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Heritabilities of and genetic correlations between the dairy traits in goats estimated in first *vs* later lactations

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The purpose of the study was to evaluate the multiple-trait model, as opposite to repeatability model approach, at an early stage of developing the breeding value estimation system for dairy goats in Poland. Milk, fat, and protein yields and fat and protein contents in first (4,443 records) and following parities (9,115 records of 5,244 goats) were analysed as two separate traits within a trait. Variance components were estimated with REML method. Classification of dairy traits in lactation I contained random effects of animal's additive genetic background, herd-sire interaction, and fixed effects of herd-year-season, breed, year of birth, litter size, and linear regression on days-in-milk. Traits recorded in later lactations were considered to be the same within a trait, yet of repeated measurements. Hence, statistical model additionally accounted for fixed effect of parity and random effect of permanent environment. Heritability of milk yield ranged from 0.214 to 0.247 in later lactations, and from 0.190 to 0.324 in lactation I depending on set of traits which were estimated simultaneously. For lactation I the h^2 for fat yield ranged from 0.208 to 0.224 and for later lactations from 0.204 to 0.216. Heritability for protein yield ranged from 0.130 to 0.208 for lactation I, and from 0.180 to 0.201 for later lactations. Heritabilities for fat content ranged from 0.278 to 0.318 in lactation I and from 0.214 to 0.243 in later lactations. Those for protein content were between 0.397 to 0.448 and 0.276 to 0.310 for lactation I and later lactations, respectively. Repeatability coefficients for all the dairy traits in the later lactations were between 0.247 to 0.355. Phenotypic correlations between lactations for each trait exceeded 0.50 while genetic correlations ranged from 0.880 to 0.996. Correlations between yields within lactation were high and positive while those between milk yield and milk constituents contents were moderate and negative. Presented correlations follow the general pattern found in

other dairy goat as well as in dairy cattle populations. It is concluded that repeatability model should better suit Polish conditions.

KEY WORDS: correlations / dairy goats / heritability / multiple-trait model / single-trait model

There are numerous papers studying the genetic parameters for cattle dairy traits in the first two or more lactations – Meyer [1983, 1984], Short *et al.* [1990], García-Cortés *et al.* [1995]. When later lactations are included in estimating the breeding value, more ties between sires are created leading to increase the accuracy of evaluation [Meyer 1984] especially when herds are of small size [Beaumont 1989]. Still, selection decisions are often based on first lactation [Da *et al.* 1992]. Some authors presented the opinion that the dairy performance of cows in all lactations is determined by more or less the same genes [Tong *et al.* 1979, Meyer 1984] and first parity yield is therefore an efficient selection criterion for lifetime production [Meyer 1984]. The genetic correlations between the first three lactations in cattle reached even the value of 1 [Meyer 1984]. Nevertheless, Beaumont [1989] suggested that lactations take place at various ages and physiological statuses of the animals, and may, therefore, be determined by different genes.

Some authors recommended the use of the repeatability model for estimating the breeding value [Tong *et al.* 1979, Meyer 1984, Strabel and Misztal 1999], but some [Suzuki *et al.* 2000] claimed that genetic evaluation may be more accurate if the first and following lactations were treated as different traits. Yet, the former seems to be more appropriate for the dairy goat populations as the links between the bucks (and herds) are much weaker than in the cattle.

The aim of this study was to evaluate the multiple-trait model approach, as opposite to repeatability model approach, at the early stage of developing the breeding value estimation system for dairy goats in Poland.

Material and methods

The data set covered 4,443 goats with first lactation performance and 5,244 goats with 9,115 records on later lactations (Tab. 1). The goats were maintained in 211 herds in 10 breeding regions in Poland. Small herds were grouped within each breeding region into two herds according to their first lactation milk production level. To conclude, 78 herds were created. The data set comprised information on lactations between 1983 and 2000, while the year of birth ranged from 1977 to 1999. Ten classes of both year of birth and year of kidding were created. The first class of year of birth included animals born till 1990, while the first class of year of kidding included animals kidded till 1991, and then every year. Kiddings were divided into two season classes – the first class contained kiddings which took place from October to March, while the second those from April to September. Three classes of litter size in first and subsequent lactations were distinguished. Parity for later lactations was divided into four classes – the fourth

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Table 1 Number of statewasters by breed, year of breed, year of breeding, scalars of breeding and later are minister increases (i) -) and lateration (

one containing lactations later than the fourth. The main breeds in Poland are the White Improved followed by the Fawn Improved (often named Colour Improved). Alpine and Saanen breeds were imported mainly from France in the mid nineties and are kept pure ever since. The White Improved goats are mated to White Improved or Saanen bucks and the Fawn Improved to Fawn Improved or Alpine bucks. The numbers of goats in particular levels of each of the effects are presented in Table 1.

