

Tuesday 3 September Registration Opens 0730		
1800-1945	Congress Official Welcome and Keynote Speaker Sir Alec Jeffreys (UK) - Opening Address	Plenary 3
1945-2145	Welcome Reception	Ground Floor
Wednesday 4 September Registration Opens 0730		
0900-0945	Keynote Speaker Eske Wilerslev (DEN) - Hunting the Molecular Past Chairs: Mecki Prinz & Adrian Linacre	Plenary 3
0945-1030	Oral session	
0945-1000	Walther Parson (AUT) Next Generation mtDNA sequencing of forensic samples with the Ion Torrent PGM	
1000-1015	Bram Bekaert (BEL) Multiplex DNA amplification and barcoding in a single reaction for 454 Roche sequencing: A comprehensive study on the control region of the mitochondrial genome	
1015-1030	Thomas Callaghan (USA) Assessment of rapid DNA reference sample prototype instruments	
1030-1100	Morning Tea, Exhibition and Poster Viewing Themes 1-3 Proudly Sponsored by Flinders University- Faculty of Science and Engineering	Ground Floor
1100-1245	Oral session	Plenary 3
1100-1115	Bruce Budowle (USA) Next generation sequencing provides comprehensive multiplex capabilities	
1115-1130	Kenneth Kidd (USA) Microhaplotypes are a powerful new type of forensic marker	
1130-1145	Renee Ottens (AUS) The development and implementation of direct PCR in casework	
1145-1200	Dmitry Zubakov (NED) Blood and semen identification from human DNA using copy number variation markers	
1200-1215	James Creecy (USA) Duplex-specific nuclease (DSN) normalization: A method for the rehabilitation of low copy number DNA profiles	
1215-1230	Anastasia Khodakova (AUS) Programmable DNA hybridisation as a new tool for forensic DNA genotyping	
1230-1245	Henrik Green (SWE) Assessment of HaloPlex amplification for sequence capture and massive parallel sequencing of sudden cardiac death / arrhythmogenic right ventricular cardiomyopathy genes	

Wednesday 4 September (continued)		
1245-1345	Promega Corporation Lunch Symposium	Room 204
1245-1345	Lunch & Exhibition	Ground Floor
1350-1435	Keynote Speaker SallyAnn Harbison (NZ) - The Changing Face of Body Fluid Identification Chairs: Linzi Wilson-Wilde & Manfred Kayser	Plenary 3
1435-1520	Oral session	
1435-1450	Titia Sijen (NED) On RNA profiling, RNA data interpretation and an inter-laboratory EUROFORGEN RNA exercise	
1450-1505	Eletra Isabel Williams (NZL) The development of a method for FISH identification of forensically relevant body fluids	
1505-1520	Shujin Li (CHN) LINE-1 DNA methylation: a marker for discriminating monozygotic twins	
1520-1545	Afternoon Tea, Exhibition & Poster Viewing Themes 4-6 Proudly Sponsored by Illumina	Ground Floor
1545-1715	Oral session	Plenary 3
1545-1600	Marie Allen (SWE) Forensic epigenetic age signature - Biological age determination using pyrosequencing analysis of methylation markers	
1600-1615	Rachel Fleming (NZL) New RNA methods for the identification of body fluids and cell types	
1615-1630	Ajin Choi (KOR) Body fluid identification by simultaneous analysis of DNA methylation and body fluid-specific bacteria	
1630-1645	Iva Gomes (GER) Selection of miRNA reference genes for accurate normalization of gene expression data for body fluid identification	
1645-1700	Benjamin Benn Hjort (DEN) Identification of blood, saliva and semen using second generation sequencing of total miRNA	
1700-1715	Jack Ballantyne (USA) Two-Factor logistic regression models enable miRNA profiling to provide accurate identification of forensically relevant body fluids and tissues	
1745-1830	General Assembly	Plenary 3

Thursday 5 September Registration Opens 0800		
0900-0945	Keynote Speaker Chris Tyler-Smith (UK) - Y-chromosomal variation from whole-genome sequences Chairs: Leonor Gusmão & Wolfgang Mayer	Plenary 3
0945-1030	Oral session	
0945-1000	Maria Geppert (GER) Expanding the knowledge of genetic variation in indigenous populations of South America by resequencing the Y chromosome	
1000-1015	Kaye Ballantyne (AUS) Rapidly mutating Y-chromosomal STRs - a multi-center assessment of global male lineage and relative differentiation	
1015-1030	Burkhard Berger (AUT) Disentangling close and distant relatives in Tyrolean mountain villages by rapidly mutating Y-STRs	
1030-1100	Morning Tea, Exhibition & Poster Viewing Themes 7-8	Ground Floor
1100-1245	Oral session	Plenary 3
1100-1115	Lutz Roewer (GER) The global PPY23 databasing project to support the implementation of high-resolution Y chromosome diagnostics in the forensic workflow	
1115-1130	Toni Diegoli (USA) A recombination study of 15 X chromosomal short tandem repeat markers using multigenerational family pedigrees	
1130-1145	Vania Pereira (DEN) Assessing the potential application of X-chromosomal haploblocks in population genetics and forensic studies	
1145-1200	Daniel Kling (NOR) FamLinkX - A new software accounting for linkage, linkage disequilibrium and mutations in calculations of relatedness using X-chromosomal marker data	
1200-1215	Mikkel Meyer Andersen (DEN) Cluster analysis of Y-chromosomal STR population data using discrete Laplace distributions	
1215-1230	Charles Brenner (USA) Understanding rare haplotype evidence	
1230-1245	Bruce Weir (USA) Population genetic theory for lineage markers	
1245-1345	QIAGEN Lunch Symposium	Room 204

