

POLYMORPHISM OF THE PRION PROTEIN GENE IN MEAT AND WOOL-MEAT SHEEP BREEDS IN POLAND

Roman Niznikowski¹✉, Grzegorz Czub¹, Marcin Świątek¹,
Magdalena Ślęzak¹, Krzysztof Głowacz²

¹Department of Animal Breeding and Production, Division of Sheep and Goat Breeding,
Warsaw University of Life Sciences – SGGW, Ciszewskiego 8, 02-786 Warszawa,
Poland

²Department of Animal Environment Biology, Division of Animal Hygiene and Welfare
Warsaw University of Life Sciences – SGGW, Ciszewskiego 8, 02-786 Warszawa,
Poland

Abstract. The study was conducted in 2009–2013 on a total of 1587 (1230 females and 357 males) sheep of meat breeds (Berrichone du cher, Suffolk and Charolaise) and wool-meat breeds (Polish Merino, old type Polish Merino, Corriedale and Żelaźnieńska sheep) at age two to 11 years. Highly significant ($P \leq 0.01$) effect of breed on the frequency of scrapie alleles and genotypes, and significant effect ($P \leq 0.05$) of sex in the case of old type Polish Merino, were found. Most alleles (ALRR, ALRQ, ALHQ, ALRQ, AFRQ, VLRR, VLRQ) were found in Polish Merino and only two (ALRR and ALRQ) in Suffolk. Amino acid phenylalanine encoded at codon 141 occurred only in combination with AFRQ allele, while leucine in the other six. Seventeen scrapie genotypes were identified, most in Polish Merino and Corriedale (12 each), Żelaźnieńska sheep and Berrichon du cher (5 each), Charolaise (3) and Suffolk (2). Very high frequency of ALRR/ALRR in Suffolk and Berrichon du cher reveals their high genetic resistance to both forms of scrapie. Low frequencies of genotypes susceptible to classical scrapie were found in Charolaise and genotypes suspected to genetic lack of resistance to atypical scrapie in Żelaźnieńska sheep. Many signs of genetic susceptibility to both forms of scrapie were found in Merino and Corriedale, which requires new appropriate breeding programs leading to elimination those conditions from sheep population, especially in old type Polish Merino.

Key words: sheep, PrP, distribution of alleles and genotypes

✉ roman_niznikowski@sggw.pl

INTRODUCTION

The European Parliament has introduced regulations for prevention, control, and eradication of transmissible spongiform encephalopathies [Commission decision of 13 February 2003. . . , Regulation (EC) No 260/2003, Regulation (EC) No 999/2001]. In sheep, there are two common forms of transmissible spongiform encephalopathy: classical and atypical scrapie. Genetically polymorphic proteins responsible for the occurrence of classical scrapie are located at codons 136, 154 and 171 [Lühken *et al.* 2004, Kaal and Windig 2005, Kaam *et al.* 2005, Palhiere *et al.* 2008]. ARR allele ensure the least sensitivity to scrapie (which is result of encoding alanine – A, arginine – R and also arginine – R), while allele VRQ is responsible for the high degree of genetic susceptibility to this disease – (which is result of encoding alanine valine – V , arginine – R, glutamine – Q) [Kaal and Windig 2005, Kaam *et al.* 2005, Palhiere *et al.* 2008, Rejduch *et al.* 2009]. In the case of atypical scrapie (Nor98), which for the first time was described by Bebestadt *et al.* [2003], suspected alleles were located at codon 141 [Goldman 2008, Mcintyre *et al.* 2008, Mazza *et al.* 2010], which encodes the phenylalanine (F) and leucine (L). Alleles with F are more frequently accompanied by clinical forms of this disease [Goldman 2008, Mcintyre *et al.* 2008] Moreover, classical scrapie can exist simultaneously with the atypical form in the herds of sheep [Mazza *et al.* 2010].