Eight hundred and three classes of herd-sire and 593 classes of herd-year-season interaction of kidding in first, and 1286 and 743, in later lactations were distinguished, respectively. The herd-sire classes were created using either the actual sire number for does with known sire or using the genetic group of unknown sire [Quaas 1988] for does without known sire. The genetic groups themselves, were created according to the year of birth and breed of does.

The variance components were estimated with the REML procedure using VCE4 software [Groeneveld 1998]. Milk, fat and protein yields and fat and protein contents were treated as two different traits each, in the first and the later parities.

The model to analyse first lactation performance contained random additive genetic effect of an animal, and random effect of herd-sire interaction, as well as fixed effects of herd-year-season, breed, year of birth, litter size and linear regression on days-in-milk. The performances in later lactations were analysed using repeatability multiple-trait animal model containing, besides the above mentioned effects, also random effect of permanent environment of a goat and fixed effect of parity.

The heritabilities were calculated as a ratio $\sigma_a^2/(\sigma_a^2 + \sigma_e^2)$, while repeatability as

$$(\sigma_{p}^{2} + \sigma_{a}^{2})/(\sigma_{p}^{2} + \sigma_{a}^{2} + \sigma_{e}^{2}),$$

where:

 σ_a^2 - the additive component; σ_p^2 - the permanent environment component; σ_e^2 - the error variance.

Results and discussion

Average performances in later lactations and lactation I, as they were defined above, are presented together with standard deviations and minimum-maximum values, in Table 2. As expected the level of all the traits differed noticeably between the lactations. About 21% of the goats did not have information about later lactations (Tab. 3). Yet, the only difference between goats having just one lactation and those with more lactations is the length of lactation I, whereas the performance differences are secondary. That may indicate that goats which breed earlier in the breeding season have a greater chance to stay in herd, while their production potential is of a lesser importance and is not subjected to pre-selection.

Trait	Mean	SD	Minimum	Maximum
Lengh of lactations II+ (days)	266	47	60	446
Lengh of lactation I (days)	263	42	60	449
Milk yield in lactations II+ (bg)	640	234	88	1488
Milk yield in lactation I (bg)	526	174	97	1236
Fat.content in lactations II+ (%)	3.49	0.62	1.03	599
Fat.content in lactation I (%)	3.56	0.59	1.85	592
Protein content in lactations II+ (%)	2.93	031	1.66	5.70
Protein content in lactation I (%)	2.96	030	1.66	5.17
Fat yield in lactations II+ ([bg)	23.17	8.58	4.00	57.73
Fat yield in lactation I (bg)	18.61	6.62	4.04	51.62
Protein yield in Actations II+ (bg)	18.47	6.75	2.60	49.45
Protein yield in Actation I (bg)	15.50	5.20	3.04	39.88

Table 2. Means, standard deviations (SD) and extreme values of traits in later latations (II+) and latation I

Table 3. Milk yield and fat and protein content in hotation I of grats with onlyfiest (I) and within one than just first location

Trait	With only lactation I		Withmore	Withmore than first	
	(n=925)		hctation(lactation (n=3518)	
	mean	SD	mem	SD	
Days in milk	256	44	264	42	
Milk vield (bg)	519	174	528	174	
Fat (%)	3.58	0 <i>5</i> 9	3.55	0 <i>.</i> 99	
Protein (%)	2.99	030	2.95	0.30	

