



# Nutritional value of cooked offal derived from free-range rams reared in South Africa

L.C. Hoffman <sup>a,\*</sup>, L.L. Laubscher <sup>a</sup>, K. Leisegang <sup>b</sup>

<sup>a</sup> University of Stellenbosch, Faculty of AgriSciences, Private Bag X1, Matieland, 7602, South Africa

<sup>b</sup> University of the Western Cape, Faculty of Community and Health Sciences, School of Natural Medicine, Private Bag 17, Bellville, 7535, South Africa

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## ABSTRACT

Nutritional value of Dorper ( $n = 10$ ) and Merino ( $n = 10$ ) by-products were evaluated. Proximate composition differed between organs and breeds with Merino heart (68.9 g/100 g), spleen (77.2 g/100 g) and testicles (83.7 g/100 g) having higher moisture contents than their Dorper counterparts. Dorper brain (10.1 g/100 g), heart (15.2 g/100 g), spleen (20.4 g/100 g) and testicles (12.9 g/100 g) had higher protein contents than Merino. Dorper organs also tended to have a lower fat content. Amino acid and fatty acid profiles differed between organs and breeds. Few differences were noted in total SFA and MUFA. Dorper heart (1.8%) had significantly lower total PUFA than Merino heart (7.3%). All the organs showed favourable P:S ratios, with the exception of the tongue, heart and stomach. Dorper and Merino brain, lungs and testicles had favourable n-6/n-3 ratios. Cholesterol content differed between both organs and breeds. The value of offal as food is discussed further.

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## 1. Introduction

The so-called fifth quarter of a carcass is traditionally consumed in a number of countries and its general consumption around the world is escalating. Organs recovered from slaughtered animals offer a range of foods which are nutritionally attractive (U S Department of Agriculture & Agricultural Research Service, 2011). Edible organs are highly prized in South East Asia and Africa, whilst demand is variable and low in Australia and USA, respectively (Fatma & Mahdey, 2010; Pearson & Dutson, 1988). In some African countries, edible offal contributes 33% more edible material per animal slaughtered and reduces the whole carcass price by 42.3% (Aduku, Aganga, Okoh, Ingawa, & Phillip, 1991). In South Africa, when visiting abattoirs, managers and owners are quick to point out that the value of the offal (organ meat) is on the increase. Offal was traditionally sold to the lower income market; however, with the increase in tourism, some of the offal products are becoming delicacies in niche markets, particularly in restaurants. In the Encyclopaedia of Meat Sciences, Ockerman and Basu (2004) give a good synopsis of some of the products that can be made from various organs/variety meats. Irrespective of who the end consumer is, there is a need in the industry for more information on the nutritional value of the major offal found in livestock. Scientific literature on the nutritional value of offal is relatively scarce with limited data available on the internet in the form of nutritional food tables – the USDA Nutrient database does contain some nutritional information under the caption of “variety meat and

by-products” (U S Department of Agriculture & Agricultural Research Service, 2011). These, however, are generally species specific with few focusing on nutritional composition differences as a result of other extrinsic and intrinsic factors. Authors such as Park, Kouassi, and Chin (1991) have, however, reported slight differences between goat breeds for the moisture, total fat and cholesterol content of the liver, kidney and heart. In a later study, Park and Washington (1993) reported significant differences in the fatty acid composition of organ meat between two goat breeds and between organs within the breeds. On the other hand, Kamalzadeh, Koops, van Bruchem, Tamminga, and Zwart (1998) noted that diet restriction had little influence on the early maturing organs as they had a priority for available nutrients over the later developing organs/body parts.

Furthermore, research findings reported in the public domain often only include selected chemical analyses of a few organs, for example proximate composition, cholesterol content and fatty acid profiles of the brain, heart, liver and tongue (Abdullah, 2008; Kiernat, Johnson, & Siedler, 1964; Mustafa, 1988; Schweigert, Bennett, & Guthneck, 1953; Williams, 2007). In South Africa, specifically, where offal consumption is generally higher than in many other countries, limited if any data is available on the nutritional composition of this offal. In the present investigation, the aim is to determine the nutritional value of the major offal from Dorper and Merino type lambs from the same region reared in a free range (natural pasture) system since both breeds are particularly popular in the South African agricultural industry. The Dorper is an early maturing breed relative to the Merino, that was selected for its hardiness and is a composite breed derived in South Africa from a cross between the Dorset Horn and the Blackheaded Persian (Milne, 2000).

