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Charles Quinto
Chapman University, quint131@mail.chapman.edu

Rebecca Tinoco
Chapman University, 19rebeccatinoco93@gmail.com

Rosalee S. Hellberg
Chapman University, hellberg@chapman.edu

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DNA Barcoding Reveals Mislabeling of Game Meat Species on the U.S. Commercial Market

Charles A. Quinto[a], Rebecca Tinoco[a], Rosalee S. Hellberg[a,*]

[a]Chapman University, Schmid College of Science and Technology, Food Science and Nutrition, One University Drive, Orange, CA 92866

***Corresponding Author**:

Rosalee S. Hellberg, Ph.D.

Chapman University

Ph: 714-628-2811

E-mail: hellberg@chapman.edu

Abstract

Game meats represent a valuable specialty market in the United States that has high economic incentives associated with mislabeling. However, there is limited information on this topic. The purpose of this study was to conduct a market survey of game meats sold within the United States and identify instances of mislabeling using DNA barcoding. Products were also examined for the presence of threatened or endangered species. Fifty-four samples of whole-cut game meats were collected from online distributors in the United States and sequenced across a 658 base-pair region of the cytochrome *c* oxidase subunit I (COI) gene. The resulting DNA sequences were identified based on top species matches in the Barcode of Life Database (BOLD) and GenBank. The results showed that 18.5% of samples were potentially mislabeled and 9.3% of samples legally contained a near-threatened or vulnerable species and were correctly labeled. The samples appeared to have been mislabeled due to reasons such as economic gain and product mishandling. However, cross-species hybridization could also have contributed to the potential mislabeling of bison and yak products. Although near threatened (bison) and vulnerable (lion) species were identified, the products were correctly labeled and legally sold, as bison populations are managed and the identified lion species is not protected by the Endangered Species Act (ESA). Overall, the results of this study revealed the occurrence of game meat mislabeling in the United States and suggest the need for further evaluation of this practice.

Keywords: DNA barcoding; game meat; species identification; adulteration; misbranding; DNA sequencing

1. Introduction

Food fraud, in the form of ingredient substitution and mislabeling of food products, has been observed globally (Cawthorn, Steinman, & Hoffman, 2013; Everstine, Spink, & Kennedy, 2013). One type of food fraud is the intentional substitution of one species for another, which may be carried out for reasons such as financial gain or avoidance of import restrictions. Mislabeling and species substitution may also lead to illegal sales of threatened (i.e., vulnerable, endangered or critically endangered) species protected by the Endangered Species Act (ESA) (Fish and Wildlife Service [FWS], 2003) and disrupt conservation efforts aimed at these animals (Crego-Prieto et al., 2012; International Union for Conservation of Nature and Natural Resources [IUCN], 2014; Rasmussen & Morrissey, 2009). Game meats represent an important specialty market in the United States, with an estimated value of US$39 thousand million (National Agricultural Statistics Service [NASS], 2012). According to the U.S. Food and Drug Administration (FDA), game meats are defined as exotic meats, animals and birds which are not in the Meat and Poultry Act (FDA, 2012). Due to differences in the retail prices between high-cost game meats and lower-priced livestock, such as beef, pork and poultry, there is high economic motivation for species substitution to occur (Economic Research Service [ERS], 2014). Furthermore, game meats are sold as cuts or ground products, which makes it difficult to identify mislabeled species based on appearance alone. There is also potential for the harvesting of threatened or endangered meat species protected by the ESA that are mislabeled and sold as otherwise legal game meats.

Game meats produced in the United States are regulated by the U.S. Department of Agriculture (USDA) while game meats imported into the United States are regulated by

the FDA (Food Safety and Inspection Servce [FSIS], 2011). While it is legal for wild game to be hunted in the United States for personal consumption, the USDA requires that domestically-produced game meats sold commercially are farm-raised (FDA, 2013; FSIS, 2011). However, unlike animals covered under the Meat and Poultry Act, mandatory inspection services are not required for game meats (USDA, 2000). Imported game meat is allowed provided it is an eligible product from an approved country (Animal and Plant Health Inspection Service [APHIS], 2012; FSIS, 2013; USDA, 2014) and the meat does not violate any U.S. regulations (FWS, 2006). Imported products must follow the Code of Federal Regulations (CFR) Title 50 Part 17 which dictates that threatened and imported species acquired through commerce or commercial activity are illegal and ineligible for import (Endangered and Threatened Wildlife and Plants, 2014). Furthermore, according to the ESA, even animals maintained in a controlled environment are prohibited for commercial activity unless actions are for conservation (FWS, 2003). However, species are only protected by the ESA provided that they are listed as threatened or endangered in the Federal Register or included in provisions of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES).