Heritability of milk yield ranged from 0.214 to 0.247 for later lactations and from 0.190 to 0.324 for lactation I (Tab. 4), depending on the set of traits which were estimated simultaneously. Heritabilities of fat and protein yields did not differ much between first and later lactations, but were still higher in lactation I. For fat yield, h^2 in lactation I ranged from 0.208 to 0.224 and for later lactations from 0.204 to 0.216. Heritability of protein yield was lower then that of fat yield and ranged from 0.130 to 0.208 for I, and from 0.180 to 0.201 for later lactations. Most reports [Rothschild and Henderson 1979, Meyer 1984, Teepker and Swalve 1988, Dong and van Vleck 1989, Suzuki *et al.* 2000] showed the h^2 for yield traits of dairy cows to be higher in first than in later lactations. On the other hand, some reports presented the highest heritability in lactation II [Meyer 1983] or even in lactation III [Reents *et al.* 1995]. The present results do not allow to conclude that the heritability estimates for yield traits differ between lactations.

Trait	Haritability*	Repeatability
Mik II+ (kg) Mik I (kg)	0.214-0.247 0.190-0.324	0349-0355
Rat II+ (%) Rat I (%)	0.214-0.243 0.278-0.318	0.247-0.267
Protein II+ (%) Protein I (%)	0.276-0.310 0.397-0.448	0323-0355
Rat II+ (bg) Rat I (bg)	0.204-0.216 0.208-0.224	0.266-0.279
Brotein II+ (bg) Brotein I (bg)	0.180-0.201 0.130-0.208	0311-0337

Table 4. Heritability and repeatability of investigated trais

*Standard errors of the estimates ranged between 0.006 and 0.033.

The heritability coefficients for contents appeared also somewhat higher in lactation I. For fat content they ranged from 0.278 to 0.318 in I, and from 0.214 to 0.243 in later lactations, and for protein content from 0.397 to 0.448 and from 0.276 to 0.310 for lactation I and later lactations, respectively.

Repeatabilities for all the dairy traits (Tab. 4) ranged from 0.247 to 0.355, and they seem low when compared to estimates for dairy cattle. Indeed, if the rearing environment influences future performance, its effect upon later lactations may get weaker as the parity increases. Thus, leaving first lactation data aside when estimating permanent environment component, can be responsible for lower estimates of repeatability. In an earlier study on goats based on all lactations data and using a a multiple-trait model Bagnicka and Łukaszewicz [1999] found the repeatability coefficients of dairy traits to oscillate around 0.40.

Phenotypic correlations between lactations for every milk trait were just above 0.5 while genetic correlations between lactations ranged from 0.880 to 0.996 (Tab. 5). The genetic correlations found in this study between first and subsequent lactations in the Polish dairy goats are of the same range than those found in dairy cattle [Rothschild and Henderson 1979, Tong *et al.* 1979, Short *et al.* 1990].

Phenotypic and genetic correlations between milk traits within lactation are presented in Tables 6 and 7. The correlations follow the general pattern found for all lactations in other dairy goat populations [Boichard *et al.* 1989, Analla *et al.* 1996, Večerova and Hyanek 1995] as well as for dairy cattle [Tong *et al.* 1979, Meyer 1983 and 1984, Teepker and Swalve 1988, Beaumont 1989, Dong and van Vleck 1989,

Table 5. Franctypic and genetic correlation coefficients between latation I and later latations for particular traits (bracketsdars SEs)							
Trais	Prenotypic correlation	Genetic correlation					
Mikyiald	0.519	0.962-0.970 (0.043-0.062)					
Fat. content.	0.529	0.932-0.936 (0.042-0.044)					
Brotain contant.	0.520	0.330-0.334 (0.027-0.044)					
Fat yield	0.514	0.934-0.969 (0.042-0.069)					
Brotainviald	0.517	0.954-0.996 (0.005-0.013)					

Table 6. Genetic correlation coefficients (above the diagonal) and phenotypic correlation coefficients (below the diagonal) between traits within lactation I (bracketed are SEs)

Trait	Milk yield	Rat. content.	Protein content.	Fatyield	Brotein yield
Milk yield Fat cantent Protein content Fat yield Protein yield	-0.113 -0.116 0.881 0.933	-0347 (0.059) 0321 0340 -0.020	-0.479 (0.086) 0.589 (0.054) 0.035 0.174	0.719 (0.042) 0.375 (0.062) 0.082 (0.075) 0.885	0.823 (0.027) 0.013 (0.072) 0.151 (0.085) 0.837 (0.044)