\* Corresponding author. Tel.: +27 21 808 4747; fax: +27 21 808 4750.  
E-mail address: [lch@sun.ac.za](mailto:lch@sun.ac.za) (L.C. Hoffman).

## 2. Materials and methods

### 2.1. Animals and organs

Twenty animals, ten Dorper sheep and ten Merino sheep, reared in a free-range extensive system in South Africa, where they only consumed natural grazing and slaughtered using standard South African techniques at LAW abattoir (Uppington, South Africa) were randomly selected from the day's slaughter ( $n = 1000$ ). Although age and production region may have had an effect on the chemical composition, it was decided to select sheep from the two major breeds reared in South Africa from the same region (Karoo) and also from the most common age class slaughtered. Therefore, the sheep sampled were all A2 or A3 carcass classes (indicating them to be lambs with no permanent molar teeth and having a fat depth of 1–7 mm measured 25 mm from the midline between the 3rd and 4th lumbar vertebrae; an A3 lamb being the fatter). Nine organs were removed immediately after slaughter from each of the animals, including the brain, tongue, stomach, liver, heart, lungs, spleen, kidneys and testicles. The experimental design was thus a 2 (breeds: Dorper and Merino)  $\times$  10 (animals: rams)  $\times$  9 (organs: brain, tongue, stomach, liver, heart, lungs, spleen, kidneys and testicles) design.

Each of the organs was individually labelled, frozen and transported to the Stellenbosch University meat laboratory for further analyses. At the laboratory, the samples were defrosted and cooked inside a plastic bag within a water bath set at 60 °C for 60 min. Cooked samples were homogenized together with the cooking losses (juices) in a bowl with suitable blade until they were paste-like. Samples were then vacuum sealed and stored at –20 °C until analyses could be performed.

### 2.2. Chemical analyses

#### 2.2.1. Proximate composition

The moisture contents (g/100 g organ meat) of all the cooked samples were determined according to the Association of Official Analytical Chemist's Standard Methods (AOAC, 1997). The moisture content was determined by drying a 2-g sample at 100–105 °C for 24 h (AOAC Official method 934.01). After drying samples were weighed and ashed at 500 °C for 6 h to determine ash content (AOAC Official method 942.05).

The fat content was determined by homogenizing the samples in a blender, followed by chloroform:methanol (2:1) extraction (Lee, Trevino, & Chaiyawat, 1996). To determine the protein content, the sample residue from the fat analysis was dried (as per moisture determination) and ground with a pestle in a mortar to a fine powder. Samples of 0.150 g were inserted into a foil wrap designed for the Leco protein analyzer (LECO FP-528 Protein/Nitrogen Detector, LECO Corporation, St. Joseph, USA). The nitrogen content was multiplied by 6.25 to calculate the protein concentration in the sample. An EDTA calibration sample (LECO Corporation, USA, Part number 502–092) was analysed with each batch of samples to ensure accuracy and recovery rate.

The accuracy and repeatability of all the techniques used above were controlled on a bi-monthly basis by means of a National Inter-laboratory scheme (AgriLASA: Agricultural Laboratory Association of South Africa) wherein blind samples are analysed.

#### 2.2.2. Fatty acid profile and cholesterol content

After thawing, a 2-g cooked sample was extracted with a chloroform:methanol (2:1; v/v) solution according to the method of Folch, Lees, and Sloane Stanley (1957). All the extraction solvents contained 0.01% butylated hydroxytoluene (BHT) as antioxidant. A polytron mixer (WiggenHauser Homogenizer, Berlin, Germany, D-500 fitted with a standard shaft 1; speed setting D) was used to homogenize the sample with the extraction solvent. Heptadecanoic acid (C17:0) was used as an internal standard (catalogue number H3500, Sigma-Aldrich Inc., St. Louis, USA) to quantify the individual

fatty acids. Of the extracted lipids, 250  $\mu$ l was transmethylated for 2 h at 70 °C with 2 ml of a methanol/sulphuric acid (19:1; v/v) solution as transmethylating agent. After cooling to room temperature, the resulting fatty acid methyl esters (FAMES) were extracted with water and hexane. The top hexane phase was transferred to a spotting tube and dried under nitrogen. Fifty microliters of hexane was added to the dried sample of which 1  $\mu$ l was injected.

