

EFFECT OF CATTLE BREED ON MUSCLE PROTEIN

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ABSTRACT

The study evaluated differences in muscle protein quality in the *m. longissimus, pars thoracis* of bulls from the Aberdeen Angus and Czech Fleckvieh breeds reared under identical extensive pasture-based conditions. A significantly higher crude protein content ($P \leq 0.05$) was found in Czech Fleckvieh bulls (886.96 ± 87.36 g/kg of dry matter) compared to Aberdeen Angus bulls (812.48 ± 59.31 g/kg of dry matter). The Czech Fleckvieh breed also exhibited greater concentrations of non-essential amino acids (389.79 ± 37.92 vs. 363.91 ± 44.48 g/kg of dry matter; $P \leq 0.05$), essential amino acids (405.95 ± 38.95 vs. 382.25 ± 41.00 g/kg of dry matter; $P \leq 0.05$), and total analysed amino acids (795.74 ± 74.85 vs. 746.16 ± 82.71 g/kg of dry matter; $P \leq 0.05$) than Aberdeen Angus. Breed significantly affected the content of most analysed amino acids ($P \leq 0.05$), whereas no breed differences were detected for tyrosine and phenylalanine ($P > 0.05$). Lysine was the most abundant essential amino acid, with contents of 73.43 ± 8.23 g/kg of dry matter in Aberdeen Angus and 76.57 ± 8.87 g/kg of dry matter in Czech Fleckvieh ($P \leq 0.05$). Among non-essential amino acids, glutamic acid was the most abundant, reaching 108.97 ± 14.35 g/kg of dry matter in Aberdeen Angus and 119.42 ± 12.47 g/kg of dry matter in Czech Fleckvieh ($P \leq 0.05$). These findings suggest that breed influences crude protein concentration and the amino acid profile of muscle tissue.

Keywords: genotype; pasture; beef; nutrients; nutritional quality

INTRODUCTION

Beef is recognised as an important dietary source of protein, with its protein concentration remaining relatively stable (Gunduz and Cayiroglu 2024; Mujic et al. 2025). It is also characterised by a nutritionally favourable amino acid profile, particularly due to the presence of essential amino acids that cannot be synthesised by the human body (Samicho et al. 2013). Glutamic acid and lysine occur at the highest concentrations among amino acids present in beef (Wu et al. 2016). Ruminants obtain a substantial proportion of amino acids through microbial



fermentation in the rumen. Dietary protein is primarily degraded by ruminal microorganisms and transformed into microbial protein, which is digested and utilised in the small intestine. Rumen undegradable protein passes to the small intestine, where it contributes to meeting nutritional requirements that cannot be fully covered by microbial protein alone. For this reason, cattle diets should provide an appropriate balance of both rumen degradable and rumen undegradable protein (Zahradkova 2009).

The nutritional quality of muscle tissue is strongly associated with cattle breed. Compared with dairy and dual-purpose breeds, beef breeds are generally characterised by a higher protein content in muscle tissue. Differences in maturation pattern are also important, as early-maturing breeds tend to deposit fat sooner, whereas late-maturing breeds remain in the muscle growth phase for a longer period before intensive fat deposition occurs (Solarczyk et al. 2020). In addition, variation in protein concentration and amino acid composition may depend on the muscle type (Samicho et al. 2013; Fortova et al. 2018). Reported effects of grazing on muscle protein content remain inconsistent (Hwang and Joo 2017; Fruet et al. 2018; Najjar-Villarreal et al. 2019; Siphambili et al. 2020), likely due to seasonal changes in forage quality, as well as differences in pasture botanical composition and grazing management.