Table 7. Genetic correlation coefficients (above the diagonal) and phenotypic consistion coefficients (below the diagonal) between traits within her lastations (bracketed are SEs)

Trait.	Milk visH	Fat. contant.	Protein cantent	Fatyield	Broteinyield
Milk yiski Fat sontant Protsin sontant Fat yiski Protsin yiski	-0.137 -0.156 0.290 0.960	-0.387 (0.042) 0.354 0.294 -0.045	-0.420 (0.039) 0.616 (0.034) 0.002 0.102	0.730 (0.023) 0.308 (0.041) 0.011 (0.044) 0.900	0246 (0.013) -0.043 (0.067) 0.116 (0.052) 0254 (0.020)

Short *et al.* 1990]. Since in the present study the pattern of correlations does not differ between lactations, it may support a conclusion that the dairy traits are the same across lactations.

Given almost identical estimates of heritability of dairy traits recorded in different lactations and high genetic correlations between lactations, first lactation performance could be a sufficient selection criterion in dairy goats. Since, however, the Polish active population and the average herd size of dairy goats are small, paralleled by weak genetic links between environments, the repeatability model approach seems to better suit that situation. It can better account for additional links between bucks brought about by covering more lactations with the system of genetic evaluation. The reliability of a bull's proof based on 15 daughters of different lactations is equivalent to reliability of a proof based on 25 first-parity daughters [Ufford *et al.* 1979].

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Odziedziczalność i korelacje między mlecznymi cechami kóz oszacowanymi w pierwszej vs w dalszych laktacjach

Streszczenie

Materiał stanowiły dane o 9115 laktacjach powyżej pierwszej 5244 kóz oraz o 4443 laktacjach pierwszych. Komponenty wariancji oszacowano metodą REML, z modelem osobniczym, zawierającym poza losowymi czynnikami zwierzęcia i stada-ojca, stałe wpływy stada-roku-sezonu wykotu, rasy, roku urodzenia wielkości miotu oraz liniowej regresji na długość laktacji. Modele szacowania komponentów wariancji w późniejszych laktacjach zawierały, poza wymienionymi, także losowy wpływ specyficznego środowiska zwierzęcia oraz stały wpływ kolejnej laktacji. Wskaźnik odziedziczalności wydajności mleka wahał się od 0,214 do 0,247 w późniejszych laktacjach i od 0,190 do 0,324 w laktacji I, zależnie od zestawu cech w danej analizie. Dla wydajności tłuszczu h^2 w laktacji I wyniósł od 0,208 do 0,224, a w późniejszych od 0,204 do 0,216. Dla wydajności białka h^2 wahał się od 0,130 do 0,208 w laktacji I i od 0,180 do 0,201 w późniejszych. Dla zawartości tłuszczu h² zawarty był między 0,248 a 0,318 w laktacji I, oraz między 0,214 a 0,248 w późniejszych laktacjach. Odziedziczalność zawartości białka przyjęła wartości między 0,397 a 0,448 oraz między 0,276 a 0,310, odpowiednio w laktacji I i laktacjach późniejszych. Powtarzalność wszystkich cech zawierała sie w przedziale od 0.247 do 0.355. Fenotypowe korelacje miedzy laktacjami dla każdej z cech wyniosły nieco powyżej 0,50, podczas gdy genetyczne wahały się od 0,880 do 0,996. Genetyczne korelacje między wartościami cech w laktacji I a w dalszych laktacjach były bardzo wysokie, zatem wydajność w pierwszej laktacji może być dobrym kryterium selekcyjnym w doskonaleniu kóz. Jednak ze względu na to, iż polska populacja aktywna jest niewielka, a stada znajdujące się pod kontrolą nie są duże i powiązania genetyczne między nimi prawdopodobnie słabe, do szacowania wartości hodowlanej cech mlecznych kozłów powinien być raczej zastosowany model powtarzalnościowy, gdyż włączanie kolejnych laktacji pozwala na zwiększenie liczby powiązań między kozłami i powinno prowadzić do zwiększenia dokładności ich oceny.