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Transferrin Polymorphism versus Growth Rate in Lambs, Polish Long-wool Sheep

II. Analysis of relation between transferrin polymorphism of lamb blood serum versus growth rate of lambs up to age of 5 months

Summary

The flock comprised 3419 lambs, either sex, from the four subsequent lambings of the Polish long-wool sheep and the subject of the study was to attempt to verify a hypothesis of the polygenic inheritance of the growth rate of lambs in the six periods of living, (0-28, 0-100, 0-152, 28-100, 28-152 and 100-152 days respectively) and to find possible relations between the transferrin polymorphism and lamb growth rate. The relations found between the transferrin polymorphism and lamb growth rate and the preliminary evaluation leading to the identification of alleles of large effectiveness show possibilities to use the transferrin polymorphism as a genetic marker of the traits concerned for the breeding - selecting scheme.

Key words: long - wool sheep, transferrin polymorphism, growth rate, major genes.

Zusammenfassung

Titel der Arbeit: Transferrinpolymorphismus und Wachstum von Lämmern der Rasse Polnisches Langwollschaf. 2. Mitt.: Zusammenhänge zwischen dem Transferrinpolymorphismus und dem Wachstum bis zum fünften Lebensmonat

Die Untersuchungen, die 3419 Lämmer beider Geschlechter der Rasse Polnisches Langwollschaf aus vier aufeinanderfolgenden Ablammungen umfaßten, sollten die Hypothese über die polygene Vererbung des Wachstumstempos der Lämmer (in den Lebensperioden: 0.-28., 0.-100., 0.-152., 28.-100., 28.-152. und 100. - 152. Lebenstag) prüfen sowie die eventuellen Beziehungen zwischen dem Transferrinpolymorphismus und dem Wachstumstempo bestimmen. Die ermittelten Beziehungen zwischen den beiden Merkmalen und die ersten Ergebnisse der Beurteilung, die zur Aufdeckung von Genen mit einem großen Wirkungseffekt führt, weisen auf die Möglichkeit der Anwendung des Transferrinpolymorphismus als einem genetischen Marker dieser Eigenschaften in der Zucht- und Selektionsarbeit der analysierten Schafherde hin.

Introduction

There have been a number of attempts to establish the relation between quality traits and transferrin in terms of requirements of modern breeding and new criteria for the early selection. Significant relations between transferrin polymorphism and lamb weight after lambing and daily gains in different periods of life were identified in Rambouillet, Targhee, Columbia, Lincoln and Suffolk breeds, (NIX et al., 1966), Iranian sheep (PASDAR et al., 1976), Finnish sheep (ATROSHI, 1979) and Polish long-wool sheep (KMIEĆ, 1986). The relation between transferrin phenotype and body weight was also found in Croatian sheep selected for meat production (SUSIC et al.,

1992). Conventional breeding methods are based on the assumption of polygenic model of inheriting quality traits in animals inclusive of sheep. The identification of major genes, however, indicates the need to verify a hypothesis of polygenic character of inheritance (SMITH and WEBB, 1981). The following genes from among major genes should be pointed out, namely genes that influence staple thickness (PARSONS et al., 1994; ROGERS et al., 1973), muscular hypertrophy gene located on 18th sheep chromosome (COCKETT et al., 1994), sheep growth hormone (GOOTWINE et al., 1993), main histocompatibility complex gene (MHC) - (GRAIN et al., 1993), three separate loci responsible for sheep reproduction *FecC* (Cambridge type productivity), *FecI* (Iceland type productivity), *FecJ* (Java type productivity) and *Fec* productivity (Booroola type productivity) - (WASSMUTH, 1996). The *FecX* is Invendale gene located in chromosome X (DAVIS et al., 1991) responsible for high productivity the feature thereof being difficulties in the reproduction of homozygous sheep in terms of the said gene (BRAW-TAL et al., 1993). The identification of major genes which affect continuous and discrete traits is a complex process which requires the information on marker loci of the genes and backed up by certain selection of animals for mating. The information, however, might be collected on the grounds of statistics which are less costly than research and still provide indices for mixed model of inheritance (ELSEN and LE ROY, 1990; LE ROY and ELSEN, 1991); SZWACZKOWSKI, 1993; SZWACZKOWSKI et al., 1997).

