032±0,032	0,044±0,027
Bacon measure FOM	3,81*	2,475	0,420±0,135	-0,109±0,201	0,199±0,166

$^{(1)\,())}$*: p<0.05, **:p<0.01; $^{(2)\,())}$Effect estimate ± standard error.

For fine mapping, 26 microsatellite markers were typed on BTA10. The markers covered 53 cM of chromosome 10, which corresponds to an average marker interval of 2.04 cM. All markers were taken from the map of Ihara et al. (2004) and ranked according to their genomic position. Univariate estimated breeding values of the traits stillbirths maternal first (TGm1), second (TGm2) and third (TGm3) parity, as well as calving ease maternal first (KVm1), second (KVm2) and third (KVm3) parity were used as phenotypes. Stillbirths first (TGp1) and further parities (TGp2) or calving history first (KVp1) and further parities (KVp2) were included in the analysis as direct traits. The estimation was carried out with a sire model in which no further parentage information was used. The fine mapping was carried out in cooperation with the FBN in Dummerstorf using the software TIGER (Baes and Reinsch 2008). This software can perform combined linkage equilibrium and linkage disequilibrium analyses. The test variable for each QTL position is determined using residual maximum likelihood.

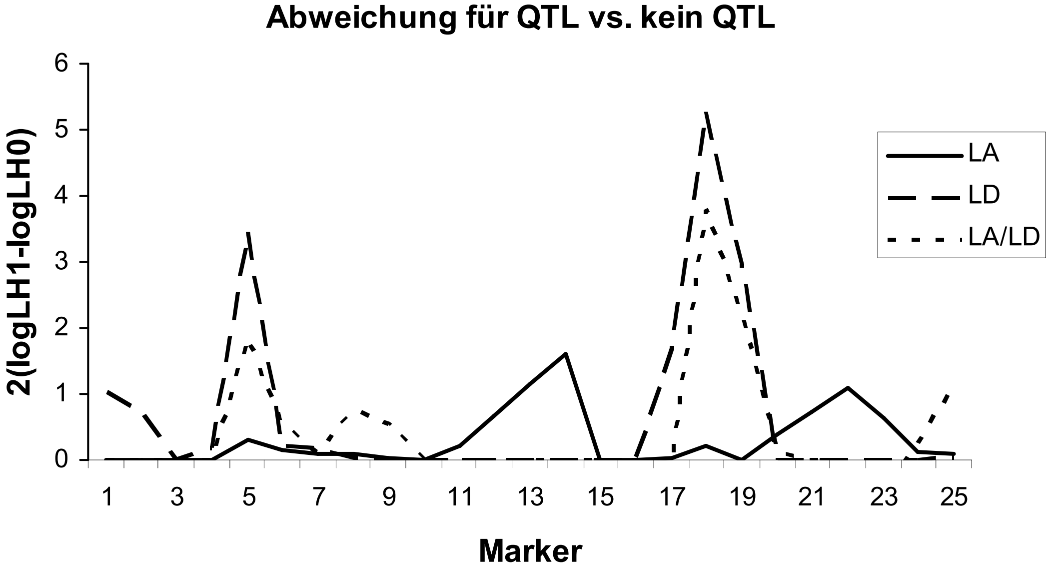

Figure 1: Deviation of logL for QTL vs. no QTL for the characteristic TGm1.

3 Results and discussion

Of the 6860 genotypes to be recorded, 6833 (99.6 %) were successfully identified. The number of polymorphic loci was 18 to 20 per breed; the number of alleles observed per locus was between 5 and 19, and the mean allele numbers varied between 3.9 (Meishan) and 9.3 (Meo). Overall, the autochthonous Vietnamese pig breeds showed almost double the mean allele number compared to the breeds of European origin. Similar ratios have already been described for the comparison of European and Chinese breeds (Li et al. 2000). It is possible that the great diversity in the indigenous breeds is due to the absence of breeding influences. Deviations from the Hardy-Weinberg equilibrium were not observed beyond what would be expected by chance. Values between 0.062 and 0.109 were observed for the inbreeding coefficient $F_{(IS)}$ (Wright 1951) in the Muong Khuong, Co, Meo and Tap Na breeds. The F_{ST}values for the grouped Vietnamese, exotic and European breeds were between 0.019 and 0.138, which according to Wright (1978) indicates a medium genetic differentiation. The smallest genetic distances were observed between the exotic breeds Landrace and Yorkshire in Vietnam. The dendrogram showed one cluster each for the Vietnamese breeds and the breeds of European origin. However, clear splits were observed within both clusters. The Vietnamese breeds were less homogeneous and the genetic distances reflected the respective spatial distances of the origins. The wild boar was clustered together with the European breeds, while the assignment of Meishan to the cluster of Vietnamese breeds showed only a low degree of confidence via bootstrapping. The results of this study contribute to the characterization of Vietnamese autochthonous pig breeds and clearly indicate that these breeds represent an important reservoir of porcine genetic resources.

4 Literature

FAO (2000): World watch list for domestic animal diversity, 3rd ed., Rome: Food andAgriculture Organization of the United Nations.

Felsenstein, J. (1995). PHYLIP (Version 3.57c): Department of Genetics, University of Washington, Seattle: distributed by the author.

Li, K./B. Fan/S. Zhao/Z. Peng/K. Li/Y. Chen/C. Moran/B. Fan/S. Zhao/Z. Peng (2000): Analysis of diversity and genetic relationships between four Chinese indigenous pig breeds and one Australian commercial pig breed, in: *Anim. Genet*, vol. 31, pp. 322-325, https://doi.org/10.1046/j.1365-2052.2000.00649.x.

Nei, M. (1972): Genetic distance between populations, in: *Am. Nat,* vol. 106, pp. 283-292, https://doi.org/10.1086/282771

Sneath, P. H. A./R. R. Sokal (1973): Numerical Taxonomy, San Fancisco, USA: Freeman, W.H.

Swofford, D. L./R. B. Selander (1989): BIOSYS-2 (Version 1.7, modified by William C. Black IV, 1997).

Wright, S. (1951): The genetic structure of populations, in: *Ann. Eugene*, vol. 15, pp. 323-354.

Wright, S. (1978): Evolution and the Genetics of Population Volume 4: Variability Within and Among Natural Populations, Chicago, USA: The University of Chicago Press.