Near infrared spectroscopy (NIRS) as a tool to predict meat chemical composition and fatty acid profile in different rabbit genotypes

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ABSTRACT - Two hundreds rabbits were obtained from 3 different maternal lines and 5 paternal lines, for a total of 11 combinations. After slaughtering the fresh hind legs (HL) and *Longissimus dorsi* muscles (LD) were scanned in the near infrared region by using a Foss NIRSystem 5000 (λ=1100-2498 nm). The WINISI software (v 1.50) was used for the spectra analysis and samples selection (49 HL and 11 LD). Selected samples were analyzed chemically for dry matter (DM), protein, lipid, ash and fatty acid profile (FA). The obtained results were used to expand and improve the existing calibration equations for fresh rabbit's meat. Afterwards these equations were used to predict meat composition of the unselected samples. Discriminant analysis didn't segregate genetic lines. The calibration results for the 400 meat samples were accurate in predicting DM, protein, lipid and some FA (R^2>0.80). Poor results were obtained for ash and for physical properties of meat. It was demonstrated that NIRS is a reliable and affordable technology to predict fresh rabbit meat composition, but because of the small differences between genotypes, NIRS wasn't able to discriminate samples according to their genetic belonging.

Key words: Rabbit, Genotypes, NIR spectroscopy, Meat quality.

Introduction - Genetic improvement of parental lines of rabbits usually targets improvement of growth traits, which might affect meat quality (Pascual and Pla, 2007). In Hungary, "Pannon White" rabbits were selected since 1991 with the aim to increase the growth rate during fattening. Selection was performed measuring the mean cross-sectional area of *Longissimus dorsi* muscle of each animal (L value) at 10.5 wks of age, using computer tomography (CT). Szendrö *et al.* (1992) proved that high L values are positively correlated to the carcass yield. NIRS could be a useful tool to obtain rapid information on meat quality during the development of selection programs. This technology doesn't use reagents and doesn't destroy samples (Pla *et al.*, 2007). The aim of this study was to use NIRS to evaluate rabbit's meat quality of different genetic lines, using fresh instead of freeze dried meat samples and to explore the use of NIRS as a discrimination technique.

Material and methods – Rabbit does of 3 maternal lines (M, P, L) were inseminated with rabbits of 5 paternal lines (M, P, L, H, C). "M" line (Maternal) was selected for litter size and teats number; "P" (Pannon White), "L" (Large Body Line) and "H" (Hycole) for daily weight gain and carcass traits; whereas "C" (Coloured Line) was obtained by crossing P x Chinchilla. Combinations were: PP, PM, PL, PH, PC, MP, MM, ML, MH, MC, LL. Two hundreds rabbits were reared by pairs, fed a commercial pellet *ad libitum* and slaughtered at 78d of age. All Lind legs (HL) and *Longissimus dorsi* muscles (LD) were dissected and stored at -18°C until analysis. L* a* b* colour, pHu, drip and cooking losses were measured on left HL and LD. The right HL and LD meat was minced and scanned by NIR spectroscopy. Measurement of the NIR spectra was performed using a Foss NIRSystem 5000, with small ring cup cells. Measurements were made in reflectance mode between 1100 and 2498 nm every 2 nm. All

samples were scanned in duplicate. The average spectrum was used for NIR analysis. Data processing and samples selection were carried out using the WINISI software. 49 HL and 11 LD were selected based on their diversity using the Select algorithm and chemically analysed after freeze-drying (FD) for moisture, lipids, ash and protein (calculated by difference, AOAC, 1984). Fatty acid (FA) profile was analyzed by gas chromatography (GC), after lipid extraction. NIRS calibrations were performed by modified partial least squares (MPLS) regression. To optimize calibration accuracy, the data were subjected to a variety of derivative transformations using common mathematical and scatter correction treatments. The best one was selected for each constituent based on the highest R^2 of cross validation (R^2cv) value and lowest standard error of calibration and cross-validation (SEC and SECV respectively). Calibration equation was obtained by considering both HL and LD meat. Discriminant analysis was processed by WINISI software, trying to segregate meat obtained by different rabbit genotypes.

