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Investigations on the impact of genetic resistance to oedema disease on performance traits and its relation to stress susceptibility in pigs of different breeds

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1 Introduction

Oedema disease and post-weaning diarrhoea are major causes of economic losses in piglet production (Bertschinger et al., 1992; Vögeli et al., 1996). They are associated with the colonization of the intestine with toxigenic *Escherichia (E.) coli* bacteria of various serotypes. Colonization depends on specific binding between adhesive fimbriae and receptors on the enterocytes (Bertschinger et al., 1990). Phenotypic tests based on the observation of adhesion after *in-vitro* inoculation of enterocytes with *E. coli* F18 were developed in the early nineties by Bertschinger et al. (1990). However, this test was not well suited for selection because it can only be applied on intestine tissue immediately after slaughter.

Meijerink et al. (1997) showed for Swiss Large White pigs that the a(1,2) fucosyltransferase (FUT1) locus on chromosome 6 is in perfect linkage disequilibrium with the hypothetical *E. coli* F18 receptor locus (ECF18R) responsible for the adhesion of bacteria to the enterocytes. They identified a polymorphism at bp 307 with a high linkage disequilibrium with ECF18R. Vögeli et al. (1997) confirmed the close linkage between FUT1 and ECF18R also for the Swiss Landrace and Piétrain breeds. The polymorphism at bp 307 identifies two different alleles A and G which show completely recessive inheritance. Only the genotype AA is resistant to adhesion of *E. coli* F18, all other genotypes are susceptible.

FUT1 is located on chromosome 6q11 and is in the same linkage group as the blood group inhibitor (S) and the ryanodine receptor (RYR1) (Meijerink et al., 1997). Vögeli et al. (1997) found moderate allele frequencies for the desired allele (A) in Swiss Large White (.34) and Piétrain (.23), whereas its frequency in Swiss Landrace was low (.07). Nevertheless, the Swiss pig breeders started to select for the desired allele in the two major breeds Large White and Landrace (Hofer, 2000, pers. comm.).

The commercial use of FUT1 as a selection tool is protected by international patents. The aim of the present study was to clarify a number of questions relevant before deciding whether a license for FUT1 should be requested. First, we wanted to estimate the allele frequencies for FUT1 for the three most important breeds in Bavaria, German Landrace, Large White, and Piétrain. Second, we were interested whether a linkage disequilibrium exists between FUT1 and RYR1 and which linkage phases are predominant in the Piétrain breed that is at present under selection for stress resistance. The two other breeds are already fixed for the resistant allele at RYR1. Finally, we wanted to examine whether there are effects of FUT1 genotypes on production and reproduction traits.

2 Material and Methods

Semen samples were collected from a total of 401 young AI-boars in Bavaria on three AI-stations from December 1999 until December 2001. In addition, we collected blood or tissue samples from 1969 progeny of these AI-boars in the two central testing stations in Bavaria. For

the progeny the usual set of traits on fattening performance, carcass composition and meat quality was recorded. For all animals FUT1-genotype was determined, whereas RYR1 was only genotyped in the Piétrain breed. Table 1 shows the number of animals genotyped for FUT1 and RYR1, respectively.

Table 1: Number of animals from three breeds genotyped for FUT1 and RYR1

		Breed			Total
		GL	PI	LW	
AI-boars	*FUT1*	135	248	18	401
	RYR1	0	254	0	254
Progeny	*FUT1*	1051	830	88	1969
	RYR1	0	830	0	830

Allele frequencies were estimated by counting and genotypes were tested for Hardy-Weinberg equilibrium with the usual ?²-test. In order to test for linkage disequilibrium between FUT1 and RYR1, we determined the haplotypes of the AI-boars based on the genotypes of their progeny. The observed and expected haplotype frequencies were then compared in another ?²-test.

The effects of FUT1-genotypes on performance traits were estimated with the following statistical model, using PROC GLM in SAS (2003). Due to the low number of progeny for the Large White breed, we only analysed German Landrace and Piétrain.

$$Y_{ijkl} = \mu + (S*Y*M)_i + Sire_j + FUT1_k + e_{ijkl}$$

where:

Y_{ijkl}	=	observed value
μ	=	overall mean
$S*Y*M_i$	=	fixed effect of station-year-month or station-date for meat quality traits
$Sire_j$	=	random effect of the sire of the animal
$FUT1_k$	=	fixed effect of FUT1-genotype
e_{ijkl}	=	random error term

