Near infrared calibrations for α_{s1} casein content in goat milk

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Introduction

Casein content greatly determines rennet properties and cheese yield of milk. Casein in ruminants milk is constituted of four different fractions α_{s1}, α_{s2}, β and κ, which are coded by different genes. A genetic polymorphism of α_{s1} casein loci (CSN1S1) was described two decades ago in goats.[1] Since them, 15 allelic variants have been described.[2–4] They have been classified into four groups, according to their average effect on α_{s1} casein content (high, medium, low and null).[5] Goats with a high level of α_{s1} casein have higher concentration of fat, protein, total casein, smaller micelles, higher curd firmness, lower coagulation time and higher cheese yield.[5] Milk recording and selection schemes require using new selection criteria based on milk casein content and technological properties. Information on the α_{s1} casein genotype of goats has been used to estimate breeding values and to select sires in French breeds. However, further research is still needed in order to know the effect of this genetic polymorphism in Spanish breeds. Present laboratory techniques used to quantify α_{s1} casein are expensive and time consuming. NIRS could provide a reliable, faster and less costly way of routinely analysis of large number of samples.

Material and methods

Calibrations were developed for α_{s1} casein content in goat milk using 157 samples collected from individual goats, with known genotypes for the α_{s1} casein gene, belonging to three different herds of Malagueña and eight of Murciano-Granadina breeds. Samples were collected from each goat in, at least, three different moments of the lactation period in two consecutive parities, in order to assure sufficiently variation of the constituent being analysed.

In order to have the necessary reference laboratory analysis of α_{s1} casein contents in calibration samples, a method, based on capillary electrophoresis, has been set up to separate and to quantify α_{s1} casein.[6] The analysis was performed with an instrument Beckman P/ACE MDQ controlled by the software Beckman Instruments Inc., Fullerton, USA.

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Samples were prepared to be presented to NIR instrument using the DESIR[7] method. This method consists of drying in an oven at 40°C for 24 hours a glass fibre filter previously soaked with the liquid under test. A variation of the typical drying conditions of this method has been proposed for goat's milk analysis[8] in order to avoid protein denaturalisation.

For NIR spectra collection a Foss NIRSystems 6500 SY-I, equipped with a spinning module, connected to a computer controlled with the Software ISI NIRS 3 ver. 3.11 (Infrasoft International, Port Matilda, PA, USA) was used. Samples (glass fibre filters) were place in a small ring cup for solid products. Spectra were obtained collecting reflectance measurements of monochromatic light in the 1100–2500 nm region with 2 nm intervals. Software WINISI II ver. 1.04 (Infrasoft International) was used for spectra treatment. Previous to calibrating, the CENTER algorithm was applied to spectra in order to detect possible outliers. Several treatments of the spectra information for scatter correction and for noise reduction (standard normal variate and detrending and first and second derivatives), as well as no treatments, were evaluated. MPLS (modified partial least squares regression) was used for calibration.

Best calibrations equations were chosen considering their calibration statistics: higher coefficient of determination for the cross-validation (r^2), lower cross-validation standard error (*SECV*) and ratio of range of reference values *to SECV* (*RER*) larger than 10, to ensure an adequate predictive capacity of the equation.[9]

Results and discussion

Table 1 shows calibration statistics for the best calibration equations found. Best mathematical treatment was 2, 10,5,1. Best results were obtained not using any treatment to correct the scatter effects.

Table 1.Calibration statistics for better equation.

Scatter	Math Treatment	Nº samples	Mean (g kg^{-1})	*SECV*	r^2	*RER*
None	2,10,5,1	130	4.74	0.98	0.78	10.58
SNV+Det	2,10,5,1	125	4.65	0.95	0.75	8.96

***SECV*: Standard error of cross-validation. r^2: coefficient of determination of the calibration equation. *RER*: ratio of range of reference values to *SECV*.**

A low r^2 value was obtained for the calibration equation (0.78), due to very high standard errors of the reference analytical values (0.992), however cross validation standard error (0.979) and *RER* (10.58) were acceptable.

Calibration could possibly be improved completing the calibration set, which, as it can be seen in Figure 1, is far for uniform and presents some small ranges of values not represented in the calibration set.

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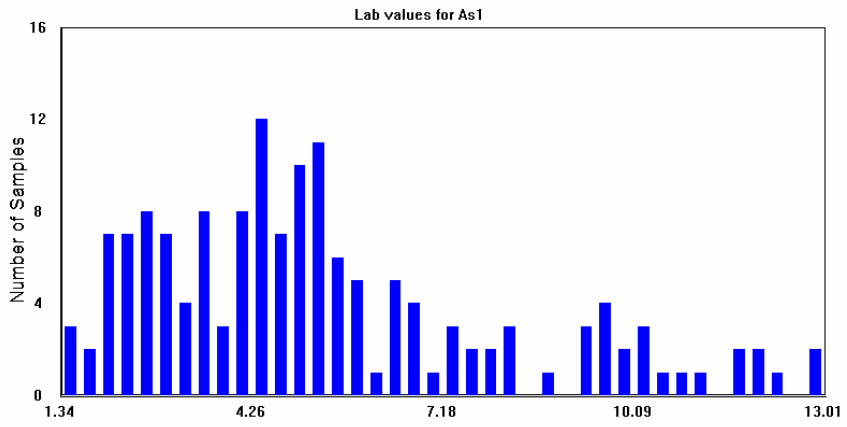

Figure 1. Histogram of αs1 casein contents in milk samples of the calibration set.

In order to test the validity of these results for the main purpose for which calibrations for quantifying α_{s1} casein content in goat milk are being developed, predictions obtained with these calibrations were used to compute means corresponding to different genotypes of the α_{s1} casein gene. Results are shown in Table 2. They are consistent with those previously published.[10]

Table 2.- Mean values (g/kg) of the different genotypes of the αs1 casein gene, computed with the predictions obtained with the best calibration equation.

αs1-cn genotype	BB	BF	EE	FF
Mean values	7.37	4.26	4.73	2.19

Conclusions

Calibration equations obtained for predicting α_{s1} casein content show not very high coefficients of determination. However, they are adequate for the purpose they have been developed: to be used in our dairy goats breeding program. Nevertheless, further work should be done using a more uniform and complete calibration set trying to improve calibrations to extend their validity to other purposes.

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