

results indicate the possibility of manipulating beef fat composition through breed selection.

Key Words: beef, fatty acid, longissimus

622 Fatty acid profile in beef meat and baby food based on beef meat. A. Nudda^{*1}, G. Battacone¹, R. Boe¹, M. G. Manca¹, M. Mele², A. Serra², and G. Pulina^{1,3}, ¹*Dipartimento di Scienze Zootecniche, University of Sassari, Italy*, ²*Dipartimento di Agronomia e Gestione dell'Agroecosistema, University of Pisa, Italy*, ³*Agricultural Research Agency of Sardinia - AGRIS Sardegna, Sassari, Italy*.

The aim of this study was to compare fatty acid (FA) profile of fresh beef meat with that of baby foods based on beef meat. For this purpose, 20 samples of homogenized beef–meat baby food (80–g jars; HO) and 18 samples of lyophilized (freeze–dried) beef–meat baby food (30–g jars; LIO), produced by various infant–food companies, and 10 samples of fresh beef meat (FM) were collected and analyzed by gas chromatography. The content of each fatty acid methyl ester (FAME) was expressed

as a percentage of total FAME. Data were analyzed with one–way ANOVA using type of product as the main effect. All fatty acids, except for α -linolenic acid (C18:3 ω 3) and c9,t11 conjugated linoleic acid (CLA), differed among the three products tested. The sum of ω 6 FA was higher in HO (21.2%) compared to FM (12.5%) and LIO (4.0%) samples, due to its higher content of linolenic acid. Therefore, ratio ω 6/ ω 3 FA was markedly higher in HO (32.1) compared to FM (9.0) and LIO (8.4) samples. On the other hand, the content of arachidonic acid (C20:4 ω 6) was more than 9–fold higher in FM compared to LIO and HO. The content of total PUFA ω 3 was highest in FM (1.5%), because of greater content of EPA, DPA and DHA compared to HO (0.8%) and LIO (0.6%) baby foods. Fatty acid composition was more similar between LIO and FM samples than between HO and FM samples, probably as a consequence of the high level of vegetable oil added to HO products. This study suggests the possibility of enhancing the FA profile of commercial baby food based on beef meat by using meat with a healthier FA profile. *Acknowledgements: Research supported by the Fondo di Ateneo per la Ricerca Scientifica (FAR, ex 60%).*

Key Words: beef meat, fatty acid, baby food

Breeding and Genetics: Breeding & Genetics Workshop

623 Solving a dilemma in graduate education: Animal Breeding and Genetics Online. R. M. Lewis^{*1}, B. B. Lockee¹, M. S. Ames¹, G. C. Márquez¹, R. M. Enns², J. M. Rumph³, T. W. Wilkinson¹, and E. J. Pollak⁴, ¹*Virginia Tech, Blacksburg*, ²*Colorado State University, Fort Collins*, ³*Michigan State University, Lake City*, ⁴*Cornell University, Ithaca, NY*.

Diminishing faculty numbers has reduced opportunities for coursework tailored to the needs of future scholars in quantitative aspects of genetics. Existing faculty must focus on basic content, limiting their ability to offer advanced instruction. A potential solution to this dilemma is utilizing distance learning technologies within a collaborative framework. Distance delivery programs have advantages: more students can access expertise within a technology-enriched learning environment. However, challenges exist. There is risk of a “psychological distance” separating students and faculty. Furthermore, distance education increases demands on faculty time, particularly with course design and implementation across institutions. A consortium of four universities has combined efforts to develop eight graduate-level online courses in animal breeding and genetics. The instructional design adopted embraces both the advantages and challenges of distance delivery. Discussion boards and virtual office hours have been used to encourage communications. A game-based genetic simulation was developed, with across-institutional teams competing through a common web-based interface. An annual face-to-face event has been held to allow social and academic interactions. Thus far, students from 19 universities have participated, with each course enjoying an enrollment of 10 to 30 students. Originally, seven courses were planned. However, based on student feedback and performance, it became clear that pre-requisite knowledge varied widely among participants. Therefore, an eighth course was added to provide foundational knowledge. Consistency in course design and implementation remains a challenge. Joint working sessions will be held to define common instructional and assessment strategies. With such a concerted effort, the Animal Breeding and Genetics Online curriculum offers promise for solving a dilemma in graduate education.

Key Words: graduate education, distance learning, quantitative genetics

624 Recent developments in genetic evaluation tools. D. Garrick^{*}, *Iowa State University, Ames*.

The principal tool for genetic evaluation is a sound and practical statistical basis to determine linear functions for combining recorded performance on an individual, its relatives and contemporaries in order to minimize the prediction error variance of the estimated genetic merit of each animal. Hazel and Lush’s methodology, known as best linear prediction or selection index, was limited to circumstances where observed performance had been corrected, prior to analysis, with the true or parametric adjustment factors for non-genetic effects such as herd-year. In practice, their method was applied using estimated adjustments for non-genetic effects and ignoring the contributions of all animals except a few close relatives. Henderson extended the method. First, to account for the estimation of fixed effects from the data, by restricting analysis to certain linear combinations of observations that resulted in translation invariant prediction, known as best linear unbiased prediction. Those evaluations had larger prediction error variance, but lacked the bias from errors in estimation of non-genetic effects. Second, a computing algorithm was developed to include information from all relatives. It used expected or average relationships between animals. A recent extension exploits the availability of genetic markers to characterize the realized rather than expected inheritance of chromosome fragments among close and distantly related animals. The combined use of genomic and phenotypic data is known as genomic prediction. It can provide genetic evaluations of animals without individual or progeny records that are more accurate than was the case using expected relationships.

Key Words: genomic prediction