This study is aimed at attempting to verify a hypothesis on the polygenic model of inheriting the quality traits within the flock in study and at answering a question if transferrin polymorphism influences the variation of traits in connection with transferrin polymorphism.

Materials and Methods

This study was carried out for four subsequent years in a pedigree flock of the Polish long-wool sheep kept at The State Animal Breeding Station at Bobrowniki. The study flock comprised 3419 lambs, either sex, from the four subsequent lambings. The growth rate in all lambs was studied in the six periods of living, i.e. 0-28, 0-100, 0-152, 28-100, 28-152 and 100-152 days respectively. The following formula was applied to calculate the growth rate: $T = [(W_2 - W_1) / (W_2 + W_1 / 2)] \times 100$, where: *T* - growth rate in certain period (percentage), *W*₁ - body weight, beginning, *W*₂ - body weight, end (MACIEJOWSKI and ZIĘBA, 1982). The analysis was made separately for males and females. The statistical analysis was carried out with the use of PEST package (GROENEVELD et al., 1990) based on BLUP formula (KENNEDY, 1989) with consideration to frequencies of phenotypes and alleles. The calculations were made to the following model: $Y_{ijk} = \mu + a_i + b_j + c_k + e_{ijk}$, where: μ - general mean, *a*_{*i*} - *i*th influence of phenotype (*i* = 1,2), *b*_{*j*} - *j*th influence of year of birth (*j* = 1,2,3,4), *c*_{*k*} - *k*th influence of birth type (*k* = 1,2), *e*_{*ijk*} - error. Each phenotype and transferrin allele were compared to the remaining ones. The least square means and standard errors were calculated with the use of LSMLMW package, (HARWEY, 1987). Quantitative traits in lambs were studied for individuals of the same sex and the following sources of

variation were taken into consideration: transferrin phenotype, age and type of delivery. Coefficients of skewness and kurtosis of distribution were analysed according to formulas given by ELANDT (1964) and the variance heterogeneity within families was estimated for groups of half-siblings. The groups of 10 individuals were studied due to the growth in reliability of the test used (LE ROY and ELSÉN, 1992). The variance heterogeneity within families (from 38 to 67 half-sibling groups – see Table 1) was conducted with the use of Bartlett test, (SZWACZKOWSKI, 1993). The hypothesis on the polygenic inheritance of traits was verified on the grounds of real data and the data corrected with reference to the year of birth, type of delivery and sex through additive corrections, (ŽUK, 1989).

Table 1

Coefficients of asymmetry and kurtosis, lamb growth rate distribution in periods of living in study and estimation of variance homogeneity within families (Koeffizient der Asymmetrie und Kurtose der Verteilung des Indikators der Wachstumsrate von Lämmern in untersuchten Lebensperioden und die Beurteilung der Homogenität der Varianz innerhalb von Familien)

Period of study	Number of half-sibling groups	Number of animals	K	Skewness		Kurtosis		Evaluation of variance homogeneity within families	
				Actual values	Corrected values	Actual values	Corrected values	Actual values	Corrected values
days 0-28	56	3119	55.39	-0.340**	-0.366**	0.331**	0.466**	**	**
days 0-100	56	2507	44.38	-0.084	-0.383**	0.082	0.836**	**	**
days 0-152	67	3021	44.81	-0.276**	-0.294**	0.367**	0.918**	**	**
days 28-100	38	1714	44.84	1.208**	1.243**	8.667**	9.856**	**	**
days 28-152	55	2541	45.95	0.854**	0.930**	6.477**	7.922**	**	**
days 100-152	50	2069	41.04	0.020	0.538**	0.549**	2.436**	**	**

k – calculated average size in half-sibling group, ** – statistical differences significant at $P \leq 0.01$