Previous studies conducted outside the United States have uncovered instances of mislabeling in processed meat and game products (Ayaz, Ayaz, & Erol, 2006; Cawthorn et al., 2013; D'Amato, Alechine, Cloete, Davison, & Corach, 2013). For example, studies conducted in South Africa found that 68.3-69.2% of meat products tested were mislabeled (Cawthorn et al., 2013; D'Amato et al., 2013). Furthermore, a study conducted in Turkey found that 22.0% of meat products tested were mislabeled, including products labeled as beef identified as poultry, deer and horse (Ayaz et al., 2006). Despite the potential for

fraudulent mislabeling of game meats on the U.S. commercial market, there is limited information on this topic, with previous studies focusing on seafood and non-game meats. For example, Hsieh, Woodward and Ho (1995) tested non-game meat products sold in the United States and found that 16.6% of samples were mislabeled. In a study conducted in North America by Wong and Hanner (2008), 25% of the commercial seafood products tested were mislabeled, including an endangered species mislabeled as a sustainable counterpart. Another study reported the illegal mislabeling of shark fins belonging to the white shark (*Carcharodon carcharias*), which is a protected species (Shivji, Chapman, Pikitch, & Raymond, 2005). Overall, the mislabeling and exploitation of protected species found in the above studies suggest the importance of investigating mislabeled game meat within the United States.

When taxonomic features have been removed due to processing, methods based on DNA or protein profiles are typically used to identify meat or seafood products at the species level (Ballin, 2010; Hellberg & Morrissey, 2011). One of these methods is DNA barcoding, which is based on genetic variation within a standardized genetic region. In animals, this standardized region is a ~650 base-pair (bp) fragment of the gene coding for cytochrome *c* oxidase subunit I (COI) (Hebert, Cywinska, Ball, & deWaard, 2003). This target is a mitochondrial gene that is relatively conserved within species and exhibits divergence between species, enabling samples to be identified at the species level in most cases. In order to identify an unknown sample using the COI DNA barcode, the query sequence is compared to a sequence database and the top species match is identified. DNA barcoding has been successfully used in previous market surveys examining species

substitution in seafood (Smith, McVeagh, & Steinke, 2008; Wong & Hanner, 2008) and meat products (D'Amato et al., 2013).

Given the limited information on game meat mislabeling practices in the United States combined with the potential for fraud to occur, the objective of this study was to perform a market survey to identify species in game meats sold within the United States using DNA barcoding. Game meats were examined for instances of mislabeling as well as for the presence of threatened or endangered species.

2. Materials and Methods

2.1. *Sample collection*

A total of 54 game meat products representing a variety of species were collected in this study from four online retail sources in the United States (Table 1). All products were received in a fresh/frozen state and upon arrival they were catalogued and stored at -80˚C. Prior to sampling, products were thawed overnight at 4˚C. A tissue sample of ~10 mg was excised with sterile scalpels and forceps and transferred to a 1.5 ml microcentrifuge tube for DNA extraction.

2.2. *DNA extraction*

DNA extractions were carried out using the DNeasy Blood and Tissue Kit (Qiagen, Valencia, CA), Spin-Column protocol according to modifications in Handy et al. (2011). Following sample collection, the tissue samples described above were lysed with 50 µl Buffer ATL and 5.56 µl Proteinase K over a period of 1-3 h at 56˚C while vortexing at 30 min increments. Following lysis, 55.6 µl Buffer AL and 55.6 µl of 95% ethanol were added to each sample tube and vortexed. The samples were transferred to columns and

centrifuged for 1 min at 8,000 rpm. The column membrane was washed with 140 µl of AW1 buffer and centrifuged for 1 min at 8,000 rpm followed by a second wash with 140 µl of AW2 buffer and centrifugation for 3 min at 14,000 rpm. The columns were transferred to a sterile 1.5 ml microcentrifuge tube prior to adding 50 µl of AE buffer preheated to 37˚C. The samples were centrifuged for 1 min at 8,000 rpm to collect the eluted DNA. A reagent blank with no tissue added was included alongside each set of extracted samples.

2.3. *PCR and sequencing*

The mammalian primer cocktails described by Ivanova, Clare and Borisenko (2012) were used to amplify a 658-bp region of the gene coding for COI. PCR was carried out as described in Ivanova et al. (2012), except that OmniMix HS (Cepheid, Sunnyvale, CA) lyophilized PCR reagent beads were used in place of adding individual reagents and the total reaction volume was increased to 25 µl. Each reaction included the following components: 0.5 OmniMix HS PCR bead, 22.5 µl molecular grade water, 0.25 µl of each 10 µM primer cocktail, and 2 µl of DNA. Cycling conditions were followed according to Ivanova et al. (2012): 94ºC for 2 min; 5 cycles of 94ºC for 30 s, 50ºC for 40 s, and 72ºC for 1 min; 35 cycles of 94ºC for 30 s, 55ºC for 40 s, and 72ºC for 1 min; and a final extension step at 72ºC for 10 min. Thermocycling was carried out with a Mastercycler nexus gradient thermal cycler (Eppendorf, Hamburg, Germany).

