MILK PROTEIN POLYMORPHISM AND RELATION BETWEEN MILK PRODUCTION TRAITS

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SUMMARY
The relation between yield traits on one side and fat content and protein content on the other is expressed by negative correlation coefficients. This paper presents some aspects of the genetic background involving polymorphism of casein loci as genetic markers. The estimated direct effects of markers and the results of linkage analysis are considered in this connection. The estimated direct effects of markers and results of linkage analysis involving casein markers and putative QTL point out that the casein genes are involved in this divergence. There are clear suggestions to different directions of casein genotypic influence to yield of milk, fat and protein and fat and protein content according to the results from estimated direct marker effects. That means that the casein genes may be closely linked to QTL for those traits (LOD score 1.09...1.90). The LOD score was 3.03 indicating a medium linkage for fat content and κ-casein. The estimated effects show a positive influence of β-CN^{A2}, κ-CN^A on milk yield, fat yield and protein yield and a simultaneous negative influence on fat content and protein content.
Keywords: Milk production traits, casein genes, marker effects, QTL-effects, genetic linkage

INTRODUCTION
The relation between yield traits on one hand and content traits on the other characterised by negative genetic correlation caused consequences in dairy cattle breeding. An orientation to high yields in breeding of Holstein Friesian cattle took place whereas gain in content of fat and protein has been noticed to be relatively small. Investigations in genetic linkage of Quantitative Trait Loci (QTL) for milk production traits with genetic markers could be suitable to examine the background for negative trait relation. The question arises whether identical, closely linked or different unlinked genes are responsible for the divergence between yield and content traits. The trait antagonism may also be based on physiological connections. Fact is that cows being superior in both complexes of milk performance are absolutely rare. The main results of such examinations regarding the casein locus on chromosome 6 suggest that it might affect the performance considerably. The methods of statistical analysis that have been used are different. Liu (1994) reported significant QTL effects for milk yield and protein yield and proved the mixed model of inheritance to be superior for milk production traits compared with the single gene model. The evidence of genetic linkage between genetic markers and putative QTL for some milk production traits was given occasional in single

family analyses. A significant linkage between QTL for fat and protein content and markers on chromosome 6 has been published by Georges *et al.* (1995) in one out of 14 families using a major gene model. Spelman *et al.* (1996) published results regarding a putative QTL for protein content and Bovenhuis and Weller (1994) for fat content in loose linkage to the casein locus. This paper presents results of estimated direct marker effects of two casein loci in contemplation with QTL- effects for five milk production traits with respect to the negative relation between yield and content traits.

MATERIAL AND METHODS

A detailed description of data examined including milk production performances, frequencies in milk protein genotypes and pedigree information has been presented by Panicke *et al.* 1996 (Table 1). Sample SMR/HF involving 1076 cows contains as well East German dairy cattle SMR based as well on minimum 50% Holstein Friesian (HF) genes as pure HF. 645 cows belonged to the herd for preservation of original German Black Pied cattle (sample DSR). The productivity was typical for the years 1990-1993 in the Eastern part of Germany. We used the two samples for estimation of direct marker effects to receiving independent results. The data had to be reduced drastically to 1258 cows for linkage analysis because of model restrictions. The data were uniformly adjusted for the fixed effects of herd, year and season of calving, age and part of population.

Table 1. Number, averages and standard deviations in milk production traits

	Number of	Milk yield (kg)		Fat yield (kg)		Protein yield (kg)		Fat content (%)		Protein content (%)	
Sample	cows	X	s	X	s	X	s	X	s	X	s
DSR	645	4803	784	193	36	159	25	3.97	0.31	3.47	0.19
SMR/HF	1076	5765	12851	250	54	199	41	4.36	0.43	3.47	0.22

The genotyping for milk protein genes has been carried out using gel-electrophoresis (Erhardt 1989). The methods used for statistical analysis of the data have also been given by Freyer *et al.* (1996) and Panicke *et al.* (1996) therefore the main points should be expounded only in this paper.

The estimation of **direct marker effects** was done by using the package PEST (Groeneveld 1993). The model can be written as follows:

$$y_{ijklm} = \mu + HYS + Ra_n + L_p + D \otimes M_{GTjklm} + A_i + e_{ijklm}$$

where y_{ijklm}- observation of cow i of marker genotype jklm , μ- general mean, HYS- fixed effect of herd year and season of calving, Ra - fixed effect of special part of population n, L_p - fixed effect of the age p at calving, D - Design matrix, M_{GTj} - fixed effect of milk protein marker genotype j, k, l, m and Ai - effect of cow i and e- residual.

