ISAG CONFERENCE 2012, Cairns, Australia

Animal Forensics Standing Committee

STANDING COMMITTEES / WORKSHOPS Information will be posted online

Organised by a standing committee **yes**

Date and meeting time: 2-3 pm, July 15, 2012

Chair, name and contact email: Sree Kanthaswamy, skanthaswamy@usdavis.edu

Agenda / programme attached:

Time	Speaker	Presentation title
14:00	Sree Kanthaswamy (Chair)	Welcome and Introductions
14:10	Christina D. Lindquist (USA)	Making your Process, Evidence, and Reports Bullet-Proof
14:30	Denise A. Andrade de Oliveira (Brazil)	A Real-Time PCR-based method to detect and quantify bovine content in buffalo derived products
14:50	Guillermo Giovambattista (Argentina) Presented by Andrés Rogberg-Muñoz	Comparison of the effectiveness between STR and SNP panels for forensic DNA analysis in bovine breeds

Number of participants at meeting: 55-60

Summary of the meeting including votes, decisions taken and plans for future conferences

Not including the committee members and the presenters, there were approximately 55-60 people at the July 15, 2012 animal forensic genetics workshop, and there was active participation by the attendees during the discussion sessions after each presentation. Presentation abstracts are presented in Appendix 1 below.

Although originally tabled as an agenda item, the business meeting was not held and no actions were taken because of the lack of quorum; only three committee members (Dr Sree Kanthaswamy, Beth Wictum and Romy Morrin O'Donnell) were present. The forensic meeting was adjourned at 3:10 p.m.

Committee members

Chair: Sree Kanthaswamy — term of service: 4 years
Department of Environmental Toxicology, and the
California National Primate Research Center, UC Davis, USA

E mail address: skanthaswamy@ucdavis.edu

Other members

1) Beth Wictum — term of service: 4 years
Veterinary Genetics Laboratory (VGL), Forensics Unit,
UC Davis, USA,
2) Romy Morrin O'Donnell — term of service: 2 years
Weatherby's, Ireland,
3) Guillermo Giovambattista, — term of service: 2 years
Instituto de Genética Veterinaria (IGEVET),
CCT La Plata/Consejo Nacional de Investigaciones
Científicas y Técnicas (CONICET) - Facultad de
Ciencias Veterinarias, Universidad Nacional
de La Plata, UNLP, Argentina,
4) Dr Leanne Van de Goor, — term of service: 2 years
Van Haeringen Laboratorium B.V. (VHL) Netherlands,
5) Sean Corley, Animal Genetics Laboratory, — term of service: 2 years
University of Queensland, Australia,
6) Dr Corinne Cherbonnel, Genindexe, France — term of service: 2 years

Appendix 1

***Making your Process, Evidence, and Reports Bullet-Proof (*Christina D. Lindquist, MS)**
While accreditation provides a solid framework for ensuring that DNA test results will stand up in court, it is a process that takes a dedicated effort and a large commitment of time and resources. That level of oversight may be unrealistic for those laboratories that perform forensic testing infrequently. This presentation will cover practical steps that laboratories can take to strengthen their procedures and assure that their reports are accepted by the courts. The points covered will include documentation, evidence handling, security and reviews. In addition to providing sensible approaches to addressing these vulnerable points, resources that are becoming available through the work of the U.S.-based SWGWILD (Scientific Working Group for Wildlife Forensic Science) will be presented.

A Real-Time PCR-based method to detect and quantify bovine content in buffalo derived products (Denise A. Andrade de Oliveira, PhD)
Fraudulent species substitution in food products is a reality in many markets throughout the world. Molecular markers are useful tools to authenticate food content and prevent these occurrences, thus ensuring food safety. PCR based techniques fit the requirements of sensitivity and specificity and are currently widely used in forensic science. Realtime PCR is

the method of choice when aiming to quantify contamination levels. We describe a method for calculating bovine and buffalo content in food products using real-time PCR with sets of primers/probe designed to specifically amplify bovine or buffalo DNA. Amplification efficiencies showed satisfactory levels for both sets using
either Taqman or SYBR Green systems in dairy or meat products. To correct potential deviations between real and obtained quantifications caused by biological differences among the involved species, we made use of a calibration curve, a set of points of controlled admixtures of bovine and buffalo material. The use of the proposed calibration curve for dairy samples always approximated the obtained to the expected quantification values. The technique was tested in commercial samples and presented efficacy and reliability appropriate for routine analysis of buffalo or bovine derived products. The method is subject of a patent document at Brazilian Patent Office and is protected under Brazilian specific regulations.

Comparison of the effectiveness between STR and SNP panels for forensic DNA analysis in bovine breeds
(Guillermo Giovambattista, PhD, Presented by Andrés Rogberg-Muñoz, PhD)
STRs have been successfully used in animal genetic identification in forensic investigations, however in the last years, SNPs have gained traction. An efficient SNP identification system requires a marker set with enough power to identify individuals. In this study, information obtained from SNPs and STRs in Taurine and Cebuine breeds was compared. Samples (N=378) from 15 breeds and 7 forensic caseworks were genotyped using18 STRs and 32 SNPs. The effects of quality, amount, and tissue sources (blood, hair, bone, beef) of DNA on genotype performance were evaluated. The SNP results showed a performance of 81.1% of call rate and a percent concordance between both replicates of 98.7%. These results were mainly explained by two factors: that assay design, and DNA samples quality rather than DNA quantity were important. Cumulative SNPs exclusion power values for sample matching, using double exclusion criteria, within each breed showed that in Taurine breeds information from the analyzed SNPs are equivalent to the 12 STRs ISAG recommended set (~10-11). In Cebuine breeds, this set exhibited only a MP between ~10-7 and ~10-9. The test also showed a range of 61 to 99% of correct assignment within each breed. These results could provide a valuable population data that support the consensus SNP panel for bovine genetic identification.