Confirmation of PCR was achieved as described in Hellberg, Kawalek, Van, Shen and Williams-Hill (2014). PCR products (4 µl) were loaded with dd H_2O (16 µl) onto pre-cast 2.0% E-gels (Life Technologies, Carlsbad, CA) and run for 6-10 min using an E-Gel iBase (Life Technologies). Results were captured using FOTO/Analyst Express

(Fotodyne, Hartland, WI) and Transilluminator FBDLT-88 (Fisher Scientific, Waltham, MA) and visualized with FOTO/Analyst PCImage (version 5.0.0.0, FOTODYNE). Amplified products were cleaned using ExoSAP-IT (Affymetrix, Santa Clara, CA) as described in Handy et al. (2011). The samples were then sent to GenScript (Piscataway, NJ) for bi-directional sequencing using BigDye Terminator v3.1 Cycle Sequencing Kit (Life Technologies) and an Applied Biosystems 3730xl Genetic Analyzer (Life Technologies).

2.4. *Sequence analysis*

Raw sequence data was assembled and edited using Geneious R7 (Biomatters Ltd., Auckland, New Zealand). Successfully assembled consensus sequences were aligned using ClustalW with the default settings in Geneious R7 and then trimmed to the COI DNA barcoding region (658 bp). The length, number of ambiguities and % high quality bases (HQ%) were recorded for each consensus sequence. Following quality guidelines set by Handy et al. (2011), only samples with assembled bi-directional sequences that were $\geq$ 500 bp with < 2% ambiguities or $\geq$ 500 bp single reads with $\geq$ 98% HQ were further analyzed. Nucleotide sequences meeting these requirements were searched against the Species Level Barcode Records in the Barcode of Life Database (BOLD) (http://www.boldsystems.org/index.php/IDS_OpenIdEngine). The top species matches showing $\geq$ 98% similarity to the query sequence were recorded. Sequences which did not yield a species match in BOLD were queried in GenBank using the Basic Local Alignment Search Tool (BLAST) and the top species matches were recorded. Any samples that were identified as potentially mislabeled products were subjected to a second round of DNA extraction and sequencing to confirm the initial result. Each identified species was queried

174 in the Encyclopedia of Life (EOL) (http://eol.org/) to identify the preferred common name
175 in addition to the IUCN (http://www.iucnredlist.org/) to determine if it was threatened or
176 endangered.

177 **3. Results and Discussion**

178 3.1. *Sequencing results*

179 Out of the 54 samples collected, a total of 22 different types of game meat were
180 represented based on the product label, with an average of 2-3 samples tested per game
181 meat type (Table 1). All 54 samples collected were successfully amplified and bi-
182 directionally sequenced to assemble a COI DNA barcode. The sequences were of high
183 quality, with an average consensus length of 657 $\pm$ 6 bp, an average ambiguity percentage
184 of 0.05 $\pm$ 0.13% and an average HQ percentage of 93.6 $\pm$ 8.1%. The majority of samples
185 (n = 51) showed genetic matches $\geq$ 98% to species-level entries in BOLD (Table 1). Of
186 these samples, 38 showed $\geq$ 98% genetic similarity to sequences from just one species
187 while 13 showed this level of similarity to at least two species (discussed below). Three
188 specimens could not be identified at the species level in BOLD and were subsequently
189 searched in GenBank using BLAST. These included two products labeled as kangaroo
190 (A24 and A33) that had top species matches of 99.00% and 96.00%, respectively, to the
191 Western grey kangaroo (*Macropus fuliginosus*), and one product labeled as partridge
192 (A29) that had a top species match of 96.00% to the chukar partridge (*Alectoris chukar*).
193 Considering that divergence within species is typically < 2% for the COI DNA barcode
194 region (Hebert, Ratnasingham, & deWaard, 2003), it is possible that samples A29 and A33
195 belong to a species not yet sequenced across this genetic region. If the sequence data for a
196 particular species has not been uploaded to BOLD, the database cannot generate a species-

level identification (Milton, Pierossi, & Ratnasingham, 2013; Ratnasingham & Hebert, 2007).

Overall, 44 of the products were found to be correctly labeled. Inadequate data on product packaging such as a missing country of origin or inconsistent naming conventions of meat cuts made it difficult to uncover trends among correctly labeled products. Based on the available information, game purchased whole, as a breast, or as a chuck/shoulder roast was always correctly labeled. However, these observations are based on a small sample size of 2-4 specimens per meat cut.