MATERIAL AND METHODS

The study involved 65 bulls of the dual-purpose breed Czech Fleckvieh and 65 bulls of the beef breed Aberdeen Angus. Czech Fleckvieh was the only dual-purpose breed, and Aberdeen Angus represented the largest group of beef breeds grazed in the study area. All animals were raised under identical conditions within an extensive pasture-based system in the Prachatice District, South Bohemia Region, Czech Republic (828 m altitude). Cattle were managed under a free-grazing system with unrestricted movement and minimal human intervention. During the main grazing season (March–November), pasture was the main component of the diet. Pasture consisted mainly of red fescue (*Festuca rubra*), meadow fescue (*Festuca pratensis*), smooth meadow-grass (*Poa pratensis*), and white clover (*Trifolium albi*). In winter, animals were fed haylage, hay, and straw. Water was supplied through tanks. Salt and mineral licks were provided ad libitum, while conserved forage in the form of bale feed was offered when necessary. The stocking density was approximately one animal per 2 ha. Bulls were slaughtered between 16 and 18 months of age over a two-year period depending on slaughterhouse capacity.

Muscle samples were obtained at the Volary slaughterhouse, ZEFA, from 65 Aberdeen Angus and 65 Czech Fleckvieh bulls slaughtered between 16 and 18 months of age. From each carcass a 500 g sample of the *m. longissimus, pars thoracis* was taken. Dry matter (g/kg) was determined gravimetrically after drying the samples at 105 °C. Crude protein content (g/kg) was calculated as nitrogen determined by the Kjeldahl method multiplied by the factor 6.25 and analysed using

a Buchi analyser (Centec automation, company s.r.o., Prague, Czech Republic). Amino acid composition was determined following acid hydrolysis using an automatic amino acid analyser AAA 400 (INGOS, a. s., Prague, Czech Republic) based on the colour reaction of amino acids with ninhydrin. The analysed amino acids included aspartic acid (Asp), threonine (Thre), serine (Ser), glutamic acid (Glu), proline (Pro), glycine (Gly), alanine (Ala), valine (Val), methionine (Met), isoleucine (Ile), leucine (Leu), tyrosine (Tyr), phenylalanine (Phe), histidine (His), lysine (Lys), and arginine (Arg).

Statistical analysis focused on the number of samples (n), mean ($\bar{x}$), and standard deviation (SD). Data normality was evaluated using the Shapiro–Wilk test in Unistat version 6.5 (Unistat Ltd., London, UK), where the data fulfilled the condition of normal distribution ($P > 0.05$). Homogeneity of variances was assessed using the F -test ($P > 0.05$). F -test was followed by the Student's t -test, and differences between mean values were considered statistically significant at $P \leq 0.05$.

RESULTS AND DISCUSSION

Table 1. demonstrates breed-related differences in muscle crude protein content, with higher values observed in Czech Fleckvieh (CF) compared to Aberdeen Angus (AA). Crude protein content reached 886.96 ± 87.36 g/kg of dry matter in CF and 812.48 ± 59.31 g/kg of dry matter in AA ($P \leq 0.05$). These findings suggest that cattle breed influences muscle protein content. CF reaches the stage of intensive fat deposition later than AA, while AA breed is characterised by greater intramuscular fat content (Bures and Barton 2018; Papanikolopoulou et al. 2025). Papanikolopoulou et al. (2025) also reported that breed can affect muscle protein content. Compared with Limousine and Holstein bulls, Aberdeen Angus bulls exhibited the lowest protein content and the highest fat content in the *m. longissimus dorsi*. However, no breed-related differences in protein content were reported in the *m. longissimus lumborum* of Aberdeen Angus and Czech Fleckvieh bulls fed the same diet in intensive feeding system and slaughtered at approximately 17 months of age (Bures and Barton 2018).

Table 1 shows differences in the content of non-essential amino acids (NEAA), essential amino acids (EAA), and total analysed amino acids (AAs) in the muscle tissue of the evaluated cattle breeds, with consistently higher values observed in the CF breed across all assessed parameters. The NEAA content reached 363.91 ± 44.48 g/kg of dry matter in AA and 389.79 ± 37.92 g/kg of dry matter in CF ($P \leq 0.05$). Similarly, EAA content was higher in CF, amounting to 405.95 ± 38.95 g/kg of dry matter compared to 382.25 ± 41.00 g/kg of dry matter in AA ($P \leq 0.05$). The AAs content was 746.16 ± 82.71 g/kg of dry matter in AA and 795.74 ± 74.85 g/kg of dry matter in CF ($P \leq 0.05$). Significant breed-related differences were identified for nearly all analysed amino acids ($P \leq 0.05$), except for Tyr and Phe, for which no significant differences were detected ($P > 0.05$). Glu was the predominant amino acid within the NEAA group, with values of 108.97 ± 14.35 g/kg of dry

