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FIBRE CHARACTERISTICS IN NORMAL-HAIRED AND ANGORA RABBITS AS DEPENDENT ON THEIR GENETIC BACKGROUND

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ABSTRACT

The authors compared the physical characteristics of the different types of hair fibre composing the fur or wool of progeny born from various matings of purebred normal-haired (N), angora (A) and their crossbred (F1) rabbits (NxN, F1xN, NxF1, F1xF1, AxF1 and AxA). These normal-haired and angora offspring carried in their genetic background different proportions of the genes of the other type: the normal-haired ones had 0, 25, 33 or 50% A genes and the angoras 50, 25 or 0% N genes. It was established that the respective types of fibre in the coat of the rabbits which also carried angora genes were longer, had greater cross-sectional area and were thicker, and the fur was more abundant in bristle fibres than was characteristic of the purebred normal-haired rabbits. In comparison with the purebred angoras, the different hair types of the angora progeny from the AxF1 and F1xF1 matings, which carried N genes in proportions of 25 and 50% respectively, were shorter and finer. These findings corroborate the hypothesis that, in addition to the angora gene, the other part of the genome also plays an influencing role in the development of the physical characteristics of the different types of hair, and the dominant allele for normal hair does not suppress the recessive angora allele to a degree of 100% (i.e. there is an incomplete penetrance).

INTRODUCTION

OLÁH (1958) found that the effect of the angora characteristic is apparent in a proportion of heterozygous F1 rabbits bred by mating normal-haired with angora rabbits. The significance of this is that in some cases the dominant allele for common hair does not suppress the recessive allele to a degree of 100% (i.e., there is not complete penetrance). Apart from two publications (DAMME *et al*., 1985; SHEN, 1992) there is only extremely sparse information available on how the quality of the coat or the wool change when the two types are paired. In China the greatest proportion of angora rabbit wool is produced by angoras back-crossed to various degrees (LIN *et al*., 1994; COLIN, 1995; SHEN *et al*., 1997); hence, examination of the wool production of angora rabbits of different genetic background is of importance not only from the theoretical aspect but also with respect to practical application.

Within the framework of a series of experiments the authors examined the following: the reproduction indicators for various matings (NxN, AxA, F1xN, NxF1, F1xF1 and AxF1) performed with purebred normal-haired (N), angora (A) and their single-crossed (F1) rabbits (EIBEN *et al*., 2000a); the growth and slaughter traits of normal-haired and angora progeny, derived from the above matings, which carried the genes of the other type in various ratios (EIBEN *et al*., 2000b); and the wool production of angora progeny with different genetic backgrounds (EIBEN *et al*., 2000c).

This research aimed to compare the bristle content of the coat of normal-haired offspring from NxN, F1xN, NxF1, F1xF1 and AxF1 matings with that of the wool of the angora progeny born in AxA, AxF1 and F1xF1 groups; the length and cross-sectional characteristics of the individual hair fibre types were also studied. The issue of importance is how the traits of fibre types of the coat or fleece of rabbits of normal-haired or angora phenotype are influenced by the presence in their genetic background of genes originating from the other type.

MATERIAL AND METHODS

The studies were performed at the experimental site of the University of Kaposvár, with progeny of equal sex ratio born from various matings between purebred normal-haired Pannon White (N), German angora (A) and their single-crossed (F1) rabbits (Table 1).

The animals were kept in a closed building with artificial lighting (16L:8D), in individual flat-deck wire mesh cages (80x50x40 cm). In winter warm air was blown in to heat the building (15-16°C), and in summer the temperature at times exceeded 25 °C. The rabbits were fed *ad libitum* with a commercially available pelleted rabbit diet (86% dry matter, 16.5% crude protein, 2.7% crude fat, 15.5% crude fibre, 0.70% lysine, 0.32% methionine, 0.60% Met+Cys, 10.3 MJ/kg digestible energy; pellet ∅ 3 mm), and drinking water was available *ad libitum* from nipple drinkers. No hay supplementation was given.