Results and Discussion

Quantitative traits are characterised by the polygenic inheritance which is understood as their genetic determination through a number of gene couples of small scale even effects and approximate symmetry of distributions of traits and variance homogeneity within families. The differentiation of gene effects and their frequencies in a way influence the departure of trait distribution from the normal distribution and the lack of homogeneity of family variance. This made researchers seek genes of large scale effects to allow for possibilities of improving the efficiency of selection (ROBERTS and SMITH, 1982). The possibility to use genes of large scale effects in selecting-

breeding schemes is connected with the identification of another gene which makes it possible to determine a quality trait called a genetic marker. One of the main indicators of selection effectiveness is allele frequency (genotype frequency as well) of large effect, (FALCONER, 1986). Coefficients of skewness and kurtosis of the distribution were estimated together with variance heterogeneity in order to verify the hypothesis on the polygenic inheritance of quality traits concerned in terms of possibilities to use them for the improvement of the effectiveness of selecting-breeding scheme in the study flock. Table 1 presents coefficients of asymmetry and kurtosis of traits and results of variance heterogeneity within families (half-sibling groups). The coefficient of asymmetry for the growth rate as estimated on the grounds of real data for the periods of 0-28, 0-152, 28-100 and 28-152 days of living was significantly different from null, ($P \leq 0.01$). It should be noted, however, that distributions of that trait were asymmetrically variant. The growth rates in the periods of 0-28 and 0-152 days were negatively skewed whereas the rates in the periods of 28-100 and 28-152 days were positively skewed. There was no departure from the normal distribution for the rates in the periods of 0-100 and 100-152 days as estimated on the grounds of real data, see Table 1. The coefficient of asymmetry estimated on the grounds of the corrected data was significantly different from null ($P \leq 0.01$) in all periods concerned. Distributions were negatively skewed for the growth rate in periods of 0-28, 0-100 and 0-152 days whereas the rates in the periods of 28-100, 28-152 and 100-152 days were positively skewed, see Table 1. Another parameter of the distribution, that is a coefficient of kurtosis is characterised by the deviation from normality and values above zero are regarded as the excess and the ones below zero as oblateness accordingly. The distribution may not only be asymmetrical but exhibit kurtosis as well, (ELANDT, 1964). The analysis of the coefficient of kurtosis for the traits concerned proved that values above zero and significantly different from null were found ($P \leq 0.01$) for the growth rate in almost all periods both for real data (with the exception for the period of 0-100 days) and corrected data, see Table 1. Calculations were made on the grounds of real and corrected data while estimating the homogeneity of variance within groups of half-siblings, see Table 1 i.e. in the same manner as for estimating coefficients of asymmetry and kurtosis. The method applied is based on assuming the variance heterogeneity within a family in case of segregating a gene of large effect. The assumption in turn is based on the fact that the different genotypes of genes in parents matched are associated with differentiated distribution of genotypes in the offspring. The small value of variance within a given family is characteristic for homozygotes (dominant or recessive) whereas the greater values are observed for families that consist of individuals of various genotypes (predominant homozygous, heterozygous, recessive homozygous). Thus the basis was found for heterogeneity of variance within half-sibling groups, ($P \leq 0.01$), for the growth rate in all periods of living concerned both for actual and corrected data - see Table 1. Generally, the results obtained lay foundations for the hypothesis on possibilities of mixed inheritance (genes of large effect and polygenes) of traits in study in the flock. Another issue being the aim of this study was an attempt to find relations between transferrin polymorphism and quality

Table 2

Growth rate in lamb rams versus transferrin phenotype (%) (Indikator der Wachstumsrate von Jungböcken in der Abhängigkeit vom Transferrinphänotyp)

