

**POSSIBILITY OF MAJOR GENES AND ASSOCIATION OF *RYR1* GENE
TO MEAT QUALITY OF DUROC SELECTED FOR MEAT
PRODUCTION AND MEAT QUALITY**

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INTRODUCTION

Meat quality is a major determinant for the choice of pork in the Japanese market because the quantity of pork consumption is nearly at a plateau. As such, a selection project for meat production and quality has been undertaken for 7 generations since 1995 at Miyagi Prefecture Animal Industry Experiment Station (Suzuki *et al.*, 2002). In the project, a correlated response for other meat quality traits was recorded through the selection while substantial genetic gain was realized in intramuscular fat content. The purpose of this study was to assess the possibility of the existence of a major locus influencing meat quality traits and to examine the association of the ryanodine receptor gene (*RYR1*) to meat quality traits.

MATERIALS AND METHODS

Selection of animals and recording of meat quality. An outline of the selection project was described by Suzuki *et al.* (2002). Correlated response was studied in approximately 80 animals (barrows and gilts) in each generation. All of the animals were slaughtered at 105 kg body weight, and their meat quality was analyzed in six generations. The numbers of animals in each generation are presented in table 1. Muscle samples were used to prepare DNA for genotype of ryanodine receptor gene (*RYR1*) (Fujii *et al.*, 1991). The number of animals with *RYR1* heterozygote genotype tended to decrease in the later generations.

Meat quality traits. The intramuscular fat content (IMF) was analyzed by the Soxhlet extraction method. Tenderness (TEND) and pliability (PLIA) of the meat were measured with the Tensipresser (Model TTp-50BX II, Taketomo-Electric Company, Japan). Other traits studied were age at slaughter (AGE), drip loss (DL), heat loss (HL), pork color standard (PCS), brightness of meat (L*) and moisture content (MOIS).

Segregation analysis of meat quality traits. Segregation analysis was undertaken for the above traits with SALP (segregation and linkage analysis program) by Stricker *et al.* (1995). A mixed inheritance model for the analysis included a major gene locus with an additive gene effect and a polygenic effect as genetic factors, the age of the animals and the effect of sex as fixed effects and random residuals. The age of the animals was excluded from the analysis of growth rate (age at slaughter). The effect of the *RYR1* genotype was additionally included in the above model to examine the effect of this genotype on meat quality traits.

Table 1. Numbers ^A of gilts and barrows in each generation

Sex	Generation of selection					
	G1	G2	G3	G4	G5	G6
Gilt	17(4)	30(5)	14(1)	16(1)	23(0)	22(1)
Barrow	43(7)	59(12)	69(10)	68(8)	52(3)	51(1)

^A Numbers in parenthesis represent the number of *RYRI* heterozygote animals.

RESULTS AND DISCUSSION

The mean values of meat quality traits were compared between normal homozygote (C/C) and heterozygote (C/T) animals in each generation. A significant difference was found in some generations for HL and PLI by Student's t-test (table 2). In HL, the mean values of the heterozygote animals were higher than those of normal animals in earlier generations of the selection; however, the difference was smaller (barrows) or reverse (gilts) in the later generations. In PLI, mean values of the *RYRI* heterozygote animals were lower than those of normal animals in earlier generations; however, the difference diminished in later generations. Thus the association of major gene loci to the traits was assessed by segregation analysis.

Table 2. Mean values^A of two genotypes of *RYRI* (normal homozygote C/C or Heterozygote C/T) for HL and PLI in six generations

Trait ^B	Sex	<i>RYRI</i> Genotype	G1 ^C	G2	G3	G4	G5	G6
HL	Gilt	C/T	27.6*	28.1*	21.3	22.7	-	21.2
		C/C	21.0	25.4	25.5	23.9	-	24.4
	Barrow	C/T	24.3	28.0	27.3*	26.7	28.6*	25.4
		C/C	21.8	26.3	24.9	25.0	24.6	25.2
PLI	Gilt	C/T	1.39*	1.46*	1.49	1.61	-	1.48
		C/C	1.64	1.55	1.57	1.54	-	1.47
	Barrow	C/T	1.52	1.49*	1.42*	1.53	1.52	1.56
		C/C	1.58	1.53	1.54	1.53	1.54	1.50

^A* indicates significant difference ($P < 0.05$) between the genotypes,

^BHL : heat loss, PLI : pliability, ^CG1–G6 : generations 1 to 6.

Results of parameter estimation are presented in table 3 ; the model without effect of *RYRI* gene was fitted to the traits. High heritabilities due to a polygenic component were estimated in AGE, L* value and TEND ; high heritabilities due to a major locus were estimated in MOIS and IMF, whereas moderate heritabilities were estimated in AGE and PCS. Low heritabilities due to a major locus were estimated in L* value and TEND. Overall heritabilities of MOIS, IMF and TEND were similar to estimates by Cameron and Enser (1991). Those of DL and IMF were higher than the estimates by Gibson *et al.* (1998) and Hermesch *et al.* (1998) ; for L* value, however, a similar estimate was reported by the latter. The estimates of variance components by the model with the *RYRI* locus were effectively the same as those of the model without it. Thus the variance components due to major loci in some of the traits were suggested to be independent of the *RYRI* locus.

Table 3. Estimated parameters ^A with mixed model

	AGE	DL	HL	PCS	L *	MOIS	IMF	TEND	PLIA
σ_a^2	78.4	0.67	1.29	0.05	4.13	0.32	0.33	57.7	0.0010
σ_m^2	50.6	0.75	3.49	0.12	0.24	0.93	1.06	0.30	0.0020
σ_e^2	5.9	1.90	8.01	0.16	4.74	0.46	0.54	86.1	0.0087
h_a^2	0.58	0.20	0.10	0.14	0.45	0.19	0.17	0.40	0.09
h_m^2	0.38	0.23	0.25	0.36	0.03	0.54	0.55	0.00	0.17

^A σ_a^2 : variance due to polygenic gene effect, σ_m^2 : variance due to a major gene locus, σ_e^2 : residual variance, h_a^2 and h_m^2 : heritability due to polygenic component and a major genotypic effect, respectively.

CONCLUSION

Evidence of a major gene locus obtained by segregation analysis was independent of the existing *RYRI* locus in AGE, PCS, MOIS and IMF, despite the phenotypic difference between the *RYRI* genotypes in HL and the PLI of pork. No possibility of a contribution by a major locus was found for L* value or TEND. Estimates of moderate to high heritability suggested the potential contribution of major genes to AGE, PCS, MOIS and IMF.

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