TUESDAY, SEPTEMBER 15

16:00 - 18:00 **REGISTRATION**

18:00 - 18:30 **OPENING CEREMONY**

18:30 - 19:00 ISFG SCIENTIFIC PRIZE 2007 LECTURE:
The X-chromosome in forensic genetics.
Prof. Dr. Habif Reinhard Szibor

19:00 Welcome Reception

WEDNESDAY, SEPTEMBER 16

08:30 - 10:00 **Qiagen Symposium**

10:00 - 10:30 Coffee break

Session 1 | Chairperson: *Niels Morling*

10:30 - 11:15 CONFERENCE:
SNP analysis of ancestry and pigmentation: recent advances and caswork applications. *Dr. Chris Phillips, PhD*

11:15 - 12:30 **POSTER SESSION 1 (P 001 - P 110)**

P 001 A review of low template STR analysis in casework using the DNA SenCE post-PCR technique.
P 002 Increased Capillary Electrophoresis Injection Settings as an Efficient Approach to Increase the Sensitivity of STR Typing.
P 003 Modification of a commercially available kit for the improvement of PCR efficiency.
P 004 When anthropometry fails: Fingerprint genotyping.
P 005 Characteristics of a Modified STR Amplification Approach for Severely Degraded Skeletal Elements.
P 006 Evaluation of reliability of STR typing in human colon carcinomas tissues used for identification purpose.
P 007 Three allele pattern in immortalized cell line detected by STR typing.
P 008 Effect of low-dose radiation on mutation rates of STR loci commonly used in forensic casework.
P 009 Allelic Alterations of STRs in Archival Paraffin Embedded Tissue as DNA Source for Paternity Testing.

P 010 The STR Profiling in Formalin Fixed and Paraffin Embedded Tissues.

P 011 Forensic STR Analysis Reveals DNA Contamination Previously Undetected During Clinical Analysis of Chronically Inflamed Tissues.

P 012 Validation of the MiniFiler Kit in archaeological samples.

P 013 Analysis of AmpFlSTR® MiniFilerTM loci and its forensic application.

P 014 Development of two new miniSTR multiplexes assay for typing archival Bouin's fluid-fixed paraffin-embedded tissues P 015 MiniSTR concept - Q11.

P 016 Characterization of NonCodis Mini STR loci on hair, fingerprint and ancient bone samples.

P 017 PowerPlex® 16 HS System: Increases to Genotyping Success Rates.

P 018 Concordance Testing with New STR Kits.

P 019 The Single Most Polymorphic STR Locus: SE33 Performance in U.S. Populations.

P 020 Development and Validation of a Next Generation-STR Pentaplex.

P 021 Validation of the AmpF?STR SEfiler Plus kit for forensic STR analysis.

P 022 Uses of the NIST 26plex STR Assay for Human Identity Testing.

P 024 Construction of Four Fluorescence labeled Multiplex Typing System for D9S1122/D10S1435/D17S1301 MiniSTR Loci and Evaluation of Its Forensic Application.

P 025 Construction and application of four fluorescence labeled multiplex typing system for 3 miniSTR loci.

P 026 Development of two new autosomal STR multiplex systems as a supplemental tool with other commercial kits.

P 027 Automation of statistical interpretation with R Software applied to validation of AmpFlSTR® Next Generation MultiplexTM (Applied Biosystems).

P 028 Power Plex 16 HS®: Internal validation of a new tool for genetic analysis of forensic and parentage testing.

P 029 Integration of the AmpFlSTR Identifiler PCR Amplification Kit with SRY-specific primers for gender identification.

P 030 Development of PCR Internal controls (PICs) for STR Profiling.

P 031 Observation of triallelic patterns in autosomal STRs during routine casework.

P 032 Characterisation of twelve new alleles in the D18S51 STR system.

P 033 Further allelic variation at the STR-loci ACTBP2 (SE33), D3S1358, D8S1132, D18S51 and D21S11.

P 034 A X-chromosome STR hexaplex as a powerfull tool in deficiency paternity cases.

P 035 Optimization and Validation Studies of The Mentype® Argus X-8 kit for Forensic Cases.

P 036 Sequence polymorphisms at the DXS6789, DXS8377 and DXS101 loci in three Asian populations.

P 037 Updated allelic structures of the DXS10135 and DXS10078 STR loci.

P 038 Y-STR anaylsis of degraded DNA using a reduced size amplicon multiplex.

P 039 Unexpected patterns in Y-STR analyses and implications for profile identification.

P 040 Validation of the new Y-miniplex system for use in forensic casework.

P 041 Development and evaluation of multiplex Y-STR assays for application in molecular genealogy.

P 042 Y- STR mutational rates determination in South Portugal Caucasian population.

P 043 Moving from male lineage characterization to male individual identification using Y-chromosome DNA-analysis.

P 044 Adaptation and evaluation of the PrepFilerTM DNA extraction technology in an automated forensic DNA analysis process with emphasis on DNA yield, inhibitor removal and contamination security.

P 045 Validated Automated Systems - LGC Introduces Change the Easy Way.

P 046 A Dedicated Automated System for Extraction, Quantification and STR Amplification of Forensic Evidence Samples.

P 047 Automated quantifiler® quantitative PCR setup, template normalization and PCR setup using HID EVOlution™ qPCR/STR setup on trace evidence samples.

P 048 Automated extraction of DNA from reference samples from various types of biological materials on the Qiagen BioRobot® Ez1.

P 049 Automated washing of FTA-card punches and PCR setup for reference samples using a LIMS-controlled Sias Xantus Automated Liquid Handler.

P 050 Automated extraction of DNA and PCR setup using a Tecan Freedom EVO® liquid handler.

P 051 Customizing a commercial laboratory information management system for a forensic laboratory.

P 052 The Fully Automated DNA Extraction with the QIAsymphony SP - Validation and first experiences in Forensic Case Work.

P 053 A Production system to generate Genetic Database information from Buccal Swab cells on FTA® Paper.

P 054 Successful STR and SNP typing of FTA-card samples with low amounts of DNA after DNA extraction using a Qiagen BioRobot® Ez1.

P 055 Automated DNA extraction of forensic samples using the QIAsymphony platform : estimations of DNA recovery and PCR inhibitor removal.

P 056 Automated reaction setup of quantitation PCR, STR and capillary electropheresis on the QIAgility.

P 057 Performance evaluation of the new EZ1 Advanced XL for forensic applications.

P 058 Efficiency of DNA IQ System in recovering semen DNA from cotton swabs.

P 059 A Novel Platform for the Modular Integration of Forensic Assay Setup and Medium- to High-Throughput Purification of Nucleic Acids.

P 060 Results of the 2009 Paternity Testing Workshop of the English Speaking Working Group.