Growth rate in ramie ramis versus antherium phenotype (74) (continued)																				
Pheno- type	n	Growth rate in periods																		
		days 0 - 28			days 0 - 100			days 0 - 152			days 28 - 100			days 28 - 152			days 100 - 152			
		LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	
AA	4	93.86	8.50	-5.93	129.15	6.94	-8.92	148.96	4.96	-1.72	52.97	8.28	-0.77	83.04	6.73	+1.89	28.02	4.49	+3.03	
AB	53	102.39	2.63	+2.84	142.16	1.84	+5.00**	152.83	1.39	+2.26	54.90	2.64	+0.86	85.24	2.06	+4.34	26.49	1.27	+1.60	
AC	43	101.54	2.75	+1.62	140.75	2.18	+3.34	151.94	1.56	+1.14	56.91	2.91	+3.06	81.56	2.20	+0.51	24.55	1.49	-0.45	
AD	30	99.49	3.19	+0.31	143.41	2.68	+7.01**	152.18	1.87	+1.93	58.93	3.45	+5.66	83.49	2.53	+2.55	23.99	1.88	-1.14	
AE	4	94.71	8.49	-4.46	133.02	6.93	-6.08	145.40	4.96	-5.84	51.49	8.26	-2.78	76.74	6.72	-5.01	21.27	4.49	-4.53	
BB	172	97.99	1.54	-1.35	137.94	1.15	+1.01	149.39	0.88	-0.89	51.54	1.61	-2.28	79.24	1.24	-1.88	23.70	0.84	-1.39	
BC	311	96.99	1.24	-2.54	136.00	0.95	-1.14	149.21	0.71	-1.15	53.29	1.29	-0.52	80.42	1.00	-0.68	25.66	0.67	+0.67	
BD	255	98.67	1.36	-0.66	138.50	0.95	+1.51	149.77	0.76	-0.67	55.80	1.35	+1.07	80.50	1.10	-0.70	24.17	0.68	-0.95	
BE	31	95.05	3.32	-5.01	133.78	2.73	-3.31	146.64	1.82	-4.09*	52.55	3.88	-1.25	80.69	2.68	-0.02	24.33	1.83	-0.61	
CC	147	94.94	1.61	-4.74*	136.35	1.21	-0.61	148.76	0.92	-1.58	54.09	1.66	+0.54	81.35	1.30	+0.52	25.53	0.85	+0.51	
CD	198	95.22	1.47	-4.24*	137.36	1.08	+0.06	149.23	0.82	-1.14	55.78	1.50	+2.12	81.79	1.18	+0.77	25.18	0.76	+0.07	
CE	36	99.18	2.94	-1.00	134.32	2.81	-2.53	149.86	1.71	-0.72	55.66	3.54	+2.55	80.72	2.36	+0.43	25.08	1.88	-0.17	
DD	70	100.42	2.25	+0.49	137.93	1.66	+0.46	150.94	1.26	+0.10	52.34	2.31	-1.72	81.66	1.81	+0.84	26.16	1.15	+1.05	
DE	18	104.36	4.45	+6.10	139.90	3.66	+4.20	150.84	2.38	+1.38	47.40	5.45	-6.54	77.45	3.52	-3.76	26.58	2.49	+2.32	
EE	1	114.62	16.94	+18.59	-	-	-	159.73	9.89	+10.98	-	-	-	81.95	13.41	+0.22	-	-	-	
Total	1373	99.30	1.65		137.18	1.00		150.38	0.97		53.83	1.28		81.05	1.31		25.05	0.70		

* - statistical differences significant at $P \leq 0.05$; ** - statistical differences significant at $P \leq 0.01$

Table 3

Quality traits of lamb rams versus transferrin alleles (Untersuchte Nutzeigenschaften von Jungböcken in Abhängigkeit vom Auftreten der Transferrinallele)

Period of study	Tf ^A allele			Tf ^B allele			Tf ^C allele			Tf ^D allele			Tf ^E allele			Total	
	n = 134			n = 822			n = 735			n = 571			n = 90			n = 1373	
	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE
days 0- 28	100.98	3.14	-7.45	97.99	1.51	-9.56	96.48	1.55	-15.39	97.91	1.70	+2.58	98.77	3.77	+20.23	99.30	1.65
days 0-100	141.33	2.44	+0.87	137.49	1.12	+4.32	136.63	1.20	-1.42	138.34	1.26	+18.99**	135.20	3.14	-9.63	137.18	1.00
days 0-152	152.06	1.76	-2.81	149.56	0.85	-6.48	149.32	0.88	-4.94	149.89	0.95	+2.14	148.86	2.12	+2.67	150.38	0.97
days 28-100	56.29	3.24	+8.61	53.78	1.56	-2.99	54.45	1.62	+11.19	55.27	1.76	+0.90	52.72	4.26	-10.41	53.83	1.28
days 28-152	83.35	2.49	+5.82	80.52	1.21	+1.60	81.06	1.24	+2.13	81.15	1.37	-0.34	79.89	3.02	-11.50	81.05	1.31
days 100-152	25.20	1.67	-2.16	24.79	0.79	-0.99	25.41	1.00	+0.90	24.83	0.88	+1.94	24.95	2.10	-3.88	25.05	0.70