The estimation of QTL-effects and the analysis of genetic linkage were carried out using a maximum likelihood approach (Liu 1994, Simianer 1993, 1995). The parameter estimation λ (q frequency of the desired QTL-allele, a additive effect of QTL, d dominance effect, θ recombination rate, h^2 polygenic heritability) is based on a likelihood function, involving the

marker genotypes of sire and offspring (genotyped cows with phenotypic data), the QTL-genotypes, the probabilities of marker and QTL genotypes for estimation, the polygenic breeding value of the sire. More information has been presented by Liu (1994) and Freyer *et al* (1996).

RESULTS AND DISCUSSION

The estimated genotypic effects of markers β-CN and κ-CN on milk production traits are jointly contemplated with the results of linkage analysis (significant QTL-effects could be estimated for all milk production traits but not shown here) and milk protein markers. This is done by monitoring the divergence between yield traits on one side and content of fat and protein on the other. The estimated direct marker effects partly suggest a clear outline (Table 2 and 3).

Table 2. Estimated effects of casein- genotypes on milk yield, fat yield and protein yield and results from linkage analysis

Marker genotype	Milk yield		Fat yield		Protein yield	
	SMR/HF	DSR	SMR/HF	DSR	SMR/HF	DSR
β-CN: A1A1	**-84**[a]	-93	**-1.83**	-2.49	**-2.15**	-1.31
A1A2	2[b]	-57	-0.07	-2.64	0.01	-0.55
A2A2	**124**[b]	51	**3.81**	1.33	**3.68**	1.01
linkage analysis	$\theta = 0.02$	LOD score 0.40	$\theta = 0$	LOD score 1.89	$\theta = 0$	LOD score 1.11
κ-CN: AA	-15	-10	-1.31	**-0.53**	-1.25	**-1.31**[a]
AB	33	-5	1.81	0.25	1.82	**-2.45**[b]
BB	-88	-33	-0.59	**-2.26**	0.74	**-4.49**[b]
linkage analysis	$\theta = 0.21$	LOD score 0.65	$\theta = 0.37$	LOD score .004	$\theta = 0.5$	LOD score 0

Effects with different suffix indicate genotypes with significant contrasts (p<5%). Bold signs mark the extreme genotypic effects of the CN loci. Frequ. = mean frequency of genotypes

A close linkage is indicated for marker β-CN and QTL for fat yield, protein yield and fat content (p<5) by $\theta = 0$ and LOD scores 1.11...1.89. The estimation of direct effects of marker κ-CN on fat yield and protein yield did not result in such clear outline (Table 3). The linkage analysis did not lead to a strong suggestion either. The κ-CN[B] is associated with the positive QTL allele for both traits. The genetic linkage was significant for fat Genotypes affecting yield traits positively cause negative effects on content traits and vice versa. The results from linkage analyses are quite different in quality (LOD scores) and quantity (recombination rates). The relevance of the genotypic effects estimated has been confirmed by results from Ortner *et al.* (1995) regarding sign and also in quantity of genotypic effects on the traits involved in the divergence.

Table 3. Estimated effects of casein- genotypes on fat content and protein content and results from linkage analysis

Marker genotype	frequ.	Fat content		Protein content	
		SMR/HF	DSR	SMR/HF	DSR
β-CN: A1A1	0.24	0.033 [a]	0.026	0.014	0.007
A1A2	0.47	-0.001 [b]	-0.012	-0.003	-0.011
A2A2	0.19	-0.028 [b]	-0.011	-0.018	-0.058
linkage analysis		$\theta = 0$	LOD score 1.09	$\theta = 0.1$	LOD score 0.04
κ-CN: AA	0.52	-0.010 [a]	-0.002	-0.008 [a]	-0.004
AB	0.37	0.004 [b]	0.007	0.008 [b]	0.008
BB	0.06	0.063 [b]	-0.009	0.050 [b]	-0.048
linkage analysis		$\theta = 0.26$	LOD score 3.03	$\theta = 0.5$	LOD score 0

In case of an existing QTL within the CN locus indicated by the results involving β-CN for fat yield, protein yield and fat content the linkage phases are deducted in the manner as shown. The linkage between κ-CN and QTL for fat content shows a medium linkage ($\theta = 0.26$ and LOD score 3.03). This result compared to those from β-CN indicating a close linkage to the estimated QTL for fat yield, protein yield and fat content may be influenced by an other putative QTL located on chromosome 6 but also by material specific constellations (Freyer et al. 1996). If breeders are interested in cows being superior in yield and content traits, there could be a possibility to find them by selecting cows carrying heterozygote genotypes in casein loci. Directed mating for producing the next generation taking in consideration the casein genotypes of the mates as emphasized above may offer the way for realizing this. It has to be assumed that much more loci might are involved in the divergence of yield and content. Latest research projects in gene mapping and further linkage studies may contribute to a better understanding of the whole basis underlying this negative relation between the traits and coping with it in dairy cattle breeding later on.

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