For the analysis in the Piétrain breed we used a model which added the effect of the RYR1-genotype and the interaction between FUT1 and RYR1.

$$Yijkl = \mu + (S*Y*M)_i + Sire_j + FUT1_k + RYR1_l + F*G_{lk} + e_{ijkl}$$

where :

$RYR1_l$	=	fixed effect of RYR1-genotype
$F*G_{lk}$	=	fixed interaction term between FUT1- and RYR1-genotype

The above models were applied for the traits average daily gain (ADG), feed conversion ratio (FCR), lean percentage (LP), backfat thickness (BF), pH in the eye muscle 45 min *post mortem* (pH1) and pH in the ham 24 h *post mortem*. For the traits piglets born alive (LBP) and piglets weaned (WP) we could only use the breeding values of the sires of dam breeds. These were analysed with a simple linear model containing the fixed effects of breed (LW, GL) and FUT1-genotype.

3 Results and Discussion

The results from the estimation of allele frequencies in FUT1 are given in table 2. Frequencies estimated from AI-boars and their progeny were very similar, except for the Piétrain breed. The frequencies for Landrace and Pietrain are very similar to the ones estimated by Vögeli et al. (1998) from Swiss data, whereas Large White showed a lower frequency, especially in the progeny. Genotype frequencies were in Hardy-Weinberg equilibrium for all three breeds.

Table 2: Estimated allele frequencies and results of the test for deviation from Hardy-Weinberg equilibrium (HWE) for the breeds German Landrace (GL), Large White (LW) and Piétrain (PI)

Breed	AI-boars	Progeny	HWE in progeny
GL	.05	.07	ns
LW	.26	.22	ns
PI	.33	.25	ns

Table 3 shows the genotype frequencies for FUT1 and RYR1 for progeny of the Piétrain breed. It can be seen that the most desired genotype AA-NN is extremely rare in the population. The frequency of RYR_N is .34 in this sample. The comparison of observed and expected genotype frequencies showed a highly significant ($P < .001$) deviation from the values expected under linkage equilibrium. Closer inspection of the contributions to the overall ?²-value revealed that deviations of the frequency of AG-NN and GG-NN contributed 31.8% and 30.3% to the overall ?²-value.

Table 3: Distribution of genotype frequencies among progeny of the Piétrain breed

	RYR1		
FUT1	NN	NP	PP
AA	2	12	28
AG	16	158	167
GG	95	256	233

The analysis of haplotypes of the progeny calculated from the haplotypes of their sires confirmed that there is an excess of G-N and correspondingly a lack of A-N haplotypes in the population, while G-P and A-P haplotypes are in good agreement with the expectations (table 4).

Table 4: Observed and expected haplotype frequencies among the progeny of the Piétrain breed

	A-N	A-P	G-N	G-P
Observed	.03	.15	.29	.53
Expected	.07	.15	.26	.52

None of the performance traits analysed in German Landrace showed significant effects of FUT1-genotype (table 5). In the Piétrain breed RYR1 showed the well-known effects on lean percentage, backfat thicknes and pH1 as expected. The only significant result for FUT1 in the Piétrain breed was found for pH24. Closer inspection revealed that this was mainly caused by one of the two animals with AA-NN genotype which had an extraordinary high value for pH24. When this animal was excluded from the analyses, results for FUT1 were no longer significant.

Table 5: Results for the analysis of the influence of FUT1 in German Landrace (GL) and FUT1 and RYR1 in Piétrain (PI) on various performance traits

	GL		PI	
Trait	A-N	FUT1	RYR1	F*G
ADG	ns	ns	ns	ns
FCR	ns	ns	ns	ns
LP	ns	ns	***	ns
BF	ns	ns	*	ns
pH1	ns	ns	***	*
pH24	ns	*	ns	ns
LBP	ns	ns	ns	ns
WP	ns	ns	ns	ns

4 Conclusion

There are good prospects for a selection for resistance to oedema disease in the Large White breed. In German Landrace the frequency of the desired allele is low and selection would take a long time to increase the frequency of the A-allele. It might be worthwhile to check, whether A-alleles could be imported from other breeds. In the Piétrain breed the allele frequency of allele A at FUT1 looks promising, but selection would be massively hampered by the unfavourable linkage disequilibrium with RYR1. It is not clear at present whether this linkage disequilibrium is caused by a founder effect or if there are other reasons. In view of the whole breeding program it must be kept in mind that resistance of final products can only be achieved if all the breeds of the final cross are homozygous.

5 References

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