Thirteen of the 51 specimens identified through BOLD had multiple species matches with genetic similarity $\geq$ 98%. One sample (A32) labeled as coyote was identified as both coyote (*Canis latrans*) and grey wolf (*Canis lupus*) with 100.0% similarity to each species. In North America, there is a continuous distribution of both coyotes and wolves, allowing for interbreeding between the two species and thus preventing complete distinction based on the DNA barcode (Vila et al., 1999). Four products labeled as elk (A19-A21 and A50) had a 100.0% match to two species: red deer (*Cervus elaphus*) and American elk (*Cervus canadensis*). Due to the lack of consensus regarding classification practices and consequences of human involvement with *Cervus* species, some authors have included *C. canadensis* as a subspecies of *C. elaphus* while others categorize them as two separate species (Polziehn & Strobeck, 2002; Randi, Mucci, Claro-Hergueta, Bonnet, & Douzery, 2001). These four products also had secondary species matches to sika deer (*Cervus nippon*), sambar (*Cervus unicolor/Rusa unicolor*), and rusa (*Cervus timorensis/Rusa timorensis*) with genetic similarities of 98.00-98.36%. These results may be explained by the oftentimes inclusion of sika as a subspecies of red deer and rusa

descending from a similar ancestry as *R. unicolor* and *Axis porcinus* (Groves, 2006; Pitra, Fickel, Meijaard, & Groves, 2004). Since the greatest genetic similarity was found with red deer/American elk, the products were determined to be correctly labeled. The four products labeled as elk with sole top species matches to red deer (A05, A07, A15 and A51) were also determined to be correctly labeled. This was on the basis that EOL lists American elk as a subspecies of *C. elaphus* and these two organisms do not show sufficient divergence to be differentiated with the COI DNA barcode. In another case of products matching multiple species, two specimens labeled as buffalo (A04 and A54) were identified as Asian water buffalo (*Bubalus bubalis*) with 100.0% genetic similarity and as water buffalo (*Bubalus arnee*) with 99.80% similarity. However, the difference in nomenclature is a result of domestication and not a difference in animal species (Gentry, Clutton-Brock, & Groves, 2004). Aside from hybridization and dissimilar classification practices, specimens may be misidentified if the sequence data used to assign species in BOLD has not been validated or is incorrect (Ratnasingham & Hebert, 2007). In addition, DNA barcoding is not effective for species identification when two or more species do not show sufficient genetic divergence across the selected barcode region (Ward, Costa, Holmes, & Steinke, 2008).

The remaining samples with multiple species identified at $\geq$ 98% genetic similarity are discussed below, as none of the identified species corresponded to what was listed on the label.

3.2. *Mislabeled products*

Ten of the 54 samples sequenced were determined to be potentially mislabeled (Table 1). These results were confirmed by a second DNA extraction and sequencing.

Interestingly, six of these products were associated with economic incentives based on differences in retail prices, while four products were priced lower than the list price for the identified species (Table 2). In instances that lacked an economic incentive, accidental mishandling by the manufacturer or the supplier may have resulted in the listed product being replaced by a higher-valued species, as the substitution would have resulted in profit loss.

Five of the potentially mislabeled products (A12, A16, A17, A28 and A49) were identified with 100.0% genetic similarity to a single species without secondary matches. Two products labeled as bison (A12, A49) and one product labeled as yak (A28) were identified as domestic cattle (*B. taurus*); a product labeled as black bear [(*Ursus americanus*) (A16)] was identified as American beaver (*Castor canadensis*); and a product labeled as pheasant [(*Phasiandae* family) (A17)] was identified as helmeted guineafowl (*Numida meleagris*). The products labeled as bison, pheasant and yak each showed potential for economic gain. The product labeled as pheasant and identified as guineafowl had the smallest potential profit of US$3.81/kg, while the product labeled as yak and identified as domestic cattle had the largest potential profit of US$46.59-$57.08/kg. Domestic cattle labeled as bison would have resulted in a profit of US$8.57-$55.43/kg depending on the product type. While there is economic incentive associated with mislabeling cattle as bison, these findings could be due to crossbreeding between cattle and bison, which is known to occur in the wild (Polziehn, Strobeck, Sheraton, & Beech, 1995). As a result of the maternal inheritance pattern of mitochondrial DNA, offspring of a male bison and a female cow would have a DNA barcode matching that of cattle (Derr et al., 2012; Polziehn et al., 1995). According to regulations listed in Exotic Animals and Horses,

9 C. F.R. § 352 (2014), products labeled as bison may refer to American bison or the hybrid species cattalo. However, if cattalo is to be sold as bison, it must be a result of direct breeding between American bison and cattle. Since it is unknown whether the products labeled as bison, but identified as cattle, were a result of species substitution, direct crossbreeding, or backcrossing, the products are considered potentially mislabeled. Similarly, yak and cattle have crossbred resulting in mitochondrial cattle DNA in a species resembling yak (Leslie & Schaller, 2009; Qi, Jianlin, Wang, Rege, & Hanotte, 2010). However, it can be difficult to differentiate these hybridized individuals morphologically and therefore mislabeling may have been unintentional, despite the potential for profit. In the case of the product labeled as beaver and identified as black bear, an economic loss would have resulted, indicating possible product mishandling. Interestingly, the FDA previously issued a warning letter to a game meats distributor for selling misbranded black bear steaks identified as brown bear (*Ursus arctos*) and misbranded black bear burgers found to contain elk/red deer (*Cervus* sp.) (FDA, 2011).