Wool samples were collected from angoras at the third and fourth harvest. At the same occasions, also hair samples were taken from normal-haired rabbits, i.e. the first one at time of 3rd shearing from the right side while the second one at time of 4th shearing, from the left side of the haunch. The total number of the wool and hair samples was 750. This paper outlines the results obtained for the third shearing of angoras and first hair sampling of normal-haired rabbits born in spring or summer.

The preparation and evaluation of the fibre samples were performed in France (at INRA, Le Magneraud and Toulouse). The measurements were taken 2 cm from the base end of the hair fibres, as their mean diameter varies very little at this point (THÉBAULT *et al*., 1995). The samples were fixed onto stiff card with rubber bands such as to ensure that the proximal, shorn ends of the hairs remained in the same plane. Hair specimens containing only bristle fibres (bristle lock) were mounted on microscope slides for the purposes of examining the cross-sectional characteristics of the bristle hair fibres, while slides reflecting the original hair follicle bundle composition (whole lock) were prepared for the examination of the hair structure (bristle + awn/down fibres, in %) besides the evaluation of other two fibre type (awn and down) characteristics. The samples, consisting of parallel hair fibres, were fixed with nail polish and drawn with thread into a 10-15 mm long plastic tube of 1.6 mm internal diameter. The samples were inserted into a fibrotom (ITF-Fibrotome, Instrument S.A.), after which, by means of a razor blade, four sections of 50-60 μm thickness were prepared; these were fixed on a microscope slide with a cover slip and nail polish. The Imagine Analysis computer procedure (THÉBAULT *et al*., 1995), facilitated by the VISILOG (C) programme (Noesys 3.6.1, France) was used in the evaluation of the slides. Depending on the type and thickness of the hair under examination, 1000-4000 individually designated hair fibres per section were examined. The cross-sectional area of each hair measured was derived from the average of the diameters recorded on that hair from nine different directions. The computer programme distinguished the three types of hair fibre (bristle, awn and down fibre) on the basis of dimensions and degree of medullation, and determined the largest, smallest and mean diameter for each hair fibre. The degree of accuracy achieved with this method is illustrated by the fact that the repeatability values proved to be between 0.80 and 0.99. The length of the hairs was measured with a ruler (5 bristle, 5 awn and 5 down hair fibres per sample).

Statistical evaluation of the data was performed according to the GLM (General Linear Models) procedure, by means of SAS software, version 6.09. The tables give the least square means (LSM) and the residual standard deviation (RSD). The chi-square test was used to examine the significance of the frequency distributions (FREQ examination, SAS version 6.09). In the analysis of variance procedure the factors affecting the physical characteristics of the hair types (cross-sectional area, diameter and length) were tested on the basis of the individual data obtained, with account taken of the fixed effects (sex and season), by means of the following model:

$Y_{ijklm}= \mu+G_i+P_j+S_k+Se_l+e_{ijklm}$

where Y_{ijklm} = production of the individual under examination
μ = overall mean
G_i = genotype of the progeny (i=NN, F1N/NF1, F1F1, AF1, AA)
P_j = phenotype of the progeny (j=normal-haired, angora)
S_k = effect of sex (k=male, female)
Se_l = effect of season (l=spring, summer)
e_{ijklm} = random error

RESULTS AND DISCUSSION

Bristle content

The bristle rate of the normal coat proved significantly higher than that measured in the angora fleece (Table 1). This is contrary to the report of ROCHAMBEAU (1988) that the angora mutation did not influence the bristle to down fibre ratio, which ranges between 1 to 2.5% for both common fur and angora wool. In both phenotypes, however, it was observed that there was no significant change in bristle rate with increase in the proportion of genes originating from the other type, which seems to support the findings reported by ROCHAMBEAU (1988).

DAMME *et al*. (1985) observed a decrease in bristle rate among progeny in groups of purebred New Zealand White, German angora x NZW, AN and AA offspring of German angora x (German angora x NZW), and in purebred German angora rabbits (4.7, 2.6, 3.4, 1.0 and 0.8% respectively). In accordance with our results, in the above study the bristle rate of the normal hair was higher than that of the wool, the difference only being significant between the two phenotypes. In a study performed by SHEN (1992), as compared to the purebred German or French angoras, the bristle rate of the wool was found to be higher in the angora progeny of (NZW x angora) x angora groups, and also when the two angora rabbit types were crossed.