P 061 Results of the 2008 Colombian Paternity Testing Quality Control Exercise.

P 062 Sequencing of mitochondrial DNA and the problem of human specificity.

P 063 A new technology in mtDNA Sequencing: success rates vs time.

P 064 Optimization and Validation of 10 Mitochondrial DNA SNPs using SNaPshot Kit.

P 065 MTexpertTM, an Automated Software System for Forensic Mitochondrial DNA Data Analysis.

P 066 Comparison of the Plexor® HY System, Quantifiler and Quantifiler Duo Kits using the Roche LightCycler 480 System and the ABI 7900 Real time PCR Instrument.

P 067 QuantifilerTM Human DNA Quantification Kit (AB) as a screening kit for DNA profiling.

P 068 Direct quantitation of genomic DNA from saliva spotted FTA® by Real-Time PCR.

P 069 Fast PCR amplification of AmpFlSTR Identifiler (2nd report).

P 070 Rapid Amplification of Commercial STR Typing Kits.

P 071 Direct Amplification of STRs from Blood or Buccal Cell Samples.

P 072 Rapid STR analysis of single source DNA samples in 2 hours.
P 073 Preliminary trials of low volume (1µl) PCR amplification using AmpliGrid (AG480F) slides.
P 074 Validation of a microchip electrophoresis system as a DNA amplification control.
P 075 MiniSTRs: a powerful tool to identify genetic profiles in samples with small amounts of DNA.
P 076 Increased sensitivity for amplified STR alleles on capillary sequencers with BigDye® XTerminatorTM.
P 077 DNA Typing From Lipstick Prints Left On The Skin.
P 078 SNPs in Paternity Investigations: The Simple Future.
P 079 Internal validation of 29 autosomal SNP-multiplex with ABI 310 Genetic Analyzer.
P 080 ABO Genotyping by Duplex Amplification and Oligonucleotide Probes Hybridization.
P 081 Comparative analysis of ABO genotyping and serological typing in Northern Chinese Han Population.
P 082 Rapid ABO genotyping directly from fresh blood, hair and stains of blood and buccal epithelial cells.
P 083 Trace DNA Success Rates Relating to Volume Crime Offences.
P 084 Biological And DNA Evidence In 1000 Sexual Assault Cases.
P 085 Male DNA recovery from different type of evidences in 300 cases of sexual assault.
P 086 Sexual assault cases related to unknown perpetrator: almost 50% of the analyzed cases corresponded to serial offenders.
P 087 Female DNA traces - it´s not always the offender!
P 088 Analysis of Forensic samples in Banco Nacional de Datos Geneticos.
P 089 Paternity investigation experience with a 40 autosomal SNP panel.
P 090 DNA profile evidence in complex disputed paternity cases: The analysis of 200 real cases.
P 091 Supplementary Markers for Deficient Immigration Cases: Additional STRs or SNPs?
P 092 A study of Argentinian attitudes regarding the custody and use of forensic DNA databases.
P 093 Genotyping of DNA samples under adverse conditions of Low Copy Number - LCN (Formolisados Tissue samples and embedded in paraffin).
P 094 STR genotyping of DNA extracted from used Triage kits.
P 095 Post-coital vaginal sampling with nylon-flocked swabs improves DNA typing.
P 096 Extraction of High Quality DNA from Biological Materials and Calcified Tissues.
P 097 Effect of Blood Stained Soils and Time Period on DNA and Allele drop out using Promega 16 Powerplex® Kit.
P 098 Prevalence of mixed DNA profiles in fingernail swabs from autoptic cases.
P 099 Standardization of teeth sampling for DNA analysis from decomposing bodies before soft tissue removal regarding anthropological analysis.
P 100 Analysis of DNA profiles extracted from degraded samples from archival of formalin fixed tissue included in paraffin (FFTIP) and hairs.
P 101 Genetic identification of degraded DNA samples buried in different types of soil.
P 102 Utility validation of extraction of genomic DNA from hard tissues, bone and nail, using PrepFilerTM Forensic DNA Extraction Kit.
P 103 A new approach in the identification of degraded paternity samples.
P 104 High yield DNA extraction from bones using a full demineralization approach.

P 105 Validation of a new magnetic particle-based method (PrepFiler™ Forensic DNA Extraction Kit) for rapid extraction of high quality DNA from a wide variety of forensic samples.

P 106 The tooth - an approach for DNA extraction.

P 107 A small change in the standard extraction method in order to obtain better results.

P 108 STR and SNP Analysis of human DNA from Lucilia sericata larvae's gut contents.

P 109 The transfer of human DNA by Lucilia blowflies.

P 110 Room temperature preservation and transportation of reference and trace DNA swabs.

12:30 - 14:00 **Promega Symposium**

Session 2 | Chairpersons: *Walther Parson & Leonor Gusmão*

14:00 - 14:45 CONFERENCE:

The furure of criminal DNA databases.
Prof. Dr. Peter M. Schneider

14:45 - 16:00 **ORAL PRESENTATIONS 1**

14:45 **O 01** **How well does your DNA predict your appearance?**
Manfred Kayser[1], [1]Department of Forensic Molecular Biology, Erasmus University Medical Center Rotterdam, The Netherlands, Rotterdam, Netherlands.

15:10 **O 02** **A new SNP multiplex assay for the determination of geographic origin and pigmentary traits to aid anthropological investigations.** Caroline Bouakaze[1], Christine Keyser[1], Bertrand Ludes[1], [1]Institute of Legal Medicine, Strasbourg, France.

15:22 **O 03** **Highly Differentiated Autosomal SNPs to Analyze Ancestry and Infer Admixture Components in American Populations.** Christopher Phillips[1], Liliana Porras-Hurtado[1,2], Manuel Fondevila[1], Antonio Salas[1], Antonio Gomez-Tato[3], Jose Alvarez-Dios[3], Ana Freire-Aradas[1], Adriana Castillo[6], Julieta Henoa[2], Guillermo Barreto[4], Fernando Rondon[4], William Zabala[5], Lisbeth Borjas[5], Angel Carracedo[1], Maria Victoria Lareu[1], [1]Forensic Genetics Unit, Institute of Legal Medicine, University of Santiago de Compostela, Santiago of Compostela, Spain, [2]Medical Genetic Laboratory, Technology University of Pereira, Pereira, Colombia, [3]Faculty of Mathematics, University of Santiago de Compostela, Santiago of Compostela, Spain, [4]Human Molecular Genetic Research Group, University of Valle, Cali, Colombia, [5]Medical Genetics Unit, University of Zulia, Zulia, Venezuela, [6]Industrial University, Santander, Colombia.

