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Variability in candidate genes for meat performance traits in pigs

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Introduction

The genes for growth hormone *GH*, heart fatty acid-binding protin *H-FABP*, leptin *LEP*, leptin receptor *LEPR* and *MYC* protooncogene are presented as candidate genes for meat production and meat quality in pigs. We studied genetic variability of these loci and genetic diversity among Large White and Landrace breed in Czech Republic.

Tab 1: PCR conditions

Loci	Temperature conditions of PCR	PCR product	Source
H-FABP	95℃/60s 57℃/60s 72℃/120s, 30x	700 bp	Gerbens et al.(1997)
MYC	95℃/40s 58℃/60s 72℃/60s, 30x	322 bp	Reiner et al.(2000)
GH	95℃/40s 60℃/60s 72℃/90s, 30x	506 bp	Schellander et al.(1994)
LEP	95℃/40s 55℃/60s 72℃/60s, 30x	152 bp	Stratil et al.(1997)
LEPR	94℃/60s 55℃/60s 72℃/120s, 30x	2000 bp	Stratil et al. (1998)

Materials and Methods

We analysed 181 pigs of Large White (LW) and 120 pigs of Landrace (La) breeds. Genotypes of candidate genes were performed using PCR-RFLP methods. Calculated population parameters were: frequencies of genotypes and alleles, Hardy-Weinberger equilibrium, observed and expected heterosygosity, Nei´s genetic identity and genetic distance through program Popgene version 1.31 (1999).

Tab 2: Determination of genotypes of individual loci

Loci	Restriction endonuclease	Genotypes
H-FABP:	*Hinf*I	***HH*** 195, 59; ***Hh*** 256, 195, 59; ***hh*** 256 bp
MYC:	*Msp*I	***AA*** 322; ***AB*** 322, 201, 121; ***BB*** 201, 121 bp
GH:	*Msp*I	***AA*** 222,147, 137; ***AB*** 282, 222, 147, 137; ***BB*** 282, 222 bp
GH:	*Hae*II	***AA*** 333, 173; ***AB*** 506, 333, 173; ***BB*** 506 bp
LEP:	*Hinf*I	***TT*** 152; ***CT*** 152, 84, 68;- ***CC*** 84, 68 bp
LEPR:	*Hpa*II	***AA*** 2000; ***AB*** 2000,1450, 550; ***BB*** 1450, 550

Results

Population Descriptive Statistics

Large White

Locus	N	Frequency of genotypes			Allele frequency relative		χ^2
			Absolute	Expective			
H-FABP	60	***HH***	28	30.0	***H***	0.708 ± 0.042	1.5733
		Hh	29	25.0	***h***	0.292 ± 0.042	
		hh	3	5.0			
LEP	181	***CC***	4	4.74	***C***	0.163 ± 0.019	0.1639
		CT	51	49.52	***T***	0.837 ± 0.019	
		TT	126	126.74			
LEPR	18	***AA***	4	3.0	***A***	0.417 ± 0.082	0.9444
		AB	7	9.0	***B***	0.583 ± 0.082	
		BB	7	6.0			
GH1	175	+/+	82	81.49	+	0.683 ± 0.025	0.0314
		+/-	75	76.01	-	0.317 ± 0.025	
		-/-	18	17.49			
GH2	172	+/+	98	95.91	+	0.747 ± 0.023	0.7163
		+/-	71	65.19	-	0.253 ± 0.023	
		-/-	13	10.91			
CMYC	167	***AA***	86	88.30	***A***	0.727 ± 0.024	0.8068
		AB	71	66.41	***B***	0.27 3 ± 0.024	
		BB	10	12.30			

Landrace

Locus	N	Frequency of genotypes			Allele frequency relative		χ^2
			Absolute	Expective			
H-FABP	83	***HH***	44	43.27	***H***	0.723 ± 0.034	0.1597
		Hh	32	33.45	***h***	0.277 ± 0.034	
		hh	7	6.27			
LEP	120	***CC***	4	1.58	***C***	0.117 ± 0.021	4.7024^{*}
		CT	20	24.84	***T***	0.883 ± 0.021	
		TT	96	93.58			
LEPR	82	***AA***	9	10.14	***A***	0.354 ± 0.080	0.3046
		AB	40	37.72	***B***	0.646 ± 0.080	
		BB	33	34.14			
GH1	87	+/+	21	13.56	+	0.397 ± 0.037	11.1207^{***}
		+/-	27	41.88	-	0.603 ± 0.037	
		-/-	39	31.56			
GH2	81	+/+	62	60.43	+	0.864 ± 0.024	2.2603
		+/-	16	19.13	-	0.136 ± 0.024	
		-/-	3	1.44			
CMYC	100	***AA***	68	66.35	***A***	0.8150 ± 0.028	1.2186
		AB	27	30.31	***B***	0.1850 ± 0.028	
		BB	5	3.35			

Summary of Heterozygosity Statistics for All Loci

Large White

Locus	Sample Size	H_O	H_E
H-FABP	120	0.4833	0.4132
LEP	362	0.2818	0.2728
LEPR	36	0.3889	0.4861
CMYC	334	0.4251	0.3964
GH1	350	0.4286	0.4331
GH2	344	0.3547	0.3779
Mean	258	0.3937	0.3966
St.Dev		0.0697	0.0711

H_O - observed heterozygosity
H_E - Nei's (1973) expected heterozygosity

Landrace

Locus	SampleSize	H_O	H_E
H-FABP	166	0.3855	0.4006
LEP	240	0.1667	0.2061
LEPR	164	0.4878	0.4572
CMYC	200	0.2700	0.3016
GH1	174	0.3103	0.4786
GH2	162	0.1975	0.2347
Mean	184	0.3030	0.3465
St.Dev		0.1198	0.1156

Nei's Original Measures of Genetic Identity and Genetic distance

Nei's genetic identity (above diagonal) and genetic distance (below diagonal).

Nei (1972)

	Large White	Landrace
Large White	****	0.9717
Landrace	0.0287	****

Nei (1978)

	Large White	Landrace
Large White	****	0.9739
Landrace	0.0265	****

Dendrogram Based Genetic distance: Method = UPGMA -- Modified from NEIGHBOR procedure of PHYLIP Version 3.5

Nei (1972)

```
  +---------------------------------- LW
--1
  +---------------------------------- La
```

Between	And	Length
1	LW	1.43582
1	La	1.43582

Nei (1978)

```
  +--------------------------------- LW
--1
  +--------------------------------- La
```

Between	And	Length
1	LW	1.32406
1	La	1.32406

REFERENCES:
More information at author's e-mail addresses.

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