So far, research in Poland has been conducted only in order to monitor the occurrence of alleles of classical scrapie in many breeds of sheep [Palhiere *et al.* 2008, Rejduch *et al.* 2009, Wiśniewska and Mroczkowski 2009], despite the first case of atypical form of scrapie in 2009 [Polak *et al.* 2010]. The result of previous studies proved the absence of the alleles encoding valine at codon 136 in Polish Heath Sheep and different frequency of their presence in other breeds [Rejduch *et al.* 2009, Wiśniewska and Mroczkowski 2009, Niżnikowski *et al.* 2013]. Relatively few papers relate to alleles of scrapie located at codon 141. It is worth to carry out breeding work aimed to eliminate not only VRQ allele but also allele encoding phenylalanine at codon 141 from sheep population. Those actions should lead to improve genetic resistance to both forms of scrapie. Therefore, the assumed direction of the research aimed to determine the prevalence of the genetic determinants of both forms of scrapie in meat and wool-meat sheep held all over the country.

MATERIAL AND METHODS

The study was conducted in 2009–2013 in meat sheep flocks: Berrichon du cher (one flock from Wielkopolskie Voivodeship); Suffolk (two flocks from Wiel-

kopolskie Voivodeship) and Charolaise (two flocks from Wielkopolskie Voivodeship) and wool- meat sheep flocks: Polish Merino (three flocks from Wielkopolskie Voivodeship, eight flocks from Kujawsko-Pomorskie Voivodeship); Old type Polish Merino (one flock from Wielkopolskie Voivodeship, five flocks from Mazowieckie Voivodeship, eight flocks from Kujawsko-Pomorskie Voivodeship); Corriedale (two flocks from Podlaskie Voivodeship); Żelaźnińska sheep (two flock from Podlaskie Voivodeship and one flock from Łódzkie Voivodeship). Animals were at age of two to 11 years (Table 1). Herds were randomly selected for sampling. For the isolation of genomic DNA animal blood samples were obtained from vein jugularis into tubes containing anticoagulant EDTA. DNA was isolated from blood leucocytes using the conserved EDTA. In order to obtain high quality DNA suitable after freezing and thawing of a reusable, blood was pretreated with the resulting DNA modification by removal of heme-compounds lysis of erythrocytes products. DNA was isolated from leukocytes by chromatography on mini-columns of silicate (A&A Biotechnology). The obtained fraction was used as template DNA for amplification of polymorphic gene allele fragment. Sample genotyping was performed with KASPar[®] (www.kbioscience.co.uk), system which use the single nucleotide polymorphism (SNP) based on primers listed in Table 2.

The high reliability of SNP method compared to the sequencing method was proved by Green et al. [2006]. Based on the reading of DNA samples genotyped within the ewes and rams frequency distributions of alleles and genotypes were presented. This action was a preparatory act to the next stages of research. For the statistical evaluation SPSS software version 22.0 was used. The impact of breed and sex within the breed for attendance of alleles and genotypes was assessed using the χ^2 test. The results are shown in the tables. With regard to the effect of breed, alleles have 36 degrees of freedom and the genotypes – 76 degrees of freedom. In contrast, the test results for breeds disaggregated by sex: from one degree of freedom for Suffolk up to five degrees of freedom for the Polish Merino for alleles and from one degree of freedom for the Suffolk up to 12 degrees of freedom for Polish Merino and Corriedale for genotypes. Degrees of freedom were fixed within breeds according to the formula: (number of sexes – one) \times (number of alleles or genotypes – one). The results are summarized in Tables.