15:34 **O 04** **STRs and AIMs informativeness for forensic purposes in an admixed Brazilian population.** Silviene Fabiana Oliveira[1], Neide Maria Godinho[2], Carlos Eduardo Amorim[1] Carolina Carvalho Gontijo[1], Gabriel Falcão Alencar[1], Rejane da Silva Sena Barcelos[2,3], Aguinaldo Luiz Simões[4], Celso Teixeira Mendes-Júnior[5], [1]Universidade de Brasilia, Brasilia, Distrito Federal, Brazil, [2]Instituto de Criminalistica de Goias, Goiania, Goias,

Brazil, [3]Universidade Católica de Goiás, Goiania, Goias, Brazil, [4]Faculdade de Medicina de Ribeirão Preto, Ribeirão Preto, São Paulo, Brazil, [5]Faculdade de Filosofia Ciências e Letras de Ribeirão Preto, Ribeirão Preto, São Paulo, Brazil.

15:46 **O 05** **Insertion/Deletion Polymorphisms as Ancestry Informative Markers**
Daniel Zaumsegel[1], Markus A. Rothschild[1], Peter M. Schneider[1], [1]Institute of Legal Medicine, University Hospital Cologne, Cologne, Germany.

16:00 - 16:30 Coffee break

Session 3 | Chairpersons: *Mike Coble & Lutz Roewer*

16:30 - 18:00 **ORAL PRESENTATIONS 2**

16:30 **O 06** **The diversified genetic landscape of mountain areas: high-resolution sampling and analysis of Y-chromosomal variation in Tyrol (Austria).** Burkhard Berger[1], Daniel Erhart[1], Harald Niederstätter[1], Christoph Gassner[2], Harald Schennach[2], Walther Parson[1], [1]Institute of Legal Medicine, Innsbruck Medical University, Innsbruck Austria, [2]Central Institute for Blood Transfusion and Division for Immunology, University Hospital, Innsbruck, Austria.

16:42 **O 07** **Inferring the demographic history of the last nomad hunter-gatherer population in Ecuador - the Waorani - using lineal and recombining DNA markers** Maria Geppert[1], Baeta Miriam[3], Nunez Carolina[3], Zweynert Sarah[2], Vacas Omar[4], González-Solorzano Jorge[5], Willuweit Sascha[1], Nagy Marion[1], Martínez-Jarreta Begona[3], Krawczak Michael[6], Gonzalez-Andrade Fabricio[5], Roewer Lutz[1], [1]Dept. Forensic Genetics, Institute of Legal Medicine and Forensic Sciences, Charité - Universitätsmedizin Berlin, Germany, [2]Clinics for Psychiatry, Charité - Universitätsmedizin Berlin, Berlin, Germany, [3]Department of Legal Medicine, University of Zaragoza, Zaragoza, Spain, [4]Catholic University of Ecuador, Quito, Ecuador, [5]Hospital Metropolitano, Quito, Ecuador, [6]Institut für Medizinische Informatik und Statistik, Universitätsklinikum Schleswig-Holstein, Kiel, Germany.

16:58 **O 08** **Multi-Continental Genetic Contributions to the Extant Population of Argentina as detected from autosomal, Y-chromosomal and mitochondrial DNA,** Daniel Corach[1], Oscar Lao[2], Cecilia Bobillo[1], Kristiaan Van der Gaag[3], Mark Vermeulen[2], Mannis Van Oven[2], Kate Van Duijn[2], Miriam Goedbloed[2], Peter M Vallone[4], Walther Parson[5], Peter De Knijff[3], Manfred Kayser[2], [1]Servicio de Huellas Digitales Genéticas and Cátedra de Genética y Biología Molecular, Faculty of Pharmacy and Biochemistry, University of Buenos Aires, Buenos Aires, Argentina, [2]Department of Forensic Molecular Biology, Erasmus University Medical Center Rotterdam, Rotterdam, Netherlands, [3]Department of Human Genetics, Leiden University Medical Center, Leiden, Netherlands, [4]Biochemical Science Division, National Institute of Standards and Technology, Gaithersburg, United States, [5]Institute of Legal Medicine, Innsbruck Medical University, Innsbruck, Austria.

17:10 **O 09** **Development of a New Forensic STR Multiplex with Enhanced Performance for Degraded and Inhibited Samples,** Julio Mulero[1], Robert Green[1], Nicola Oldroyd[1], Lori Hennessy[1], [1]Applied Biosystems, Foster City, CA, United States.

17:22 **O 10** **A Suite of New STR Systems Designed to Meet the Changing Needs of the DNA-Typing Community** Lotte Downey[1], Carla Abdo[1], Doug Storts[1], Cindy Sprecher[1], Bob McLaren[1], Dawn Rabbach[1], Benjamin Krenke[1], Erin McCombs[1], [1]Promega Corporation, Madison, WI, United States.

17:34 **O 11** **Analysis of microRNA expression in forensically-relevant human body fluids,** Dmitry Zubakov[1], Antonius W.M. Boersma[2], Ying Choi[1], Erik A.C. Wiemer[2], Manfred Kayser[1], [1]Department of Forensic Molecular Biology, Erasmus University Medical Center Rotterdam, Rotterdam, Netherlands, [2]Department of Medical Oncology, Erasmus University Medical Center Rotterdam, Rotterdam, Netherlands.

17:46 **O 12** **Identification of Forensically Relevant Body Fluids Using a Panel of Differentially Expressed microRNAs,** Erin Hanson[1], Helge Lubenow[3], Jack Ballantyne[1,2], [1]National Center for orensic Science, Orlando, FL, United States, [2]University of Central Florida, Department of Chemistry, Orlando, FL, United States, [3]Qiagen, Hilden, Germany.

THURSDAY, SEPTEMBER 17

08:30 - 10:00 **Applied Biosystems Symposium**

10:00 - 10:30 Coffee break

Session 1 | Chairperson: *Daniel Corach*

10:30 - 11:15 CONFERENCE:
Genetic Dissection of human disorders using genome-wide association studies, *Dr. Luis Carvajal Carmona, PhD*

11:15 - 12:30 **POSTER SESSION 2 (P 111 - P208)**

P 111 The problem of DNA contamination in forensic case work-How to get rid of unwanted DNA?

P 112 An alternative strategy for whole mitochondrial genome amplification and sequencing suited for lower quality mtDNA.

P 113 Alterations of Length Heteroplasmy in Mitochondrial DNA Under Various Amplification Conditions.

P 114 MtSNP typing before mtDNA sequencing: Why do it?

P 115 Collecting cell material for DNA-typing from clothing using filtertips and vacuum.

P 116 Washing with Ethanol - a suitable Method of DNA-Extraction?

P 117 Trace DNA collection - performance of minitape and three different swabs.

P 118 Optimisation of Cellular DNA Recovery from Tape-Lifts.

P 119 One method of collecting the fallen off the epithelial cells.