Length of bristle, awn and down fibres

The results of this study confirm the observation (OLÁH, 1958) that the angora characteristic is apparent in a proportion of **normal-haired** F1 rabbits. In the F1xN and NxF1 matings, from which, in theory, half of the progeny were of NN or AN/NA genotype, all three types of hair were longer than in the NxN group, the difference proving significant in the case of the bristle fibres (Table 1). Further increase in the proportion of the angora genome exerted no influence on the length of the respective hair types.

Table 1:Bristle rate and fibre length of different hair types in normal-haired and angora rabbits of different genetic background

Group	n	Offspring phenotype	Offspring genome part	Bristle rate, %	Fibre length, mm *bristle*	Fibre length, mm *awn*	Fibre length, mm *down*
NxN	33	normal	0% A	1.37^{a}	36.8^{d}	33.0^{d}	26.8^{c}
F1xN/NxF1	43	normal	25% A	1.50^{a}	39.8^{c}	35.1^{cd}	28.8^{bc}
F1xF1	38	normal	33% A	1.44^{a}	38.8^{c}	33.9^{cd}	28.3^{b}
AxF1	21	normal	50% A	1.67^{a}	39.8^{c}	34.4^{c}	28.2^{bc}
F1xF1	11	angora	50% N	0.33^{b}	97.1^{ab}	83.3^{ab}	69.2^{a}
AxF1	25	angora	25% N	0.55^{b}	89.9^{b}	80.6^{b}	69.8^{a}
AxA	41	angora	0% N	0.36^{b}	96.2^{a}	84.2^{a}	70.6^{a}
P				NS	*	*	*
Phenotype	135	normal		1.50^{b}	39.0^{a}	34.3^{a}	28.2^{a}
	77	angora		0.41^{a}	94.4^{b}	82.7^{b}	69.9^{b}
Sex	106	male		1.06^{a}	67.8	59.9^{a}	50.0^{a}
	106	female		0.85^{b}	65.6	57.1^{b}	48.1^{b}
Birth season				NS	NS	NS	NS
RSD				0.58	8.28	6.26	5.39

Values with different superscripts within columns show significant difference.
(NS: $P>0.05$ a,b,c,d and $*P<0.05$.)

In comparison with the **wool** of the purebred angora rabbits, the bristle and the awn hairs in the fleece of the AxF1 progeny of 25% N genetic background were significantly shorter. However, the same trait in the F1xF1 angora progeny, which carried the genes of normal-haired rabbits in a ratio of 50%, corresponded to that of the AxA group (Table 1). The slight differences found in the length of the down fibres were not statistically verifiable. On comparing purebred NZW, German angora x NZW and angora x F1 normal-haired progeny, DAMME *et al.* (1985) also observed a small, but non-significant change in the length of the bristle and down fibres with increase in the proportion of the gene originating from angoras. In their study the down fibres of the AxA rabbits were insignificantly longer but their bristle fibres were shorter than those of the angora progeny of the angora x F1 group. On the other hand, SHEN (1992) reported longer bristle and down fibres in F1 x German angora group than in purebred German angora rabbits.

Cross-sectional area and mean diameter of bristle, awn and down fibres

In the **normal-haired** rabbits the cross-sectional area of the hairs increased in all three fibre types proportionate to increase in the ratio of the angora genome. The difference proved significant for bristle and down fibres in the AxF1 normal-haired progeny (50% A) in comparison with the NxN group (Table 2). The same change was recorded with respect to the mean diameter of the hair types. Bristle and down fibres proved thicker than in the NxN or the F1xN/NxF1 group not only for the AxF1 progeny, but even in the F1xF1 (33% A genome part) offspring (Table 2).

The cross-sectional area and thickness of the respective types of hair fibre in the **angora wool** also increased proportionate to decrease in the ratio of the N gene. The cross-sectional area and thickness of the bristle and awn hairs showed no statistical difference between the angora progeny of the AxA and AxF1 groups, but their values were significantly greater than the corresponding data recorded in the F1xF1 angora progeny, which carried N genes in a ratio of 50% (Table 2). The cross-sectional area and thickness of the down hair fibres, which constitute 95 to 100% of the fleece, were significantly smaller in the wool of the AxF1 and F1xF1 angora rabbits in comparison with the AxA group, but there was no significant difference between the angora progeny of 25 or 50% N genetic background (Table 2).