* - statistical differences significant at $P \leq 0.05$

Table 5

Quality traits of lamb ewes versus transferrin alleles (Untersuchte Nutzeigenschaften weiblicher Lämmer in Abhängigkeit vom Auftreten der Transferrinallele)

Period of study	Tf ^A allele			Tf ^B allele			Tf ^C allele			Tf ^D allele			Tf ^E allele			Total	
	n = 163			n = 907			n = 794			n = 629			n = 74			n = 1492	
	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE
days 0- 28	99.18	2.66	+19.46	96.27	1.50	-1.30	95.42	1.52	-16.82	97.25	1.68	+3.20	96.15	3.99	-10.19	97.55	1.47
days 0- 100	135.13	2.14	+13.18	133.42	1.06	+0.83	133.39	1.12	-5.64	133.97	1.19	+11.39	133.07	3.42	-14.22	133.45	1.19
days 0- 152	147.13	1.60	+18.10*	145.26	0.85	-3.75	144.82	0.87	-7.74	145.57	0.94	+2.77	144.51	2.38	-5.97	145.80	0.89
days 28- 100	50.37	3.14	+8.86	50.77	1.72	+7.67	49.94	1.76	+5.07	50.61	1.93	+10.84	48.48	5.25	-10.73	48.83	1.69
days 28- 152	73.35	2.48	+8.28	72.85	1.46	-5.47	72.79	1.49	+6.19	72.79	1.57	+5.74	71.47	3.63	+5.53	72.02	1.41
days 100-152	21.73	1.39	-0.41	21.51	0.70	+5.93	21.11	0.73	+0.07	20.92	0.79	+4.67	22.68	2.29	+3.31	21.02	0.77

* - statistical differences significant at $P \leq 0.05$

traits of the lambs. Table 2 shows values of the quality traits in lamb rams versus transferrin phenotype. The significantly smaller growth rate ($P \leq 0.05$) in the period of 0-28 days was found in lamb rams exhibiting Tf CC (94.94%) and Tf CD (95.22%) transferrin genotypes compared to all remaining ones and the estimated differences were -4.74% and -4.24% respectively, see Table 2. The significantly greater growth rate ($P \leq 0.01$) in the period of 0-100 days was found in lamb rams exhibiting Tf AB (142.16%) and Tf AD (143.41%) transferrin genotypes compared to all remaining phenotypes and the estimated differences were 5.00% and 7.01% respectively, see Table 2. The significantly smaller growth rate ($P \leq 0.05$) in the period of 0-152 days was found in lamb rams exhibiting BE (146.64%) transferrin and the estimated difference was -4.09%. The estimated differences in growth rate in periods of 28-100, 28-152 and 100-152 days accordingly were not statistically confirmed, see Table 2. Table 3 shows growth rates versus transferrin alleles in lamb rams. Lamb rams exhibiting Tf^D transferrin genotype were characterized by the significantly greater growth rate ($P \leq 0.01$) in the period of 0-100 days, the estimated difference being 18.99%. Significant relations ($P \leq 0.05$ and $P \leq 0.01$) were also found in lamb ewes between the growth rate and transferrin genotype in periods of 0-28 and 0-152 days respectively, see Table 4. The significantly smaller growth rates ($P \leq 0.05$ and $P \leq 0.01$) in the period of 0-28 days were found in lamb ewes exhibiting BC (-3.17%) and CC (-5.37%) transferrin genotypes respectively. The significantly smaller growth rate ($P \leq 0.01$) in the period of 0-152 days was found in lamb ewes exhibiting Tf CC (-2.91%). The differences in the growth rate in lamb ewes in the remaining periods were not confirmed statistically, see Table 4. The analysis of the relation between the growth rate in lamb ewes and transferrin alleles proved significant differences ($P \leq 0.05$) only in Tf^A allele in the period of 0-152 days (18.10%). It should be noted that estimated differences in the growth rate in lamb ewes in the study periods were always positive for animals exhibiting Tf^D allele. The differences, however, were not statistically confirmed, see Table 5. Similar relations between transferrin polymorphism and daily weight gain in different periods of lamb living were found in sheep of rambouillet, targhee, columbia, lincoln, suffolk breeds, (NIX et al., 1968), in Finnish sheep, (ATROSHI, 1979) and in the study flock in the earlier research, (KMIEÆ, 1986). The relation between transferrin phenotypes and daily weight gain in the study periods of living was not found in the Iranian sheep, (PASDAR et al., 1976). Individuals of the heterozygous transferrin genotype exhibited the greater growth rate both in lamb rams and ewes in all periods of living although the differences were not confirmed statistically, see Table 6. The results obtained are consistent with results reported by other authors who proved that sheep of the heterozygous transferrin genotype were heavier than the homozygous ones, (BOGDANOV and POLJAKOVSKI, 1970; ARORA et al., 1971, TIJANKOV, 1972; BUDNIKOVA and BAŠKHEEVA, 1979; RIBIN et al., 1979).