P 120 The analysis of biological samples from crime scene for a future human DNA profile confrontation. Effects of presumptive test reagents on the ability to obtain STR profiles for human identification.

P 121 Influence of the luminol chemiluminescence reaction in confirmatory tests for detection and characterization of bloodstains in forensic analysis.

P 122 Grading a rape case followed by death from the study of autosomal STRs and STRs of the Y chromosome - Case Study.

P 123 Case report of a homicide resolved 15 years later: the robustness of the Chelex extraction.

P 124 Statistical analysis of DNA mixtures using peak area information in a case of savage murder.

P 125 Identification of Gestational Trophoblastic Disease in a sexual assault case.

P 126 Forensic application of Y chromosome SNPs in inconclusive cases.

P 127 Traffic accident vs homicide: the contribution of DNA analysis to clarify this mystery. A case report.

P 128 Human being eaten by his own dogs: genetic confirmation through analysis of bones recovered in a dog's stomach content.

P 129 DNA analysis of biological material on bullets and crime scene reconstruction.

P 130 Forensic application of mitochondrial DNA SNPs.

P 131 Case Report: Crime investigation set on Mitochondrial DNA analysis.

P 132 Two completely different mitochondrial genomes within blood cells of three healthy Individuals.

P 133 An homoplasmic large deletion in mtDNA control region: case report.

P 134 A Paternal Mutation in the Penta D STR Locus.

P 135 Non-exclusion maternity case with two apparent genetic incompatibilities, a mutation and a null allele.

P 136 Tetragametic Chimerism. ¿Nature rarities or not an unusual finding in paternity testing Studies?

P 137 Chimerism Detected in Fraternal Twins using ABI AmpFlSTR® Identifiler.

P 138 A case of chimerism in a paternity study.

P 139 Paternity Testing involving human remains identification and putative half sisters: Usefulness of an X-hexaplex STR markers.

P 140 Prenatal Testing in Paternity Testing: A Positive Perspective.

P 141 X-STRs analysis in paternity testing when the alleged father is related to the biological father.

P 142 Utility of Y- and X-STRs in the research of complex biological relationship.

P 143 DNA recovery from a 44-year old umbilical cord.

P 144 Evaluation of deleted region from Yp11.2 of two amelogenin negative related males.

P 145 Admissibility of Y-STRs at court: a case report from Australia.

P 146 Kinship Matching for Mass Identification Projects.

P 147 Disaster Carbonized Victims Identification in State of Rondonia, Brazil.

P 148 Analysis of Complex Kinship Cases for Human Identification of Civil War Victims in Guatemala Using M-FISys Software.

P 149 Genetic identification of fire deaths.

P 150 Missing and Unidentified Persons Database.

P 151 The search for missing casualties of the Korean War: Systematic approaches to DNA typing of old skeletal remains.

P 152 Use of alternative samples in the restitution of missing persons descendants.

P 153 Missing people: problems of identification of unknown bodies with the use of DNA database.

P 154 Mitochondrial DNA Analysis of human skeletal remains unearthed from northern area of Kanagawa Prefecture, Japan.

P 155 A mini primer set covering the mtDNA hypervariable regions for the genetic typing of old skeletal remains.

P 156 Assesment of the efectiveness of human remains DNA typing: analysis of 134 cases.

P 157 Sampling of the Cranium for Mitochondrial DNA Analysis of Human Skeletal Remains.

P 158 First identification of human remains using mtDNA sequence analysis in Genetic Laboratory of Royal Gendarmerie in Morocco.

P 159 The Romanovs -what did we learn?

P 160 Mitochondrial DNA analysis in severely degraded bone samples.

P 162 Evaluation of different DNA-based methods in identification of soldiers missing in action since the World War II.

P 163 Population data for 12 STR loci in Northern European brown bear (Ursus arctos) and application of DNA-profiles for forensic case-work.

P 164 The use of mitochondrial DNA genes to identify closely related avian species.

P 165 Identifying NUMT contamination in mtDNA analyses.

P 166 Human STR polymorphisms investigated in chimpanzees.

P 167 Forensic Investigation of UK Cervus Elaphus species.

P 168 Canine DNA profiling in forensic casework - joining efforts for standardization.

P 169 Genetic typing of dogs'traces in biological samples.

P 170 Belgian Dog mitochondrial DNA database for forensics.

P 171 Genetic Diversity Analysis of 10 STR´s loci used for Forensic Identification in Canine Hair Samples.

P 172 Advances in the application of canine DNA analysis to serious crime investigation in the UK.

P 173 Gene expression analysis as a tool for age estimation of blowfly pupae.

P 174 The use of polymorphic DNA fragments (STRs/SNPs) to prevent counterfeiting.

P 175 FishPopTrace - Developing SNP-based population genetic assignment methods to investigate illegal fishing.

P 176 Application of molecular markers for detection of South American camelid illegal traffic.

P 177 Microbial forensics: do Aspergillus fumigatus strains present local or regional differentiation?

P 178 Detection of Bacterial Variation by Next Generation SOLiDTM Sequencing for Microbial Forensics Investigations.

P 179 Simultaneous identification of multiple mammalian species from mixed forensic samples based on mtDNA control region length polymorphism.

P 180 Identifying Endangered Species from Degraded Mixtures at Sub Cellular Levels.

P 181 Cytochrome b or Cytochrome c Oxidase Subunit 1 for Mammalian Species Identification - An Answer to the Debate.

P 182 Identification of sample donor in dexamethasone controversy.

P 183 Genus identification of toxic plant by DNA.

P 184 Forensic DNA Analysis of Botanical Evidence.

P 185 Tiger species identification based on molecular approach.

P 186 The Impact of Jumping Alignments on Clustering and Database Searching.

P 187 Enhancing the Size, Sampling, and Quality of Global Forensic mtDNA Databases.

P 188 Clustering for Forensic Mitotype Quality Analysis.

P 189 A cost-efficient fast and reliable two-stage strategy for the high-throughput identification of samples belonging to mtDNA haplogroup K and its subhaplogroups K1 and K2.

P 190 Mitochondrial DNA diversity in South Africa: Control and coding region data from the KhoiSan people.

P 191 A South East Asian mtDNA population report from Laos.

P 192 HVIII discrimination power to distinguish HVI and HVII common sequences.

P 193 Characterization of a Native American mtDNA haplogroup C lineage.

P 194 Haplotype diversity in human mitochondrial DNA control region in "black" and "white" individuals from the metropolitan area of São Paulo (Brazil).

P 195 Mitochondrial DNA control region data from two population samples from West Africa and the Middle East.

P 196 mtDNA SNP analysis in a Central Portuguese population.

P 197 Mitochondrial DNA control region database in Banco Nacional de Datos Genéticos-Argentina.

P 198 Preliminary results of mitochondrial DNA sequence variation in Spanish pyrenean populations.