RESULTS AND DISCUSSION

In Table 3 the distributions of alleles of assessed sheep breeds disaggregated by sex are summarized. In all tested breeds highly significant ($P \leq 0.01$) differences in the distributions of alleles have been found, moreover significant differences ($P \leq 0.05$) between the sexes within breed were found only in old-type Polish Merino. Generally seven alleles were found (ALRR, ALRQ, ALHQ,

Table 1. Experimental material used in the study in 2009–2013

Tabela 1. Materiał doświadczalny wykorzystany w badaniach w latach 2009–2013

Breed – Rasa	Sex – Płeć		
	♀	♂	
Polish Merino Merynos polski	296	61	2010: 43 (♀), 6 (♂) 2011: 112 (♀), 11 (♂) 2012: 79 (♀), 28 (♂) 2013: 62 (♀), 16 (♂)
Old type Polish Merino Merynos polski w starym typie	394	74	2009: 228 (♀), 12 (♂) 2010: 48 (♀), 19 (♂) 2011: 36 (♀), 11 (♂) 2012: 56 (♀), 27 (♂) 2013: 26 (♀), 5 (♂)
Corriedale Corriedale	110	9	2011: 25 (♀), 5 (♂) 2013: 85 (♀), 4 (♂)
Żelaźnińska sheep Owca żelaźnińska	244	145	2010: 49 (♀), 57 (♂) 2011: 37 (♀), 40 (♂) 2012: 35 (♀), 26 (♂) 2013: 123 (♀), 22 (♂)
Berrichon du cher Berrichon du cher	131	41	2010: 14 (♀), 6 (♂) 2011: 41 (♀), 16 (♂) 2012: 24 (♀), 6 (♂) 2013: 52 (♀), 13 (♂)
Suffolk Suffolk	37	18	2010: 8 (♀) 2011: 15 (♀), 8 (♂) 2013: 14 (♀), 10 (♂)
Charolaise Charolaise	18	9	2010: 3 (♀) 2011: 11 (♀), 5 (♂) 2013: 4 (♀), 4 (♂)
Total within sex – Razem w obrębie płci	1230	357	
Total – Razem	1587		

Table 2. The primers and SNP genotyping of the locus of the prion protein

Tabela 2. Startery oraz miejsca genotypowania SNP dla locus białka prionowego

Locus	Primers 5'-3' Startery 5'-3'	SNP	Changes Zmiany	Localization Lokalizacja
<i>PRNP</i> prion protein <i>PRNP</i> białko prionowe	CACAGTCAGTGAACAAGCC/ CTTGCCAGGTTGGGG	AY909542:g.385A>G	A/G	Exon 3
		AY909542:g.386G>T	G/T	Exon 3
		AY909542:g.479C>T	C/T	Exon 3
		AY909542:g.493C>T	C/T	Exon 3
		AY909542:g.534G>A	G/A	Exon 3

ALRH, AFRQ, VLRQ i VLRR). The largest polymorphism has been demonstrated in Polish Merino in which all alleles were found. Five alleles were found in old type Polish Merino and Corriedale (ALRR, ALRQ, ALHQ, AFRQ, VLRQ), four

in Żelaźnieńska sheep (ALRR, ALRQ, ALHQ and AFRQ), three in Berrichon du cher (ALRR, ALRQ and ALHQ) and Charolaise (ALRR, ALRQ and VLRQ) and only two in Suffolk (ALRR and ALRQ). In old type Polish Merino rams compared to old type Polish Merino ewes were found: higher frequency of ALRR allele, lower ALRQ, similar ALRH and absence of AFRQ and higher frequency of VLRQ. In the all research material, the frequencies of the occurrence of alleles were following: ALRR – 63.9%, ALRQ – 26.9%, VLRQ – 3.8%, ALHQ – 3.6% , AFRQ – 1.8%), ALRH and VLRR – <1% . The highest frequency of allele ALRR was observed in both sexes of Suffolk and ewes of Berrichon du cher and Charolaise. The lowest were in old type Polish Merino and Corriedale ewes and Polish Merino rams. In the case of allele ALRQ, the highest frequency of occurrence was found in Polish Merino and Charolaise rams and old type Polish Merino ewes, while the lowest was observed in both sexes of Corriedale, Berrichon du cher and Suffolk. ALRH allele appeared only in Polish Merino.