The remaining five mislabeled samples had a genetic similarity $\geq$ 98% to multiple species, none of which corresponded to the species listed on the label. Two of the four products labeled as alligator [(*Alligator* sp.) (A10 and A11)] were identified as spectacled caiman (*Caiman crocodilus*) with genetic similarities of 99.54-99.69%. These products also showed a secondary match to the yacare caiman (*Caiman yacare*) with genetic similarity of 98.57-99.23%. According to Busack and Pandya (2001), conflicting classifications have caused *C. yacare* to be considered either a separate species or a subspecies of *C. crocodilus*. The distributor which sold the alligator products also sold products labeled as spectacled caiman. Since replacing alligator with caiman would result

289 in profit loss (Table 2), the mislabeling may have been a result of accidental mishandling
290 or intentional substitution based on a lack of supply for the desired product.
291 Two products labeled as red deer (A31 and A41) also showed multiple species
292 matches with ≥ 98% genetic similarity. One product (A31) had a primary identification of
293 llama *(Lama glama*) with genetic similarity matches of 98.62-100.0% and secondary
294 matches to guanaco *(Lama guanicoe*) and alpaca *(Lama pacos, Vicugna pacos*) with 98.77-
295 99.39% similarity. The second product (A41) was identified as alpaca (*L. pacos*) with
296 100.0% genetic similarity and vicuňa (*Vicugna vicugna*) with 98.32% similarity.
297 Identification of multiple species for these products is a result of the domestication of
298 guanaco and vicuňa to produce llama and alpaca, respectively (Barreta et al., 2013).
299 During the domestication process, hybridization occurred between llamas and alpacas
300 making it difficult to distinguish the two based on DNA barcoding. Products labeled as
301 llama and alpaca were sold by the same distributor that had the mislabeled red deer
302 products, but since llama is sold for a much higher price than alpaca, product A41 shows a
303 potential for economic gain while A31 does not. Based on the genetic similarity of llama
304 and alpaca, it is possible that both products originated from the same species or that they
305 were incorrectly identified by the supplier/distributor. Regardless of these genetic
306 similarities, both products were considered mislabeled, since none of the top species
307 matches were for red deer.
308 Finally, a product labeled as antelope [(*Bovidae* family) (A14)] showed a top
309 species match to sika deer with genetic similarities of 98.01-100.0% and secondary genetic
310 matches of 98.01-98.62% to red deer, usuri sika deer (*Cervus hortulorum*) and hokkaido
311 sika deer (*Cervus yesoensis*). The difficulty in assigning a single species may be due to

312 existing uncertainties involving deer species (Cook, Wang, & Sensabaugh, 1999; Pitra et
313 al., 2004). Early classifications relied on morphology and have been deemed inadequate.
314 The use of DNA analysis has shown molecular differences between sika, usuri sika and
315 hokkaido sika deer which are located in different geographic regions of Asia (Groves,
316 2006). Despite molecular differences between species, nomenclature assignments have not
317 been consistent and declining populations prevent complete resolution (Cook et al., 1999;
318 Groves, 2006). Furthermore, red and sika deer may share an ancestral species making it
319 difficult to discern groups. Despite these issues, none of the primary or secondary species
320 matches would have resulted in a correctly labeled antelope product. Of note, products
321 labeled as antelope and sika deer were both sold by the same distributor and the
322 replacement of antelope with sika deer would have resulted in a potential economic profit
323 of US$6.62/kg (Table 2).

324 Each distributor was examined for the frequency of mislabeling among the
325 products sampled (Fig. 1). At least one product from each distributor was potentially
326 mislabeled, with distributors A and B having the highest numbers of potentially
327 misbranded products, at 16.0% and 57.1%, respectively. All four potentially mislabeled
328 products from distributor A were substituted with a species also offered for sale by the
329 same distributor. Since only one potentially mislabeled product from distributor A was
330 associated with economic incentives, the fraudulent products may have been due to
331 improper handling or supply issues. On the other hand, three of the four potentially
332 mislabeled products from distributor B showed profit incentives through species
333 substitution (Table 2). Overall, nine out of ten potentially mislabeled products were
334 substituted for a species the distributor also processed, with the exception being a product

335 labeled as bison (A12) sold by distributor B that was identified as domestic cattle. Though
336 not every substituted species was offered as the same cut as the expected species,
337 unintentional mix-ups may have occurred due to the inability to distinguish meats based on
338 visual inspection alone. Provided that the distributor has adequate quality systems in place,
339 incidences of mislabeling may have occurred at the supplier or farm level.