P 199 Mitochondrial DNA sequence data of the Waorani population - an isolated indigenous group from North West Amazonia.

P 200 Argentinean Mitochondrial DNA sequence database.

P 201 Common mitochondrial DNA haplogrous observed in an Argentinian population sample.

P 202 Mitochondrial DNA Control Region sequence Analysis of Mataco-Guaicurú Speaking tribes from Argentina.

P 203 Haplotype diversity in mitochondrial DNA hypervariable region I and II in Maracaibo population (Venezuela).

P 204 Geographic substructure in the mitochondrial DNA distribution of U.S. "Hispanic" populations.

P 205 Variability of mitochondrial DNA HVIII segment in a human isolate from the Pas Valley (northern Spain).

P 206 Segments HVI and HVII of mitochondrial DNA in a population from Santa Catarina (Brazil): predominance of European lineages.

P 207 Mitochondrial DNA control region in native population from Quebrada de Humahuaca (northwestern Argetina).

P 208 The genetic composition of Argentina prior to the massive immigration era: insights from matrilineages of extant criollos in central-western Argentina.

12:30 - 14:00 **Abbot Symposium**

Session 2 | Chairpersons: *Peter Gill & Mecki Prinz*

14:00 - 14:45 CONFERENCE:

Integrated Forensic Sciences in Missing Persons Identification
Dr. Tom Parsons, PhD

14:45 - 16:00 **ORAL PRESENTATIONS 3**

14:45 **O 13** **New analytical tools for the YHRD: Mixture interpretation and refinement of ancestry prediction by Y-SNP inclusion** Sascha Willuweit[1], Lutz Roewer[1], [1]Institute of Legal Medicine, Dept. of Forensic Genetics, Berlin, Germany.

14:57 **O 14** **Resolving mtDNA Mixtures by means of Phylogenetic Software**
Alexander Röck[1], Arne Dür[1], Cordula Berger[2], Walther Parson[2], [1]Institute of Mathematics, University of Innsbruck, Innsbruck, Austria, [2]Institute of Legal Medicine, Innsbruck Medical University, Innsbruck, Austria.

15:09 **O 15** **Performance of the Banco Nacional de Datos Geneticos in Argentina**
Mariel Andrea Abovich[1], Adrián Maximiliano Arellano[1], Silvia Graciela Cabeller[1], María Victoria Cólica[1], Carlos Gregorio Echenique[1], María Gabriela Fraga[1], Claudia Cristina Gillo[1], Hernán Eduardo Lavalle[1], Luis Mariano Ochoa[1], Jorge Horacio Solimine[1], Andrea Hilda Szocs[1], Marina Laura Bettelani[1], Alejandro García Bates[1], Sandra Evangelina Filippini[1], Daniel Horacio Alcázar[1], Florencia Liliana Gagliardi[1], Oscar Santapá[1], Sergio Fernando Valente[1], María Belén Rodriguez Cardozo[1], [1]Banco Nacional de Datos Genéticos, Buenos Aires, Argentina.

15:21 **O 16** **Investigation of illegal graves in Argentina by using STR, miniSTR, Y-STR and mitochondrial DNA analysis.** Carola Romanini[1], Laura Catelli[1], Magdalena Romero[1], Patricia Bernardi[1], Carlos Vullo[2], [1]EAAF, Córdoba, Argentina, [2]LIDMO, Córdoba, Argentina.

15:33 **O 17** **DNA Profiling of Skeletal Samples from the Disappeared in Latin America**
Steven Weitz[1], Lisa Ricci[1], Jon Davoren[1], [1]Bode Technology, Lorton, Virginia, United States.

15:45 **O 18** **Genomic technologies in the analysis of forensic historical relics: identification of remains of all members of Nicholas II Royal family and their servants.** Evgeny Rogaev[1,2], Anastasia Grigorenko[2,3], Yuri Moliaka[2], Gulnaz Faskhutdinova[2], Ellen Kittler[4], Irina Morozova[1,2], [1]Vavilov Institute of General Genetics, Russian Academy of Science, Moscow, Russian Federation, [2]Brudnick Neuropsychiatric Research Institute, University of Massachusetts Medical School, Worcester, MA, United States, [3]Research Center of Mental Health, Russian Academy of Medical Science, Moscow, Russian Federation, [4]University of Massachusetts. Medical School, CFAR, Worcester, MA, United States.

16:00 - 16:30 Coffee break

Session 3 | Chairpersons: *John Butler & Lourdes Prieto Solla*

16:30 - 18:00 **ORAL PRESENTATIONS 4**

16:30 **O 19** **Tri-allelic SNP markers enable analysis of mixed and degraded DNA samples** Antoinette Westen[1], Anuska Matai[1], Jeroen Laros[3], Hugo Meiland[2], Peter de Knijff[3], Titia Sijen[1], [1]Netherlands Forensic Institute, the Hague, Netherlands, [2]Leiden Institute of Advanced Computer Science, Leiden, Netherlands, [3]Forensic Laboratory for DNA Research, Leiden, Netherlands.

16:41 **O 20** **A New SNP Assay for Human Identification of Highly Degraded DNA,** Ana Freire-Aradas[1], Manuel Fondevila[1], Christopher Phillips[1], Peter Gill[2], Lourdes Prieto[3], Ángel Carracedo[1], María Victoria Lareu[1], [1]Forensic Genetics Unit, Institute of Legal Medicine, University of Santiago de Compostela, Santiago de Compostela, Spain, [2]Centre for Forensic Science, University of Strathclyde, Glasgow, United Kingdom, [3]University Institute of Research Police Sciences (IUICP), DNA Laboratory, Comisaría General de Policía Científica, Madrid, Spain.

16:52 **O 21** **SNP typing of forensic samples with the GenPlexTM HID System: A collaborative study** Carmen Tomas[1], Michael Stangegaard[1], Claus Boersting[1], Helle Smidt[1], Stine Frisk Fredslund[1], Peter M Schneider[2], Angel Carracedo[3], Hoff-Olsen Per[4], Bertil Lindblom[5], Cordula Haas[6], Ingo Bastisch[7], Toineke Westen[8], Denise Syndercombe Court[9], Mechthild Prinz[10], Peter M Vallone[11], Rixun Fang[12], Michael D Coble[13], Art Eisenberg[14], Anders J Hansen[1], Niels Morling[1], [1]Section of Forensic Genetics, Department of Forensic Medicine, Faculty of Health Sciences, University of Copehnagen and the SNPforID Consortium, Copenhagen, Denmark, [2]Institute of Legal Medicine, University Hospital, Cologne, Germany, [3]Facultad de Medicina y Odontologia, Santiago de Compostela, Spain, [4]Institute of Forensic Medicine, University of Oslo, Rikshospitalet, Oslo, Norway, [5]Department of Forensic Genetics and Forensic Toxicology, Linköping, Sweden, [6]Institut für Rechtsmedizin, Universität Zürich, Zürich, Switzerland, [7]Bundeskriminalamt, Wiesbaden, Germany, [8]Human Biological Trace Research, NFI, The Hague, Netherlands, [9]Center for Haematology, Institute of Cell and Molecular Sciences, Bart and The London, London, United Kingdom, [10]New York City Office of Chief Medical Examiner, Department of Forensic Biology, New York, NY, United States, [11]National Institute of Standards and Technology, Gaithersburg, MD, United States, [12]Applied Biosystems, a part of Life Technologies, Foster City, CA, United States, [13]Armed Forces DNA Identification Laboratory, Armed Forces Institute of Pathology, Rockville, MD, United States, [14]UNT Center for Human ID, Fort Worth, TXz United States.