Conclusions

The results obtained allow to advance the hypothesis of the mixed model of inheritance (genes of large effect plus polygenes) regarding the growth rate in lambs in the study

Table 4
Growth rate of lamb ewes versus transferrin phenotype (%) (Indikator der Wachstumsrate der Jungschafe in Abhängigkeit vom Auftreten des Transferrin-
phänotyps)

Pheno- type	n	Growth rate in periods																	
		days 0 - 28			days 0 - 100			days 0 - 152			days 28 - 100			days 28 - 152			days 100 - 152		
		LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference	LSM	SE	Difference
AA	3	108.41	7.90	+10.62	139.82	5.86	+5.76	151.47	5.64	+4.92	44.81	7.59	-4.48	62.39	8.22	-8.86	15.83	4.14	-4.75
AB	59	99.61	2.28	+2.22	134.97	1.87	+1.85	146.43	1.38	+0.79	50.80	2.73	+2.28	71.06	2.11	-1.18	22.63	1.23	+1.70
AC	55	98.22	2.37	+0.73	134.32	1.85	+0.93	146.95	1.40	+1.31	48.42	2.88	-0.05	74.64	2.23	+2.75	21.23	1.22	+0.16
AD	42	99.47	2.69	+2.08	136.42	2.21	+2.89	147.83	1.59	+2.14	52.48	3.20	+3.90	74.87	2.50	+2.91	21.42	1.38	+0.80
AE	4	96.20	7.88	-1.66	131.41	6.75	-1.96	149.40	4.86	+3.87	52.92	8.81	+4.69	81.67	7.10	+10.30	23.04	4.12	+2.21
BB	195	99.34	1.51	+2.09	134.71	1.12	+1.29	146.61	0.87	+0.99	50.05	1.79	+1.36	71.30	1.45	-0.94	20.65	0.73	-0.45
BC	355	94.35	1.28	-3.17*	133.10	0.89	-0.43	144.67	0.72	-1.08	50.85	1.43	+2.23	73.62	1.34	+1.47	21.82	0.58	+0.78
BD	271	95.84	1.42	-1.67	132.69	0.92	-0.86	145.02	0.77	-0.71	51.58	1.57	+1.84	73.88	1.34	+1.78	21.35	0.61	+0.28
BE	27	96.56	3.35	-0.46	132.36	2.68	-1.37	143.10	1.95	-2.74	46.91	4.52	-2.22	67.55	3.04	-5.04	22.87	1.89	+1.92
CC	143	92.40	1.57	-5.37**	131.75	1.30	-1.81	142.81	0.92	-2.91**	48.46	1.96	-0.38	71.85	1.47	-0.40	21.32	0.84	+0.29
CD	221	98.70	1.48	+1.27	135.04	1.02	+1.65	146.01	0.82	+0.30	49.86	1.67	+1.27	71.54	1.39	-0.66	19.79	0.66	-1.30
CE	20	92.08	3.72	-5.46	129.38	3.08	-4.22	142.71	2.23	-3.05	49.49	4.34	+0.63	73.51	3.46	+1.27	21.24	1.88	+0.12
DD	74	96.19	2.15	-1.51	132.75	1.54	-1.01	144.51	1.24	-1.38	48.48	2.35	-0.24	71.30	1.98	-0.80	21.48	1.02	+0.52
DE	21	99.45	3.64	+2.10	138.64	3.28	+5.39	147.35	2.18	+1.62	49.72	5.45	+0.96	72.94	3.29	+0.89	24.34	2.40	+3.44
EE	2	96.49	11.11	-1.80	124.36	11.66	-8.09	142.07	6.86	-4.05	37.59	15.19	-11.79	68.14	10.00	-3.49	16.32	7.11	-5.32
Total	1492	97.55	1.47	x	133.45	1.19	x	145.80	0.89	x	48.83	1.69	x	72.02	1.41	x	21.02	0.77	x