Discussed alleles are among the genetically resistant or neutral to scrapie and confirm the results of the national [Wiśniewska and Mroczkowski 2009, Niżnikowski et al. 2014] and foreign studies [Lühken et al. 2004, Kaal and Windig 2005, Kaam et al. 2005, Palhiere et al. 2008]. It is worth to emphasize definitely higher frequency of ALRR allele in meat sheep compared to meat-wool breed. VLRQ allele had higher frequency of occurrence in both sexes of old type Polish Merino, rams of Polish Merino and Charolaise and ewes of Polish Merino. In these last one VLRR allele was also observed. These data (except VLRR allele) are in line with the results of earlier cited national and foreign papers. Abovementioned genotypes are consistent with the information about classical scrapie in contrast to the atypical. According to foreign studies atypical form is associated with the occurrence of phenylalanine at codon 141 and with AFRQ allele [Goldman 2008, Mcintyre et al. 2008, Mazza et al. 2010]. This allele occurred with highest frequency in both sexes of Corriedale and at very low frequency in both sexes of Żelaźnieńska sheep and both Merino breed. Other breeds did not have that allele. Generally, breeding work should be urgently directed to eliminate animals containing encoded valine at codon 136 (in particular both Merino breeds, Corriedale and Charolaise) and phenylalanine at codon 141 (in particular both Merino breeds, Corriedale and Żelaźnieńska sheep). The distributions of scrapie genotypes are in Table 4.

There was no significant impact of sex within breed on scrapie genotypes distribution, while the differences between breeds were highly significant ($P \leq 0.01$). After analysing the research data 17 genotypes were found: Polish Merino and Corriedale – 12; old type Polish Merino – 11, Żelaźnieńska sheep and Berrichon du cher – five; Charolaise – three; Suffolk – two. The genotypes with highest frequencies were: ALRR/ALRR (39.6%), ALRR/ALRQ (35.9%), ALRQ/ALRQ

Table 3. Frequency of PrP alleles occurrence in tested sheep breeds

Tabela 3. Częstotliwość występowania alleli PrP u badanych owiec

Breed Rasa			Alleles – Allele						Total Razem	
			ALRR	ALRQ	ALHQ	ALRH	AFRQ	VLRR		VLRQ
Polish Merino Merynos polski	♀	n	362	173	21	1	3	1	31	592
		%	61.1	29.3	3.5	0.2	0.5	0.2	5.2	100.0
	♂	n	71	42	7	0	0	0	2	122
		%	58.3	34.4	5.7	0.0	0.0	0.0	1.6	100.0
Old type Polish Merino Merynos polski w starym typie	♀	n	409	303	11	0	15	0	50	788
		%	51.9	38.5	1.4	0.0	1.9	0.0	6.3	100.0
	♂	n	95	38	2	0	0	0	13	148
		%	64.2	25.7	1.4	0.0	0.0	0.0	8.7	100.0
Corriedale Corriedale	♀	n	118	25	26	0	27	0	24	220
		%	53.6	11.4	11.8	0.0	12.3	0.0	10.9	100.0
	♂	n	12	0	2	0	4	0	0	18
		%	66.7	0.0	11.1	0.0	22.2	0.0	0.0	100.0
Żelaznieńska sheep Owca żelaznieńska	♀	n	345	127	11	0	5	0	0	488
		%	70.7	26.0	2.3	0.0	1.0	0.0	0.0	100.0
	♂	n	199	86	3	0	2	0	0	290
		%	68.6	29.7	1.0	0.0	0.7	0.0	0.0	100.0
Berrichon du cher Berrichon du cher	♀	n	214	25	23	0	0	0	0	262
		%	81.7	9.5	8.8	0.0	0.0	0.0	0.0	100.0
	♂	n	62	11	9	0	0	0	0	82
		%	75.6	13.4	11.0	0.0	0.0	0.0	0.0	100.0
Suffolk Suffolk	♀	n	66	8	0	0	0	0	0	74
		%	89.2	10.8	0.0	0.0	0.0	0.0	0.0	100.0
	♂	n	34	2	0	0	0	0	0	36
		%	94.4	5.6	0.0	0.0	0.0	0.0	0.0	100.0
Charolaise Charolaise	♀	n	30	6	0	0	0	0	0	36
		%	83.3	16.7	0.0	0.0	0.0	0.0	0.0	100.0
	♂	n	11	6	0	0	0	0	1	18
		%	61.1	33.3	0.0	0.0	0.0	0.0	5.6	100.0
Total within sex Razem w obrębie płci	♀	n	1544	667	92	1	50	1	105	2460
		%	62.9	27.1	3.7	0.0	2.0	0.0	4.3	100.0
	♂	n	484	185	23	0	6	0	16	714
		%	67.9	25.9	3.2	0.0	0.8	0.0	2.2	100.0
Total Razem	n	2028	852	115	1	56	1	121	3174	
	%	63.9	26.9	3.6	0.0	1.8	0.0	3.8	100.0	