340 The overall rate of potential mislabeling found in this study (18.5%) was similar to
341 previous studies investigating non-game meat products in the United States and Turkey,
342 which reported mislabeling rates of 16.6% (Hsieh et al., 1995) and 22.0% (Ayaz et al.,
343 2006), respectively. However, these rates are much lower than those reported by studies
344 investigating meat and game products sold in South Africa [68.3-69.2%] (Cawthorn et al.,
345 2013; D'Amato et al., 2013). The higher rates of mislabeling found in the latter studies may
346 be due to differences in market regulations, inspection programs or product monitoring. In
347 comparison to seafood, the rate of mislabeling in the current study was slightly lower than
348 the rate of 25.3% reported by Wong and Hanner (2008) for North American seafood.
349 Given that seafood is one of the top food categories subject to fraud (Johnson, 2014), it
350 may be expected that seafood has a rate of mislabeling equal to or higher than game meat.

351 3.3. *Threatened and endangered species*

352 According to IUCN classifications, one sample (A38) was identified as vulnerable
353 (included in the threatened category), four samples (A13, A22, A23, A52) were identified
354 as near threatened, fifteen samples were identified as species with a population status not
355 yet assessed, and the remaining samples were identified as species with stable populations
356 (Table 1). The five products identified as a near threatened or threatened species were all
357 determined to be correctly labeled and legally sold. The four products with a status of near

threatened were all labeled as bison and identified as American bison (*Bison bison*) (Gates & Aune, 2008). Although the bison population has increased since the steep decline in the 19th century, herds are currently managed under conservation programs. Despite the National Agricultural Statistics Service (NASS, 2012) indicating 162,110 bison were present on farms in 2012, IUCN classifications do not account for commercial herds when determining if a species is threatened or endangered (Gates & Aune, 2008). The managed herds allow for population control while still offering bison products for consumption. The sample included in the threatened category was the product labeled and identified as lion [(*Panthera leo*) (A38) (Bauer, Nowell, & Packer, 2012)]. Despite being listed as a threatened species by the IUCN, lion is not protected under the ESA (FWS, 2003, 2013). Until this species is listed as threatened in the Federal Register, lion products sold commercially do not violate conservation laws. In an attempt to conserve the lion species, the FWS submitted a proposal to add *Panthera leo leo* to the list of threatened species to provide protection against commercial activity (FWS, 2013). In summary, since the bison population is managed and the lion is not protected by the ESA, the sale of these products would not be considered illegal.

The observed incidence of threatened species identified in products analyzed in this study (1.85%) is similar to previous market studies examining mislabeled threatened fish and seafood species. Wong and Hanner (2008) found that 1.10% of the 91 North American seafood products analyzed in their study were from a threatened species. Another market survey reported that 0.58% of 1,215 seafood items collected in the United States were endangered or critically endangered (Warner, Timme, Lowell, & Hirshfield, 2013). On the other hand, one study focused on just one product type found that 18.25% out of 400 whale

meat products analyzed from Japan and Korea were from protected stocks (Dalebout, Lento, Cipriano, Funahashi, & Baker, 2002).

4. Conclusion

Overall, the results of this study demonstrate the occurrence of mislabeling of commercially-sold game meat products in the United States, with 18.5% of the game meats analyzed determined to be potentially mislabeled. Although one of the products tested contained a species from a threatened population, the product was correctly labeled and legally sold. An examination of the potentially misbranded products suggested the possibility of intentional mislabeling for economic gain for over half of the misbranded products. The other products appear to have been misbranded for other reasons, such as inadequate traceability systems and/or mishandling by the distributor or supplier. It is also possible that products may appear to be mislabeled due to cross-species hybridization or inconsistencies with classification. The results of this study suggest that existing policies may require some amendment to identify and deter such practices, such as the implementation of mandatory inspection of game meats and verification of species labeling. Additional market research on game meat mislabeling within the United States is recommended in order to delineate trends and determine appropriate steps to improve control of this specialty food group.

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Figure Captions

Figure 1. Summary of products by distributor showing the percentage of correctly labeled and mislabeled game meat products tested

561 **Table 1.** Summary of samples collected and analyzed in this study. Top species matches and % genetic similarity were determined using the
562 Barcode of Life Database (BOLD), unless otherwise noted

Sample ID	Product label	Samples (n)	Top species match	Genetic similarity	Population status[a]
A27, A44	Alligator	2	American alligator (*Alligator mississippiensis)*	100.0%	Stable
A10	Alligator	1	Spectacled caiman (*Caiman crocodilus*)[b]	99.54%	Stable
A11	Alligator	1	Spectacled caiman (*Caiman crocodilus*)[b]	99.69%	Stable
A03	Alpaca	1	Alpaca (*Lama pacos*)	99.54%	Not assessed
A30	Antelope	1	Nilgai antelope (*Boselaphus tragocamelus*)	99.69%	Stable
A14	Antelope	1	Sika deer (*Cervus nippon*)[b]	100.0%	Stable
A02	Beaver	1	American beaver (*Castor canadensis*)	99.80%	Stable
A13, A22, A23, A52	Bison	4	American bison (*Bison bison*)	100.0%	Near threatened
A12, A49	Bison	2	Domestic cattle (*Bos taurus*)[b]	100.0%	Not assessed
A16	Black bear	1	American beaver (*Castor canadensis*)[b]	100.0%	Stable
A06	Bobcat	1	Bobcat (*Lynx rufus*)	100.0%	Stable
A04, A54	Buffalo	2	Asian water buffalo (*Bubalus bubalis*)	100.0%	Not assessed
A01, A08, A09	Camel	3	Dromedary camel (*Camelus dromedarius*)	100.0%	Not assessed
A32	Coyote	1	Coyote (*Canis latrans*); Grey wolf (*Canis lupus*)[c]	100.0%	Stable