17:03 **O 22** **A panel of X chromosomal Indel-Polymorphism are useful in typing of degraded DNA** Sandra Hering[1], Christa Augustin[2], Reinhard Szibor[3], Jeanett Edelmann[4], [1]Institute of Legal Medicine, Technical University Dresden, Dresden, Germany, [2]Institute of Legal

Medicine, University-Hospital Hamburg-Eppendorf, Hamburg, Germany, [3]Institute of Legal Medicine, Otto-von-Guericke-University Magdeburg, Magdeburg, Germany, [4]Institute of Legal Medicine, University of Leipzig, Leipzig, Germany.

17:14 **O 23** **Insertion deletion polymorphisms: a multiplex assay and forensic applications** Rui Pereira[1,2], Christopher Phillips[2], Cíntia Alves[1], António Amorim[1,3], Ángel Carracedo[2,4], Leonor Gusmão[1], [1]IPATIMUP - Institute of Molecular Pathology and Immunology of the University of Porto, Porto, Portugal, [2]Institute of Legal Medicine, University of Santiago de Compostela, Santiago de Compostela, Spain, [3]Faculty of Sciences of the University of Porto, Porto, Portugal, [4]Genomics Medicine Group, CIBERER, University of Santiago de Compostela, Santiago de Compostela, Spain.

17:25 **O 24** **The Combination of Single Cell Micromanipulation with LVPCR System and Its Application in Forensic Science,** Lan Hu[1], Cai-xia Li[1], Bing Qi[2], An-quan Ji[1], Xiu-lan Xu[1], [1]Institute of Forensic Science, Ministry of Public Security, Beijing, China, [2]Chinese Peoples Public Security University, Beijing, China.

17:36 **O 26** **Application of full mitochondrial genome sequencing using 454 GS FLX pyrosequencing** Martin Mikkelsen[1], Eszter Rockenbauer[1], Andrea Wächter[1], Liane Fendt[2], Bettina Zimmermann[2], Walther Parson[2], Sandra Abel Nielsen[3], Tom Gilbert[3], Eske Willerslev[3], Niels Morling[1], [1]Section of Forensic Genetics, Department of Forensic Medicine, Faculty of Health Sciences, University of Copenhagen, Copenhagen, Denmark, [2]Institute of Legal Medicine, Innsbruck Medical University, Innsbruck, Austria, [3]Natural History Museum of Denmark,University of Copenhagen, Copenhagen, Denmark.

18:00 - 19:00 Language Working Groups Meetings

20:30 **Gala Dinner - Alvear Palace Hotel**
Av. Alvear 1891, Ciudad Autónoma de Buenos Aires, Argentina

FRIDAY, SEPTEMBER 18

08:30 - 10:00 Language Working Groups Meetings

10:00 - 10:30 Joint EDNAP / ENFSI Meeting

Session 1 | Chairperson: *Wolfgang Mayr*

10:30 - 11:15 CONFERENCE:
Statistics of linked markers in relationship testing.
Prof. Max Baur, PhD, Prof. Dr. Peter M. Schneider, Dr. Rolf Fimmers

11:15 - 12:30 **POSTER SESSION 3 (P 209 - P 317)**

P 209 A genetic study of the East Timor population using autosomal SNPs.
P 210 Swedish population data on the SNPforID Consortium autosomal SNP-multiplex**.**
P 211 The polymorphisms of 9 SNP loci on mitochondrial DNA in the Chinese Han population.
P 212 48 autosomal Single nucleotide Polymorphisms typing of a Moroccan sample using the GenPlexTM system. Population and Forensic data.
P 213 Allele frequency investigation of an autosomal SNP by using pyrosequencing typing platform.
P 214 The Africa male lineages of Bahia's people - Northeast Brazil - A preliminary SNP's study.
P 215 SNPSTR rs59186128_D7S820 in European Caucasoid, Hispanic and Afro-American Populations.
P 216 Population Data of 52 Autosomal SNPs in Italian Populations**.**
P 217 Database of the polymorphic genetic markers D19S433 and D2S1338 of the population of Buenos Aires Province, Argentina.
P 218 A highly polymorphic STR-locus within the MHC-region close to HLA-DR/DQ: Austrian population data of DQIV (alias M2_4_32)
P 219 Population genetic data for F13A01, FES/FPS, F13B and LPL in Colombia (Department of Santander).
P 220 Genetic analysis of 9 non-CODIS miniSTR loci in the Brazilian population of Parana.
P 221 pop.STR - an online population frequency browser for established and new forensic STRs.
P 222 Population data for 15 STRs loci in an immigrant population sample from Northern Italy.
P 223 Allele frequencies of six miniSTR loci (D10S1248, D14S1434, D22S1045, D4S2364, D2S441, D1S1677) in two Italian population.
P 224 Phylogenetic position of Berber-speaking population of Azrou using 15 STRs of Identifiler.
P 225 Allele frequencies for 15 Short Tandem Repeats loci in an Argentine population sample.
P 226 The present of tri-allelic TPOX genotypes in Dominican Population.
P 227 Genetic profile of Federal District of Brazil based on 18 STR autosomal loci.
P 228 Two non-CODIS miniSTR multiplex systems for analysis of degraded DNA samples in the Chinese Han population.
P 229 Usefulness of a hundred of autosomal tetranucleotide STR markers for genetic analysis among geographically close human regional populations in East Asia.
P 230 Allele frequencies of three miniSTR loci (D22S1045, D14S1434 and D10S1248) in North-East Italy.
P 231 Use of non CODIS miniSTR markers: creation of a data base in Argentina.
P 232 Update of an on-line autosomal STR and Y-STR reference database of Argentina.
P 233 Population data about the distribution of 15 autosomal STRs and 17 Y-STRs in South of Italy (Calabria)
P 234 Population Data of 5 Next Generation STRs in Southern Italy.
P 235 Forensic evaluation of 15 STR loci in Venezuelan military aircraft pilots.
P 236 Genetic composition of Middle-West Brazilian populations, estimated with autosomics STRs, shows no difference.
P 237 Association between STRs from the X chromosome in a sample of Portuguese Gypsies.
P 238 Genetic data of 10 X-chromosomal loci in Vitória population (Espírito Santo State, Brazil)
P 239 Genetic studies of eight X-STRs in a Northeast Italian population.
P 240 Chromosome X centromere region - Haplotype frequencies for different populations.
P 241 Analysis of 12 X-chromosomal STRs in an Algerian population sample.