Effect of breed – $P \leq 0.01$; effect of sex in old type Polish Merino – $P \leq 0.05$.Wpływ rasy – $P \leq 0,01$; wpływ płci w obrębie merynosa polskiego starego typu – $P \leq 0,05$.

(7.2%), ALRR/ALHQ (5.9%), VLRQ/ALRR (4.3%) and ALRR/AFRQ, VLRQ/ALRQ (both 2.3%). Other genotypes occurred with frequencies less than 0.6 per-

cent. Genotypes: ALRQ/ALHQ, ALRQ/ALRH, ALRQ/AFRQ, ALHQ/ALHQ, ALHQ/AFRQ, AFRQ/AFRQ, VLRR/ALRR, VLRQ/ALHQ, VLRQ/AFRQ, VLRQ/VLRQ have not been found in either sex of Żelaźnieńska sheep, Berrichon du cher, Suffolk; Corriedale rams and Charolaise ewes. The highest frequency of ALRR/ALRR genotype was found in both sexes of Berrichon du cher and Suffolk and in Charolaise ewes, which proves their high genetic resistance to classical form of scrapie [Lühken et al. 2004, Kaam et al. 2005, Kaal and Windig 2005, Goldaman 2008, Palhiere et al. 2008, Wiśniewska and Mroczkowski 2009, Mazza et al. 2010, Niżnikowski et al. 2013]. This genotype was present in all studied breeds except that, its lowest frequency has been found in both sexes of Polish Merino and Corriedale and old type of Polish Merino ewes and Charolaise rams. The heterozygote ALRR/ALRQ genotype also occurred in all breeds, with the highest frequency in both sexes of Żelaźnieńska sheep and Charolaise rams and the lowest in both sexes of Corriedale, Berrichon du cher and Suffolk. Genotype ALRR/ALHQ occurred most often in both sexes of Corriedale and Berrichon du cher, while its absence was noted in Suffolk and Charolaise. The highest frequency of ALRQ/ALRQ genotype was in Polish Merino rams and old type Polish Merino ewes. It was not present in both sexes of Suffolk and Charolaise, Corriedale rams and Berrichon du cher ewes. ALRQ/ALHQ genotype was only found in both sexes of Polish Merino and in old type Polish Merino ewes. ALRQ/ALRH genotype was only in one Polish Merino ewe and ALHQ/ALHQ genotype – only in one Corriedale ewe.