A15, A05	Elk	2	Red deer (*Cervus elaphus*)	100.0%	Stable
A07	Elk	1	Red deer (*Cervus elaphus*)	99.85%	Stable
A51	Elk	1	Red deer (*Cervus elaphus*)	99.69%	Stable
A19, A20, A21, A50	Elk	4	Red deer (*Cervus elaphus*); American elk (*Cervus canadensis*)[c]	100.0%	Stable; Not assessed
A34	Emu	1	Emu (*Dromaius novaehollandiae*)	100.0%	Stable
A24	Kangaroo	1	Western grey kangaroo (*Macropus fuliginosus*)[d]	99.00%	Stable
A33	Kangaroo	1	Western grey kangaroo (*Macropus fuliginosus*)[d]	96.00%	Stable
A38	Lion	1	Lion (*Panthera leo*)	100.0%	Vulnerable (threatened)
A43	Muskrat	1	Common muskrat (*Ondatra zibethicus*)	99.85%	Stable
A29	Partridge	1	Chukar partridge (*Alectoris chukar*)[d]	96.00%	Stable
A42	Partridge	1	Chukar partridge (*Alectoris chukar*)	99.54%	Stable
A40	Partridge	1	Red-legged partridge (*Alectoris rufa*)	99.84%	Stable
A26, A36, A48	Pheasant	3	Ring-necked pheasant (*Phasianus colchicus*)	100.0%	Stable
A17	Pheasant	1	Helmeted guineafowl (*Numida meleagris*)[b]	100.0%	Stable
A35	Raccoon	1	Northern raccoon (*Procyon lotor*)	99.69%	Stable
A31	Red deer	1	Llama (*Lama glama*)[b]	100.0%	Not assessed
A41	Red deer	1	Alpaca (*Lama pacos*)[b]	100.0%	Not assessed
A39, A45	Turtle	2	Common snapping turtle (*Chelydra serpentina*)	100.0%	Stable

A18, A25, A46	Wild boar	3	Wild boar (*Sus scrofa*)	100.0%	Stable
A47	Wild boar	1	Wild boar (*Sus scrofa*)	99.84%	Stable
A53, A55	Yak	2	Yak (*Bos grunniens*)	100.0%	Not assessed
A28	Yak	1	Domestic cattle (*Bos taurus*)[b]	100.0%	Not assessed

563 [a]According to the International Union for Conservation of Nature (IUCN)
564 [b]Potentially mislabeled
565 [c]Sequences for a single sample matched multiple species with 100.0% similarity
566 [d]No sequence matches were available in BOLD for this sample. The top species match from GenBank is reported