* - statistical differences significant at $P \leq 0.05$; ** - statistical differences significant at $P \leq 0.01$

Table 6

Growth rate in homo- and heterozygous lambs with reference to transferrin genotype (Indikator der Wachstumsrate von hinsichtlich des Transferringenotyps homo- und heterozygoten Lämmern)

Period of study	Lamb rams						Lamb ewes							
	Homozygous				Differ- ence	Total		Homozygous				Differ- ence	Total	
	n = 394		n = 979			n = 1373		n = 417		n = 1075			n = 1492	
	LSM	SE	LSM	SE		LSM	SE	LSM	SE	LSM	SE		LSM	SE
days 0-28	97.28	1.80	97.51	1.74	+9.59	99.30	1.65	96.45	1.74	96.43	1.69	+5.66	97.55	1.47
days 0-100	137.25	1.32	137.62	1.33	-10.86	137.18	1.00	133.33	1.34	133.70	1.23	-5.54	133.45	1.19
days 0-152	149.45	1.03	149.72	0.97	+9.42	150.38	0.97	144.95	1.01	145.36	1.01	-3.43	145.80	0.89
days 28-100	52.65	1.82	54.81	1.83	-5.53	53.83	1.28	49.13	2.05	50.63	1.97	-2.71	48.83	1.69
days 28-152	80.50	1.45	81.07	1.39	+2.29	81.05	1.31	71.41	1.64	73.08	1.62	-2.28	72.02	1.41
days 100-152	24.87	0.94	25.05	0.93	+4.16	25.05	0.70	20.97	0.87	21.35	0.81	-13.58	21.02	0.77

periods of living. The statistically significant relations ($P \leq 0.05$ and $P \leq 0.01$) between lamb rams transferrin phenotypes and growth rates in periods of 0-28, 0-100 and 0-152 days were found. The statistically significant relations ($P \leq 0.05$ and $P \leq 0.01$) were found in ewes for periods of 0-28 and 0-152 days as far as the growth rate was concerned. The significant relations were observed with respect to Tf CC phenotype regarding the growth traits both in lamb rams and ewes in periods of 0-28 days and in lamb ewes in the period of 0-152 days and the estimated differences in the level of the traits concerned were negative compared to all other individuals. The relations between alleles together with transferrin phenotypes and lamb growth rate indicators as well as results of statistical estimation leading to detecting genes of large effect show possibilities of using the transferrin polymorphism as a genetic marker for the traits concerned in the selecting-breeding scheme. Such possibilities occur irrespective of biological functions of transferrin, functions of dominant genes or the phenotype large effect of the dominant genes being shown through the exposure of certain biological functions of transferrin or a result of its genotypes.

The results of the study show how complex the relations between transferrin polymorphism and quality traits as well as mechanisms of natural and breeding selections are. They may also suggest the feedback between transferrin locus and „major genes“ locus, the dominant genes being responsible for conditioning lamb traits in study.

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Buchbesprechung

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