In the research material a great deal of genotypes contain alleles VLRR, VLRQ and AFRQ – a total of ten. VLRR/ALRR genotype was observed just in one Polish Merino ewe. VLRQ/ALRR genotype, was found in both sexes of old type Polish Merino, Polish Merino ewes and Charolaise rams. VLRQ/ALRQ and VLRQ/ALHQ genotypes were found in ewes and rams of both Merino breeds and Corriedale ewes, whereas VLRQ/VLRQ genotype in two ewes and one ram of old type Polish Merino. The homozygote VLRQ genotype is the least desirable due to the total lack of genetic resistance to scrapie. Other genotypes in combination with this allele must be removed from the population of sheep. Based on papers [Goldman 2008, McIntyre et al. 2008] in which relationship between atypical form of scrapie and conditions at codon 141 was confirmed, five genotypes were determined. Among them, ALRR/AFRQ genotype had a highest frequency in both sexes of Corriedale, and was absent in the meat breeds as well as in rams of both Merino breeds. ALRQ/AFRQ genotype was observed only in old type Polish Merino ewes. While ALHQ/AFRQ and AFRQ/AFRQ genotype only in Corriedale ewes. Genotype AFRQ/AFRQ, despite the presence in only two sheep, is highly undesirable, like VLRQ/VLRQ, and should be eliminated at first. Very specific VLRQ/AFRQ genotype was found in four Corriedale ewes. The results

Table 4. Frequency of PrP genotypes occurrence in tested sheep breeds
 Tabela 4. Częstotliwość występowania genotypów PrP u badanych owiec

Breed Rasa	Genotype – Genotyp																								Total Razem
	ALRR/ALRR		ALRR/ALRQ		ALRR/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		ALRQ/ALRQ		
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	
Polish Merino	n	102	121	15	2	19	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	296
♀	%	34.5	40.9	5.1	0.7	6.4	1.4	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Merynos polski	n	21	24	5	0	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61
♂	%	34.5	39.4	8.2	0.0	13.1	1.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Old type	n	122	128	6	9	71	4	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	394
♀	%	31.0	32.5	1.5	2.3	18.0	1.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Mier. polski w starym typie	n	29	26	2	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74
♂	%	39.2	35.1	2.7	0.0	6.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Comedale	n	23	21	19	15	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	110
♀	%	20.9	19.2	17.3	13.6	0.9	0.0	0.0	0.0	0.9	3.6	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Corriedale	n	3	0	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9
♂	%	33.4	0.0	22.2	44.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Zelaźnińska sheep	n	106	117	11	5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	244
♀	%	43.5	48.0	4.5	2.0	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Owca zelaźnińska	n	58	78	3	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	145
♂	%	40.0	53.8	2.1	1.4	2.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Berrichon du cher	n	84	24	22	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	131
♀	%	64.1	18.3	16.8	0.0	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Berrichon du cher	n	22	9	9	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	41
♂	%	53.6	22.0	22.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Suffolk	n	29	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	37
♀	%	78.4	21.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Suffolk	n	16	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18
♂	%	88.9	11.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Charolaise	n	12	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18
♀	%	66.7	33.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Charolaise	n	2	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9
♂	%	22.2	66.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Total within sex	n	478	425	73	31	96	9	1	6	1	4	2	1	58	34	4	5	2	1230						
♀	%	38.9	34.5	5.9	2.5	7.8	0.7	0.1	0.5	0.1	0.3	0.2	0.1	4.7	2.8	0.3	0.4	0.2	100.0						
Razem w obrębie płci	n	151	145	21	6	18	1	0	0	0	0	0	0	10	3	1	0	1	357						
♂	%	42.3	40.6	5.9	1.7	5.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	2.8	0.8	0.3	0.0	0.3	100.0						
Total	n	629	570	94	37	114	10	1	6	1	4	2	1	68	37	5	3	1587							
Razem	%	39.6	35.9	5.9	2.3	7.2	0.6	0.1	0.4	0.1	0.3	0.1	0.1	4.3	2.3	0.3	0.2	100.0							

Effect of breed – $P \leq 0.01$. Wpływ rasy – $P \leq 0,01$.

obtained by Mazza et al. [2010] indicate the possibility of co-existence of both classic and atypical scrapie, not only in one herd, but also in one sheep.

Summing up, research confirmed the possibility of both forms of scrapie practically in most breeds of sheep, with the exception Berrichon du cher and Suffolk. In this regard, urgent work should be carried out in flocks of both Merino breeds and Corriedale. In herds of Żelaźnieńska sheep elimination of AFRQ allele carriers is require, similarly VLRQ allele carriers in Charolaise. These activities require minor adjustments at Żelaźnieńska sheep and Charolaise breeds and precise breeding program in both Merino breeds and Corriedale.