Analysis was done on a Thermo Finnigan Focus GC (Thermo Electron S.p.A, Strada Rivoltana, Milan, Italy) equipped with a flame ionization detector using a BPX70 capillary column (60 m  $\times$  0.25 mm internal diameter, 0.25  $\mu$ m film, SGE International Pty Ltd, Victoria, Australia). Gas flow rates were 20 ml/min for hydrogen, 200 ml/min for air and 25 ml/min for nitrogen carrier gas. Temperature programming was linear at 7 °C/min, with an initial temperature of 60 °C and a final temperature of 160 °C. The injector temperature was 220 °C (split flow 20:120) and the detector temperature was 260 °C. The FAMES were identified by comparing the retention times to those of a standard FAME mixture (Supelco™ 37 Component FAME Mix, 10 mg/ml in CH<sub>2</sub>Cl<sub>2</sub>, Catalogue Number 47885-U, Supelco, Bellefonte, USA).

From the lipid extraction used for the fatty acid determination, 1 ml was used for cholesterol determination. Stigmasterol was added as internal standard before drying the sub-sample under nitrogen (C<sub>29</sub>H<sub>48</sub>O, Sigma-Aldrich Inc.). After drying, 0.5 ml of a 6% ethanolic potassium hydroxide (KOH) solution was used to saponify the lipid fraction in a heating block for 1 h at 70 °C. After cooling, distilled water and hexane were added and the top phase was transferred to a spotting tube and dried under nitrogen. Fifty microliters of hexane was added to the dried sample of which 1  $\mu$ l was injected.

Analysis was done on a Thermo Finnigan Focus GC equipped with a flame ionized detector using a DB-17 capillary column (15 m  $\times$  0.53 mm internal diameter, 1.50  $\mu$ m film, Agilent Technologies Inc., CA, USA). Gas flow rates were 20 ml/min for hydrogen, 200 ml/min for air and 25 ml/min for nitrogen carrier gas. Temperature settings were as follows: injector, 220 °C, oven, 250 °C and detector, 265 °C.

#### 2.2.3. Amino acid profile

Amino acids were determined on cooked dried, defatted organ samples. Samples were hydrolyzed (AOAC official method 994.12, 2003) with 6 M HCl in a sealed tube under nitrogen for 24 h at 110 °C. Thereafter samples were diluted and derivatized using the EZ:Faast LC method (Phenomenex, USA). EZ:Faast consists of a solid phase extraction step followed by a derivatization step and a liquid–liquid extraction step to get rid of interfering compounds in the matrix. In the solid phase extraction step the samples are pulled through a sorbent tip that binds the amino acids whilst the remaining interfering compounds flow through. The amino acids are then derivatized allowing them to migrate to the organic layer which is removed, dried, redissolved and subject to Liquid chromatography–mass spectrometry–mass spectrometry (LC/MS/MS) analysis. In addition a daughter ion is formed that makes LC/MS/MS analysis possible. Labelled methionine-d<sub>3</sub> was included as internal standard. A Waters Micromass Quattro Micro LC/MS/MS triple quadrupole mass spectrometer (mass range: 2–2000 m/z), complete with Waters Alliance 2695 Separations Module (HPLC) was used for the determination of amino acid composition (Waters Corporation, Milford, USA).

### 2.3. Statistical analyses

The data was analysed using a one way analysis of variance per organ with breed (Dorper or Merino) as the main effect. The results were generated using PROC GLM of SAS software, Version 9.1.3 of the SAS Institute Inc. (2002–2005). The model was:

$$Y_{ij} = \mu + a_i + \varepsilon_{ij}$$

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