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Amino acid composition of muscle and intestine protein in pigs at different ages*J.A. Conde-Aguilera^{1,2}, C. Cobo-Ortega^{1,2}, S. Tesserand³, Y. Mercier⁴ and J. Van Milgen^{1,2}**¹Agrocampus Ouest, UMR1348 PEGASE, Rennes, 35000, France, ²INRA, UMR1348 PEGASE, Saint-Gilles, 35590, France, ³INRA, UR83 Recherches Avicoles, Nouzilly, 37380, France, ⁴Adisseo France, Antony, 92160, France; alberto.conde@rennes.inra.fr*

Changes in the amino acid (AA) composition of whole body protein during growth have been reported. We hypothesize that part of this change is due to changes in the AA composition of different tissues. The objective of this study was to evaluate the AA composition of tissues in pigs at different ages. Two groups of 6 pigs each received diets formulated to meet nutrient requirements and were slaughtered at 10 and 23 wk of age, respectively. Samples of the longissimus dorsi (LM) and rhomboideus (RM) muscles, proximal (I1) and distal jejunum (I2), and ileum (I3) were taken for analysis. The relative weight of LM increased by 32% at 23 wks of age, but decreased for RM (-52%) and the small intestine (-39, -22, and -30% for I1, I2 and I3, respectively). Protein content increased with age by 13% and 7% in LM and RM, respectively. Total AA content (per 16 g N) increased with age from 85.5 to 90.7% on average for the tissues at 23 wk of age. For LM and RM, the increase in AA content was due to an increase in essential AA content (especially His, Lys, and Ile in LM, and His, Phe, and Tyr in RM), while the content of non-essential AA decreased with age (especially Gly and Pro). In I1, the contents of Thr, Ile, Phe, and His decreased with increasing age, while that of Gly and Pro increased. In I2, the Met and Asp content increased while that of Thr and Glu decreased. In I3, the content of Met, Cys, Ser, and Gly increased within increasing age and that of Lys, Phe, Tyr, Arg, and Asp decreased. The AA composition of tissue protein is affected by age (or body weight), and the changes in composition differs among tissues. This may contribute to the change in the whole body AA composition during growth.

Comparison of gastrointestinal tracts and pH values of Ross 308 broiler and indigenous Venda chicken*M. Mabelebe^{1,2}, O.J. Alabi¹, J.W. Ngambi¹ and D. Norris¹**¹University of Limpopo, Agricultural Economics and Animal Production, P/Bag X1106 Sovenga Turfloop, 0727 Polokwane, South Africa, ²University of New England, Environmental and Rural Science, University of New England, Armidale, NSW 2351, Australia, Australia, Australia; jones.ngambi@ul.ac.za*

An experiment was conducted to determine and compare the pH values in the digestive tracts of Ross 308 broiler and indigenous Venda chickens. A complete randomized design (CRD) with two treatments (Ross 308 broiler and indigenous Venda chickens) having five replicates was used in this experiment. The chickens were both raised under intensive management system and fed a commercial diet until the age of 70 d. Five birds per treatment (breed) were taken, weighed and killed by cervical dislocation, then scalded and defeathered. Weights, lengths and pH values of different segments of the gastrointestinal tract were measured immediately by using a sensitive level electronic scale (RADWAG), millimeter graduate rule and a Model 191 pH meter equipped with a spear-like electrode (Knick, Berlin, Germany), respectively. Breed difference had effect ($P < 0.05$) on live weight, crop, gizzard and large intestine weight. However, proventriculus, small intestine, caecum, and liver weights were not influenced ($P > 0.05$) by the breed differences. All the length parameters measured were similar ($P > 0.05$), however, the GIT of the broiler chickens was longer ($P < 0.05$) than the indigenous Venda chickens. In addition, breed differences had effect ($P < 0.05$) on the crop, gizzard and small intestine pH. However, the proventriculus, large intestine, caecum and pH at 2, 4, 6 and 24 h were not influenced by the breed differences ($P > 0.05$). The differences observed in the present study could be attributed to genetic variation of the chickens.