P 242 Genetic patterns of 10 X chromosome short tandem repeats in an Asian population from Macau.

P 243 Genetic data of 10 X-STR in two Native American populations of Argentina.

P 244 Genetic origin based on Y-specific STR haplotypes in a sample of Caucasian-Mestizo and African descent male individuals of Colombia.

P 245 A Y-chromosome SNP multiplex for haplogroup assignment of West Eurasian men from Tyrol (Austria)

P 246 Y-chromosome haplotype database in Venezuelan central region and its comparison with others Venezuelan populations.

P 247 Y-chromosomal STR haplotypes in an Arab population from Somalia.

P 248 Knowing your DNA database: issues with determining ancestral Y haplotypes in a Y-Filer database**.**

P 249 Population data of 12 Y-STR loci from a Somali population.

P 250 New single nucleotide polymorphisms on Y chromosome in the Chinese Han population**.**

P 251 Evaluating Y-Chromosome STRs mutation rates: a collaborative study of the Ge.F.I.-ISFG Italian Group.

P 252 Analysis of Y Chromosome SNPs in Alagoas, Northeastern Brazil.

P 253 Investigation of population structure in the Victorian Italian & Greek population using Y chromosome STR haplotype analysis.

P 254 Mutation rates at 17 Y-STR loci in father-son pairs from Southern Spain.

P 255 Comparative Y-STR and Y-SNP analysis of the seklers and csangos to the present Hungarians.

P 256 Banco Nacional de Datos Genéticos: YFILER Database.

P 257 Y-Chromosome SNP analysis in the Brazilian Population of São Paulo State (Ribeirão Preto).

P 258 Haplotyping of Y-chromosomal short tandem repeats DYS481, DYS570, DYS576 and DYS643 in three Baltic populations.

P 259 Comparison of Y chromosome haplogroup frequencies in 8 Provinces from Argentina.

P 260 Genetic Structure of Mendoza Province Population Inferring using Autosomal and Y-chromosome STRs.

P 261 Distribution of Y-chromosomal SNP-haplogroups between males from Ethiopia.

P 262 Dissecting the Finnish male uniformity: the value of additional Y-STR loci.

P 263 Allele frequencies and population data for 17 Y-STR loci in Casablanca resident population.

P 264 Y-STR haplotype variation in a sample from Gran Buenos Aires (Argentina)

P 265 Phylogeography of French male lineages.

P 266 Haplotype frequencies for 17 Y-STR loci (AmpFlSTR®Y-filerTM) in a Moroccan population sample.

P 267 Analysis of Y chromosome lineages in a samples from Sub-Saharan Africa descendents in Rio de Janeiro.

P 268 Development of Y-SNP typing assay for forensic application in Venezuelan population.

P 269 Evaluation of extended haplotype data for the African Botswana population.

P 270 Evaluation of 21 Y-STRs for population and forensic studies in South Africa.

P 271 STR Allele Frequencies and Y Haplotypes in Five Chilean Sample Populations.

P 272 South to North increasing gradient of Paternal European ancestry throughout the Mexican territory: Evidence of Y-linked Short Tandem Repeats.

P 273 Origin of paternal lineages in an admixed population of Northern Argentina (La Esperanza, Jujuy).

P 274 Bayes' Theorem simplified even more.

P 275 Validation and consistency of sample sizes in forensic and population genetic studies using microsatellites markers.

P 276 Searching a DNA Data Bank with complex mixtures from two individuals.

P 277 Bayesian networks for victim identification on the basis of DNA profiles.

P 278 Estimating the number of contributors to forensic DNA mixtures: does maximizing the likelihood performs better than the maximum allele count?

P 279 Use of freeware for calculating likelihood ratio for paternity and kinship in complicated human Pedigrees.

P 280 Analysis of complex family cases with Probabilistic Expert Systems.

P 281 Population stratification in Argentina strongly influences likelihood ratio estimates in paternity testing as revealed by a simulation-based approach.

P 282 A preliminary mitochondrial DNA SNP assay for inferring biogeographical ancestry.

P 283 Partial forensic validation of a 16plex SNP assay for the inference of biogeographical ancestry.

P 284 Forensic application of an individual ancestry index in Brazilian populations.

P 285 DRD2TaqI haplotypes in three urban Brazilian populations.

P 286 The Kurgan people from southern Siberia: What did they look like? Where did they come from?

P 287 Forensic typing tests for 42 SNPs with two SNaPshot assays to predict common pigmentation trait variation in Europeans.

P 288 Analysis of CYP2D6 gene variation in Venezuelan population: implications for forensic toxicology.

P 289 CYP2D6 polymorphism studies: how forensic genetics helps clinical medicine.

P 290 Genetic susceptibility for addiction: searching of risk loci for the widespread drugs of abuse.

P 291 The Relevance Between Dopamine D3 Receptor Gene Variations and Drug Addiction.

P 292 Genetics of addiction in legal medicine and forensic investigation: SNPs variations ass ociated with nicotine and cannabis dependence.

P 293 Changes of the Na+ and K+ channels levels in human heart failure and ischemia.

P 294 Considerations about mRNA extraction from post-mortem human heart.

P 295 The role of Cav3 gene in channelopathies.

P 296 Involvement of hypertrophic cardiomyopathy genes in Sudden Infant Death Syndrome (SIDS).

P 297 Sequenom Massarray application in the Long QT Syndrome mutation detection.

P 298 Analysis of three major sarcomeric genes (MYH7, TNNT2, MYBPC3) in cardiomyopathy.

P 299 Forensic mitochondrial DNA analysis in HIV-infected patients treated with nucleoside reverse transcriptase inhibitors.

P 300 Loss of heterozygosity detected in a short tandem repeat (STR) locus in rheumatoid arthritis peripheral blood.

P 301 Single cell gel electrophoresis in determining DNA degradation: Potential for use in postmortem interval estimation and time since the deposition of blood stains.

P 302 Selective enrichment of human DNA from non-human DNAs for DNA typing of decomposed skeletal remains.

P 303 Reparation of degraded DNA improves PCR amplification of larger STR loci.

P 304 Increased discrimination power of forensic STR testing by liquid chromatography-mass spectrometry in rare autochthonous populations.