Thursday 5 September (continued)		
1245-1345	Lunch & Exhibition	Ground Floor
1350-1435	Keynote Speaker Rebecca Johnson (AUS) - Wildlife Forensic Science – Current and Future Directions Chairs: SallyAnn Harbison & Roland van Oorschot	Plenary 3
1435-1520	Oral session	
1435-1450	Michael Bunce (AUS) NGS metagenomics and metabarcoding: What are the prospects and problems in forensic applications	
1450-1505	Andreas Tillmar (SWE) Species determination of DNA-mixtures using next generation sequencing	
1505-1520	Samuel Wasser (USA) presented by Bruce Weir (USA) Combatting transnational organized wildlife crime using DNA assignment of poaching hotspots	
1520-1545	Afternoon Tea, Exhibition & Poster Viewing Themes 9-11	Ground Floor
1545-1715	Oral session	Plenary 3
1545-1600	Anastasia Khodakova (AUS) Application of next generation sequencing for forensic soil DNA analysis	
1600-1615	Jennifer Young (AUS) The use of NGS for enhanced forensic soil DNA analysis	
1615-1630	Alexander Roeck (AUT) Concept for reengineering and expanding the EMPPOP mtDNA population database	
1630-1645	Sai Palagummi (NZL) A multiplex analysis of RNA expression during injury healing in human dermal injuries for injury age estimation	
1645-1700	Weibo Liang (CHN) mRNA degradation pattern analysis in post-mortem normalized using the DNA	
1700-1715	Joanne Simons (NZL) Standard 28-cycle amplification of X/Y-FISH labelled epithelial cells for DNA profiling	
1730-1830	Workshop: Writing & Reviewing Scientific Papers	

Friday 6 September Registration Opens 0815		
0900-0945	Keynote Speaker John Buckleton (NZ) - How do we interpret DNA evidence properly? Chairs: Niels Morling & Peter Schneider	Plenary 3
0945-1030	Oral session	
0945-1000	Michael Coble (USA) An investigation of software programs using “drop-out” and “continuous” methods for complex mixture interpretation	
1000-1015	Duncan Taylor (AUS) Going totally Bayesian: Lab experiences when moving to a continuous DNA interpretation model	
1015-1030	James Curran (NZL) Statistical building blocks for continuous DNA interpretation systems	
1030-1100	Morning Tea, Exhibition & Poster Viewing Theme 12	Main Foyer
1100-1245	Oral session	Plenary 3
1100-1115	Roberto Puch Solis (UK) Evaluating forensic DNA profiles using peak heights, allowing for dropin, allelic dropout and stutters	
1115-1130	Peter Gill (NOR) On the meaning of the likelihood ratio: is a large number always an indication of strength of evidence?	
1130-1145	Torben Tvedebrink (DEN) Estimating drop-out probabilities of STR alleles accounting for truncation, degradation and stutters	
1145-1200	Bas Kokshoorn (NED) Implementation of probabilistic models in casework; A case study	
1200-1215	Jo-Anne Bright (NZL) Matching mixtures against DNA databases	
1215-1230	Roland Van Oorschot (AUS) Advances in understanding DNA transfer: The role of persistence, drying time, temperature and sample type	
1230-1245	Thomas Parsons (BIH) Models for reporting and integration of DNA matching in missing persons/DVI identification projects	
1245-1345	Life Technologies Lunch Symposium	Room 204
1245-1345	Lunch & Exhibition	Ground Floor

Friday 6 September (continued)		
1350-1435	Keynote Speaker Jeremy Austin (AUS) - Beyond STRs: Ancient DNA and advanced forensic identification of missing persons remains Chairs: Walther Parson & Runa Daniel	Plenary 3
1435-1520	Oral session	
1435-1450	Christopher Phillips (ESP) A global ancestry SNP panel for next generation sequencing technologies	
1450-1505	Birgitte Lundsberg (DEN) presented by Niels Morling (DEN) Development and optimisation of four multiplex assays with 99 of the AIM SNPs from the EUROFORGEN AIMs set on the Sequenom Massarray system	
1505-1520	Hye-Young Lee (KOR) Development of ancestry inference system for subgrouping of Asian	
1520-1545	Afternoon Tea, Exhibition & Poster Viewing Themes 13-15	Ground Floor
1545-1715	Oral session	Plenary 3
1545-1600	Susan Walsh (NED) Predicting skin colour from DNA using a model-based approach	
1600-1615	Ewelina Pospiech (POL) presented by Wojciech Branicki (POL) Epistasis in the determination of human pigmentation is common and improves the DNA based phenotype prediction	
1615-1630	Mark Barash (AUS) Identification of Single Nucleotide Polymorphisms (SNPs) involved in the determination of physical appearance	
1630-1645	Carla Santos (ESP) Pacifiplex: A forensic ancestry SNP panel centered on Australia and the Pacific region	
1645-1700	Runa Daniel (AUS) Preliminary assessment of the Ion Torrent PGM system for SNP genotyping in forensic DNA analysis	
1700-1715	Marie Allen (SWE) Haloplex and MiSeq NGS for simultaneous analysis of 10 STRs, 386 SNPs and the complete mtDNA Genome	
1900-2330	Congress Gala Dinner	Melbourne Room 1