



# Influence of *MYOD* family on meat performance of Czech Large White and Czech Landrace pigs

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## Objectives

The objective of our study was to analyse the associations of *MYOD* family polymorphic variants with meat production in Czech breeds of pigs.

## Introduction

The pork production largely depends on muscle fibre numbers, which are formed only during embryonic development. *MYOD* family consists of four related genes: *MYOD1*, *MYOG* (*MYF4*, myogenin), *MYF5* and *MYF6* (*MRF4*, herculin). Two members, *MYOD1* and *MYF5*, are mainly expressed during cell proliferation of myoblasts, muscle precursor cells. *MYOD1* gene induces differentiation of fibroblasts into myoblasts, while fusion of myoblasts into myofibres is controlled by myogenin.

## Material and Methods

### Animals

A total of 254 pigs, sibs and half-sibs, from Large White (201 animals) and Landrace (53 animals) breeds were included into the analysis.

### Trait definition

The following traits were analysed: intramuscular fat (**IMF**), backfat thickness (**BFT**), weights of neck (**NW**), loin (**LW**), shoulder (**SW**) and ham (**HW**), test daily gain (**TDG**), lean meat content (**LMC**), remission (**REM**) and dry matter (**DM**). Intramuscular fat was established using soxhlet-petroleum extraction. Backfat thickness was determined as a mean from the three measurements: BFT 1 - height to the middle of second thoracic vertebra, BFT 2 - height to the middle of last thoracic vertebra and BFT 3 - height to the middle of first sacral vertebra. TDG was calculated between 30-kg and 100-kg body weights. Lean meat content was determined as percentage of sum of neck, loin, shoulder and ham weights in cold half carcass. Remission was established on the fresh cut using absorption spectroscopy at 525 nm. Dry matter was weighed after drying at 105 °C for 24 h.

### Statistical analysis

The associations of studied polymorphisms were estimated using a mixed linear model (REML) in SAS for Windows 9.1.3. The genotypes of relevant gene (**genotypes**), sex (**SEX**), breed (**BREED**) and year-month of the slaughter (**YMS**) were used as fixed effects. The effect of the sire of pigs (**SIRE**) was included in model as a random effect. For all traits with the exception of test daily gain, the linear regression on hot half carcass weight (**HHCW**; kg) and test daily gain (**TDG**; kg) were used. Because of lower number of individuals in Landrace breed, a separated analysis for single breed was not carried out.

## Results and Conclusion

Significant differences were observed between *MYOD1*, *MYF4* and *MYF5* genes and meat production traits. No significance between *MYF6* and performance traits was found out. Results are shown in tables 2 and 3.

Table 1 Absolute (n) and relative (R) frequencies of genotypes at the loci *MYOD1*, *MYOG*, *MYF5* and *MYF6*

Breed		<i>MYOD1</i> / <i>Ddel</i>			<i>MYOG</i> / <i>MspI</i>			<i>MYF5</i> / <i>HpaII</i>			<i>MYF6</i> / <i>BseRI</i>		
		AA	AB	BB	AA	AB	BB	AA	AB	BB	AA	AB	BB
Large White	n	44	107	50	69	83	27	0	7	187	43	128	8
	R	0.22	0.53	0.25	0.39	0.46	0.15	0.00	0.04	0.96	0.24	0.72	0.04
Landrace	n	21	26	6	27	22	3	0	1	51	12	39	1
	R	0.40	0.49	0.11	0.52	0.42	0.06	0.00	0.02	0.98	0.23	0.75	0.02

Table 2 Least-squares means and standard errors for selected traits and genotypes of *MYOD1* and *MYOG* genes

	<i>MYOD1</i> / <i>Ddel</i>			<i>MYOG</i> / <i>MspI</i>		
	AA	AB	BB	AA	AB	BB
IMF (%)	1.58 ± 0.10	1.47 ± 0.07 <sup>a</sup>	1.76 ± 0.10 <sup>b</sup>	1.55 ± 0.08	1.65 ± 0.08 <sup>a</sup>	1.34 ± 0.13 <sup>b</sup>
NW (kg)	3.84 ± 0.04	3.78 ± 0.04	3.76 ± 0.05	3.85 ± 0.04 <sup>a</sup>	3.75 ± 0.04 <sup>b</sup>	3.76 ± 0.07
LW (kg)	4.73 ± 0.06	4.73 ± 0.05	4.80 ± 0.07	4.81 ± 0.05 <sup>a</sup>	4.71 ± 0.05	4.62 ± 0.10 <sup>**</sup>
LMC (%)	54.15 ± 0.34	53.74 ± 0.29	53.92 ± 0.39	54.32 ± 0.30 <sup>**</sup>	53.74 ± 0.31 <sup>a</sup>	54.08 ± 0.49
DM (%)	12.64 ± 0.54 <sup>a</sup>	11.86 ± 0.50	11.56 ± 0.61 <sup>**</sup>	11.74 ± 0.52	12.08 ± 0.53	12.91 ± 0.76

Note: Values with the different superscripts show significance level within rows: P ? 0.01 (A, B), P ? 0.05 (a, b); P ? 0.1 (\*, \*\*)

Table 3 Least-squares means and standard errors for selected traits and genotypes of *MYF5* and *MYF6* genes

	<i>MYF5</i> / <i>HpaII</i>			<i>MYF6</i> / <i>BseRI</i>		
	AA	AB	BB	AA	AB	BB
IMF (%)	-	2.03 ± 0.24 <sup>a</sup>	1.54 ± 0.06 <sup>b</sup>	1.63 ± 0.11	1.54 ± 0.07	1.55 ± 0.32
LW (kg)	-	4.34 ± 0.15 <sup>a</sup>	4.75 ± 0.04 <sup>b</sup>	4.78 ± 0.07	4.73 ± 0.05	4.85 ± 0.14
LMC (%)	-	52.46 ± 0.81 <sup>a</sup>	53.99 ± 0.26 <sup>b</sup>	54.00 ± 0.38	54.06 ± 0.28	54.28 ± 0.80

Note: Values with the different superscripts show significance level within rows: P ? 0.01 (A, B), P ? 0.05 (a, b); P ? 0.1 (\*, \*\*)

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