P 305 Analysis of DNA Forensic Markers Using High Throughput Mass Spectrometry.

P 307 Validation of Mass Spectrometry Analysis of mtDNA.

P 308 Enhanced resolution and statistical power through evaluation of SNPs distributed within the short tandem repeats utilizing mass spectrometry.

P 310 mRNA profiling for the identification of sperm and seminal plasma.

P 311 How specific are the vaginal secretion mRNA-markers HBD1 and MUC4?

P 312 Influence of different parameters on the integrity of RNA extracted from human autopsy tissue.

P 313 RNA extraction in practice - comparison of four different RNA extraction methods and their impact on the RNA integrity in postmortem human tissue.

P 314 Human Tissue and Body Fluid Characterization Involving DNA Methylation Methods - Towards Forensic Epigenetics.

P 315 Multiplexed SNP Detection Panels for Human Identification.

P 316 Investigation of SNP haplotypes in the H19 imprinted gene.

P 317 SNPSTRs in caucasian and negroid populations.

12:30 - 14:00 Lunch break

Session 2 | Chairpersons: *Max Baur & Niels Morling*

14:00 - 14:45 CONFERENCE:
"The investigation of remains of missing people in Argentina during the last 25 years". *Dr. Luis Fondebrider*

14:45 - 16:45 **ORAL PRESENTATIONS 5**

14:00 **O 27** **X-chromosomal markers in relationship testing: The effects of linkage and linkage disequilibrium on computed likelihood ratios** Andreas Tillmar[1], Thore Egeland[2], Bertil Lindblom[1], Gunilla Holmlund[1], Petter Mostad[3], [1]National Board of Forensic Medicine, Department of Forensic Genetics and Forensic Toxicology, Linköping, Sweden, [2]University of Oslo, Institute of Forensic Medicine, Oslo, Norway, [3]Mathematical Sciences, Chalmers University of Technology, and Mathematical Sciences Göteborg University, Göteborg, Sweden.

14:12 **O 28** **Distinguishing kinship from genealogical likelihoods**
Nádia Pinto[1,2], Leonor Gusmão[1], António Amorim[1,2], [1]IPATIMUP, Instituto de Patologia e Imunologia Molecular da Universidade do Porto, Porto, Portugal, [2]Faculdade de Ciências da Universidade do Porto, Porto, Portugal.

14:24 **O 29** **Evaluating the usage of Fst to correct for population stratification when estimating PI values**, Ulises Toscanini[1], Antonio Salas[2], Manuel García-Magariños[2], Eduardo Raimondi[1], [1]PRICAI-FUNDACIÓN FAVALORO, Buenos Aires, Argentina, [2]Unidad de Xenética, Inst. Med. Leg., Univ. de Santiago de Compostela, Santiago de Compostela, Spain.

14:36 **O 30** **Overdispersion in allelic counts and ?-correction in forensic genetics**
Torben Tvedebrink[1], [1]Department of Mathematical Sciences, Aalborg University, Aalborg, Denmark.

14:48 **O 31** **More for the same? Enhancing the investigative potential of forensic DNA databases**
Tim Clayton[1], Sue Pope[1], Jonathan Whitaker[1], Roberto Puch-Solis[1], John Lowe[1], [1]Forensic Science Service, Birmingham, United Kingdom.

15:00 **O 32** **Development of a quantitative method for taking account of the sizes of peaks when interpreting STR mixtures for court purposes,** Roberto Puch-Solis[1], Ian Evett[1], Lauren Rodgers[1], [1]Forensic Science Service, Birmingham, United Kingdom.

15:12 **O 33** **Dropout for dummies -- modular methods for dropout analysis**
Charles Brenner[1], [1]UC Berkeley, Berkeley, CA, United States.

15:24 **O 34** **RMNE probability of forensic DNA profiles with allelic drop-out**
Filip Van Nieuwerburgh[1], Els Goetghebeur[2], Mado Vandewoestyne[1], Dieter Deforce[1], [1]Laboratory for Pharmaceutical Biotechnology, Ghent University, Ghent, Belgium, [2]Department of Applied Mathematics and Computer Science, Ghent University, Ghent, Belgium.

15:36 Discussion - Biostatistics

15:48 **O 35** **Interpretation of low-copy-number DNA profile after post-PCR purification.**
Sabine Michel[1], Anne De Bast[1], Olivier Froment[1], [1]Bio.be SA - CRI, 6041 Gosselies, Belgium.

16:45 - 17:15 Coffee break

Session 3 | Chairpersons: *Angel Carracedo & Peter Schneider*

17:15 - 18:45 **ORAL PRESENTATIONS 6**

17:15 **O 36** **Trace DNA and street robbery: A criminalistic approach to DNA evidence.**
Jennifer Raymond[1,2], Roland van Oorschot[3], Simon Walsh[4], Peter Gunn[2], Claude Roux[1], [1]University of Technology, Sydney, Sydney, NSW, Australia, [2]NSW Police Force Forensic Services Group, Sydney, NSW, Australia, [3]Victoria Police Forensic Services Centre, Melbourne, VIC, Australia, [4]Australian Federal Police Forensic & Data Centres, Canberra, ACT, Australia.

17:27 **O 37** **Impact of relevant variables on the transfer of biological substances**
Roland van Oorschot[1], Mariya Goray[1,2], Ece Eken[1], John Mitchell[2], [1]Victoria Police Forensic Services Department, Macleod 3085, Victoria, Australia, [2]Genetics Department La Trobe University, Melbourne 3086, Victoria, Australia.

17:39 **O 38** **Forensic DNA transfer**
Ignacio Quinones[1,2], Barbara Daniel[2], [1]London Metropolitan Police, London, United Kingdom, [2]King's College London, London, United Kingdom.

17:51 **O 39** **Review of Low Template DNA Typing**
Adrian Linacre[1], [1]University of Strathclyde, Glasgow, United Kingdom.

18:03 **O 40** **The Challenges to the Use of Low Copy Number Analysis**
Bruce Budowle[1], Arthur Eisenberg[1], Suzanne Gonzalez[1], John Planz[1], Rhonda Roby[1], Angela van Daal[1], [1]University of North Texas Health Science Center, Fort Worth, TX, United States, [2]Bond University, Gold Coast, Queensland, Australia.

18:15 **O 41** **The interpretation of 'low-level' DNA profiles - where next?**
Peter Gill[1,2], John Buckleton[3], [1]University of Strathclyde, Glasgow, United Kingdom, [2]University of Oslo, Oslo, Norway, [3]ESR, Auckland, New Zealand.

18:27 Discussion - DNA of low quality and/or quantity

18:45 - 19:15 **Congress Highlights / Closing Ceremony**

19:15 - 20:45 **General Assembly of the ISFG**