CONCLUSIONS

Based on the studies carried out in four wool-meat breeds and three meat breed was found:

1. Highly significant impact of breed on frequencies of alleles and genotypes of scrapie ($P \leq 0.01$) and significant ($P \leq 0.05$) impact of sex on frequency of allele within old type Polish Merino.
2. The higher number of alleles – seven (ALRR, ALRQ, ALHQ, ALRQ, AFRQ, VLRR and VLRQ) in Polish Merino was found, while the lowest number was observed in the Suffolk (ALRR and ALRQ).
3. Phenylalanine amino acid which is encoded at codon 141 were occurred only in AFRQ allele combination, while leucine in another six.
4. Seventeen genotypes of scrapie were identified, 12 in the Polish Merino and Corriedale, five in Żelaźnieńska sheep and Berrichon du cher, three in Charolaise and two in Suffolk.
5. Very high frequencies of ALRR/ALRR genotype were observed in Berrichon du cher and Suffolk which indicate their high genetic resistance to both forms of scrapie.
6. In both Merino breeds and Corriedale were found a great deal of conditions genetically susceptibility to both forms of scrapie, which require the development of appropriate breeding programs leading to their elimination from populations of sheep, with particular reference to old type Polish Merino.

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POLIMORFIZM GENU BIAŁKA PRIONOWEGO W STADACH OWIEC MIĘSNYCH I WELNISTO-MIĘSNYCH W POLSCE

Streszczenie. Badania przeprowadzono w latach 2009–2013 w stadach owiec ras welnisto-mięsnych (merynos polski, merynos polski starego typu, corriedale, owca żelaźnieńska) oraz ras mięsnych (berrichone du cher, suffolk i charolaise). Ocenie poddano zwierzęta w wieku od 2 do 11 lat. Analizy przeprowadzono na materiale 1587 owiec (1230 samic i 357 samców). Na podstawie przeprowadzonych prac badawczych stwierdzono wysoko istotny ($P \leq 0,01$) wpływ rasy owiec na frekwencje występowania alleli i genotypów trzęsawki, oraz istotny wpływ ($P \leq 0,05$) płci w przypadku frekwencji alleli w obrębie merynosa polskiego starego typu. Wykazano występowanie największej liczby – siedmiu alleli (ALRR, ALRQ, ALHQ, ALRQ, AFRQ, VLRR i VLRQ) u merynosa polskiego, natomiast najniższa liczba – dwóch alleli została stwierdzona u rasy suffolk (ALRR i ALRQ). Aminokwas fenyloalanina kodowany w kodonie 141 wystąpił jedynie w kombinacji allelu AFRQ, natomiast leucyna u sześciu pozostałych. Zidentyfikowano łącznie 17 genotypów trzęsawki, w tym najwięcej, bo po 12 u merynosa polskiego i corriedale, po 5 u owcy żelaźnieńskiej i rasy berrichone du cher, trzech u rasy charolaise i dwóch u rasy suffolk. Stwierdzono bardzo wysoką frekwencję występowania genotypu ALRR/ALRR u ras suffolk i berrichone du cher, wskazując na ich wysoką oporność genetyczną na obie formy trzęsawki. Niskie frekwencje genotypów genetycznie podatnych na trzęsawkę klasyczną stwierdzono u rasy charolaise oraz genotypów podejrzanych, o genetyczną nieoporność na trzęsawkę atypową – u owcy żelaźnieńskiej. Wykazano też sporo uwarunkowań wskazujących na podatność genetyczną na obie formy trzęsawki, u obu ras merynosowych i corriedale, co wymaga opracowania stosownych programów prowadzących do ich wyeliminowania z populacji utrzymywanych owiec, ze szczególnym wskazaniem na merynosa polskiego starego typu.

Słowa kluczowe: owce, PrP, rozkład alleli i genotypów

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