matter in AA and 119.42 ± 12.47 g/kg of dry matter in CF ($P \leq 0.05$). Among EAA, Lys was the most abundant amino acid, reaching 73.43 ± 8.23 g/kg of dry matter in AA and 76.57 ± 8.87 g/kg of dry matter in CF ($P \leq 0.05$). These findings suggest that breed may significantly influence amino acid composition and affect the nutritional quality of muscle protein. Consistent with our study, Koutsidis et al. (2008), Vopalensky et al. (2017), Chen et al. (2022) and Ge et al. (2023) reported that breed can affect amino acid composition and content of total analysed amino acids. Our study is consistent with the results reported by Vopalensky et al. (2017). In both studies, the Aberdeen Angus breed was raised under identical pasture conditions and feeding management. The main difference between the studies was the number of analysed samples. The results were highly comparable, indicating that breed is likely a primary factor affecting the amino acid composition of the *m. longissimus thoracis*. Consistent with our study, Lys was the most abundant EAA and Glu was most abundant NEAA in different muscles across cattle breeds (Samicho et al. 2013; Vopalensky et al. 2017; Ge et al. 2023; Merayo et al. 2023).

Tab. 1: Amino acid profile and crude protein content (g/kg of dry matter) in the muscle tissue of Aberdeen Angus and Czech Fleckvieh bulls

Nutrients	Aberdeen Angus $\bar{x} \pm SD$	Czech Fleckvieh $\bar{x} \pm SD$	P value
Crude protein	812.48 ± 59.31	886.96 ± 87.36	*
AAs	746.16 ± 82.71	795.74 ± 74.85	*
EAA	382.25 ± 41.00	405.95 ± 38.95	*
Thre	33.67 ± 4.12	36.00 ± 3.64	*
Val	37.41 ± 4.36	40.14 ± 4.20	*
Met	19.06 ± 2.67	21.54 ± 2.57	*
Iso	35.44 ± 3.95	37.86 ± 3.71	*
Leu	61.43 ± 6.47	65.51 ± 6.93	*
Phe	30.66 ± 3.32	31.61 ± 3.76	ns
His	31.89 ± 4.65	34.34 ± 4.63	*
Lys	73.43 ± 8.23	76.57 ± 8.87	*
Arg	59.26 ± 6.56	62.37 ± 7.55	*
NEAA	363.91 ± 44.48	389.79 ± 37.92	*
Asp	70.10 ± 8.06	74.49 ± 7.50	*
Ser	29.19 ± 3.58	31.81 ± 6.20	*
Glu	108.97 ± 14.35	119.42 ± 12.47	*
Pro	38.03 ± 8.16	41.40 ± 5.19	*
Gly	40.73 ± 6.32	43.16 ± 5.73	*
Ala	45.48 ± 5.86	48.55 ± 5.17	*
Tyr	31.42 ± 4.22	30.97 ± 4.01	ns

mean($\bar{x}$) $\pm$ standard deviation(SD), AAs–total analysed amino acids, EAA–essential amino acids, NEAA – non-essential amino acids, ns = not significant, * $P \leq 0.05$

CONCLUSION

The results demonstrated that cattle breed significantly influenced crude protein concentration and the amino acid composition of muscle tissue in bulls reared under identical extensive pasture-based conditions. Czech Fleckvieh bulls exhibited higher crude protein content as well as greater concentrations of essential, non-essential, and total analysed amino acids in the *m. longissimus, pars thoracis* compared with Aberdeen Angus bulls. Breed-related differences were identified for the majority of analysed amino acids, whereas tyrosine and phenylalanine were not affected by breed. These findings suggest that cattle breed contributes to variation in the nutritional quality of beef muscle tissue.

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