DAMME *et al*. (1985) also observed increased thickness in the down fibres in the normal-haired progeny of a German angora x F1 group in comparison with purebred New Zealand Whites, but the down fibres were found to correspond in thickness between AxA and AxF1 angora rabbits. SHEN (1992) found the mean diameter of the bristle fibres to be greater in an F1x German angora group than in purebred German angoras, but this diameter was smaller in F1x French angora groups than in purebred French angora rabbits.

Table 2: Cross-sectional area and mean diameter of different hair types in normal-haired and angora rabbits of different genetic background

	Offspring		**Area, µm^2**			**Average diameter, µm**		
Group	pheno- type	genome part	*bristle*	*awn*	*down*	*bristle*	*awn*	*down*
NxN	normal	0% A	1761^{b}	647^{ab}	127^{cd}	54.3^{b}	32.7^{ab}	14.0^{cd}
F1xN/NxF1	normal	25% A	1760^{b}	588^{bc}	135^{bc}	54.8^{b}	31.2^{bc}	14.5^{bc}
F1xF1	normal	33% A	1889^{ab}	570^{bc}	148^{a}	57.0^{a}	30.6^{bc}	15.2^{a}
AxF1	normal	50% A	2025^{a}	727^{a}	141^{ab}	59.0^{a}	34.7^{a}	14.8^{ab}
F1xF1	angora	50% N	914^{d}	494^{d}	89.8^{f}	39.4^{d}	28.6^{d}	11.7^{f}
AxF1	angora	25% N	1056^{c}	533^{c}	110^{f}	42.7^{c}	29.4^{c}	13.0^{f}
AxA	angora	0% N	1075^{cd}	564^{bc}	120^{d}	43.0^{cd}	30.5^{bc}	13.6^{d}
P			*	*	***	**	*	***
Phenotype	normal		1859^{b}	633^{b}	138^{b}	56.3^{b}	32.3^{b}	14.6^{a}
	angora		1015^{a}	530^{a}	107^{a}	41.7^{a}	29.5^{a}	12.8^{b}
Sex	male		1323^{a}	566	122	47.0^{a}	30.5	13.7
	female		1550^{b}	597	123	51.0^{b}	31.3	13.8
Birth season			*	NS	*	*	NS	*
RSD			222	88.9	25.3	3.69	2.47	1.33

Values with different superscripts within columns show significant difference.
(NS: $P>0.05$ *$P<0.05$ **$P<0.01$ ***$P<0.001$.)

CONCLUSIONS

Our results confirm those previous observations that the angora effect is apparent in a proportion of crossbred rabbits, as the three types of hair fibre proved longer and thicker in the normal-haired ones which carried the angora gene in their genetic background. The reverse is also true, since, in contrast with the purebred angoras, the various fibre types in the AxF1 and F1xF1 angora progeny carrying 25 and 50% ratios of the genes of the other type grew shorter and finer. On the basis of the data obtained it seems that the bristle rate differs only between normal coat and angora fleece of homozygous origin; in heterozygous rabbits carrying the genome of the other type in various degrees this ratio does not vary significantly. In some instances earlier observations (DAMME *et al*., 1985; SHEN, 1992) were statistically verified: the length of the bristle and down fibres increases with higher proportion in the angora genetic background in normal-haired rabbits and with a decrease in the ratio of genes originating from the normal-haired type in angoras. For all three types of fibre and in both the normal-haired and the angora rabbits it was unambiguous that the cross-sectional area and thickness of the hairs increased distinctly proportionate to increase in the ratio of the angora gene present.

The recent results together with our previous report regarding wool production (Eiben *et al.*, 2000c) corroborate the hypothesis (Mirgiyants cit. Rochambeau, 1988) that complemental genes also play an influencing role in angora wool production and in the development of the physical traits of the hair fibre types, and also that the dominant allele for normal coat does not suppress the recessive allele to a degree of 100% (i.e., there is an incomplete penetrance).

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