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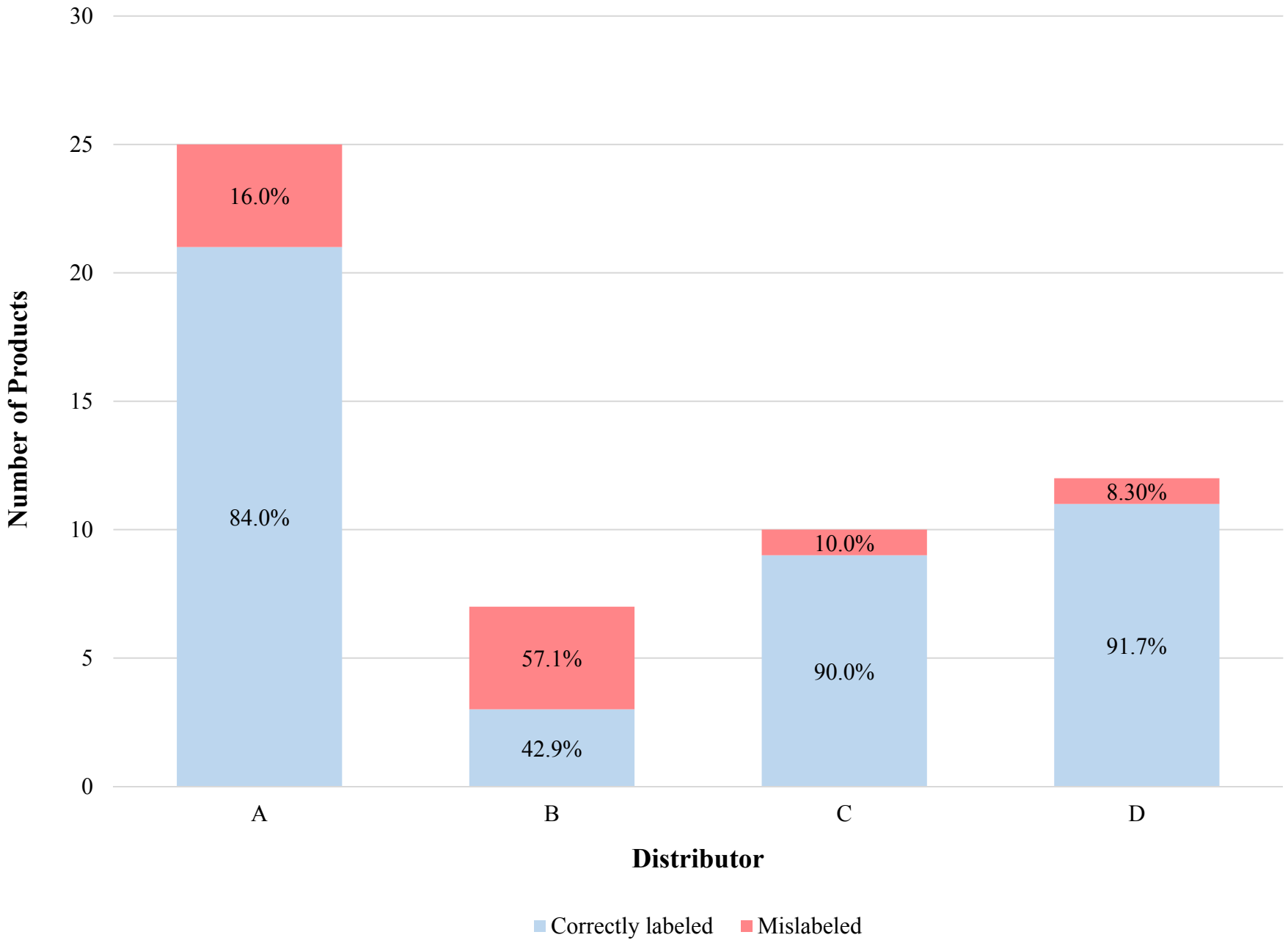
580 **Table 2.** Retail price comparisons of potentially mislabeled game meats. Retail prices were obtained from online distributors unless otherwise
581 noted

Distributor	Sample ID	Product label	Retail price (USD)	Cut	Identified species	Retail price of identified species (USD)	Notes
A	A10	Alligator	$77.14/kg	Tenderloin meat	Spectacled caiman (*Caiman crocodilus*)	$88.16/kg	N/A
A	A11	Alligator	$44.07/kg	Body and tail meat	Spectacled caiman (*Caiman crocodilus*)	$66.12/kg	Price of identified species is for "Caiman Meat." Body and tail meat was not offered.
B	A14	Antelope	$41.78/kg	Center cut steak	Sika deer (*Cervus nippon*)	$35.16/kg[a]	N/A
B	A12	Bison	$19.73/kg	Stew meat	Domestic cattle (*Bos taurus*)	$11.16/kg[a,b]	Price of identified species is for boneless beef stew.
C	A49	Bison	$70.55/kg	Rib eye steak	Domestic cattle (*Bos taurus*)	$15.12/kg[a,b]	Price of identified species is for uncooked beef steaks.
B	A16	Black bear	$28.55/kg	Stew meat	American beaver (*Castor canadensis*)	$88.16/kg	Beaver as stew meat was not an available cut by this distributor. Price is for stew meat from another online distributor
B	A17	Pheasant	$13.18/kg	Leg quarters	Helmeted guineafowl (*Numida meleagris*)	$9.37/kg[a]	N/A
A	A31	Red deer	$61.73 to $77.16/kg	Loin chop	Llama (*Lama glama*)	$110.21/kg	Prices of identified species are for llama strip loin steak.

							No loin chop cut offered.
A	A41	Red deer	$61.73 to $77.16/kg	Loin chop	Alpaca (*Lama pacos*)	$44.07/kg[a]	Prices of identified species are for alpaca strip loin steak. No loin chop cut offered.
D	A28	Yak	$62.99 to $73.48/kg	Sirloin steak	Domestic cattle (*Bos taurus*)	$16.40/kg[a,b]	Price of identified species is for choice sirloin steak.

582 [a]Product has an economic incentive to be sold mislabeled
583 [b]Based on the average retail price listed by the USDA Economic Research Service for January 2014 - August 2014 (ERS, 2014)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Number of Products
16.0%
84.0%
57.1%
42.9%
10.0%
90.0%
8.30%
91.7%
A
B
C
D
Distributor
Correctly labeled
Mislabeled