Results and conclusions - High value of standard deviation (SD) was found for lipid amount, which could be related to the two meat sample types used in this study (LD and HL). Pla *et al.* (1998) found significant differences in fat content between the two types of meat (LD=0.9%, HL=3.24%). NIRS ability to predict the main rabbit meat's proximate composition (Table 1) was high for dry matter (DM), crude protein and lipid (R^2=0.95, 0.91 and 0.96, respectively). These interesting performances were also confirmed by a cross-validation (R^2cv=0.93, 0.88 and 0.94, respectively). In agreement with part of the literature, the ability of NIRS to predict ash content was low (R^2=0.40); Berzaghi *et al.* (2005) and Molette *et al*. (2001) obtained very low R^2 calibrating ash in FD chicken breast (0.05) and fatty livers (0.15), respectively. Few minerals have spectral absorptions in the NIR spectral range. Thus, their determination by NIRS depends on indirect correlations between meat organic compounds and mineral, and this is the main cause of inefficiency in ash prediction. As regards the NIR estimation of the proximate composition, other studies reported worse results than in the present study as far as fresh meat is concerned, while better R^2 were always obtained with FD meat. In fact, **Bázár** *et al*. (2007) achieved R^2 values for lipid and protein of 0.89 and 0.85 in fresh meats and 0.99 and 0.96 for FD rabbit meat, respectively. Moisture has a key role on the ability of NIRS to predict the other meat components, and this explains why FD samples give better results. The slightly higher R^2 value of FD meat doesn't justify the use of freeze drying, that is an expensive and losing time procedure. Lipid and FA profile are directly influenced by the diet and could also be influenced by selection for growth rate (Hernandez *et al*., 2008). The calibrations were accurate for total SFA, MUFA and PUFA (R^2=0.98, 0.93 and 0.90, respectively), confirming that NIRS has high capacity to predict the main classes of FA also in the fresh meat (Table 1). On hen FD breast meat Berzaghi *et al.* (2005) obtained R^2 for the same FA classes of 0.97, 0.95, 0.98, respectively. Interesting results were also obtained in validation for C15:0; C17:0; C18:1 *n*-9; MUFA; C20:3 *n*-6; C20:4 *n*-6, PUFA that obtained a R^2cv value higher than 0.80. The low amount of PUFA, and the high amount of SFA found in the present study could depend on the 4 months storage at -18°C, during which part of PUFA could have been hydrolysed. Alteration of lipids could also be affected by sample handling. In the present study the HL was submitted to deboning which could have increased the FA alteration. In order to obtain more reliable data the LD muscle is preferable as meat sample. Some physical traits of rabbit meat were set in calibration, such as pH, L* a* b* colour, drip and cooking losses but the R^2 were <0.1. The ability of NIRS to discriminate the rabbit meat according to its genetic origin was also tested, but it didn't provide good results. WINISI software wasn't able to assign correctly the spectra to the right group. This result was expected as the different genetic lines were strictly connected to P line, and this explains the similarities of the meat samples' analysed. The trial demonstrated that NIRS is a useful technology to predict fresh rabbit meat composition, however NIRS wasn't able to predict physical properties of meat and to discriminate samples derived from the considered fattening rabbits' genetic lines.

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Table 1. Statistical overview of chemical composition and fatty acid (FA) of fresh rabbit meat.

Constituent	N	Mean	SD	Minimum	Maximum	SEC[1]	R^2 [2]	SECV[3]	R^2cv[4]
DM	197	26.61	1.31	22.67	30.55	0.29	0.95	0.35	0.93
Protein	194	22.19	0.82	19.72	24.66	0.24	0.91	0.28	0.88
Lipid	186	3.08	1.31	0.00	7.02	0.26	0.96	0.33	0.94
Ash	187	1.21	0.05	1.06	1.35	0.04	0.40	0.04	0.24
C14:0	106	2.17	0.52	0.60	3.75	0.20	0.86	0.24	0.79
C15:0	103	0.81	0.60	0.00	2.63	0.11	0.97	0.22	0.86
C16:0	110	28.97	3.98	17.03	40.91	1.85	0.78	2.40	0.64
C17:0	106	0.82	0.30	0.00	1.71	0.05	0.98	0.12	0.85
C18:0	112	8.36	1.46	3.99	12.73	0.96	0.56	1.18	0.35
Total SFA	109	42.55	6.44	23.24	61.86	0.95	0.98	3.73	0.66
C16:1	108	2.28	0.94	0.00	5.09	0.35	0.86	0.56	0.64
C18:1 n-9	104	22.41	3.22	12.75	32.06	1.06	0.89	1.23	0.85
C18:1n-7	108	1.67	0.43	0.39	2.95	0.17	0.84	0.23	0.70
C20:1 n-9	93	0.24	0.07	0.03	0.45	0.02	0.90	0.04	0.67
Total MUFA	105	27.23	4.07	15.01	39.45	1.11	0.93	1.65	0.84
C18:2 n-6	105	23.02	7.65	0.08	45.96	1.90	0.94	3.79	0.75
C18:3 n-3	107	1.42	0.75	0.00	3.67	0.31	0.83	0.50	0.55
C20:3 n-3	54	0.08	0.03	0.00	0.18	0.02	0.79	0.02	0.49
C20:3 n-6	99	0.26	0.12	0.00	0.62	0.03	0.95	0.05	0.85
C20:4 n-6	100	2.41	1.51	0.00	6.95	0.59	0.85	0.68	0.80
C20:5 n-3	98	0.08	0.05	0.00	0.22	0.03	0.66	0.04	0.40
C22:5 n-3	77	0.32	0.24	0.00	1.02	0.09	0.87	0.11	0.77
C22:6 n-3	108	0.10	0.04	0.00	0.23	0.04	0.16	0.04	0.14
Total PUFA	104	29.28	9.63	0.39	58.16	3.05	0.90	3.76	0.85
Total n-6	109	26.73	8.85	0.19	53.28	3.57	0.84	4.07	0.79
Total n-3	109	2.08	0.84	0.00	4.59	0.41	0.76	0.55	0.56

[1]SEC standard error of calibration; [2]R^2 Coefficient of determination in calibration; [3]SECV Standard error of cross validation; [4]R^2cv Coefficient of determination of cross validation.

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